

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *HELICOBACTER PYLORI* AND VACCINE COMPOSITIONS THEREOF

Background of the Invention

5 *Helicobacter pylori* is a gram-negative, S-shaped, microaerophilic bacterium that was discovered and cultured from a human gastric biopsy specimen. (Warren, J.R. and B. Marshall, (1983) *Lancet* 1: 1273-1275; and Marshall et al., (1984) *Microbios Lett.* 25: 83-88). *H. pylori* has been strongly linked to chronic gastritis and duodenal ulcer disease. (Rathbone et. al., (1986) *Gut* 27: 635-641). Moreover, evidence is
10 accumulating for an etiologic role of *H. pylori* in nonulcer dyspepsia, gastric ulcer disease, and gastric adenocarcinoma. (Blaser M. J., (1993) *Trends Microbiol.* 1: 255-260). Transmission of the bacteria occurs via the oral route, and the risk of infection increases with age. (Taylor, D.N. and M. J. Blaser, (1991) *Epidemiol. Rev* 13: 42-50). *H. pylori* colonizes the human gastric mucosa, establishing an infection that usually
15 persists for decades. Infection by *H. pylori* is prevalent worldwide. Developed countries have infection rates over 50% of the adult population, while developing countries have infection rates reaching 90% of the adults over the age of 20. (Hopkins R. J. and J. G. Morris (1994) *Am. J. Med.* 97: 265-277).

 The bacterial factors necessary for colonization of the gastric environment, and
20 for virulence of this pathogen, are poorly understood. Examples of the putative virulence factors include the following: urease, an enzyme that may play a role in neutralizing gastric acid pH (Eaton et al., (1991) *Infect. Immunol.* 59: 2470-2475; Ferrero, R.L. and A. Lee (1991) *Microb. Ecol. Hlth. Dis.* 4: 121-134; Labigne et al., (1991) *J. Bacteriol.* 173: 1920-1931); the bacterial flagellar proteins responsible for
25 motility across the mucous layer. (Hazell et al., (1986) *J. Inf. Dis.* 153: 658-663; Leying et al., (1992) *Mol. Microbiol.* 6: 2863-2874; and Haas et al., (1993) *Mol. Microbiol.* 8: 753-760); Vac A, a bacterial toxin that induces the formation of intracellular vacuoles in epithelial cells (Schmitt, W. and R. Haas, (1994) *Molecular Microbiol.* 12(2): 307-319); and several gastric tissue-specific adhesins. (Boren et al., (1993) *Science* 262: 1892-
30 1895; Evans et al., (1993) *J. Bacteriol.* 175: 674-683; and Falk et al., (1993) *Proc. Natl. Acad. Sci. USA* 90: 2035-203).

 Numerous therapeutic agents are currently available that eradicate *H. pylori* infections *in vitro*. (Huesca et. al., (1993) *Zbl. Bakt.* 280: 244-252; Hopkins, R. J. and J. G. Morris, supra). However, many of these treatments are suboptimally effective *in vivo*
35 because of bacterial resistance, altered drug distribution, patient non-compliance or poor drug availability. (Hopkins, R. J. and J. G. Morris, supra). Treatment with antibiotics combined with bismuth are part of the standard regime used to treat *H. pylori* infection.

(Malfertheiner, P. and J. E. Dominguez-Munoz (1993) *Clinical Therapeutics* 15 Supp. B: 37-48). Recently, combinations of a proton pump inhibitors and a single antibiotic have been shown to ameliorate duodenal ulcer disease. (Malfertheiner, P. and J. E. Dominguez-Munoz supra). However, methods employing antibiotic agents can have the
5 problem of the emergence of bacterial strains which are resistant to these agents. (Hopkins, R. J. and J. G. Morris, supra). These limitations demonstrate that new more effective methods are needed to combat *H. pylori* infections *in vivo*. In particular, the design of new vaccines that may prevent infection by this bacterium is highly desirable.

10 Summary of the Invention

This invention relates to novel genes, e.g., genes encoding polypeptides such as bacterial surface proteins, from the organism *Helicobacter pylori* (*H. pylori*), and other related genes, their products, and uses thereof. The nucleic acids and peptides of the present invention have utility for diagnostic and therapeutics for *H. pylori* and other
15 *Helicobacter* species. They can also be used to detect the presence of *H. pylori* and other *Helicobacter* species in a sample; and for use in screening compounds for the ability to interfere with the *H. pylori* life cycle or to inhibit *H. pylori* infection. More specifically, this invention features compositions of nucleic acids corresponding to entire coding sequences of *H. pylori* proteins, including surface or secreted proteins or
20 parts thereof, nucleic acids capable of binding mRNA from *H. pylori* proteins to block protein translation, and methods for producing *H. pylori* proteins or parts thereof using peptide synthesis and recombinant DNA techniques. This invention also features antibodies and nucleic acids useful as probes to detect *H. pylori* infection. In addition, vaccine compositions and methods for the protection against infection by *H. pylori* are
25 within the scope of this invention.

Detailed Description of the Drawings

Figure 1 is a bar graph that depicts the antibody titer in serum of mice following immunization with specific *H. pylori* antigens.

30 Figure 2 is a bar graph that depicts the antibody titer in mucous of mice following immunization with specific *H. pylori* antigens.

Figure 3 is a bar graph that depicts therapeutic immunization of *H. pylori* infected mice with specific antigens dissolved in HEPES buffer.

Figure 4 is a bar graph that depicts therapeutic immunization of *H. pylori*
35 infected mice with specific antigens dissolved in buffer containing DOC.

Figure 5 is a graph depicting the activity of recombinant PPIase.

Figure 6 is a graph depicting PPIase activity in an *H. pylori* extract.

Figure 7 is a graph depicting a decrease of glutamate racemase activity with L-Serine-O-Sulfate.

Figure 8 depicts the amino acid sequence alignment in a portion of the sequence of 12 *H. pylori* proteins (depicted in the single letter amino acid code and designated by their amino acid Sequence ID Numbers; shown N-terminal to C-terminal, left to right).

Figure 9 depicts the N-terminal portion of nine *H. pylori* proteins (depicted in the single letter amino acid code and designated by their amino acid Sequence ID Numbers; shown N-terminal to C-terminal, left to right).

Detailed Description of the Invention

In one aspect, the invention features a recombinant or substantially pure preparation of *H. pylori* polypeptide of SEQ ID NO: 492. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide of SEQ ID NO: 492, such nucleic acid is contained in SEQ ID NO: 1. The *H. pylori* polypeptide sequences described herein are contained in the Sequence Listing, and the nucleic acids encoding *H. pylori* polypeptides are contained in the Sequence Listing.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 492 through SEQ ID NO: 541. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 492 through SEQ ID NO: 541, such nucleic acids are contained in SEQ ID NO: 1 through SEQ ID NO: 50.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 542 through SEQ ID NO: 591. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 542 through SEQ ID NO: 591, such nucleic acids are contained in SEQ ID NO: 51 through SEQ ID NO: 100.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 592 through SEQ ID NO: 641. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 592 through SEQ ID NO: 641, such nucleic acids are contained in SEQ ID NO: 101 through SEQ ID NO: 150.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 642 through SEQ ID NO: 691. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 642 through SEQ ID NO: 691, such nucleic acids are contained in SEQ ID NO: 151 through SEQ ID NO: 200.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 692 through SEQ ID NO: 741. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 692 through SEQ ID NO: 741, such nucleic acids are contained in SEQ ID NO: 201 through SEQ ID NO: 250.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 742 through SEQ ID NO: 759, SEQ ID NO: 761, SEQ ID NO: 763, SEQ ID NO: 765 through SEQ ID NO: 791. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 742 through SEQ ID NO: 759, SEQ ID NO: 761, SEQ ID NO: 763, SEQ ID NO: 765 through SEQ ID NO: 791, such nucleic acids are contained in SEQ ID NO: 251 through SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, and SEQ ID NO: 274 through SEQ ID NO: 300.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 792 through SEQ ID NO: 818 and SEQ ID NO: 820 through SEQ ID NO: 841. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 792 through SEQ ID NO: 818 and SEQ ID NO: 820 through SEQ ID NO: 841, such nucleic acids are contained in SEQ ID NO: 301 through SEQ ID NO: 327 and SEQ ID NO: 329 through SEQ ID NO: 350.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 842 through SEQ ID NO: 846 and SEQ ID NO: 848 through SEQ ID NO: 891. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 842 through SEQ ID NO: 846 and SEQ ID NO: 848 through

SEQ ID NO: 891, such nucleic acids are contained in SEQ ID NO: 351 through SEQ ID NO: 364 and SEQ ID NO: 366 through SEQ ID NO: 400.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 892 through SEQ ID NO: 896 and SEQ ID NO: 898 through SEQ ID NO: 941. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 892 through SEQ ID NO: 896 and SEQ ID NO: 898 through SEQ ID NO: 941, such nucleic acids are contained in SEQ ID NO: 401 through SEQ ID NO: 405 and SEQ ID NO: 407 through SEQ ID NO: 450.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 942 through SEQ ID NO: 963 and SEQ ID NO: 966 through SEQ ID NO: 982. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 942 through SEQ ID NO: 963 and SEQ ID NO: 966 through SEQ ID NO: 982, such nucleic acids are contained in SEQ ID NO: 451 through SEQ ID NO: 472 and SEQ ID NO: 475 through SEQ ID NO: 491.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1037, SEQ ID NO: 1038, SEQ ID NO: 1041 through SEQ ID NO: 1087 and SEQ ID NO: 1090. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1037, SEQ ID NO: 1038, SEQ ID NO: 1041 through SEQ ID NO: 1087 and SEQ ID NO: 1090, such nucleic acids are contained in SEQ ID NO: 983, SEQ ID NO: 984, SEQ ID NO: 987 through SEQ ID NO: 1033 and SEQ ID NO: 1036.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1296 through SEQ ID NO: 1298. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1296 through SEQ ID NO: 1298, such nucleic acids are contained in SEQ ID NO: 1293 through SEQ ID NO: 1295.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides as set forth in the Sequence Listing. The invention also includes

substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides as set forth in the Sequence Listing. It should be understood that this invention encompasses each of the *H. pylori* polypeptides and nucleic acids encoding such polypeptides as identified in the Sequence Listing by a given sequence identification number. For example, a representative *H. pylori* polypeptide is contained in SEQ ID NO: 494. Therefore, this invention encompasses a recombinant or substantially pure preparation of an *H. pylori* polypeptide of SEQ ID NO: 494. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide of SEQ ID NO: 494.

10 In another aspect, the invention pertains to any individual *H. pylori* polypeptide member or nucleic acid encoding such member from the above-identified groups of *H. pylori* polypeptides (e.g., SEQ ID NO: 542-SEQ ID NO: 591) or nucleic acids (e.g., SEQ ID NO: 51-SEQ ID NO: 100), as well as any subgroups from within the above-identified groups. Furthermore, the subgroups can preferably consists of 1, 3, 5, 10, 15, 20, 30 or 40 members of any of the groups identified above, as well as, any combinations thereof. For example, the group consisting of *H. pylori* polypeptides SEQ ID NO: 692 through SEQ ID NO: 741 can be divided into one or more subgroups as follows: SEQ ID NO: 692-SEQ ID NO: 680; SEQ ID NO: 681-SEQ ID NO: 710; SEQ ID NO: 711-SEQ ID NO: 730; SEQ ID NO: 731-SEQ ID NO: 741; or any combinations thereof.

20 Particularly preferred is an isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* cell envelope polypeptide or a fragment thereof. Such nucleic acid is selected from the group consisting of SEQ ID NO: 255, SEQ ID NO: 263, SEQ ID NO: 266, SEQ ID NO: 277, SEQ ID NO: 280, SEQ ID NO: 285, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 299, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 321, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 353, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 375, SEQ ID NO: 384, SEQ ID NO: 391, SEQ ID NO: 392, SEQ ID NO: 397, SEQ ID NO: 398, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 409, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 427, SEQ ID NO: 433, SEQ ID NO: 434, SEQ ID NO: 441, SEQ ID NO: 444, SEQ ID NO: 445, SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 453, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 983, SEQ ID NO: 989, SEQ ID NO: 1008, SEQ ID NO: 1011, SEQ ID NO: 1014, SEQ ID NO: 1015, SEQ ID NO: 1029, SEQ ID NO: 1032, SEQ ID NO: 259, SEQ ID NO: 286, SEQ ID NO: 326, SEQ ID NO: 374, SEQ ID NO: 399, SEQ ID NO: 422, SEQ ID NO: 454, SEQ ID NO: 465, SEQ ID NO: 998, SEQ ID NO: 1009, SEQ ID NO:

1023, SEQ ID NO: 1294, SEQ ID NO: 1295, SEQ ID NO: 319, SEQ ID NO: 325, SEQ ID NO: 425, SEQ ID NO: 437, SEQ ID NO: 438, SEQ ID NO: 447, SEQ ID NO: 448, SEQ ID NO: 467, SEQ ID NO: 996, SEQ ID NO: 1027, SEQ ID NO: 1031, SEQ ID NO: 254, SEQ ID NO: 352, SEQ ID NO: 415, SEQ ID NO: 1019, SEQ ID NO: 381,
 5 SEQ ID NO: 389, SEQ ID NO: 1010, SEQ ID NO: 1012, SEQ ID NO: 354, SEQ ID NO: 372, SEQ ID NO: 400, SEQ ID NO: 421, SEQ ID NO: 1022, SEQ ID NO: 463, SEQ ID NO: 281, SEQ ID NO: 988, SEQ ID NO: 411, SEQ ID NO: 407, SEQ ID NO: 1017, SEQ ID NO: 290, SEQ ID NO: 417, SEQ ID NO: 430, SEQ ID NO: 992, SEQ ID NO: 1025, SEQ ID NO: 477, SEQ ID NO: 414, SEQ ID NO: 253, SEQ ID NO: 293,
 10 SEQ ID NO: 334, SEQ ID NO: 343, SEQ ID NO: 418, SEQ ID NO: 424, and SEQ ID NO: 443.

In another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* outer membrane polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 255, SEQ ID NO: 263,
 15 SEQ ID NO: 266, SEQ ID NO: 277, SEQ ID NO: 280, SEQ ID NO: 285, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 299, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 321, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 353, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 375, SEQ ID NO: 384, SEQ ID NO: 391, SEQ ID NO: 392, SEQ ID NO: 397, SEQ ID NO: 398, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 409, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 427, SEQ ID NO: 433, SEQ ID NO: 434, SEQ ID NO: 441, SEQ ID NO: 444, SEQ ID NO: 445, SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 453, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 983, SEQ ID NO: 989, SEQ ID NO: 1008, SEQ ID NO: 1011, SEQ ID NO: 1014, SEQ ID NO: 1015, SEQ ID NO: 1029, SEQ ID NO: 1032, SEQ ID NO: 259, SEQ ID NO: 286, SEQ ID NO: 326, SEQ ID NO: 374, SEQ ID NO: 399, SEQ ID NO: 422, SEQ ID NO: 454, SEQ ID NO: 465, SEQ ID NO: 998, SEQ ID NO: 1009, SEQ ID NO: 1023, SEQ ID NO: 1294, SEQ ID NO: 1295, SEQ ID NO: 319, SEQ ID NO: 325, SEQ ID NO: 425, SEQ ID NO: 437, SEQ ID NO: 438, SEQ ID NO: 447, SEQ ID NO: 448, SEQ ID NO: 467, SEQ ID NO: 996, SEQ ID NO: 1027, SEQ ID NO: 1031, SEQ ID NO: 254, SEQ ID NO: 352, SEQ ID NO: 415, SEQ ID NO: 1019, SEQ ID NO: 381, SEQ ID NO: 389, SEQ ID NO: 1010, and SEQ ID NO: 1012.

In another embodiment, the *H. pylori* outer membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a terminal phenylalanine residue or a
 35 fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 255, SEQ ID NO: 263, SEQ ID NO: 266, SEQ ID NO: 277, SEQ ID NO: 280,

SEQ ID NO: 285, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 299, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 321, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 353, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 375, SEQ ID NO: 384, SEQ ID NO: 391, SEQ ID NO: 392,
5 SEQ ID NO: 397, SEQ ID NO: 398, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 409, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 427, SEQ ID NO: 433, SEQ ID NO: 434, SEQ ID NO: 441, SEQ ID NO: 444, SEQ ID NO: 445, SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 453, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 983, SEQ ID NO: 989, SEQ ID NO: 1008, SEQ ID NO: 1011, SEQ ID NO: 1014, SEQ ID NO: 1015, SEQ ID NO: 1029, and SEQ ID NO: 1032.

In another embodiment, the *H. pylori* outer membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a C-terminal tyrosine cluster or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 286, SEQ ID NO: 326, SEQ ID NO: 374, SEQ ID NO: 399, SEQ ID NO: 422, SEQ ID NO: 454, SEQ ID NO: 465, SEQ ID NO: 998, SEQ ID NO: 1009, SEQ ID NO: 1023, SEQ ID NO: 1294, and SEQ ID NO: 1295.

In another embodiment, the *H. pylori* outer membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a terminal phenylalanine residue and a C-terminal tyrosine cluster or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 319, SEQ ID NO: 325, SEQ ID NO: 425, SEQ ID NO: 437, SEQ ID NO: 438, SEQ ID NO: 447, SEQ ID NO: 448, SEQ ID NO: 467, SEQ ID NO: 996, SEQ ID NO: 1027, and SEQ ID NO: 1031.

In another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* inner membrane polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 354, SEQ ID NO: 372, SEQ ID NO: 400, SEQ ID NO: 421, SEQ ID NO: 1022, SEQ ID NO: 463, SEQ ID NO: 281, SEQ ID NO: 988, SEQ ID NO: 411, SEQ ID NO: 407, SEQ ID NO: 1017, SEQ ID NO: 290, SEQ ID NO: 417, SEQ ID NO: 430, SEQ ID NO: 992, and SEQ ID NO: 1025.

In another embodiment, the *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in outer membrane and cell wall synthesis or a fragment thereof encoded by the nucleic acid comprising a nucleotide sequence of SEQ ID NO: 354.

In another embodiment, the *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in energy conversion or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 372, SEQ ID NO: 400, SEQ ID NO: 421, and SEQ ID NO: 1022.

In another embodiment, the *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in cofactor metabolism or a fragment thereof encoded by the nucleic acid comprising a nucleotide sequence of SEQ ID NO: 463.

5 In another embodiment, the *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in secretion or adhesion or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 281 and SEQ ID NO: 988.

10 In another embodiment, the *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in transport or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 407 and SEQ ID NO: 1017.

In another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* flagellar polypeptide or a fragment thereof encoded by the nucleic acid comprising a nucleotide sequence of SEQ ID NO: 477.

15 In another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* transport polypeptide or a fragment thereof encoded by the nucleic acid comprising a nucleotide sequence of SEQ ID NO: 414.

20 Particularly preferred is an isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* cytoplasmic polypeptide or a fragment thereof. Such nucleic acid is selected from the group consisting of SEQ ID NO: 470, SEQ ID NO: 1033, SEQ ID NO: 357, SEQ ID NO: 457, SEQ ID NO: 461, SEQ ID NO: 1030, SEQ ID NO: 345, SEQ ID NO: 383, SEQ ID NO: 387, SEQ ID NO: 455, SEQ ID NO: 1003, SEQ ID NO: 351, SEQ ID NO: 416, SEQ ID NO: 278, SEQ ID NO: 335, SEQ ID NO: 346, SEQ ID NO: 350, SEQ ID NO: 419, SEQ ID NO: 460, SEQ ID NO: 472, SEQ ID NO: 1000, SEQ ID NO: 1004, SEQ ID NO: 1020, SEQ ID NO: 1293, SEQ ID NO: 318, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 330, SEQ ID NO: 347, SEQ ID NO: 440, SEQ ID NO: 446, SEQ ID NO: 464, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 995, SEQ ID NO: 997, SEQ ID NO: 1005, and SEQ ID NO: 1028.

30 In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in energy conversion or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 470 and SEQ ID NO: 1033.

35 In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in amino acid metabolism and transport or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 357 and SEQ ID NO: 457.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in nucleotide metabolism and transport or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 461 and SEQ ID NO: 1030.

5 In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in cofactor metabolism or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 345, SEQ ID NO: 383, SEQ ID NO: 387, SEQ ID NO: 455, and SEQ ID NO: 1003.

10 In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in lipid metabolism or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 351 and SEQ ID NO: 416.

15 In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in genome replication, transcription, recombination and repair or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 278, SEQ ID NO: 335, SEQ ID NO: 346, SEQ ID NO: 350, SEQ ID NO: 419, SEQ ID NO: 460, SEQ ID NO: 472, SEQ ID NO: 1000, SEQ ID NO: 1004, SEQ ID NO: 1020, and SEQ ID NO: 1293.

20 Particularly preferred is an isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* secreted polypeptide or a fragment thereof. Such nucleic acid is selected from the group consisting of SEQ ID NO: 355, SEQ ID NO: 1006, SEQ ID NO: 257, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 261, SEQ ID NO: 264, SEQ ID NO: 265, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 275, SEQ ID NO: 276, SEQ ID NO: 279, SEQ ID NO: 283, 25 SEQ ID NO: 284, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 323, SEQ ID NO: 338, SEQ ID NO: 342, SEQ ID NO: 348, SEQ ID NO: 349, SEQ ID NO: 356, SEQ ID NO: 30 358, SEQ ID NO: 359, SEQ ID NO: 360, SEQ ID NO: 361, SEQ ID NO: 362, SEQ ID NO: 363, SEQ ID NO: 367, SEQ ID NO: 370, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 377, SEQ ID NO: 378, SEQ ID NO: 379, SEQ ID NO: 380, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 394, SEQ ID NO: 395, SEQ ID NO: 396, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 408, SEQ ID NO: 420, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 429, SEQ ID NO: 432, SEQ ID NO: 439, SEQ 35 ID NO: 442, SEQ ID NO: 451, SEQ ID NO: 471, SEQ ID NO: 478, SEQ ID NO: 488,

SEQ ID NO: 987, SEQ ID NO: 990, SEQ ID NO: 991, SEQ ID NO: 993, SEQ ID NO: 1001, SEQ ID NO: 1002, SEQ ID NO: 1007, SEQ ID NO: 1013, SEQ ID NO: 1016, SEQ ID NO: 1018, SEQ ID NO: 1021, and SEQ ID NO: 1026.

In another embodiment, the *H. pylori* secreted polypeptide or a fragment thereof
 5 is an *H. pylori* polypeptide involved in secretion and adhesion or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 355 and SEQ ID NO: 1006.

Particularly preferred is an isolated nucleic acid comprising a nucleotide
 sequence encoding an *H. pylori* cellular polypeptide or a fragment thereof. Such nucleic
 10 acid is selected from the group consisting of SEQ ID NO: 256, SEQ ID NO: 267, SEQ ID NO: 282, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 332, SEQ ID NO: 333, SEQ ID NO: 336, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 340, SEQ ID NO: 341, SEQ ID NO: 344, SEQ ID NO: 369, SEQ ID NO: 376, SEQ ID NO: 382, SEQ
 15 ID NO: 386, SEQ ID NO: 423, SEQ ID NO: 431, SEQ ID NO: 435, SEQ ID NO: 436, SEQ ID NO: 458, SEQ ID NO: 462, SEQ ID NO: 475, SEQ ID NO: 476, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 984, SEQ ID NO: 994, SEQ ID NO: 1024, and SEQ ID NO: 1036.

Particularly preferred is a purified or isolated *H. pylori* cell envelope polypeptide
 20 or a fragment thereof, wherein the polypeptide is selected from the group consisting of SEQ ID NO: 746, SEQ ID NO: 754, SEQ ID NO: 757, SEQ ID NO: 768, SEQ ID NO: 771, SEQ ID NO: 776, SEQ ID NO: 783, SEQ ID NO: 785, SEQ ID NO: 790, SEQ ID NO: 802, SEQ ID NO: 803, SEQ ID NO: 804, SEQ ID NO: 812, SEQ ID NO: 818, SEQ
 25 ID NO: 820, SEQ ID NO: 882, SEQ ID NO: 844, SEQ ID NO: 855, SEQ ID NO: 857, SEQ ID NO: 859, SEQ ID NO: 866, SEQ ID NO: 875, SEQ ID NO: 882, SEQ ID NO: 883, SEQ ID NO: 888, SEQ ID NO: 889, SEQ ID NO: 893, SEQ ID NO: 895, SEQ ID NO: 900, SEQ ID NO: 901, SEQ ID NO: 903, SEQ ID NO: 918, SEQ ID NO: 924, SEQ ID NO: 925, SEQ ID NO: 932, SEQ ID NO: 935, SEQ ID NO: 936, SEQ ID NO: 940,
 30 SEQ ID NO: 941, SEQ ID NO: 943, SEQ ID NO: 944, SEQ ID NO: 957, SEQ ID NO: 959, SEQ ID NO: 960, SEQ ID NO: 1037, SEQ ID NO: 1043, SEQ ID NO: 1062, SEQ ID NO: 1065, SEQ ID NO: 1068, SEQ ID NO: 1069, SEQ ID NO: 1083, SEQ ID NO: 1086, SEQ ID NO: 750, SEQ ID NO: 777, SEQ ID NO: 817, SEQ ID NO: 865, SEQ ID NO: 890, SEQ ID NO: 913, SEQ ID NO: 945, SEQ ID NO: 956, SEQ ID NO: 1052,
 35 SEQ ID NO: 1063, SEQ ID NO: 1077, SEQ ID NO: 1297, SEQ ID NO: 1298, SEQ ID NO: 810, SEQ ID NO: 816, SEQ ID NO: 916, SEQ ID NO: 928, SEQ ID NO: 929, SEQ

ID NO: 938, SEQ ID NO: 939, SEQ ID NO: 958, SEQ ID NO: 1050, SEQ ID NO: 1081, SEQ ID NO: 1085, SEQ ID NO: 745, SEQ ID NO: 843, SEQ ID NO: 906, SEQ ID NO: 1073, SEQ ID NO: 872, SEQ ID NO: 880, SEQ ID NO: 1064, SEQ ID NO: 1066, SEQ ID NO: 845, SEQ ID NO: 863, SEQ ID NO: 891, SEQ ID NO: 912, SEQ ID NO: 1076, SEQ ID NO: 954, SEQ ID NO: 772, SEQ ID NO: 1042, SEQ ID NO: 902, SEQ ID NO: 898, SEQ ID NO: 1071, SEQ ID NO: 781, SEQ ID NO: 908, SEQ ID NO: 921, SEQ ID NO: 1046, SEQ ID NO: 1079, SEQ ID NO: 968, SEQ ID NO: 905, SEQ ID NO: 744, SEQ ID NO: 784, SEQ ID NO: 825, SEQ ID NO: 834, SEQ ID NO: 909, SEQ ID NO: 915, and SEQ ID NO: 934.

10 In another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* outer membrane polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 746, SEQ ID NO: 754, SEQ ID NO: 757, SEQ ID NO: 768, SEQ ID NO: 771, SEQ ID NO: 776, SEQ ID NO: 783, SEQ ID NO: 785, SEQ ID NO: 790, SEQ ID NO: 802, SEQ ID NO: 803, SEQ ID NO: 804, SEQ ID NO: 812, 15 SEQ ID NO: 818, SEQ ID NO: 820, SEQ ID NO: 882, SEQ ID NO: 844, SEQ ID NO: 855, SEQ ID NO: 857, SEQ ID NO: 859, SEQ ID NO: 866, SEQ ID NO: 875, SEQ ID NO: 882, SEQ ID NO: 883, SEQ ID NO: 888, SEQ ID NO: 889, SEQ ID NO: 893, SEQ ID NO: 895, SEQ ID NO: 900, SEQ ID NO: 901, SEQ ID NO: 903, SEQ ID NO: 918, SEQ ID NO: 924, SEQ ID NO: 925, SEQ ID NO: 932, SEQ ID NO: 935, SEQ ID NO: 20 936, SEQ ID NO: 940, SEQ ID NO: 941, SEQ ID NO: 943, SEQ ID NO: 944, SEQ ID NO: 957, SEQ ID NO: 959, SEQ ID NO: 960, SEQ ID NO: 1037, SEQ ID NO: 1043, SEQ ID NO: 1062, SEQ ID NO: 1065, SEQ ID NO: 1068, SEQ ID NO: 1069, SEQ ID NO: 1083, SEQ ID NO: 1086, SEQ ID NO: 750, SEQ ID NO: 777, SEQ ID NO: 817, SEQ ID NO: 865, SEQ ID NO: 890, SEQ ID NO: 913, SEQ ID NO: 945, SEQ ID NO: 25 956, SEQ ID NO: 1052, SEQ ID NO: 1063, SEQ ID NO: 1077, SEQ ID NO: 1297, SEQ ID NO: 1298, SEQ ID NO: 810, SEQ ID NO: 816, SEQ ID NO: 916, SEQ ID NO: 928, SEQ ID NO: 929, SEQ ID NO: 938, SEQ ID NO: 939, SEQ ID NO: 958, SEQ ID NO: 1050, SEQ ID NO: 1081, SEQ ID NO: 1085, SEQ ID NO: 745, SEQ ID NO: 843, SEQ ID NO: 906, SEQ ID NO: 1073, SEQ ID NO: 872, SEQ ID NO: 880, SEQ ID NO: 30 1064, and SEQ ID NO: 1066.

In another embodiment, the *H. pylori* outer membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a terminal phenylalanine residue or a fragment thereof selected from the group consisting of SEQ ID NO: 746, SEQ ID NO: 754, SEQ ID NO: 757, SEQ ID NO: 768, SEQ ID NO: 771, SEQ ID NO: 776, SEQ ID NO: 783, SEQ ID NO: 785, SEQ ID NO: 790, SEQ ID NO: 802, SEQ ID NO: 803, SEQ ID NO: 804, SEQ ID NO: 812, SEQ ID NO: 818, SEQ ID NO: 820, SEQ ID NO: 882,

SEQ ID NO: 844, SEQ ID NO: 855, SEQ ID NO: 857, SEQ ID NO: 859, SEQ ID NO: 866, SEQ ID NO: 875, SEQ ID NO: 882, SEQ ID NO: 883, SEQ ID NO: 888, SEQ ID NO: 889, SEQ ID NO: 893, SEQ ID NO: 895, SEQ ID NO: 900, SEQ ID NO: 901, SEQ ID NO: 903, SEQ ID NO: 918, SEQ ID NO: 924, SEQ ID NO: 925, SEQ ID NO: 932, 5 SEQ ID NO: 935, SEQ ID NO: 936, SEQ ID NO: 940, SEQ ID NO: 941, SEQ ID NO: 943, SEQ ID NO: 944, SEQ ID NO: 957, SEQ ID NO: 959, SEQ ID NO: 960, SEQ ID NO: 1037, SEQ ID NO: 1043, SEQ ID NO: 1062, SEQ ID NO: 1065, SEQ ID NO: 1068, SEQ ID NO: 1069, SEQ ID NO: 1083, and SEQ ID NO: 1086.

10 In another embodiment, the *H. pylori* outer membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a C-terminal tyrosine cluster or a fragment thereof selected from the group consisting of SEQ ID NO: 777, SEQ ID NO: 817, SEQ ID NO: 865, SEQ ID NO: 890, SEQ ID NO: 913, SEQ ID NO: 945, SEQ ID NO: 956, SEQ ID NO: 1052, SEQ ID NO: 1063, SEQ ID NO: 1077, SEQ ID NO: 1297, and SEQ ID NO: 1298.

15 In another embodiment, the *H. pylori* outer membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a terminal phenylalanine residue and a C-terminal tyrosine cluster or a fragment thereof selected from the group consisting of SEQ ID NO: 810, SEQ ID NO: 816, SEQ ID NO: 916, SEQ ID NO: 928, SEQ ID NO: 929, SEQ ID NO: 938, SEQ ID NO: 939, SEQ ID NO: 958, SEQ ID NO: 1050, SEQ ID NO: 1081, and SEQ ID NO: 1085. 20

In another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* inner membrane polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 845, SEQ ID NO: 863, SEQ ID NO: 891, SEQ ID NO: 912, SEQ ID NO: 1076, SEQ ID NO: 954, SEQ ID NO: 772, SEQ ID NO: 1042, 25 SEQ ID NO: 902, SEQ ID NO: 898, SEQ ID NO: 1071, SEQ ID NO: 781, SEQ ID NO: 908, SEQ ID NO: 921, SEQ ID NO: 1046, and SEQ ID NO: 1079.

In another embodiment, the *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in outer membrane and cell wall synthesis or a fragment thereof comprising an amino acid sequence of SEQ ID NO: 845.

30 In another embodiment, the *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in energy conversion or a fragment thereof selected from the group consisting of SEQ ID NO: 863, SEQ ID NO: 891, SEQ ID NO: 912, and SEQ ID NO: 1076.

In another embodiment, the *H. pylori* inner membrane polypeptide or a fragment 35 thereof is an *H. pylori* polypeptide involved in cofactor metabolism or a fragment thereof comprising an amino acid sequence of SEQ ID NO: 954.

In another embodiment, the *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in secretion or adhesion or a fragment thereof selected from the group consisting of SEQ ID NO: 772 and SEQ ID NO: 1042.

5 In another embodiment, the *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in transport or a fragment thereof selected from the group consisting of SEQ ID NO: 898 and SEQ ID NO: 1071.

In another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* flagellar polypeptide or a fragment thereof comprising an amino acid sequence of SEQ ID NO: 968.

10 In another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* transport polypeptide or a fragment thereof comprising an amino acid sequence of SEQ ID NO: 905.

Particularly preferred is a purified or isolated *H. pylori* cytoplasmic polypeptide or a fragment thereof, wherein the polypeptide is selected from the group consisting of
15 SEQ ID NO: 961, SEQ ID NO: 1087, SEQ ID NO: 848, SEQ ID NO: 948, SEQ ID NO: 952, SEQ ID NO: 1084, SEQ ID NO: 836, SEQ ID NO: 874, SEQ ID NO: 878, SEQ ID NO: 946, SEQ ID NO: 1057, SEQ ID NO: 842, SEQ ID NO: 907, SEQ ID NO: 769, SEQ ID NO: 826, SEQ ID NO: 837, SEQ ID NO: 841, SEQ ID NO: 910, SEQ ID NO: 951, SEQ ID NO: 963, SEQ ID NO: 1054, SEQ ID NO: 1058, SEQ ID NO: 1074, SEQ
20 ID NO: 1296, SEQ ID NO: 809, SEQ ID NO: 813, SEQ ID NO: 815, SEQ ID NO: 821, SEQ ID NO: 838, SEQ ID NO: 931, SEQ ID NO: 937, SEQ ID NO: 955, SEQ ID NO: 981, SEQ ID NO: 982, SEQ ID NO: 1049, SEQ ID NO: 1051, SEQ ID NO: 1059, and SEQ ID NO: 1082.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment
25 thereof is an *H. pylori* polypeptide involved in energy conversion or a fragment thereof selected from the group consisting of SEQ ID NO: 961 and SEQ ID NO: 1087.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in amino acid metabolism and transport or a fragment thereof selected from the group consisting of SEQ ID NO: 848 and SEQ ID
30 NO: 948.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in nucleotide metabolism and transport or a fragment thereof selected from the group consisting of SEQ ID NO: 952 and SEQ ID
NO: 1084.

35 In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in cofactor metabolism or a fragment

thereof selected from the group consisting of SEQ ID NO: 836, SEQ ID NO: 874, SEQ ID NO: 878, SEQ ID NO: 946, and SEQ ID NO: 1057.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in lipid metabolism or a fragment thereof
5 selected from the group consisting of SEQ ID NO: 842, SEQ ID NO: 907.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in genome replication, transcription, recombination and repair or a fragment thereof selected from the group consisting of
10 SEQ ID NO: 769, SEQ ID NO: 826, SEQ ID NO: 837, SEQ ID NO: 841, SEQ ID NO: 910, SEQ ID NO: 951, SEQ ID NO: 963, SEQ ID NO: 1054, SEQ ID NO: 1058, SEQ ID NO: 1074, and SEQ ID NO: 1296.

Particularly preferred is a purified or isolated *H. pylori* secreted polypeptide or a fragment thereof, wherein the polypeptide is selected from the group consisting of SEQ ID NO: 846, SEQ ID NO: 1060, SEQ ID NO: 748, SEQ ID NO: 749, SEQ ID NO: 751,
15 SEQ ID NO: 752, SEQ ID NO: 755, SEQ ID NO: 756, SEQ ID NO: 759, SEQ ID NO: 761, SEQ ID NO: 763, SEQ ID NO: 765, SEQ ID NO: 766, SEQ ID NO: 767, SEQ ID NO: 770, SEQ ID NO: 774, SEQ ID NO: 775, SEQ ID NO: 778, SEQ ID NO: 779, SEQ ID NO: 780, SEQ ID NO: 782, SEQ ID NO: 786, SEQ ID NO: 787, SEQ ID NO: 788, SEQ ID NO: 789, SEQ ID NO: 791, SEQ ID NO: 792, SEQ ID NO: 793, SEQ ID NO:
20 794, SEQ ID NO: 795, SEQ ID NO: 796, SEQ ID NO: 805, SEQ ID NO: 806, SEQ ID NO: 814, SEQ ID NO: 829, SEQ ID NO: 833, SEQ ID NO: 839, SEQ ID NO: 840, SEQ ID NO: 847, SEQ ID NO: 849, SEQ ID NO: 850, SEQ ID NO: 851, SEQ ID NO: 852, SEQ ID NO: 853, SEQ ID NO: 854, SEQ ID NO: 858, SEQ ID NO: 861, SEQ ID NO: 862, SEQ ID NO: 864, SEQ ID NO: 868, SEQ ID NO: 869, SEQ ID NO: 870, SEQ ID
25 NO: 871, SEQ ID NO: 879, SEQ ID NO: 881, SEQ ID NO: 885, SEQ ID NO: 886, SEQ ID NO: 887, SEQ ID NO: 892, SEQ ID NO: 894, SEQ ID NO: 896, SEQ ID NO: 899, SEQ ID NO: 911, SEQ ID NO: 917, SEQ ID NO: 919, SEQ ID NO: 920, SEQ ID NO: 923, SEQ ID NO: 930, SEQ ID NO: 933, SEQ ID NO: 942, SEQ ID NO: 962, SEQ ID NO: 969, SEQ ID NO: 979, SEQ ID NO: 1041, SEQ ID NO: 1044, SEQ ID NO: 1045,
30 SEQ ID NO: 1047, SEQ ID NO: 1055, SEQ ID NO: 1056, SEQ ID NO: 1061, SEQ ID NO: 1067, SEQ ID NO: 1070, SEQ ID NO: 1072, SEQ ID NO: 1075, and SEQ ID NO: 1080.

In another embodiment, the *H. pylori* secreted polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in secretion and adhesion or a fragment thereof
35 selected from the group consisting of SEQ ID NO: 846 and SEQ ID NO: 1060.

Particularly preferred is a purified or isolated *H. pylori* cellular polypeptide or a fragment thereof, wherein the polypeptide is selected from the group consisting of SEQ ID NO: 747, SEQ ID NO: 758, SEQ ID NO: 773, SEQ ID NO: 797, SEQ ID NO: 798, SEQ ID NO: 799, SEQ ID NO: 800, SEQ ID NO: 801, SEQ ID NO: 807, SEQ ID NO: 808, SEQ ID NO: 823, SEQ ID NO: 824, SEQ ID NO: 827, SEQ ID NO: 828, SEQ ID NO: 830, SEQ ID NO: 831, SEQ ID NO: 832, SEQ ID NO: 835, SEQ ID NO: 860, SEQ ID NO: 867, SEQ ID NO: 873, SEQ ID NO: 877, SEQ ID NO: 914, SEQ ID NO: 922, SEQ ID NO: 926, SEQ ID NO: 927, SEQ ID NO: 949, SEQ ID NO: 953, SEQ ID NO: 966, SEQ ID NO: 967, SEQ ID NO: 970, SEQ ID NO: 971, SEQ ID NO: 972, SEQ ID NO: 973, SEQ ID NO: 974, SEQ ID NO: 975, SEQ ID NO: 976, SEQ ID NO: 977, SEQ ID NO: 978, SEQ ID NO: 980, SEQ ID NO: 1038, SEQ ID NO: 1048, SEQ ID NO: 1078, and SEQ ID NO: 1090.

In another aspect, the invention pertains to any individual *H. pylori* polypeptide member or nucleic acid encoding such a member from the above-identified groups of *H. pylori* polypeptides.

In another aspect, the invention features nucleic acids capable of binding mRNA of *H. pylori*. Such nucleic acid is capable of acting as antisense nucleic acid to control the translation of mRNA of *H. pylori*. A further aspect features a nucleic acid which is capable of binding specifically to an *H. pylori* nucleic acid. These nucleic acids are also referred to herein as complements and have utility as probes and as capture reagents.

In another aspect, the invention features an expression system comprising an open reading frame corresponding to *H. pylori* nucleic acid. The nucleic acid further comprises a control sequence compatible with an intended host. The expression system is useful for making polypeptides corresponding to *H. pylori* nucleic acid.

In another aspect, the invention features a cell transformed with the expression system to produce *H. pylori* polypeptides.

In another aspect, the invention features a method of generating antibodies against *H. pylori* polypeptides which are capable of binding specifically to *H. pylori* polypeptides. Such antibody has utility as reagents for immunoassays to evaluate the abundance and distribution of *H. pylori*-specific antigens.

In another aspect, the invention features a method of generating vaccines for immunizing an individual against *H. pylori*. The method includes: immunizing a subject with an *H. pylori* polypeptide, e.g., a surface or secreted polypeptide, or active portion thereof, and a pharmaceutically acceptable carrier. Such vaccines have therapeutic and prophylactic utilities.

In another aspect, the invention provides a method for generating a vaccine comprising a modified immunogenic *H. pylori* polypeptide, e.g., a surface or secreted polypeptide, or active portion thereof, and a pharmacologically acceptable carrier.

In another aspect, the invention features a method of evaluating a compound, e.g.
5 a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *H. pylori* polypeptide. The method includes: contacting the candidate compound with an *H. pylori* polypeptides and determining if the compound binds or otherwise interacts with an *H. pylori* polypeptide. Compounds which bind *H. pylori* are candidates as activators or inhibitors of the bacterial life cycle. These assays can be performed *in vitro*
10 or *in vivo*.

In another aspect, the invention features a method of evaluating a compound, e.g.
a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *H. pylori* nucleic acid, e.g., DNA or RNA. The method includes: contacting the candidate
15 compound with an *H. pylori* nucleic acid and determining if the compound binds or otherwise interacts with an *H. pylori* polypeptide. Compounds which bind *H. pylori* are candidates as activators or inhibitors of the bacterial life cycle. These assays can be performed *in vitro* or *in vivo*.

The invention features *H. pylori* polypeptides, preferably a substantially pure preparation of an *H. pylori* polypeptide, or a recombinant *H. pylori* polypeptide. In
20 preferred embodiments: the polypeptide has biological activity; the polypeptide has an amino acid sequence at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% homologous to an amino acid sequence contained in the Sequence Listing; the polypeptide has an amino acid sequence essentially the same as an amino acid sequence in the Sequence Listing; the polypeptide is at least 5, 10, 20, 50, 100, or 150 amino acid residues in length; the
25 polypeptide includes at least 5, preferably at least 10, more preferably at least 20, more preferably at least 50, 100, or 150 contiguous amino acid residues of a polypeptide contained in the Sequence Listing.

In preferred embodiments: the *H. pylori* polypeptide is encoded by a nucleic acid contained in the Sequence Listing, or by a nucleic acid having at least 60%, 70%,
30 80%, 90%, 95%, 98%, or 99% homology with a nucleic acid shown in the Sequence Listing.

In a preferred embodiment, the subject *H. pylori* polypeptide differs in amino acid sequence at 1, 2, 3, 5, 10 or more residues from a sequence in the Sequence Listing. The differences, however, are such that the *H. pylori* polypeptide exhibits an *H. pylori*
35 biological activity, e.g., the *H. pylori* polypeptide retains a biological activity of a naturally occurring *H. pylori* enzyme.

In preferred embodiments, the polypeptide includes all or a fragment of an amino acid sequence contained in the Sequence Listing; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' to the genomic DNA which encodes a sequence contained in the Sequence Listing.

5 In yet other preferred embodiments, the *H. pylori* polypeptide is a recombinant fusion protein having a first *H. pylori* polypeptide portion and a second polypeptide portion, e.g., a second polypeptide portion having an amino acid sequence unrelated to *H. pylori*. The second polypeptide portion can be, e.g., any of glutathione-S-transferase, a DNA binding domain, or a polymerase activating domain. In preferred embodiment
10 the fusion protein can be used in a two-hybrid assay.

Polypeptides of the invention include those which arise as a result of alternative transcription events, alternative RNA splicing events, and alternative translational and posttranslational events.

The invention also encompasses an immunogenic component which includes an
15 *H. pylori* polypeptide in an immunogenic preparation; the immunogenic component being capable of eliciting an immune response specific for the *H. pylori* polypeptide, e.g., a humoral response, an antibody response, or a cellular response. In preferred embodiments, the immunogenic component comprises at least one antigenic determinant from a polypeptide contained in the Sequence Listing.

20 In another aspect, the invention provides a substantially pure nucleic acid having a nucleotide sequence which encodes an *H. pylori* polypeptide. In preferred embodiments: the encoded polypeptide has biological activity; the encoded polypeptide has an amino acid sequence at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% homologous to an amino acid sequence contained in the Sequence Listing; the encoded
25 polypeptide has an amino acid sequence essentially the same as an amino acid sequence in the Sequence Listing; the encoded polypeptide is at least 5, 10, 20, 50, 100, or 150 amino acids in length; the encoded polypeptide comprises at least 5, preferably at least 10, more preferably at least 20, more preferably at least 50, 100, or 150 contiguous amino acids contained in the Sequence Listing.

30 In preferred embodiments: the nucleic acid is that as shown in the Sequence Listing; the nucleic acid is at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% homologous with a nucleic acid sequence contained in the Sequence Listing.

In a preferred embodiment, the encoded *H. pylori* polypeptide differs (e.g., by amino acid substitution, addition or deletion of at least one amino acid residue) in amino
35 acid sequence at 1, 2, 3, 5, 10 or more residues, from a sequence in the Sequence Listing. The differences, however, are such that: the *H. pylori* encoded polypeptide

exhibits a *H. pylori* biological activity, e.g., the encoded *H. pylori* enzyme retains a biological activity of a naturally occurring *H. pylori*.

In preferred embodiments, the encoded polypeptide includes all or a fragment of an amino acid sequence contained in the Sequence Listing; fused, in reading frame, to
5 additional amino acid residues, preferably to residues encoded by genomic DNA 5' to the genomic DNA which encodes a sequence contained in the Sequence Listing.

In preferred embodiments, the subject *H. pylori* nucleic acid will include a transcriptional regulatory sequence, e.g. at least one of a transcriptional promoter or transcriptional enhancer sequence, operably linked to the *H. pylori* gene sequence, e.g.,
10 to render the *H. pylori* gene sequence suitable for expression in a recombinant host cell.

In yet a further preferred embodiment, the nucleic acid which encodes an *H. pylori* polypeptide of the invention, hybridizes under stringent conditions to a nucleic acid probe corresponding to at least 8 consecutive nucleotides of a nucleic acid contained in the Sequence Listing; more preferably to at least 12 consecutive nucleotides
15 of a nucleic acid contained in the Sequence Listing; more preferably to at least 20 consecutive nucleotides of a nucleic acid contained in the Sequence Listing; more preferably to at least 40 consecutive nucleotides of a nucleic acid contained in the Sequence Listing.

In a preferred embodiment, the nucleic acid encodes a peptide which differs by at
20 least one amino acid residue from the sequences shown in the Sequence Listing.

In a preferred embodiment, the nucleic acid differs by at least one nucleotide from a nucleotide sequence shown in the Sequence Listing which encodes amino acids shown in the Sequence Listing.

In another aspect, the invention encompasses: a vector including a nucleic acid
25 which encodes an *H. pylori* polypeptide or an *H. pylori* polypeptide variant as described herein; a host cell transfected with the vector; and a method of producing a recombinant *H. pylori* polypeptide or *H. pylori* polypeptide variant; including culturing the cell, e.g., in a cell culture medium, and isolating the *H. pylori* or *H. pylori* polypeptide variant e.g., from the cell or from the cell culture medium.

30 In another aspect, the invention features, a purified recombinant nucleic acid having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with a sequence contained in the Sequence Listing.

The invention also provides a probe or primer which includes a substantially purified oligonucleotide. The oligonucleotide includes a region of nucleotide sequence
35 which hybridizes under stringent conditions to at least 10 consecutive nucleotides of sense or antisense sequence contained in the Sequence Listing, or naturally occurring

mutants thereof. In preferred embodiments, the probe or primer further includes a label group attached thereto. The label group can be, e.g., a radioisotope, a fluorescent compound, an enzyme, and/or an enzyme co-factor. Preferably, the oligonucleotide is at least 10 and less than 20, 30, 50, 100, or 150 nucleotides in length.

5 The invention further provides nucleic acids, e.g., RNA or DNA, encoding a polypeptide of the invention. This includes double stranded nucleic acids as well as coding and antisense single strands.

The *H. pylori* strain, from which genomic sequences have been sequenced, has been deposited in the American Type Culture Collection(ATCC) as strain HP-J99.

10 Included in the invention are: allelic variations; natural mutants; induced mutants; proteins encoded by DNA that hybridizes under high or low stringency conditions to a nucleic acid which encodes a polypeptide as shown in the Sequence Listing (for definitions of high and low stringency see Current Protocols in Molecular Biology, John Wiley & Sons, New York, 1989, 6.3.1 - 6.3.6, hereby incorporated by
15 reference); and, polypeptides specifically bound by antisera to *H. pylori* polypeptides, especially by antisera to an active site or binding domain of *H. pylori* polypeptide. The invention also includes fragments, preferably biologically active fragments. These and other polypeptides are also referred to herein as *H. pylori* polypeptide analogs or variants.

20 Putative functions have been determined for several of the *H. pylori* polypeptides of the invention, as shown in Table 1.

Accordingly, uses of the claimed *H. pylori* polypeptides in these identified functions are also within the scope of the invention.

In addition, the present invention encompasses *H. pylori* polypeptides
25 characterized as shown in Table 1 below, including: *H. pylori* cell envelope proteins, *H. pylori* secreted proteins, *H. pylori* cytoplasmic proteins and *H. pylori* cellular proteins. Members of these groups were identified by BLAST homology searches and by searches for secretion signal or transmembrane protein motifs. Polypeptides related by
significant homology to the polypeptides of Table 1 (as reflected by FASTA compar-
30 isons of the amino acid sequences and indicated in many cases in Tables 3-6 below) are also considered to be classified in the manner of the homolog shown in Table 1.

TABLE 1

ORF NAME	nt Seq ID#	aa Seq ID #
A.CELL ENVELOPE		
A.1 Outer membrane		
A.1.2 Terminal phe residue		
0lae12001_24218781_f2_18	255	746

02gel1622_875260_f3_36	263	754
02gp20706_23632775_f3_32	266	757
07ap11015_23938312_f3_2	271	762
05eel0816_4103408_f2_11	277	768
06ap20306_23437632_f3_9	280	771
07ap20216_7227202_f3_10	285	776
14ap10815_20585777_cl_13	292	783
hplp14013_11726503_c2_20	294	785
hp5p15641_21698387_c2_20	299	790
02gp20706_16803513_fl_1	311	802
02gp20706_20365905_f2_8	312	803
02gp20814_3984818_fl_1	313	804
05ae30220_9882767_f2_34	321	812
07ep11916_5913592_f3_18	327	818
09ze10333_22460750_f2_6	329	820
14ap10221_13689381_c3_4	331	882
06ce20610_1367157_fl_8.aa	353	844
02gel0116_16803513_f2_34	364	855
02gel0116_36367936_cl_92	366	857
05cel0910_25598277_f3_3	368	859
06cp11217_4881263_f2_9	375	866
06ep30223_34409437_f3_94	384	875
06gp71906_970325_c3_190	391	882
07ae10923_24426508_fl_1	392	883
09cp10224_1062966_c3_61	397	888
09cp10224_1412715_c3_56	398	889
09cp61003_14562637_c2_93	402	893
09cp61003_24063587_cl_74	404	895
11ae80818_7952_cl_49	409	900
11ap20714_4960432_c3_97	410	901
11ap20714_7227202_f3_43.aa	412	903
hp5p15641_12195281_cl_24	427	918
hp6p10903_4398263_f3_6.aa	433	924
hp6p10903_4398263_f3_6.aa	434	925
02ae31010_30208317_fl_14	441	932
02cp10615_26573462_cl_45	444	935
03ae10804_12609533_cl_26	445	936
04ep41903_4101593_f2_10.aa	449	940
05ep10815_26570332_c2_99	450	941
05ep10815_4719175_cl_83	452	943
06cp30603_679218_f2_34	453	944
11ae80818_19632781_c3_57	466	957
11ap20714_34023312_f3_46	468	959
11eel1408_4977193_cl_41.aa	469	960
11ael1922_12586675_f2_1	983	1037
07eel1402_2458267_c3_108	985	1039
11ap20714_7227202_f3_40	989	1043
hp7e10192_25598277_c2_15	1008	1062
06ep30223_34409437_f2_64	1011	1065
09cp10224_1062966_cl_44	1014	1068
01ce61016_12931513_c2_106	1015	1069
05ep10815_4719175_cl_115	1029	1083

- 22 -

05ae30220_4977193_c3_198	1032	1086
A.1.3 No terminal phe residue		
02ae11612_22477267_f2_27	259	750
A.1.4 C-terminal tyrosine cluster motif		
07ep11916_5273452_c3_31	286	777
07ce11019_22051291_f1_1	326	817
06cp11217_19720300_f3_11	374	865
09cp10224_429510_c2_46.aa	399	890
hp4e53394_22864682_c2_86.aa	422	913
06ep10615_961562_f2_41	454	945
09cp61003_492187_c2_80.aa	465	956
14gp11423_26803801_f3_7	998	1052
hp4e53394_19720300_c3_98	1009	1063
hp4e53394_19720300_c3_98	1023	1077
01ce61016_492187_c3_120	1294	1297
06ep10615_961562_f1_15	1295	1298
A.1.5 Terminal phe residue and C-terminal tyrosine cluster		
04ge10816_33726080_c2_29	319	810
06ee10709_21675012_f1_2	325	816
hp5p15575_33445317_f2_20.aa	425	916
01cp20708_36134808_f2_11	437	928
02ae31010_12504512_f3_28.aa	438	929
04ep41903_26757937_f3_16	447	938
04ep41903_26757937_f3_16	448	939
11ae80818_7290627_c2_51	467	958
13ae10610_35912_f2_3	996	1050
01cp20708_13086002_f3_27	1027	1081
14cp11908_24218954_c1_68	1031	1085
A.1.6 Via homolgy		
01ae11010_40688_c2_38	254	745
02gp20814_24415958_f3_9	269	760
09cp11003_5945252_f2_4	328	819
06cp30603_23476568_c2_133.aa	352	843
09cp61003_5945252_f1_5	406	897
14ee41924_23527267_c3_107	415	906
07ee11402_10759567_c2_86	1019	1073
A.1.7 Other outer membrane proteins		
06ep10615_9842_f3_46	381	872
06gp10409_3398427_f2_12	389	880
06ep10615_9842_f1_5	1010	1064
06gp10409_3398427_f2_12	1012	1066
A.2 Inner Membrane		
A.2.1 Proteins involved in outer membrane and cell wall synthesis		
06ep30223_4698838_f2_55	354	845
A.2.2 Proteins involved in energy conversion		
06ce20610_4331338_f3_18	372	863
09cp10224_4484718_c1_38	400	891
hp4e13394_5964452_c2_97	421	912
hp4e13394_15828963_c2_90	1022	1076
A.2.3 Proteins involved in cofactor metabolism		
06gp71906_25478192_c1_131	463	954

A.2.4 Proteins involved in secretion and adhesion		
06cp30603_23452_c3_80	281	772
09cp10713_23452_c3_195	988	1042
A.2.5 Via homolgy		
11ap20714_5271967_c1_60	411	902
A.2.6 Proteins involved in transport		
11ae80818_11188791_c3_60	407	898
14cp11908_25593768_c3_97	1017	1071
A.2.7 Other inner membrane proteins		
13ae10712_14100018_f2_12	290	781
hp1p13939_25397327_f3_22	417	908
hp5p15870_14350428_f1_1	430	921
06ge20501_14100018_c1_34	992	1046
05ae30220_14350428_f3_91	1025	1079
A.3 Flagellar proteins		
hp4e13394_3368767_c1_80	477	968
A.4 Transport proteins		
14ce31519_15635927_f3_15	414	905
A.5 Other cell envelope proteins		
04cp11202_24256567_c3_117	253	744
29ge30321_34157812_f3_10	293	784
29ge30321_12913562_f1_1	334	825
hp6p10233_12273302_f1_1	343	834
hp2e10911_24855312_c1_69	418	909
hp5p15575_29300311_c1_29	424	915
02ae31010_5085162_c1_47	443	934
B. CYTOPLASMIC PROTEINS		
B.1 Proteins involved in energy conversion		
11ge10308_5256_f2_1	470	961
11ge10308_24609417_f2_1	1033	1087
B.2 Proteins involved in amino acid metabolism and transport		
06ep11917_24803153_c3_24	357	848
06ep11202_4884677_c1_17	457	948
B.3 Proteins involved in nucleotide metabolism and transport		
06ep30223_23476067_c1_119	461	952
06ep30223_23476067_c1_115	1030	1084
B.4 Proteins involved in cofactor metabolism		
07ap11213_35156577_c1_24	345	836
06ep30223_23557202_c2_130	383	874
06ep30223_5109443_c1_109	387	878
06ep11202_133293_c1_19	455	946
07ee50709_35156577_f3_80	1003	1057
B.5 Proteins involved in lipid metabolism		
hp6e12267_14650278_f3_29	351	842
14ee41924_23834800_f2_32	416	907
B.6 Proteins involved in mRNA translation and ribosome biogenesis		
14ee41924_16282067_c1_72	473	964
07ee11402_19565702_c2_88	1034	1088
" B.7 Proteins involved in genome replication, transcription, recombination and repair"		
05ee10816_4687651_c1_22	278	769

29ge30321_135253_f2_6	335	826
07ap80601_976413_f3_9	346	837
14ce21516_85786_f1_1	350	841
hp2e10911_3349_c1_63	419	910
06ep30223_16512_c3_160	460	951
14ce61516_13073577_f2_12	472	963
07ee50709_4818967_f2_43	1000	1054
05ae30220_976413_c3_204	1004	1058
07ee50709_4818967_f2_43	1020	1074
hp7e10590_13073577_c3_107	1293	1296
B.8 Other cytoplasmic proteins		
04ge10816_22086531_f2_10	318	809
05cp21223_4725443_f3_14	322	813
06ap11119_24426508_f3_26	324	815
12ge10321_4821082_f3_14	330	821
hp3p10807_189075_f2_4	347	838
02ae31010_2117087_f3_34	440	931
03ae10804_21698400_c2_32	446	937
06gp71906_25504187_f3_112	464	955
hp7p10290_35156558_f3_15	490	981
hp7p10290_4351718_f1_6	491	982
13ae10610_859692_c2_32	995	1049
06ap11119_24426508_f3_27	997	1051
hp3e11188_47327_f2_9	1005	1059
07ee50709_26438968_f2_36	1028	1082
C. SECRETED PROTEINS		
C.1 Proteins involved in secretion and adhesion		
12ap10324_4805318_f2_3	355	846
12ap10324_4805318_f2_6	1006	1060
C.2 Other secreted proteins		
01gp11016_4103403_c2_13	257	748
02ae11612_1074212_f1_1	258	749
02ae11612_23598175_f1_2	260	751
02ae11612_33203250_c1_51	261	752
02gp20706_1203402_c3_58	264	755
02gp20706_15781452_c2_51	265	756
02gp20706_4892558_f3_19	268	759
04cp11202_24261588_f2_23	270	761
05ae30220_21619067_f3_56	272	763
07ap11213_35401528_c1_21	273	764
05ae30220_24882812_c3_103	274	765
05ae30220_25953163_c3_98	275	766
05ee10816_14649077_f3_18	276	767
06ap11119_16594193_f1_9	279	770
06cp30603_4689068_c3_79	283	774
07ap11111_234693_c3_14	284	775
09cp11003_19532625_c3_17	287	778
09cp20502_24001388_c1_31	288	779
12gp31106_3024126_f2_25	289	780
13ae10712_29569208_c2_27	291	782
hp2p10272_23697200_f3_22	295	786
hp2p10272_26829136_f1_1	296	787

hp5e15211_819455_c2_24	297	788
hp5p15212_34064750_f2_9	298	789
hp6e10967_23476502_f2_6	300	791
hp6e10967_24882750_f2_7	301	792
hp6e12267_4876718_f2_23	302	793
hp6e20339_1190660_c2_46	303	794
hp6e20339_21492187_c1_40	304	795
hp6e20339_34024187_c1_37	305	796
04cp11202_16603425_c2_72	314	805
04cp11202_19797128_f1_5	315	806
05ee10816_259703_f2_7	323	814
hp2p10272_22692325_f3_21	338	829
hp6e20339_24317062_c3_57	342	833
02ge11622_21695936_c1_54	348	839
12ge10321_24308513_f3_20	349	840
14ee41924_2458267_c2_93	356	847
01ce11104_36125337_c1_8	358	849
01ce21104_33203250_c3_87	359	850
02ae31010_34616666_f2_27	360	851
02ae31010_35270000_f3_33	361	852
02ae31010_36132785_f2_29	362	853
02ge10116_15781452_c1_87	363	854
03ae10804_23485968_c3_47	367	858
06ce20610_29298537_c2_32	370	861
06ce20610_3913967_c3_36	371	862
06cp11118_212827_c1_17	373	864
06cp30603_21492187_f2_41	377	868
06cp30603_34024187_f1_20	378	869
06cp30603_34024187_f1_20	379	870
06ep10615_14649077_f3_52	380	871
06ep30223_5271902_c1_106	388	879
06gp71906_24261588_c2_174	390	881
09ce10413_414011_f1_3	394	885
09ce10413_5865665_f1_4	395	886
09ce52017_29324062_c1_21	396	887
09cp21607_7224187_c2_12	401	892
09cp61003_19532625_c1_78	403	894
09cp61003_24335762_c3_111	405	896
11ae80818_783127_c3_63	408	899
hp4e13394_35957200_f1_21	420	911
hp5p15575_6140713_f2_18	426	917
hp5p15641_24304527_c3_35	428	919
hp5p15641_25635452_c3_34	429	920
hp6p10606_19546933_c3_31	432	923
02ae31010_16833312_f2_19	439	930
02ae31010_36132785_f2_29	442	933
05ep10815_4195292_c1_84	451	942
12ap10324_13178562_f3_6	471	962
hp2e10911_4882027_c2_87	474	965
hp5p15212_6928132_c3_34	478	969
hp7p10290_25548812_f3_14	488	979
07ee50709_10213593_f3_77	986	1040

06ep10615_14649077_f2_30	987	1041
01ce61016_23609580_c3_139	990	1044
06gp71906_3024126_c1_128	991	1045
09cp10713_34024187_f1_31	993	1047
02ap11117_23495187_c3_81	1001	1055
09cp10713_34024187_f1_31	1002	1056
hple80523_23485968_c2_49	1007	1061
09ce10413_5865665_f1_4	1013	1067
01ce61016_23609580_c3_139	1016	1070
14cp11908_783127_c1_72	1018	1072
hp4e13394_5088562_f3_54	1021	1075
hp8e10080_19546933_c2_88	1026	1080
07ee50709_960952_f2_47	1035	1089
D. OTHER CELLULAR PROTEINS		
01ge11619_23711062_c3_14	256	747
02gp20706_23866562_c2_53	267	758
06cp30603_23476568_c1_44	282	773
01ge10203_35281542_c3_16	306	797
01ge10203_860166_f3_9	307	798
01ge11619_13788141_c2_11	308	799
01ge11619_24415880_c2_12	309	800
01ge11619_24417813_c1_8	310	801
04cp11202_23553177_c1_75	316	807
04cp11202_23553177_c3_109	317	808
29ep10720_24220926_f2_8	332	823
29ep10720_24432762_c3_39	333	824
29ge30321_21673965_f2_7	336	827
29ge30321_24336712_f1_5	337	828
hp2p10272_24406280_c1_26	339	830
hp3p10807_29343768_f1_1	340	831
hp3p10807_29352212_f2_5	341	832
02ep20506_24611325_f2_6	344	835
06ae11016_30579712_f2_21	369	860
06cp11217_4897077_f1_6	376	867
06ep11202_26353438_c1_22	382	873
06ep30223_4876077_c3_149	386	877
hp5e15044_4554652_f3_3	423	914
hp6p10590_23440913_c2_31	431	922
hp6p10904_2214676_c1_14	435	926
hp6p10904_23704412_f2_5	436	927
06ep11202_792962_c2_26.aa	458	949
06gp71906_15115637_f2_59	462	953
hp3e11188_47327_f2_5	475	966
hp3e11188_5082842_f3_12	476	967
hp5p15641_30273312_c2_28	479	970
hp5p15641_5211687_c2_29	480	971
hp6p10590_30521093_f2_14	481	972
hp6p10904_7089062_c1_16	482	973
hp6p12129_16603417_f3_14	483	974
hp6p12244_3948467_c1_52	484	975
hp6p22217_23470967_f1_4	485	976
hp7e10192_4412568_f2_5	486	977

hp7p10287_24611325_c2_24	487	978
hp7p10290_25585941_f3_12	489	980
02ge10116_23866562_c3_146	984	1038
hp4p62853_5914693_c3_52	994	1048
07ce10312_4554652_f3_2	1024	1078
hp6p12244_3948467_c3_88	1036	1090

[In Table 1, "nt" represents nucleotide Seq. ID number and "aa" represents amino acid Seq. ID number]

5 Definitions

A purified preparation or a substantially pure preparation of a polypeptide, as used herein, means a polypeptide that has been separated from other proteins, lipids, and nucleic acids with which it naturally occurs. Preferably, the polypeptide is also separated from substances, e.g., antibodies or gel matrix, e.g., polyacrylamide, which are used to purify it. Preferably, the polypeptide constitutes at least 10, 20, 50 70, 80 or 95% dry weight of the purified preparation. Preferably, the preparation contains: sufficient polypeptide to allow protein sequencing; at least 1, 10, or 100 µg of the polypeptide; at least 1, 10, or 100 mg of the polypeptide.

A purified preparation of cells refers to, in the case of plant or animal cells, an *in vitro* preparation of cells and not an entire intact plant or animal. In the case of cultured cells or microbial cells, it consists of a preparation of at least 10% and more preferably 50% of the subject cells.

A substantially pure nucleic acid, e.g., a substantially pure DNA, is a nucleic acid which is one or both of the following: not immediately contiguous with both of the coding sequences with which it is immediately contiguous (i.e., one at the 5' end and one at the 3' end) in the naturally-occurring genome of the organism from which the nucleic acid is derived; or which is substantially free of a nucleic acid with which it occurs in the organism from which the nucleic acid is derived. The term includes, for example, a recombinant DNA which is incorporated into a vector, e.g., into an autonomously replicating plasmid or virus, or into the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (e.g., a cDNA or a genomic DNA fragment produced by PCR or restriction endonuclease treatment) independent of other DNA sequences. Substantially pure DNA also includes a recombinant DNA which is part of a hybrid gene encoding additional *H. pylori* DNA sequence.

A "contig" as used herein is a nucleic acid representing a continuous stretch of genomic sequence of an organism.

An "open reading frame", also referred to herein as ORF, is a region of nucleic acid which encodes a polypeptide. This region may represent a portion of a coding sequence or a total sequence.

As used herein, a "coding sequence" is a nucleic acid which is transcribed into messenger RNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the five prime terminus and a translation stop code at the three prime terminus. A coding sequence can include but is not limited to messenger RNA, synthetic DNA, and recombinant nucleic acid sequences.

A "complement" of a nucleic acid as used herein refers to an anti-parallel or antisense sequence that participates in Watson-Crick base-pairing with the original sequence.

A "gene product" is a protein or structural RNA which is specifically encoded for by a gene.

As used herein, the term "probe" refers to a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest. Probes are often associated with or capable of associating with a label. A label is a chemical moiety capable of detection. Typical labels comprise dyes, radioisotopes, luminescent and chemiluminescent moieties, fluorophores, enzymes, precipitating agents, amplification sequences, and the like. Similarly, a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest and immobilizes such molecule is referred herein as a "capture ligand". Capture ligands are typically associated with or capable of associating with a support such as nitro-cellulose, glass, nylon membranes, beads, particles and the like. The specificity of hybridization is dependent on conditions such as the base pair composition of the nucleotides, and the temperature and salt concentration of the reaction. These conditions are readily discernable to one of ordinary skill in the art using routine experimentation.

Homologous refers to the sequence similarity or sequence identity between two polypeptides or between two nucleic acid molecules. When a position in both of the two compared sequences is occupied by the same base or amino acid monomer subunit, e.g., if a position in each of two DNA molecules is occupied by adenine, then the molecules are homologous at that position. The percent of homology between two sequences is a function of the number of matching or homologous positions shared by the two sequences divided by the number of positions compared x 100. For example, if 6 of 10 of the positions in two sequences are matched or homologous then the two sequences are 60% homologous. By way of example, the DNA sequences ATTGCC and TATGGC

share 50% homology. Generally, a comparison is made when two sequences are aligned to give maximum homology.

Nucleic acids are hybridizable to each other when at least one strand of a nucleic acid can anneal to the other nucleic acid under defined stringency conditions.

- 5 Stringency of hybridization is determined by: (a) the temperature at which hybridization and/or washing is performed; and (b) the ionic strength and polarity of the hybridization and washing solutions. Hybridization requires that the two nucleic acids contain complementary sequences; depending on the stringency of hybridization, however, mismatches may be tolerated. Typically, hybridization of two sequences at high
- 10 stringency (such as, for example, in a solution of 0.5X SSC, at 65° C) requires that the sequences be essentially completely homologous. Conditions of intermediate stringency (such as, for example, 2X SSC at 65° C) and low stringency (such as, for example 2X SSC at 55° C), require correspondingly less overall complementarity between the hybridizing sequences. (1X SSC is 0.15 M NaCl, 0.015 M Na citrate).

- 15 The terms peptides, proteins, and polypeptides are used interchangeably herein. As used herein, the term "surface protein" refers to all surface accessible proteins, e.g. inner and outer membrane proteins, proteins adhering to the cell wall, and secreted proteins.

- A polypeptide has *H. pylori* biological activity if it has one, two and preferably more of the following properties: (1) if when expressed in the course of an *H. pylori*
- 20 infection, it can promote, or mediate the attachment of *H. pylori* to a cell; (2) it has an enzymatic activity characteristic of an *H. pylori* protein; (3) or the gene which encodes it can rescue a lethal mutation in an *H. pylori* gene. A polypeptide has biological activity if it is an antagonist, agonist, or super-agonist of a polypeptide having one of the above-
- 25 listed properties.

- A biologically active fragment or analog is one having an *in vivo* or *in vitro* activity which is characteristic of the *H. pylori* polypeptides shown in the Sequence Listing, or of other naturally occurring *H. pylori* polypeptides, e.g., one or more of the biological activities described herein. Especially preferred are fragments which exist *in*
- 30 *vivo*, e.g., fragments which arise from post transcriptional processing or which arise from translation of alternatively spliced RNA's. Fragments include those expressed in native or endogenous cells as well as those made in expression systems, e.g., in CHO cells. Because peptides such as *H. pylori* polypeptides often exhibit a range of physiological properties and because such properties may be attributable to different
- 35 portions of the molecule, a useful *H. pylori* fragment or *H. pylori* analog is one which exhibits a biological activity in any biological assay for *H. pylori* activity. Most

- 30 -

preferably the fragment or analog possesses 10%, preferably 40%, more preferably 90% or greater of the activity of *H. pylori*, in any *in vivo* or *in vitro* assay.

5 Analogues can differ from naturally occurring *H. pylori* polypeptides in amino acid sequence or in ways that do not involve sequence, or both. Non-sequence modifications include changes in acetylation, methylation, phosphorylation, carboxylation, or glycosylation. Preferred analogues include *H. pylori* polypeptides (or biologically active fragments thereof) whose sequences differ from the wild-type sequence by one or more conservative amino acid substitutions or by one or more non-conservative amino acid substitutions, deletions, or insertions which do not substantially diminish the biological activity of the *H. pylori* polypeptide. Conservative substitutions typically include the substitution of one amino acid for another with similar characteristics, e.g., substitutions within the following groups: valine, glycine; glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid; asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine. Other conservative substitutions are outlined in 10 Table 2 below.

TABLE 2
CONSERVATIVE AMINO ACID REPLACEMENTS

For Amino Acid	Code	Replace with any of
Alanine	A	D-Ala, Gly, beta-Ala, L-Cys, D-Cys
Arginine	R	D-Arg, Lys, D-Lys, homo-Arg, D-homo-Arg, Met, Ile, D-Met, D-Ile, Orn, D-Orn
Asparagine	N	D-Asn, Asp, D-Asp, Glu, D-Glu, Gln, D-Gln
Aspartic Acid	D	D-Asp, D-Asn, Asn, Glu, D-Glu, Gln, D-Gln
Cysteine	C	D-Cys, S-Me-Cys, Met, D-Met, Thr, D-Thr
Glutamine	Q	D-Gln, Asn, D-Asn, Glu, D-Glu, Asp, D-Asp
Glutamic Acid	E	D-Glu, D-Asp, Asp, Asn, D-Asn, Gln, D-Gln
Glycine	G	Ala, D-Ala, Pro, D-Pro, β -Ala, Acp
Isoleucine	I	D-Ile, Val, D-Val, Leu, D-Leu, Met, D-Met
Leucine	L	D-Leu, Val, D-Val, Leu, D-Leu, Met, D-Met
Lysine	K	D-Lys, Arg, D-Arg, homo-Arg, D-homo-Arg, Met, D-Met, Ile, D-Ile, Orn, D-Orn
Methionine	M	D-Met, S-Me-Cys, Ile, D-Ile, Leu, D-Leu, Val, D-Val
Phenylalanine	F	D-Phe, Tyr, D-Thr, L-Dopa, His, D-His, Trp, D-Trp, Trans-3,4, or 5-phenylproline, cis-3,4, or 5-phenylproline
Proline	P	D-Pro, L-1-thioazolidine-4-carboxylic acid, D-or L-1-oxazolidine-4-carboxylic acid
Serine	S	D-Ser, Thr, D-Thr, allo-Thr, Met, D-Met, Met(O), D-Met(O), L-Cys, D-Cys
Threonine	T	D-Thr, Ser, D-Ser, allo-Thr, Met, D-Met, Met(O), D-Met(O), Val, D-Val
Tyrosine	Y	D-Tyr, Phe, D-Phe, L-Dopa, His, D-His
Valine	V	D-Val, Leu, D-Leu, Ile, D-Ile, Met, D-Met

Other analogs within the invention are those with modifications which increase peptide stability; such analogs may contain, for example, one or more non-peptide bonds (which replace the peptide bonds) in the peptide sequence. Also included are: analogs that include residues other than naturally occurring L-amino acids, e.g., D-amino acids
5 or non-naturally occurring or synthetic amino acids, e.g., β or γ amino acids; and cyclic analogs.

As used herein, the term "fragment", as applied to an *H. pylori* analog, will ordinarily be at least about 20 residues, more typically at least about 40 residues, preferably at least about 60 residues in length. Fragments of *H. pylori* polypeptides can
10 be generated by methods known to those skilled in the art. The ability of a candidate fragment to exhibit a biological activity of *H. pylori* polypeptide can be assessed by methods known to those skilled in the art as described herein. Also included are *H. pylori* polypeptides containing residues that are not required for biological activity of the peptide or that result from alternative mRNA splicing or alternative protein processing
15 events.

An "immunogenic component" as used herein is a moiety, such as an *H. pylori* polypeptide, analog or fragment thereof, that is capable of eliciting a humoral and/or cellular immune response in a host animal.

An "antigenic component" as used herein is a moiety, such as an *H. pylori*
20 polypeptide, analog or fragment thereof, that is capable of binding to a specific antibody with sufficiently high affinity to form a detectable antigen-antibody complex.

As used herein, the term "transgene" means a nucleic acid (encoding, e.g., one or more polypeptides), which is partly or entirely heterologous, i.e., foreign, to the transgenic animal or cell into which it is introduced, or, is homologous to an endogenous
25 gene of the transgenic animal or cell into which it is introduced, but which is designed to be inserted, or is inserted, into the cell's genome in such a way as to alter the genome of the cell into which it is inserted (e.g., it is inserted at a location which differs from that of the natural gene or its insertion results in a knockout). A transgene can include one or more transcriptional regulatory sequences and any other nucleic acid, such as introns,
30 that may be necessary for optimal expression of the selected nucleic acid, all operably linked to the selected nucleic acid, and may include an enhancer sequence.

As used herein, the term "transgenic cell" refers to a cell containing a transgene.

As used herein, a "transgenic animal" is any animal in which one or more, and preferably essentially all, of the cells of the animal includes a transgene. The transgene
35 can be introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by

infection with a recombinant virus. This molecule may be integrated within a chromosome, or it may be extrachromosomally replicating DNA.

The term "antibody" as used herein is intended to include fragments thereof which are specifically reactive with *H. pylori* polypeptides.

5 As used herein, the term "cell-specific promoter" means a DNA sequence that serves as a promoter, i.e., regulates expression of a selected DNA sequence operably linked to the promoter, and which effects expression of the selected DNA sequence in specific cells of a tissue. The term also covers so-called "leaky" promoters, which regulate expression of a selected DNA primarily in one tissue, but cause expression in
10 other tissues as well.

Misexpression, as used herein, refers to a non-wild type pattern of gene expression. It includes: expression at non-wild type levels, i.e., over or under-expression; a pattern of expression that differs from wild type in terms of the time or stage at which the gene is expressed, e.g., increased or decreased expression (as
15 compared with wild type) at a predetermined developmental period or stage; a pattern of expression that differs from wild type in terms of decreased expression (as compared with wild type) in a predetermined cell type or tissue type; a pattern of expression that differs from wild type in terms of the splicing size, amino acid sequence, post-translational modification, or biological activity of the expressed polypeptide; a pattern of
20 expression that differs from wild type in terms of the effect of an environmental stimulus or extracellular stimulus on expression of the gene, e.g., a pattern of increased or decreased expression (as compared with wild type) in the presence of an increase or decrease in the strength of the stimulus.

As used herein, "host cells" and other such terms denoting microorganisms or
25 higher eukaryotic cell lines cultured as unicellular entities refers to cells which can become or have been used as recipients for a recombinant vector or other transfer DNA, and include the progeny of the original cell which has been transfected. It is understood by individuals skilled in the art that the progeny of a single parental cell may not necessarily be completely identical in genomic or total DNA compliment to the original
30 parent, due to accident or deliberate mutation.

As used herein, the term "control sequence" refers to a nucleic acid having a base sequence which is recognized by the host organism to effect the expression of encoded sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism; in prokaryotes, such control sequences generally
35 include a promoter, ribosomal binding site and terminators; in eukaryotes, generally such control sequences include promoters, terminators and in some instances, enhancers.

The term control sequence is intended to include at a minimum, all components whose presence is necessary for expression, and may also include additional components whose presence is advantageous, for example, leader sequences.

As used herein, the term "operably linked" refers to sequences joined or ligated to function in their intended manner. For example, a control sequence is operably linked to coding sequence by ligation in such a way that expression of the coding sequence is achieved under conditions compatible with the control sequence and host cell.

The metabolism of a substance, as used herein, means any aspect of the, expression, function, action, or regulation of the substance. The metabolism of a substance includes modifications, e.g., covalent or non-covalent modifications of the substance. The metabolism of a substance includes modifications, e.g., covalent or non-covalent modification, the substance induces in other substances. The metabolism of a substance also includes changes in the distribution of the substance. The metabolism of a substance includes changes the substance induces in the distribution of other substances.

A "sample" as used herein refers to a biological sample, such as, for example, tissue or fluid isolated from an individual (including without limitation plasma, serum, cerebrospinal fluid, lymph, tears, saliva and tissue sections) or from *in vitro* cell culture constituents, as well as samples from the environment.

The practice of the invention will employ, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See e.g., Sambrook, Fritsch, and Maniatis, *Molecular Cloning; Laboratory Manual* 2nd ed. (1989); *DNA Cloning*, Volumes I and II (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); the series, *Methods in Enzymology* (Academic Press, Inc.), particularly Vol. 154 and Vol. 155 (Wu and Grossman, eds.) and *PCR-A Practical Approach* (McPherson, Quirke, and Taylor, eds., 1991).

I. Isolation of Nucleic Acids of *H. pylori* and Uses Therefor

H. pylori Genomic Sequence

This invention provides nucleotide sequences of the genome of *H. pylori* which thus comprises a DNA sequence library of *H. pylori* genomic DNA. The detailed description that follows provides nucleotide sequences of *H. pylori*, and also describes how the sequences were obtained and how ORFs and protein-coding sequences were

- 34 -

identified. Also described are methods of using the disclosed *H. pylori* sequences in methods including diagnostic and therapeutic applications. Furthermore, the library can be used as a database for identification and comparison of medically important sequences in this and other strains of *H. pylori*.

5 To determine the genomic sequence of *H. pylori*, DNA was isolated from a strain of *H. pylori* and mechanically sheared by nebulization to a median size of 2 kb. Following size fractionation by gel electrophoresis, the fragments were blunt-ended, ligated to adapter oligonucleotides, and cloned into each of 20 different pMPX vectors (Rice et al., abstracts of Meeting of Genome Mapping and Sequencing, Cold Spring
10 Harbor, NY, 5/11-5/15, 1994, p. 225) to construct a series of "shotgun" subclone libraries.

DNA sequencing was achieved using multiplex sequencing procedures essentially as disclosed in Church et al., 1988, *Science* 240:185; U.S. Patents No. 4,942,124 and 5,149,625). DNA was extracted from pooled cultures and subjected to
15 chemical or enzymatic sequencing. Sequencing reactions were resolved by electrophoresis, and the products were transferred and covalently bound to nylon membranes. Finally, the membranes were sequentially hybridized with a series of labelled oligonucleotides complimentary to "tag" sequences present in the different shotgun cloning vectors. In this manner, a large number of sequences could be obtained
20 from a single set of sequencing reactions. The cloning and sequencing procedures are described in more detail in the Exemplification.

Individual sequence reads obtained in this manner were assembled using the FALCON™ program (Church et al., 1994, *Automated DNA Sequencing and Analysis*, J.C. Venter, ed., Academic Press) and PHRAP (P. Green, Abstracts of DOE Human
25 Genome Program Contractor-Grantee Workshop V, Jan. 1996, p.157). A resulting assembly of contigs, each representing a continuous stretch of DNA or DNA sequence was obtained. The average contig length was about 3 kb.

A variety of approaches are used to order the contigs so as to obtain a continuous sequence representing the entire *H. pylori* genome. Synthetic oligonucleotides are
30 designed that are complementary to sequences at the end of each contig. These oligonucleotides may be hybridized to libraries of *H. pylori* genomic DNA in, for example, lambda phage vectors or plasmid vectors to identify clones that contain sequences corresponding to the junctional regions between individual contigs. Such clones are then used to isolate template DNA and the same oligonucleotides are used as
35 primers in polymerase chain reaction (PCR) to amplify junctional fragments, the nucleotide sequence of which was then determined.

The *H. pylori* sequences were analyzed for the presence of open reading frames (ORFs) comprising at least 180 nucleotides. ORFs of at least 180 nucleotides (based on stop-to-stop codon reads) were predicted. As a result of the analysis of ORFs based on stop-to-stop codon reads, it should be understood that these ORFs may not correspond to the ORF of a naturally-occurring *H. pylori* polypeptide. These ORFs may contain start codons which indicate the initiation of protein synthesis of a naturally-occurring *H. pylori* polypeptide. Such start codons within the ORFs provided herein can be identified by those of ordinary skill in the relevant art and the resulting ORF and the encoded *H. pylori* polypeptide is within the scope of this invention. For example, within the ORFs a codon such as AUG or GUG (encoding methionine or valine) which is part of the initiation signal for protein synthesis can be identified and the ORF modified to correspond to a naturally-occurring *H. pylori* polypeptide. The predicted coding regions were defined by evaluating the coding potential of such sequences with the program GENEMARK™ (Borodovsky and McIninch, 1993, *Comp. Chem.* 17:123).

15 Other *H. pylori* Nucleic Acids

The nucleic acids of this invention may be obtained directly from the DNA of the above referenced *H. pylori* strain by using the polymerase chain reaction (PCR). See "PCR, A Practical Approach" (McPherson, Quirke, and Taylor, eds., IRL Press, Oxford, UK, 1991) for details about the PCR. High fidelity PCR can be used to ensure a faithful DNA copy prior to expression. In addition, amplified products can be checked by conventional sequencing methods. Clones carrying the desired sequences described in this invention may be obtained by screening the libraries by means of the PCR or by hybridization of synthetic oligonucleotide probes to filter lifts of the library colonies or plaques as known in the art (see, e.g., Sambrook et al., *Molecular Cloning, A Laboratory Manual* 2nd edition, 1989, Cold Spring Harbor Press, NY).

It is also possible to obtain nucleic acids encoding *H. pylori* polypeptides from a cDNA library in accordance with protocols herein described. A cDNA encoding an *H. pylori* polypeptide can be obtained by isolating total mRNA from an appropriate cell line. Double stranded cDNAs can then be prepared from the total mRNA. Subsequently, the cDNAs can be inserted into a suitable plasmid or viral (e.g., bacteriophage) vector using any one of a number of known techniques. Genes encoding *H. pylori* polypeptides can also be cloned using established polymerase chain reaction techniques in accordance with the nucleotide sequence information provided by the invention. The nucleic acids of the invention can be DNA or RNA. Preferred nucleic acids are shown in the Sequence Listing.

The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See e.g., Itakura *et al.* U.S. Patent No. 4,598,049; Caruthers *et al.* U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

Nucleic acids isolated or synthesized in accordance with features of the present invention are useful, by way of example, without limitation, as probes, primers, capture ligands, antisense genes and for developing expression systems for the synthesis of proteins and peptides corresponding to such sequences. As probes, primers, capture ligands and antisense agents, the nucleic acid normally consists of all or part (approximately twenty or more nucleotides for specificity as well as the ability to form stable hybridization products) of the nucleic acids shown in the Sequence Listing. These uses are described in further detail below.

Probes

A nucleic acid isolated or synthesized in accordance with the nucleotide sequences set forth in the Sequence Listing can be used as a probe to specifically detect *H. pylori*. With the sequence information set forth in the present application, sequences of twenty or more nucleotides are identified which provide the desired inclusivity and exclusivity with respect to *H. pylori*, and extraneous nucleic acids likely to be encountered during hybridization conditions. More preferably, the sequence will comprise at least twenty to thirty nucleotides to convey stability to the hybridization product formed between the probe and the intended target molecules.

Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques. Individuals skilled in the art will readily recognize that the nucleic acids, for use as probes, can be provided with a label to facilitate detection of a hybridization product.

Nucleic acid isolated and synthesized in accordance with the Sequence Listing can also be useful as probes to detect homologous regions (especially homologous genes) of other *Helicobacter* species using appropriate stringency hybridization conditions as described herein.

Capture Ligand

For use as a capture ligand, the nucleic acid selected in the manner described above with respect to probes, can be readily associated with a support. The manner in which nucleic acid is associated with supports is well known. Nucleic acid having twenty or more nucleotides in a sequence contained in the Sequence Listing have utility

to separate *H. pylori* nucleic acid from the nucleic acid of each other and other organisms. Nucleic acid having twenty or more nucleotides in a sequence shown in the Sequence Listing can also have utility to separate other *Helicobacter* species from each other and from other organisms. Preferably, the sequence will comprise at least twenty
5 nucleotides to convey stability to the hybridization product formed between the probe and the intended target molecules. Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques.

Primers

Nucleic acid isolated or synthesized in accordance with the sequences described
10 herein have utility as primers for the amplification of *H. pylori* nucleic acid. These nucleic acids may also have utility as primers for the amplification of nucleic acids in other *Helicobacter* species. With respect to polymerase chain reaction (PCR) techniques, nucleic acids of ≥ 10 -15 nucleotides contained in the Sequence Listing have utility in conjunction with suitable enzymes and reagents to create copies of *H. pylori*
15 nucleic acid. More preferably, the sequence will comprise twenty or more nucleotides to convey stability to the hybridization product formed between the primer and the intended target molecules. Binding conditions of primers greater than 100 nucleotides are more difficult to control to obtain specificity. High fidelity PCR can be used to ensure a faithful DNA copy prior to expression. In addition, amplified products can be
20 checked by conventional sequencing methods.

The copies can be used in diagnostic assays to detect specific sequences, including genes from *H. pylori* and/or other *Helicobacter* species. The copies can also be incorporated into cloning and expression vectors to generate polypeptides corresponding to the nucleic acid synthesized by PCR, as is described in greater detail
25 herein.

Antisense

Nucleic acid or nucleic acid-hybridizing derivatives isolated or synthesized in accordance with the sequences described herein have utility as antisense agents to prevent the expression of *H. pylori* genes. These sequences also have utility as antisense
30 agents to prevent expression of genes of other *Helicobacter* species.

In one embodiment, nucleic acid or derivatives corresponding to *H. pylori* nucleic acids is loaded into a suitable carrier such as a liposome or bacteriophage for introduction into bacterial cells. For example, a nucleic acid having twenty or more nucleotides is capable of binding to bacteria nucleic acid or bacteria messenger RNA.
35 Preferably, the antisense nucleic acid is comprised of 20 or more nucleotides to provide necessary stability of a hybridization product of non-naturally occurring nucleic acid and

bacterial nucleic acid and/or bacterial messenger RNA. Nucleic acid having a sequence greater than 1000 nucleotides in length is difficult to synthesize but can be generated by recombinant DNA techniques. Methods for loading antisense nucleic acid in liposomes is known in the art as exemplified by U.S. Patent 4,241,046 issued December 23, 1980
5 to Papahadjopoulos et al.

II. Expression of *H. pylori* Nucleic Acids

Nucleic acid isolated or synthesized in accordance with the sequences described herein have utility to generate polypeptides. The nucleic acids exemplified in the
10 Sequence Listing or fragments of said nucleic acid encoding active portions of *H. pylori* polypeptides can be cloned into suitable vectors or used to isolate nucleic acid. The isolated nucleic acid is combined with suitable DNA linkers and cloned into a suitable vector.

The function of a specific gene or operon can be ascertained by expression in a
15 bacterial strain under conditions where the activity of the gene product(s) specified by the gene or operon in question can be specifically measured. Alternatively, a gene product may be produced in large quantities in an expressing strain for use as an antigen, an industrial reagent, for structural studies, etc. This expression can be accomplished in a mutant strain which lacks the activity of the gene to be tested, or in a strain that does
20 not produce the same gene product(s). This includes, but is not limited to other *Helicobacter* strains, and other bacterial strains such as *E. coli*, *Norcardia*, *Corynebacterium*, and *Streptomyces* species. In some cases the expression host will utilize the natural *Helicobacter* promoter whereas in others, it will be necessary to drive the gene with a promoter sequence derived from the expressing organism (e.g., an *E.*
25 *coli* beta-galactosidase promoter for expression in *E. coli*).

To express a gene product using the natural *H. pylori* promoter, a procedure such as the following can be used. A restriction fragment containing the gene of interest, together with its associated natural promoter element and regulatory sequences (identified using the DNA sequence data) is cloned into an appropriate recombinant
30 plasmid containing an origin of replication that functions in the host organism and an appropriate selectable marker. This can be accomplished by a number of procedures known to those skilled in the art. It is most preferably done by cutting the plasmid and the fragment to be cloned with the same restriction enzyme to produce compatible ends that can be ligated to join the two pieces together. The recombinant plasmid is intro-
35 duced into the host organism by, for example, electroporation and cells containing the

recombinant plasmid are identified by selection for the marker on the plasmid. Expression of the desired gene product is detected using an assay specific for that gene product.

In the case of a gene that requires a different promoter, the body of the gene (coding sequence) is specifically excised and cloned into an appropriate expression plasmid. This subcloning can be done by several methods, but is most easily accomplished by PCR amplification of a specific fragment and ligation into an expression plasmid after treating the PCR product with a restriction enzyme or exonuclease to create suitable ends for cloning.

A suitable host cell for expression of a gene can be any procaryotic or eucaryotic cell. For example, an *H. pylori* polypeptide can be expressed in bacterial cells such as *E. coli*, insect cells (baculovirus), yeast, or mammalian cells such as Chinese hamster ovary cell (CHO). Other suitable host cells are known to those skilled in the art.

Expression in eucaryotic cells such as mammalian, yeast, or insect cells can lead to partial or complete glycosylation and/or formation of relevant inter- or intra-chain disulfide bonds of a recombinant peptide product. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, et al., (1987) *Embo J.* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz et al., (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Baculovirus vectors available for expression of proteins in cultured insect cells (SF 9 cells) include the pAc series (Smith et al., (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow, V.A., and Summers, M.D., (1989) *Virology* 170:31-39). Generally, COS cells (Gluzman, Y., (1981) *Cell* 23:175-182) are used in conjunction with such vectors as pCDM 8 (Aruffo, A. and Seed, B., (1987) *Proc. Natl. Acad. Sci. USA* 84:8573-8577) for transient amplification/expression in mammalian cells, while CHO (dhfr⁻ Chinese Hamster Ovary) cells are used with vectors such as pMT2PC (Kaufman et al. (1987), *EMBO J.* 6:187-195) for stable amplification/expression in mammalian cells. Vector DNA can be introduced into mammalian cells via conventional techniques such as calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, or electroporation. Suitable methods for transforming host cells can be found in Sambrook et al. (Molecular Cloning: A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory press (1989)), and other laboratory textbooks.

Expression in procaryotes is most often carried out in *E. coli* with either fusion or non-fusion inducible expression vectors. Fusion vectors usually add a number of NH₂ terminal amino acids to the expressed target gene. These NH₂ terminal amino acids often are referred to as a reporter group. Such reporter groups usually serve two purposes: 1) to increase the solubility of the target recombinant protein; and 2) to aid in

the purification of the target recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the reporter group and the target recombinant protein to enable separation of the target recombinant protein from the reporter group subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Amrad Corp., Melbourne, Australia), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase, maltose E binding protein, or protein A, respectively, to the target recombinant protein. A preferred reporter group is poly(His), which may be fused to the amino or carboxy terminus of the protein and which renders the recombinant fusion protein easily purifiable by metal chelate chromatography.

Inducible non-fusion expression vectors include pTrc (Amann et al., (1988) *Gene* 69:301-315) and pET11d (Studier et al., Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 60-89). While target gene expression relies on host RNA polymerase transcription from the hybrid trp-lac fusion promoter in pTrc, expression of target genes inserted into pET11d relies on transcription from the T7 gn10-lac 0 fusion promoter mediated by coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 under the transcriptional control of the lacUV 5 promoter.

For example, a host cell transfected with a nucleic acid vector directing expression of a nucleotide sequence encoding an *H. pylori* polypeptide can be cultured under appropriate conditions to allow expression of the polypeptide to occur. The polypeptide may be secreted and isolated from a mixture of cells and medium containing the peptide. Alternatively, the polypeptide may be retained cytoplasmically and the cells harvested, lysed and the protein isolated. A cell culture includes host cells, media and other byproducts. Suitable media for cell culture are well known in the art. Polypeptides of the invention can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and immunoaffinity purification with antibodies specific for such polypeptides. Additionally, in many situations, polypeptides can be produced by chemical cleavage of a native protein (e.g., tryptic digestion) and the cleavage products can then be purified by standard techniques.

In the case of membrane bound proteins, these can be isolated from a host cell by contacting a membrane-associated protein fraction with a detergent forming a solubilized complex, where the membrane-associated protein is no longer entirely embedded in the membrane fraction and is solubilized at least to an extent which allows it to be chromatographically isolated from the membrane fraction. Several different criteria are used for choosing a detergent suitable for solubilizing these complex. For example, one property considered is the ability of the detergent to solubilize the *H. pylori* protein within the membrane fraction at minimal denaturation of the membrane-associated protein allowing for the activity or functionality of the membrane-associated protein to return upon reconstitution of the protein. Another property considered when selecting the detergent is the critical micells concentration (CMC) of the detergent in that the detergent of choice preferably has a high CMC value allowing for ease of removal after reconstitution. A third property considered when selecting a detergent is the hydrophobicity of the detergent. Typically, membrane-associated proteins are very hydrophobic and therefore detergents which are also hydrophobic; e.g., the triton series, would be useful for solubilizing the hydrophobic proteins. Another property important to a detergent can be the capability of the detergent to remove the *H. pylori* protein with minimal protein-protein interaction facilitating further purification. A fifth property of the detergent which should be considered is the charge of the detergent. For example, if it is desired to use ion exchange resins in the purification process then preferably detergent should be an uncharged detergent. Chromatographic techniques which can be used in the final purification step are known in the art and include hydrophobic interaction, lectin affinity, ion exchange, dye affinity and immunoaffinity.

One strategy to maximize recombinant *H. pylori* peptide expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 119-128). Another strategy would be to alter the nucleic acid encoding *H. pylori* peptide to be inserted into an expression vector so that the individual codons for each amino acid would be those preferentially utilized in highly expressed *E. coli* proteins (Wada et al., (1992) *Nuc. Acids Res.* 20:2111-2118). Such alteration of nucleic acids of the invention can be carried out by standard DNA synthesis techniques.

The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See, e.g., Itakura et al. U.S.

Patent No. 4,598,049; Caruthers et al. U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

III. *H. pylori* Polypeptides

5 This invention encompasses isolated *H. pylori* polypeptides encoded by the disclosed *H. pylori* genomic sequences, including the polypeptides contained in the Sequence Listing. Polypeptides of the invention are preferably at least 5 amino acid residues in length. Using the DNA sequence information provided herein, the amino acid sequences of the polypeptides encompassed by the invention can be deduced using
10 methods well-known in the art. It will be understood that the sequence of an entire nucleic acid encoding an *H. pylori* polypeptide can be isolated and identified based on an ORF that encodes only a fragment of the cognate protein-coding region. This can be achieved, for example, by using the isolated nucleic acid encoding the ORF, or fragments thereof, to prime a polymerase chain reaction with genomic *H. pylori* DNA as
15 template; this is followed by sequencing the amplified product.

 The polypeptides of the invention can be isolated from wild-type or mutant *H. pylori* cells or from heterologous organisms or cells (including, but not limited to, bacteria, yeast, insect, plant and mammalian cells) into which an *H. pylori* nucleic acid has been introduced and expressed. In addition, the polypeptides can be part of
20 recombinant fusion proteins.

H. pylori polypeptides of the invention can be chemically synthesized using commercially automated procedures such as those referenced herein.

 Many of the polypeptides of the invention are related to one another. Some of these relationships are described in Tables 3-6 below. All of the polypeptide lengths in
25 Table 3 are from stop codon to stop codon in the nucleotide sequence of *H. pylori*. As is known in the art, the actual polypeptide lengths are usually shorter than the stop-to-stop codon lengths because a start codon for an initiator charged tRNA usually appears a few nucleotides downstream from the prior stop codon and within a few nucleotides following a ribosome binding site (also known as a "Shine-Delgarno sequence"). Since
30 most of the ribosome binding sites in *H. pylori* have many of the same general features of those known in *E. coli*, one skilled in the art can predict the actual start codon with good reliability from the stop-to-stop nucleotide sequence of an open reading frame. The polypeptide sequences of SEQ ID NOs:492-743 of this invention represent the stop-to-stop codon lengths of the open reading frames of SEQ ID NOs:1-252. All other
35 polypeptide sequences of this invention represent the predicted start to stop protein lengths from the nucleotide sequences. One skilled in the art can recognize start sites in

the stop-to-stop open reading frames of the nucleotide sequences presented herein. In addition, one skilled in the art will occasionally detect alternative start sites, some of which may be utilized *in vivo* by the cellular machinery. The number of these alternative start sites is sufficiently small that one skilled in the art can readily test them in a recombinant expression systems known in the art to determine which ones provide authentic functional protein products.

The relationship between the polypeptides shown in Table 3 can be described as follows. First, all of the polypeptides of Table 3 are at least 90% identical with each other over most of their lengths, and most are over 95% identical with each other. Second, the stop-to-stop lengths are different for some of the homologous pairs of polypeptides. In some cases, the shorter polypeptide contains the relevant portion of the protein exhibiting utility in this invention; in some cases, the longer polypeptide may exhibit improved utility. Third, some polypeptides in the second column are homologous to two shorter polypeptides in the fifth column.

In all cases, the homology relationships described in Table 3 are highly significant. For example, a typical *H. pylori* gene product will exhibit amino acid sequence identities of between 92% and 100% among different strains of *H. pylori* selected from human patients. The nucleotide sequences encoding the related polypeptides of this invention are also very similar to one another. For example, nucleotide probes derived from the coding sequence of a polypeptide of this invention can be used in PCR or hybridization experiments to identify clones carrying the nucleotide sequence encoding the homologous related polypeptide.

TABLE 3

ORF Name	aa Seq ID #	Length	ORF Name	aa Seq ID #	Length	Length Difference	%ID	Overlap
01ael1010_40688_c2_38	745	261	hp3el1075orf3	632	261	0	100%	261
01ael2001_24218781_f2_18	746	148	05gp11901orf19	553	370	-222	95%	149
01ael2001_24218781_f2_18	746	148	07gp11807orf17	568	195	-47	100%	143
01ge10203_35281542_c3_16	797	261	01ge10203orf7	659	154	107	91%	138
01ge10203_35281542_c3_16	797	261	01ge10203orf14	657	71	190	99%	69
01ge10203_860166_f3_9	798	233	01ge10203orf6	658	233	0	100%	233
01ge11619_13788141_c2_11	799	105	11ge10309orf4	687	105	0	100%	105
01ge11619_23711062_c3_14	747	319	11ge10309orf12	579	319	0	100%	319
01ge11619_24415880_c2_12	800	173	11ge10309orf5	688	173	0	100%	173
01ge11619_24417813_c1_8	801	324	11ge10309orf24	684	324	0	100%	324
01gp11016_4103403_c2_13	748	145	01gp11016orf13	508	123	22	100%	123
02ael1612_1074212_f1_1	749	103	02ael1612orf1	509	103	0	100%	103
02ael1612_22477267_f2_27	750	304	03xel1215orf7	529	152	152	94%	148
02ael1612_23598175_f1_2	751	332	02ael1612orf15	510	332	0	100%	332
02ael1612_33203250_c1_51	752	509	05cp11911orf35	549	206	303	99%	205
02ep20506_24611325_f2_6	835	256	01cel1513orf17	500	256	0	100%	256
02ge10116_36367936_c1_19	753	173	02ge20116orf25	521	173	0	100%	173
02ge11622_21695936_c1_54	839	313	13eel0216orf57	743	313	0	98%	313
02ge11622_875260_f3_36	754	523	13eel0216orf7	586	523	0	100%	523
02gp20706_1203402_c3_58	755	162	09ge70821orf2	574	162	0	100%	162
02gp20706_15781452_c2_51	756	97	06ge10115orf17	563	97	0	100%	97
02gp20706_16803513_f1_1	802	488	01cp11710orf16	652	64	424	98%	63
02gp20706_16803513_f1_1	802	488	01cp11710orf6	655	247	241	99%	247
02gp20706_16803513_f1_1	802	488	01cp11710orf5	654	146	342	99%	145
02gp20706_20365905_f2_8	803	198	01cp11710orf9	656	130	68	95%	130
02gp20706_20365905_f2_8	803	198	01cp11710orf18	653	85	113	100%	75
02gp20706_23632775_f3_32	757	230	06ge10115orf4	565	230	0	100%	230

TABLE 3 (continued)

02gp20706_23866562_c2_53	758	120	06ge10115orf19	564	84	36	96%	84
02gp20706_4892558_f3_19	759	218	01cp11710orf1	502	218	0	100%	218
02gp20814_24415958_f3_9	760	176	14ee10308orf4	594	176	0	99%	176
02gp20814_3984818_f1_1	804	215	14ee10308orf1	593	68	147	97%	67
02gp20814_3984818_f1_1	804	215	14ee10308orf7	694	155	60	100%	143
04cp11202_16603425_c2_72	805	185	14cp10119orf1	692	161	24	96%	158
04cp11202_19797128_f1_5	806	199	04ge11713orf10	665	132	67	100%	127
04cp11202_23553177_c1_75	807	372	06ap10209orf4	674	88	284	96%	79
04cp11202_23553177_c1_75	807	372	06ap10209orf1	673	186	186	98%	179
04cp11202_23553177_c3_109	808	372	06ap10209orf4	674	88	284	96%	79
04cp11202_23553177_c3_109	808	372	06ap10209orf1	673	186	186	98%	179
04cp11202_24256567_c3_117	744	536	04ge11713orf35	601	200	336	99%	195
04cp11202_24256567_c3_117	744	536	04ge11713orf28	666	122	414	91%	111
04cp11202_24256567_c3_117	744	536	04ge11713orf36	667	250	286	97%	234
04cp11202_24261588_f2_23	761	96	01ae12021orf5	492	96	0	100%	96
04ge10816_22086531_f2_10	809	208	04ge11210orf1	664	208	0	100%	208
04ge10816_33726080_c2_29	810	369	13ae10610orf1	690	133	236	98%	120
05ae30220_21619067_f3_56	763	293	05ae20220orf58	544	293	0	100%	293
05ae30220_24882812_c3_103	765	486	05ae20220orf119	542	486	0	100%	486
05ae30220_25953163_c3_98	766	81	05ae20220orf95	545	81	0	100%	81
05ae30220_9882767_f2_34	812	69	05ae20220orf37	671	69	0	100%	69
05cp21223_4725443_f3_14	813	113	hp1e10506orf5	696	113	0	100%	113
05ee10816_14649077_f3_18	767	263	04cel1617orf4	534	152	111	97%	144
05ee10816_259703_f2_7	814	158	04cel1617orf10	661	142	16	93%	142
05ee10816_4103408_f2_11	768	115	04cel1617orf16	531	115	0	100%	115
05ee10816_4687651_c1_22	769	953	04cel1617orf27	519	676	277	100%	676
05ee10816_4687651_c1_22	769	953	04cel1617orf26	532	238	715	100%	238
06ap11119_16594193_f1_9	770	87	11ge10309orf7	580	87	0	100%	87
06ap11119_24426508_f3_26	815	120	11ge10309orf28	685	137	-17	100%	121
06ap11119_24426508_f3_26	815	120	hp4e12063orf1	699	86	34	100%	65
06ap20306_23437632_f3_9	771	291	04gp11803orf13	541	243	48	99%	228

TABLE 3 (continued)

06cp30603_23452_c3_80	772	176	06cp30603orf16	560	159	17	97%	155
06cp30603_23476568_c1_44	773	442	05cp20518orf39	550	442	0	100%	442
06cp30603_4689068_c3_79	774	100	06cp30603orf15	559	100	0	100%	100
06ee10709_21675012_f1_2	816	284	06ee10709orf2	675	284	0	100%	284
07ap11015_23938312_f3_2	762	271	07ap11015orf2	622	95	176	100%	94
07ap11015_23938312_f3_2	762	271	07ap11015orf4	624	211	60	99%	177
07ap11111_234693_c3_14	775	209	07ap11111orf13	566	209	0	100%	209
07ap11213_35156577_c1_24	836	401	hp2e10911orf35	718	420	-19	99%	399
07ap11213_35401528_c1_21	764	803	hp2e10911orf25	672	458	345	100%	458
07ap11213_35401528_c1_21	764	803	hp2e10911orf24	620	344	459	100%	344
07ap20216_7227202_f3_10	776	532	05ap21216orf4	547	529	3	100%	529
07ap80601_976413_f3_9	837	274	07ap80601orf2	633	268	6	100%	265
07ce11019_22051291_f1_1	817	600	07cp21714orf1	678	193	407	99%	190
07ce11019_22051291_f1_1	817	600	07cp21714orf3	679	418	182	100%	414
07ep11916_5273452_c3_31	777	255	01cp11414orf2	501	255	0	100%	255
07ep11916_5913592_f3_18	818	272	01cp11710orf5	654	146	126	93%	111
09cp11003_19532625_c3_17	778	357	14ge10705orf14	599	357	0	99%	357
09cp11003_5945252_f2_4	819	219	14ge10705orf3	695	219	0	100%	219
09cp20502_24001388_c1_31	779	61	14gp11820orf1	600	61	0	100%	61
09ze10333_22460750_f2_6	820	729	03ge10505orf2	660	323	406	97%	312
12ge10321_24308513_f3_20	840	242	06gp11920orf11	741	242	0	99%	242
12ge10321_4821082_f3_14	821	172	hp4p11352orf9	683	115	57	100%	115
12ge10321_4821082_f3_14	821	172	hp4p11352orf5	701	68	104	92%	64
12gp31106_3024126_f2_25	780	147	13ap11517orf15	585	147	0	100%	147
13ae10712_14100018_f2_12	781	201	14cp10705orf4	592	201	0	99%	201
13ae10712_29569208_c2_27	782	264	13ae10712orf15	584	264	0	100%	264
14ap10221_13689381_c3_4	822	366	05gp11901orf19	553	370	-4	96%	360
14ap10221_13689381_c3_4	822	366	06ep10306orf1	676	66	300	100%	66
14ap10815_20585777_c1_13	783	677	hp3e10349orf27	628	677	0	100%	677
14ce21516_85786_f1_1	841	700	14ce21516orf1	533	361	339	98%	350
14ce21516_85786_f1_1	841	700	04ap20904orf3	740	284	416	95%	271

TABLE 3 (continued)

29ep10720_24220926_f2_8	823	86	hp4e12063orf1	699	86	0	100%	86
29ep10720_24220926_f2_8	823	86	11ge10309orf28	685	137	-51	100%	81
29ep10720_24432762_c3_39	824	227	11ge10309orf39	686	227	0	100%	227
29ge30321_12913562_f1_1	825	79	01cel1618orf22	648	79	0	100%	79
29ge30321_135253_f2_6	826	101	01cel1618orf7	650	101	0	97%	101
29ge30321_21673965_f2_7	827	488	01cel1618orf9	651	409	79	100%	409
29ge30321_24336712_f1_5	828	422	01cel1618orf11	647	188	234	93%	181
29ge30321_24336712_f1_5	828	422	01cel1618orf27	649	235	187	96%	235
29ge30321_34157812_f3_10	784	342	01cel1618orf24	498	86	256	97%	85
hp1p14013_11726503_c2_20	785	149	hp1p14013orf17	617	149	0	99%	149
hp2p10272_22692325_f3_21	829	188	09ap20802orf13	680	163	25	99%	149
hp2p10272_23697200_f3_22	786	329	09ap20802orf14	570	278	51	100%	276
hp2p10272_24406280_c1_26	830	194	09ap20802orf21	681	194	0	100%	194
hp2p10272_26829136_f1_1	787	343	hp2p10272orf1	625	343	0	100%	343
hp3p10807_189075_f2_4	838	312	hp3p10807orf6	728	325	-13	99%	312
hp3p10807_29343768_f1_1	831	187	hp3p10807orf4	697	187	0	100%	187
hp3p10807_29352212_f2_5	832	230	hp3p10807orf7	698	230	0	100%	230
hp5e15211_819455_c2_24	788	269	hp5e15211orf23	641	269	0	100%	269
hp5p15212_34064750_f2_9	789	148	02ce10213orf19	515	148	0	98%	148
hp5p15641_21698387_c2_20	790	185	hp5p15641orf23	644	185	0	98%	185
hp6e10967_23476502_f2_6	791	165	hp2p10625orf5	626	165	0	99%	165
hp6e10967_24882750_f2_7	792	157	hp2p10625orf6	627	157	0	100%	157
hp6e12267_14650278_f3_29	842	277	12ge20305orf26	742	277	0	98%	277
hp6e12267_4876718_f2_23	793	143	12ge10305orf5	582	146	-3	98%	146
hp6e20339_1190660_c2_46	794	69	04gp11213orf22	540	69	0	100%	69
hp6e20339_21492187_c1_40	795	106	04gp11213orf14	539	136	-30	99%	106
hp6e20339_24317062_c3_57	833	382	04gp11213orf5	669	382	0	99%	382
hp6e20339_34024187_c1_37	796	122	04gp11213orf11	538	122	0	100%	122
hp6p10233_12273302_f1_1	834	143	07cp10312orf5	677	138	5	95%	105

Additional relationships between polypeptides of the invention are described in Table 4 below. All of the polypeptide lengths in Table 4 below are measured from stop codon to stop codon in the nucleotide sequence of *H. pylori*.

The relationship between the polypeptides shown in Table 4 can be described as follows. First, all of the polypeptides of Table 4 are at least 90% identical with each other over most of their lengths, and most are over 95% identical with each other. Second, the stop-to-stop lengths are different for some of the homologous pairs of polypeptides. In some cases, the shorter polypeptide contains the relevant portion of the protein exhibiting utility in this invention; in some cases, the longer polypeptide may exhibit improved utility. Third, some polypeptides in the second column are homologous to two shorter polypeptides in the fifth column.

In all cases, the homology relationships described in Table 4 are highly significant. For example, a typical *H. pylori* gene product will exhibit amino acid sequence identities of between 92% and 100% among different strains of *H. pylori* selected from human patients. The nucleotide sequences encoding the related polypeptides of this invention are also very similar to one another. For example, nucleotide probes derived from the coding sequence of a polypeptide of this invention can be used in PCR or hybridization experiments to identify clones carrying the nucleotide sequence encoding the homologous related polypeptide.

TABLE 4

ORF Name	aa Seq ID#	Length (aa)	ORF Name	aa Seq ID#	Length (aa)	% Iden- tity	Over- lap (aa)	Change in Length
01cel1104_36125337_c1_8	849	74	hp1el0523orf3	612	63	100	63	11
01ce21104_33203250_c3_87	850	509	05cp11911orf35	549	206	100	204	303
01cp20708_36134808_f2_11	928	230	14ce10419orf5	704	229	100	229	1
02ae31010_12504512_f3_28.aa	929	490	01ge10801orf2	514	60	95	56	430
02ae31010_16833312_f2_19	930	181	02ce11022orf2	530	184	98	181	-3
02ae31010_2117087_f3_34	931	137	07ce10203orf17	635	76	97	77	61
02ae31010_30208317_f1_14	932	343	hp1p13947orf10	717	343	100	343	0
02ae31010_34616666_f2_27	851	184	01cel11618orf1	503	124	99	125	60
02ae31010_34616666_f2_27	851	184	hp1p13947orf11	616	81	94	77	103
02ae31010_35270000_f3_33	852	231	01ep11504orf5	505	156	99	156	75
02ae31010_36132785_f2_29	853	438	01cel11618orf3	499	67	98	64	371
02ae31010_36132785_f2_29	853	438	01cel11618orf13	504	378	97	387	60
02ae31010_5085162_c1_47	934	416	07ce10203orf11	634	416	100	416	0
02cp10615_26573462_c1_45	935	168	hp3p10304orf2	727	126	91	129	42
02ge10116_15781452_c1_87	854	97	06ge10115orf17	563	97	100	97	0
02ge10116_16803513_f2_34	855	488	01cp11710orf16	652	64	100	62	424
02ge10116_16803513_f2_34	855	488	01cp11710orf5	654	146	99	145	342
02ge10116_36367936_c1_92	857	173	02ge20116orf25	521	173	100	173	0
03ae10804_12609533_c1_26	936	257	06ep10306orf10	610	257	100	257	0

hp6p10903_4398263_f3_6.aa	924	370	05gp11901orf19	553	370	100	370	0
hp6p10903_4398263_f3_6.aa	924	370	05gp11901orf19	553	370	100	370	0
03ae10804_21698400_c2_32	937	386	06ep10306orf11	611	386	100	386	0
03ae10804_23485968_c3_47	858	88	06ep10306orf5	561	88	100	88	0
04ep41903_26757937_f3_16	938	703	29ap10306orf3	711	325	97	319	378
04ep41903_26757937_f3_16	938	703	29ap11902orf1	712	280	92	280	423
04ep41903_4101593_f2_10.aa	940	1240	14ee21118orf1	706	365	96	358	875
05ce10910_25598277_f3_3	859	258	07ee11519orf1	567	170	96	166	88
05ep10815_26570332_c2_99	941	183	12ge10610orf2	702	97	98	97	86
05ep10815_4195292_c1_84	942	441	hp1e10554orf1	715	103	99	94	338
05ep10815_4719175_c1_83	943	663	06ee10207orf1	606	99	99	99	564
06ae11016_30579712_f2_21	860	239	03ce21717orf1	526	193	99	193	46
06ce20610_1367157_f1_8.aa	844	248	29ge10111orf3	714	124	90	121	124
06ce20610_29298537_c2_32	861	234	05gp20111orf4	555	234	100	234	0
06ce20610_3913967_c3_36	862	283	05gp20111orf6	556	283	100	283	0
06ce20610_4331338_f3_18	863	353	05gp20111orf12	554	243	99	245	110
06cp11118_212827_c1_17	864	73	06cp11118orf7	558	73	100	73	0
06cp11217_19720300_f3_11	865	308	hp1p13852orf6	614	646	96	278	-338
06cp11217_4881263_f2_9	866	93	hp1p13852orf7	615	93	100	93	0
06cp11217_4897077_f1_6	867	100	hp1p13852orf4	613	100	100	100	0
06cp30603_21492187_f2_41	868	106	04gp11213orf14	539	136	98	106	-30
06cp30603_34024187_f1_20	869	483	04gp11213orf11	538	122	100	122	361
06cp30603_34024187_f1_20	869	483	04gp11213orf5	669	382	95	377	101
06cp30603_679218_f2_34	944	380	hp3e10302orf17	721	231	98	236	149
06ep10615_14649077_f3_52	871	300	04ce11617orf4	534	152	96	145	148
06ep10615_961562_f2_41	945	636	29ep20112orf2	713	135	98	87	501
06ep10615_9842_f3_46	872	159	05ep11717orf2	552	192	99	159	-33
06ep11202_133293_c1_19	946	167	06cp20302orf3	602	167	100	167	0
06ep11202_26353438_c1_22	873	286	hp2e11858orf6	623	155	100	154	131
06ep11202_26353438_c1_22	873	286	02ae21214orf1	522	109	92	110	177
06ep11202_792962_c2_26.aa	949	151	06cp20302orf6	604	66	92	66	85
06ep11202_4884677_c1_17	948	171	06cp20302orf5	603	171	99	171	0
06ep11917_24803153_c3_24	848	409	hp4e14535orf3	536	253	98	239	156
06ep11917_24803153_c3_24	848	409	hp4e14535orf7	730	60	97	60	349
06ep30223_16512_c3_160	951	231	hp3e10128orf1	720	231	100	231	0
06ep30223_23476067_c1_119	952	151	01ep30520orf8	511	94	93	95	57
06ep30223_23557202_c2_130	874	329	hp3e11024orf49	630	329	100	329	0
06ep30223_34409437_f3_94	875	148	hp3e11024orf5	631	148	100	148	0
06ep30223_4698838_f2_55	845	663	14gp12015orf13	662	344	100	334	319
06ep30223_4698838_f2_55	845	663	14gp12015orf16	663	117	99	112	546
06ep30223_4876077_c3_149	877	113	hp3e11024orf34	629	113	100	113	0
06ep30223_5109443_c1_109	878	342	05ee10411orf5	551	293	95	287	49
06ep30223_5271902_c1_106	879	207	hp2e10229orf4	619	80	95	38	127
06gp10409_3398427_f2_12	880	115	13ae10511orf3	583	115	92	115	0
06gp71906_15115637_f2_59	953	158	hp4p11393orf2	733	158	100	158	0
06gp71906_24261588_c2_174	881	96	01ae12021orf5	492	96	100	96	0
06gp71906_25478192_c1_131	954	236	hp3e11122orf3	723	236	100	236	0
06gp71906_25504187_f3_112	955	443	hp4p11393orf1	732	169	91	155	274
06gp71906_970325_c3_190	882	158	02ap21113orf2	512	113	92	98	45
07ae10923_24426508_f1_1	883	137	11ge10309orf28	685	137	100	137	0
07ae10923_24426508_f1_1	883	137	11ge10309orf28	685	137	100	137	0
09ce10413_414011_f1_3	885	169	02ce10216orf6	516	172	100	169	-3

09ce10413_5865665_f1_4	886	353	02ce10216orf7	517	74	100	74	279
09ce52017_29324062_c1_21	887	141	01ep30520orf24	506	141	100	141	0
09cp10224_1062966_c3_61	888	367	05ce10420orf1	548	194	100	194	173
09cp10224_1412715_c3_56	889	185	01ce10516orf20	495	185	100	185	0
09cp10224_429510_c2_46.aa	890	316	01ce10516orf21	496	108	98	108	208
09cp10224_4484718_c1_38	891	581	01ce10516orf15	493	301	99	297	280
09cp21607_7224187_c2_12	892	72	07gp31516orf9	569	72	100	72	0
09cp61003_14562637_c2_93	893	106	03gp20123orf3	527	80	98	83	26
09cp61003_19532625_c1_78	894	357	14ge10705orf14	599	357	99	357	0
09cp61003_24063587_c1_74	895	201	11ee10423orf1	577	116	100	116	85
09cp61003_24335762_c3_111	896	204	11ee10423orf4	578	105	100	104	99
09cp61003_492187_c2_80.aa	956	667	06gp10108orf2	621	266	98	266	401
09cp61003_5945252_f1_5	897	219	14ge10705orf3	695	219	100	219	0
11ae80818_11188791_c3_60	898	221	11ap11902orf3	575	185	99	185	36
11ae80818_19632781_c3_57	957	100	06cp11722orf11	595	100	100	100	0
11ae80818_7290627_c2_51	958	152	06cp11722orf5	598	98	100	93	54
11ae80818_783127_c3_63	899	182	03ap21820orf4	523	182	100	182	0
11ae80818_7952_c1_49	900	148	03ap21820orf8	524	148	100	148	0
11ap20714_34023312_f3_46	959	285	hp3e10057orf3	719	285	100	285	0
11ap20714_4960432_c3_97	901	151	14ee11217orf2	596	100	100	88	51
11ap20714_5271967_c1_60	902	260	14ee11217orf3	597	231	100	227	29
11ap20714_7227202_f3_43.aa	903	798	05ap21216orf4	547	529	100	529	269
11ap20714_7227202_f3_43.aa	903	798	05ap21216orf4	547	529	100	529	269
11ee11408_4977193_c1_41.aa	960	497	14ep11115orf3	708	91	100	91	406
11ge10308_5256_f2_1	961	71	11ge10308orf1	693	71	100	71	0
12ap10324_13178562_f3_6	962	269	12ap10324orf8	700	164	99	164	105
12ap10324_4805318_f2_3	846	326	12ap10324orf6	581	95	100	77	231
12ap10324_4805318_f2_3	846	326	12ap10324orf5	645	215	99	213	111
14ce31519_15635927_f3_15	905	293	02ce10809orf6	518	293	100	293	0
14ce61516_13073577_f2_12	963	784	14ep11905orf13	709	721	100	526	63
14ee41924_16282067_c1_72	964	64	02ep30607orf32	546	104	97	63	-40
14ee41924_23527267_c3_107	906	233	02ep30607orf27	520	138	98	97	95
14ee41924_23834800_f2_32	907	298	11ce10917orf10	639	298	100	298	0
14ee41924_2458267_c2_93	847	1304	02ep30607orf19	590	407	99	397	897
hp1p13939_25397327_f3_22	908	228	06ce10808orf2	557	151	100	145	77
hp2e10911_24855312_c1_69	909	161	11cp12006orf13	576	105	95	112	56
hp2e10911_3349_c1_63	910	113	01ce11618orf22	648	79	100	65	34
hp2e10911_4882027_c2_87	965	583	01cp11108orf6	507	101	99	99	482
hp3e11188_47327_f2_5	966	368	hp3p10807orf6	728	325	96	323	43
hp3e11188_5082842_f3_12	967	89	06ee11611orf1	608	89	100	89	0
hp4e13394_3368767_c1_80	968	804	09ap11406orf2	668	804	100	804	0
hp4e13394_35957200_f1_21	911	233	06ep11108orf17	562	165	100	147	68
hp4e13394_5964452_c2_97	912	79	02ap71220orf2	513	79	100	79	0
hp4e53394_22864682_c2_86.aa	913	427	hp1p13852orf6	614	646	100	422	-219
hp5e15044_4554652_f3_3	914	146	07cp10312orf5	677	138	100	138	8
hp5p15212_6928132_c3_34	969	270	11ce10908orf1	682	165	93	169	105
hp5p15575_29300311_c1_29	915	152	14ce10720orf3	591	163	95	152	-11
hp5p15575_33445317_f2_20.aa	916	294	hp3p11086orf1	636	217	92	202	77
hp5p15575_6140713_f2_18	917	288	14ce10720orf12	589	288	100	288	0
hp5p15641_12195281_c1_24	918	92	hp5p15612orf2	643	92	100	92	0
hp5p15641_24304527_c3_35	919	139	29ge10307orf4	609	103	98	102	36
hp5p15641_25635452_c3_34	920	92	29ge10307orf3	607	92	100	92	0

hp5p15641_30273312_c2_28	970	301	05cel0613orf1	572	79	91	70	222
hp5p15641_30273312_c2_28	970	301	05cel0613orf2	573	61	100	54	240
hp5p15641_5211687_c2_29	971	297	05ap10914orf3	571	60	98	60	237
hp5p15870_14350428_f1_1	921	84	05ae20220orf56	543	101	99	79	-17
hp6p10590_23440913_c2_31	922	371	04ee70114orf10	535	243	98	235	128
hp6p10590_30521093_f2_14	972	138	07cel1206orf1	637	107	97	107	31
hp6p10606_19546933_c3_31	923	283	13ep12003orf21	587	222	92	228	61
hp6p10904_2214676_c1_14	926	179	hp4p13446orf3	640	179	99	179	0
hp6p10904_23704412_f2_5	927	384	hp4p13446orf13	638	384	99	384	0
hp6p10904_7089062_c1_16	973	364	hp4p13446orf5	736	364	100	364	0
hp6p12129_16603417_f3_14	974	358	hp3e10302orf26	722	268	98	266	90
hp6p12244_3948467_c1_52	975	476	hp4p12005orf2	735	108	96	84	368
hp6p22217_23470967_f1_4	976	272	13ee12016orf7	703	272	100	272	0
hp7e10192_4412568_f2_5	977	291	02cel10114orf3	525	291	100	291	0
hp7p10287_24611325_c2_24	978	256	01cel1513orf17	500	256	100	256	0
hp7p10290_25548812_f3_14	979	489	hp3p10156orf2	724	333	100	333	156
hp7p10290_25585941_f3_12	980	374	hp3p10156orf3	725	91	91	87	283
hp7p10290_35156558_f3_15	981	411	11cp12002orf3	689	109	96	107	302
hp7p10290_4351718_f1_6	982	324	hp3p10156orf7	726	302	95	299	22

Additional relationships between polypeptides of the invention are described in Table 5 below. All of the polypeptide lengths in Table 5 below are measured from start codon to stop codon in the nucleotide sequence of *H. pylori*.

- 5 The relationship between the polypeptides shown in Table 5 can be described as follows. First, all of the polypeptides of Table 5 are at least 90% identical with each other over most of their lengths, and most are over 95% identical with each other. Second, the start-to-stop lengths are different for some of the homologous pairs of polypeptides. In some cases, the shorter polypeptide contains the relevant portion of the protein exhibiting utility in this invention; in some cases, the longer polypeptide may exhibit improved utility. Third, some polypeptides in the second column are
- 10 homologous to two shorter polypeptides in the fifth column.

- In all cases, the homology relationships described in Table 5 are highly significant. For example, a typical *H. pylori* gene product will exhibit amino acid sequence identities of between 92% and 100% among different strains of *H. pylori*
- 15 selected from human patients. The nucleotide sequences encoding the related polypeptides of this invention are also very similar to one another. For example, nucleotide probes derived from the coding sequence of a polypeptide of this invention can be used in PCR or hybridization experiments to identify clones carrying the
- 20 nucleotide sequence encoding the homologous related polypeptide.

TABLE 5

ORF Name	aa Seq ID #	Length (aa)	ORF Name	aa Seq ID #	Length (aa)	Length Differ.	% Ident.	Overlap (aa)
01ce21104_33203250_c3_87	850	502	02ae11612_33203250_c1_51	752	502	0	99.8	502
02ge10116_15781452_c1_87	854	97	02gp20706_15781452_c2_51	756	80	17	100	80
02ge10116_16803513_f2_34	855	479	02gp20706_16803513_f1_1	802	486	-7	100	479
02ge10116_16803513_f2_34	855	479	07ep11916_5913592_f3_18	818	269	210	97.66	128
02ge10116_36367936_c1_92	857	171	02ge10116_36367936_c1_19	753	169	2	100	169
06cp30603_21492187_f2_41	868	89	hp6e20339_21492187_c1_40	795	89	0	97.75	89
06cp30603_23476568_c2_133.aa	843	437	06cp30603_23476568_c1_44	773	436	1	100	436
06cp30603_34024187_f1_20	869	479	hp6e20339_24317062_c3_57	833	357	122	100	357
06cp30603_34024187_f1_20	869	479	hp6e20339_34024187_c1_37	796	118	361	100	118
06ep10615_14649077_f3_52	871	300	05ee10816_14649077_f3_18	767	263	37	96.74	245
06gp71906_24261588_c2_174	881	89	04cp11202_24261588_f2_23	761	88	1	100	88
07ae10923_24426508_f1_1	883	133	06ap11119_24426508_f3_26	815	117	16	100	117
07ae10923_24426508_f1_1	883	133	29ep10720_24220926_f2_8	823	80	53	100	80
09cp61003_19532625_c1_78	894	352	09cp11003_19532625_c3_17	778	333	19	100	333
09cp61003_5945252_f1_5	897	211	09cp11003_5945252_f2_4	819	198	13	100	198
11ap20714_7227202_f3_43.aa	903	792	07ap20216_7227202_f3_10	776	533	259	100	527
14ee41924_2458267_c2_93	847	1288	07ap11015_23938312_f3_2	762	257	1031	100	257
hp2e10911_3349_c1_63	910	110	29ge30321_12913562_f1_1	825	70	40	100	65
hp3e11188_47327_f2_5	966	368	hp3p10807_189075_f2_4	838	312	56	100	312
hp5e15044_4554652_f3_3	914	114	hp6p10233_12273302_f1_1	834	143	-29	95.58	113
hp5p15870_14350428_f1_1	921	80	05ae30220_14350428_f1_9	811	748	-668	98.75	80
hp6p10903_4398263_f3_6.aa	924	366	01ae12001_24218781_f2_18	746	119	247	96.64	119
hp6p10903_4398263_f3_6.aa	924	366	14ap10221_13689381_c3_4	822	338	28	96.45	338
hp7p10287_24611325_c2_24	978	256	02ep20506_24611325_f2_6	835	242	14	100	242

Additional relationships between polypeptides of the invention are described in Table 6 below. All of the polypeptide lengths in Table 6 below are measured from stop codon to stop codon in the nucleotide sequence of *H. pylori*.

5 The relationship between the polypeptides shown in Table 6 can be described as follows. First, all of the polypeptides of Table 6 are at least 90% identical with each other over most of their lengths, and most are over 95% identical with each other. Second, the stop-to-stop lengths are different for the homologous pairs of polypeptides. In some cases, the shorter polypeptide contains the relevant portion of the protein exhibiting utility in this invention; in some cases, the longer polypeptide may exhibit
10 improved utility.

In all cases, the homology relationships described in Table 6 are highly significant. For example, a typical *H. pylori* gene product will exhibit amino acid sequence identities of between 92% and 100% among different strains of *H. pylori* selected from human patients. The nucleotide sequences encoding the related
15 polypeptides of this invention are also very similar to one another. For example, nucleotide probes derived from the coding sequence of a polypeptide of this invention can be used in PCR or hybridization experiments to identify clones carrying the nucleotide sequence encoding the homologous related polypeptide.

TABLE 6

ORF Name	aa Seq ID#	Leng.	ORF Name	aa Seq ID #	Leng.	Leng. Diff.	Overlap	% ID
01ael2001_24218781_f2_18	746	149	11ael1922_12586675_f2_1	1037	249	100	149	100.00
02gp20706_23866562_c2_53	758	120	02ge10116_23866562_c3_146	1038	641	521	102	100.00
07apl1015_23938312_f3_2	762	271	07eel1402_2458267_c3_108	1039	1304	1033	271	100.00
07apl1213_35401528_c1_21	764	803	07ee50709_10213593_f3_77	1040	1484	681	726	100.00
05eel0816_14649077_f3_18	767	263	06ep10615_14649077_f2_30	1041	300	37	245	96.74
06cp30603_23452_c3_80	772	177	09cp10713_23452_c3_195	1042	526	349	177	94.35
07ap20216_7227202_f3_10	776	533	11ap20714_7227202_f3_40	1043	798	265	533	100.00
09cp11003_19532625_c3_17	778	357	01ce61016_23609580_c3_139	1044	343	-14	342	100.00
12gp31106_3024126_f2_25	780	147	06gp71906_3024126_c1_128	1045	405	258	143	100.00
13ael0712_14100018_f2_12	781	201	06ge20501_14100018_c1_34	1046	553	352	201	100.00
hp6e20339_34024187_c1_37	796	122	09cp10713_34024187_f1_31	1047	483	361	122	100.00
01ge10203_35281542_c3_16	797	261	hp4p62853_5914693_c3_52	1048	272	11	261	99.62
04ge10816_22086531_f2_10	809	208	13ael10610_859692_c2_32	1049	401	193	208	98.56
04ge10816_33726080_c2_29	810	369	13ael10610_35912_f2_3	1050	459	90	361	100.00
06apl1119_24426508_f3_26	815	121	06apl1119_24426508_f3_27	1051	137	16	121	100.00
07cel1019_22051291_f1_1	817	600	14gp11423_26803801_f3_7	1052	712	112	568	99.82
14apl0221_13689381_c3_4	822	366	06apl0609_12586675_f2_19	1053	375	9	363	96.69
29ge30321_135253_f2_6	826	101	07ee50709_4818967_f2_43	1054	487	386	86	98.84
hp2p10272_22692325_f3_21	829	188	02apl1117_23495187_c3_81	1055	253	65	188	99.47
hp6e20339_24317062_c3_57	833	382	09cp10713_34024187_f1_31	1056	483	101	377	96.55
07apl1213_35156577_c1_24	836	401	07ee50709_35156577_f3_80	1057	567	166	400	100.00
07ap80601_976413_f3_9	837	274	05ae30220_976413_c3_204	1058	384	110	274	100.00
hp3p10807_189075_f2_4	838	312	hp3el1188_47327_f2_9	1059	368	56	312	100.00
12apl0324_4805318_f2_3	846	327	12apl0324_4805318_f2_6	1060	420	93	327	100.00
03ael0804_23485968_c3_47	858	88	hpl1e80523_23485968_c2_49	1061	223	135	85	100.00
05cel0910_25598277_f3_3	859	258	hp7e10192_25598277_c2_15	1062	422	164	254	100.00
06cp11217_19720300_f3_11	865	308	hp4e53394_26209843_c3_98	1063	686	378	278	96.76
06ep10615_9842_f3_46	872	159	06ep10615_9842_f1_5	1064	345	186	159	99.37
06ep30223_34409437_f3_94	875	148	06ep30223_34409437_f2_64	1065	295	147	147	97.28

TABLE 6 (continued)

06gp10409_3398427_f2_12	880	116	06gp10409_3398427_f2_12	1066	292	176	116	100.00
09ce10413_5865665_f1_4	886	74	09ce10413_5865665_f1_4	1067	353	279	74	100.00
09cp10224_1062966_c3_61	888	367	09cp10224_1062966_c1_44	1068	485	118	372	94.09
09cp61003_14562637_c2_93	893	106	01ce61016_12931513_c2_106	1069	376	270	94	93.62
09cp61003_19532625_c1_78	894	357	01ce61016_23609580_c3_139	1070	343	-14	342	100.00
11ae80818_11188791_c3_60	898	221	14cp11908_25593768_c3_97	1071	538	317	204	99.51
11ae80818_783127_c3_63	899	182	14cp11908_783127_c1_72	1072	337	155	167	98.20
14ee41924_23527267_c3_107	906	233	07ee11402_10759567_c2_86	1073	292	59	232	100.00
hp2e10911_3349_c1_63	910	113	07ee50709_4818967_f2_43	1074	487	374	109	95.41
hp4e13394_35957200_f1_21	911	233	hp4e13394_5088562_f3_54	1075	225	-8	215	100.00
hp4e13394_5964452_c2_97	912	79	hp4e13394_15828963_c2_90	1076	135	56	77	100.00
hp4e53394_22864682_c2_86.aa	913	427	hp4e53394_19720300_c3_98	1077	647	220	422	100.00
hp5e15044_4554652_f3_3	914	146	07ce10312_4554652_f3_2	1078	174	28	146	100.00
hp5p15870_14350428_f1_1	921	84	05ae30220_14350428_f3_91	1079	752	668	84	98.81
hp6p10606_19546933_c3_31	923	283	hp8e10080_19546933_c2_88	1080	428	145	280	99.29
01cp20708_36134808_f2_11	928	230	01ce10320_30273587_f3_38	1081	275	45	230	100.00
02ae31010_2117087_f3_34	931	137	07ee50709_26438968_f2_36	1082	265	128	128	98.44
05ep10815_4719175_c1_83	943	663	05ep10815_4719175_c1_115	1083	925	262	653	100.00
06ep30223_23476067_c1_119	952	151	06ep30223_23476067_c1_115	1084	210	59	150	98.67
11ae80818_7290627_c2_51	958	152	hp7e10590_26172564_c1_68	1085	356	204	141	88.65
11ee11408_4977193_c1_41.aa	960	530	05ae30220_4977193_c3_198	1086	531	1	528	99.05
11ge10308_5256_f2_1	961	71	hp7e10557_21698387_f1_1	1087	239	168	69	98.55
14ee41924_16282067_c1_72	964	64	07ee11402_19565702_c2_88	1088	465	401	63	100.00
hp2e10911_4882027_c2_87	965	583	07ee50709_960952_f2_47	1089	1213	630	585	97.78
hp6p12244_3948467_c1_52	975	476	hp6p12244_3948467_c3_88	1090	508	32	445	100.00
14ce61516_13073577_f2_12	963	785	hp7e10590_13073577_c3_107	1296	897	112	785	100.00
09cp61003_492187_c2_80	956	667	01ce61016_492187_c3_120	1297	668	1	667	100.00
06ep10615_961562_f2_41	945	636	06ep10615_961562_f1_15	1298	637	1	636	100.00

IV. Identification of Nucleic Acids Encoding Vaccine Components and Targets for Agents Effective Against *H. pylori*

The disclosed *H. pylori* genome sequence includes segments that direct the synthesis of ribonucleic acids and polypeptides, as well as origins of replication, promoters, other types of regulatory sequences, and intergenic nucleic acids. The invention encompasses the identification of nucleic acids encoding immunogenic components of vaccines and targets for agents effective against *H. pylori*. An important aspect of this identification is to determine the function of the disclosed sequences, which can be achieved using a variety of approaches. Non-limiting examples of these methods are described briefly below.

Homology to known sequences: Computer-assisted comparison of the disclosed *H. pylori* sequences with previously reported sequences present in publicly available databases is a useful tool for identifying functional *H. pylori* nucleic acid and polypeptide sequences. It will be understood that protein-coding sequences, for example, may be compared as a whole, and that a high degree of sequence homology between two proteins (such as, for example, >80-90%) at the amino acid level is strongly suggestive that the two proteins also possess some degree of functional homology, such as, for example, among enzymes involved in metabolism, DNA synthesis, or cell wall synthesis, and proteins involved in transport, cell division, etc. In addition, many structural features of particular protein classes have been identified and correlate with specific consensus sequences, such as, for example, binding domains for nucleotides, DNA, metal ions, and other small molecules; sites for covalent modifications such as phosphorylation, acylation, and the like; sites of protein:protein interactions, etc. These consensus sequences may be quite short and thus may represent only a fraction of the entire protein-coding sequence. Identification of such a feature in an *H. pylori* sequence is therefore useful in determining the function of the encoded protein and identifying potentially useful targets of antibacterial drugs.

Of particular relevance to the present invention are structural features that are common to secretory, transmembrane, and surface proteins, including secretion signal peptides and hydrophobic transmembrane domains. *H. pylori* proteins identified as containing putative signal sequences and/or transmembrane domains are useful as immunogenic components of vaccines.

Identification of essential genes: Nucleic acids that encode proteins essential for growth or viability of *H. pylori* are preferred drug targets. *H. pylori* genes can be tested for their biological relevance to the organism by examining the effect of deleting and/or disrupting the genes, i.e., by so-called gene "knockout", using techniques known to those skilled in the relevant art. In this manner, essential genes may be identified.

Strain-specific sequences: Because of the evolutionary relationship between different *H. pylori* strains, it is believed that the presently disclosed *H. pylori* sequences are useful for identifying, and/or discriminating between, previously known and new *H. pylori* strains. It is believed that other *H. pylori* strains will exhibit at least 70% sequence homology with the presently disclosed sequence, although whether or not this is correct is not essential to the invention. Systematic and routine analyses of DNA sequences derived from samples containing *H. pylori* strains, and comparison with the present sequence allows for the identification of sequences that can be used to discriminate between strains, as well as those that are common to all *H. pylori* strains.

- 5 In one embodiment, the invention provides nucleic acids, including probes, and peptide and polypeptide sequences that discriminate between different strains of *H. pylori*. Strain-specific components can also be identified functionally by their ability to elicit or react with antibodies that selectively recognize one or more *H. pylori* strains.

- 10 In another embodiment, the invention provides nucleic acids, including probes, and peptide and polypeptide sequences that are common to all *H. pylori* strains but are not found in other bacterial species.

Specific Example: Determination Of Candidate Protein Antigens For Antibody And Vaccine Development

- 20 The selection of candidate protein antigens for vaccine development can be derived from the nucleic acids encoding *H. pylori* polypeptides. First, the ORF's can be analyzed for homology to other known exported or membrane proteins and analyzed using the discriminant analysis described by Klein, et al. (Klein, P., Kanehsia, M., and DeLisi, C. (1985) *Biochimica et Biophysica Acta* 815, 468-476) for predicting exported and membrane proteins.

- 25 Homology searches can be performed using the BLAST algorithm contained in the Wisconsin Sequence Analysis Package (Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711) to compare each predicted ORF amino acid sequence with all sequences found in the current GenBank, SWISS-PROT and PIR databases. BLAST searches for local alignments between the ORF and the databank sequences and reports a probability score which indicates the probability of finding this sequence by chance in the database. ORF's with significant homology (e.g. probabilities better than 1×10^{-6}) to membrane or exported proteins represent likely protein antigens for vaccine development. Possible functions can be provided to *H. pylori* genes based on sequence homology to genes cloned in other organisms.

35 Discriminant analysis (Klein, et al. supra) can be used to examine the ORF amino acid sequences. This algorithm uses the intrinsic information contained in the

ORF amino acid sequence and compares it to information derived from the properties of known membrane and exported proteins. This comparison predicts which proteins will be exported, membrane associated or cytoplasmic. ORF amino acid sequences identified as exported or membrane associated by this algorithm are likely protein
5 antigens for vaccine development.

Surface exposed outer membrane proteins are likely to represent the best antigens to provide a protective immune response against *H. pylori*. Among the algorithms that can be used to aid in prediction of these outer membrane proteins include the presence of an amphipathic beta-sheet region at their C-terminus. This region which
10 has been detected in a large number of outer membrane proteins in Gram negative bacteria is often characterized by hydrophobic residues (Phe or Tyr) approximately at positions 1, 3, 5, 7 and 9 from the C-terminus (e.g., see Figure 8, block F). Importantly, these sequences have not been detected at the C-termini of periplasmic proteins, thus allowing preliminary distinction between these classes of proteins based on primary
15 sequence data. This phenomenon has been reported previously by Struyve et al. (*J. Mol. Biol.* 218:141-148, 1991).

Also illustrated in Figure 8 are additional amino acid sequence motifs found in many outer membrane proteins of *H. pylori*. The amino acid sequence alignment in Figure 8 depicts portions of the sequence of 12 *H. pylori* proteins (depicted in the single
20 letter amino acid code) labeled with their amino acid Sequence ID Numbers and shown N-terminal to C-terminal, left to right. Six distinct blocks (labeled A through F) of similar amino acid residues are found including the distinctive hydrophobic residues (Phe or Tyr; F or Y according to the single letter code for amino acid residues) frequently found at positions near the C-terminus of outer membrane proteins. The
25 presence of several shared motifs clearly establishes the similarity between members of this group of proteins.

In addition, outer membrane proteins isolated from *H. pylori* frequently share a motif near the mature N-terminus (i.e., after processing to remove the secretion signal) as illustrated in the blocked amino acid residues in Figure 9. Figure 9 depicts the N-
30 terminal portion of nine *H. pylori* proteins (designated by their amino acid Sequence ID Numbers and shown N-terminal to C-terminal, left to right).

One skilled in the art would know that these shared sequence motifs are highly significant and establish a similarity among this group of proteins.

Infrequently it is not possible to distinguish between multiple possible
35 nucleotides at a given position in the nucleic acid sequence. In those cases the ambiguities are denoted by an extended alphabet as follows:

These are the official IUPAC-IUB single-letter base codes

Code	Base Description	
G	Guanine	
A	Adenine	
T	Thymine	
C	Cytosine	
R	Purine	(A or G)
Y	Pyrimidine	(C or T or U)
M	Amino	(A or C)
K	Ketone	(G or T)
S	Strong interaction	(C or G)
W	Weak interaction	(A or T)
H	Not-G	(A or C or T)
B	Not-A	(C or G or T)
V	Not-T (not-U)	(A or C or G)
D	Not-C	(A or G or T)
N	Any	(A or C or G or T)

5 The amino acid translations of this invention account for the ambiguity in the nucleic acid sequence by translating the ambiguous codon as the letter "X". In all cases, the permissible amino acid residues at a position are clear from an examination of the nucleic acid sequence based on the standard genetic code.

V. Production of Fragments and Analogs of *H. pylori* Nucleic Acids and Polypeptides

10 Based on the discovery of the *H. pylori* gene products provided in the Sequence Listing, one skilled in the art can alter the disclosed structure (of *H. pylori* genes), e.g., by producing fragments or analogs, and test the newly produced structures for activity. Examples of techniques known to those skilled in the relevant art which allow the production and testing of fragments and analogs are discussed below. These, or
15 analogous methods can be used to make and screen libraries of polypeptides, e.g., libraries of random peptides or libraries of fragments or analogs of cellular proteins for the ability to bind *H. pylori* polypeptides. Such screens are useful for discovery of inhibitors of *H. pylori*.

Generation of Fragments

20 Fragments of a protein can be produced in several ways, e.g., recombinantly, by proteolytic digestion, or by chemical synthesis. Internal or terminal fragments of a polypeptide can be generated by removing one or more nucleotides from one end (for a terminal fragment) or both ends (for an internal fragment) of a nucleic acid which encodes the polypeptide. Expression of the mutagenized DNA produces polypeptide
25 fragments. Digestion with "end-nibbling" endonucleases can thus generate DNA's which encode an array of fragments. DNA's which encode fragments of a protein can

also be generated by random shearing, restriction digestion or a combination of the above-discussed methods.

Fragments can also be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, peptides of the present invention may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or divided into overlapping fragments of a desired length.

Alteration of Nucleic Acids and Polypeptides: Random Methods

Amino acid sequence variants of a protein can be prepared by random mutagenesis of DNA which encodes a protein or a particular domain or region of a protein. Useful methods include PCR mutagenesis and saturation mutagenesis. A library of random amino acid sequence variants can also be generated by the synthesis of a set of degenerate oligonucleotide sequences. (Methods for screening proteins in a library of variants are elsewhere herein).

(A) PCR Mutagenesis

In PCR mutagenesis, reduced Taq polymerase fidelity is used to introduce random mutations into a cloned fragment of DNA (Leung et al., 1989, *Technique* 1:11-15). The DNA region to be mutagenized is amplified using the polymerase chain reaction (PCR) under conditions that reduce the fidelity of DNA synthesis by Taq DNA polymerase, e.g., by using a dGTP/dATP ratio of five and adding Mn^{2+} to the PCR reaction. The pool of amplified DNA fragments are inserted into appropriate cloning vectors to provide random mutant libraries.

(B) Saturation Mutagenesis

Saturation mutagenesis allows for the rapid introduction of a large number of single base substitutions into cloned DNA fragments (Mayers et al., 1985, *Science* 229:242). This technique includes generation of mutations, e.g., by chemical treatment or irradiation of single-stranded DNA *in vitro*, and synthesis of a complementary DNA strand. The mutation frequency can be modulated by modulating the severity of the treatment, and essentially all possible base substitutions can be obtained. Because this procedure does not involve a genetic selection for mutant fragments both neutral substitutions, as well as those that alter function, are obtained. The distribution of point mutations is not biased toward conserved sequence elements.

(C) Degenerate Oligonucleotides

A library of homologs can also be generated from a set of degenerate oligonucleotide sequences. Chemical synthesis of a degenerate sequences can be carried out in an automatic DNA synthesizer, and the synthetic genes then ligated into an

appropriate expression vector. The synthesis of degenerate oligonucleotides is known in the art (see for example, Narang, SA (1983) *Tetrahedron* 39:3; Itakura et al. (1981) *Recombinant DNA, Proc 3rd Cleveland Sympos. Macromolecules*, ed. AG Walton, Amsterdam: Elsevier pp273-289; Itakura et al. (1984) *Annu. Rev. Biochem.* 53:323; Itakura et al. (1984) *Science* 198:1056; Ike et al. (1983) *Nucleic Acid Res.* 11:477. Such techniques have been employed in the directed evolution of other proteins (see, for example, Scott et al. (1990) *Science* 249:386-390; Roberts et al. (1992) *PNAS* 89:2429-2433; Devlin et al. (1990) *Science* 249: 404-406; Cwirla et al. (1990) *PNAS* 87: 6378-6382; as well as U.S. Patents Nos. 5,223,409, 5,198,346, and 5,096,815).

10 Alteration of Nucleic Acids and Polypeptides: Methods for Directed Mutagenesis

Non-random or directed, mutagenesis techniques can be used to provide specific sequences or mutations in specific regions. These techniques can be used to create variants which include, e.g., deletions, insertions, or substitutions, of residues of the known amino acid sequence of a protein. The sites for mutation can be modified individually or in series, e.g., by (1) substituting first with conserved amino acids and then with more radical choices depending upon results achieved, (2) deleting the target residue, or (3) inserting residues of the same or a different class adjacent to the located site, or combinations of options 1-3.

15 (A) Alanine Scanning Mutagenesis

20 Alanine scanning mutagenesis is a useful method for identification of certain residues or regions of the desired protein that are preferred locations or domains for mutagenesis, Cunningham and Wells (*Science* 244:1081-1085, 1989). In alanine scanning, a residue or group of target residues are identified (e.g., charged residues such as Arg, Asp, His, Lys, and Glu) and replaced by a neutral or negatively charged amino acid (most preferably alanine or polyalanine). Replacement of an amino acid can affect the interaction of the amino acids with the surrounding aqueous environment in or outside the cell. Those domains demonstrating functional sensitivity to the substitutions are then refined by introducing further or other variants at or for the sites of substitution. Thus, while the site for introducing an amino acid sequence variation is predetermined, the nature of the mutation per se need not be predetermined. For example, to optimize the performance of a mutation at a given site, alanine scanning or random mutagenesis may be conducted at the target codon or region and the expressed desired protein subunit variants are screened for the optimal combination of desired activity.

25 (B) Oligonucleotide-Mediated Mutagenesis

30 Oligonucleotide-mediated mutagenesis is a useful method for preparing substitution, deletion, and insertion variants of DNA, see, e.g., Adelman et al., (*DNA*

- 62 -

2:183, 1983). Briefly, the desired DNA is altered by hybridizing an oligonucleotide encoding a mutation to a DNA template, where the template is the single-stranded form of a plasmid or bacteriophage containing the unaltered or native DNA sequence of the desired protein. After hybridization, a DNA polymerase is used to synthesize an entire
5 second complementary strand of the template that will thus incorporate the oligonucleotide primer, and will code for the selected alteration in the desired protein DNA. Generally, oligonucleotides of at least 25 nucleotides in length are used. An optimal oligonucleotide will have 12 to 15 nucleotides that are completely complementary to the template on either side of the nucleotide(s) coding for the
10 mutation. This ensures that the oligonucleotide will hybridize properly to the single-stranded DNA template molecule. The oligonucleotides are readily synthesized using techniques known in the art such as that described by Crea et al. (*Proc. Natl. Acad. Sci. USA*, 75: 5765[1978]).

(C) Cassette Mutagenesis

15 Another method for preparing variants, cassette mutagenesis, is based on the technique described by Wells et al. (*Gene*, 34:315[1985]). The starting material is a plasmid (or other vector) which includes the protein subunit DNA to be mutated. The codon(s) in the protein subunit DNA to be mutated are identified. There must be a unique restriction endonuclease site on each side of the identified mutation site(s). If no
20 such restriction sites exist, they may be generated using the above-described oligonucleotide-mediated mutagenesis method to introduce them at appropriate locations in the desired protein subunit DNA. After the restriction sites have been introduced into the plasmid, the plasmid is cut at these sites to linearize it. A double-stranded oligonucleotide encoding the sequence of the DNA between the restriction sites but
25 containing the desired mutation(s) is synthesized using standard procedures. The two strands are synthesized separately and then hybridized together using standard techniques. This double-stranded oligonucleotide is referred to as the cassette. This cassette is designed to have 3' and 5' ends that are comparable with the ends of the linearized plasmid, such that it can be directly ligated to the plasmid. This plasmid now
30 contains the mutated desired protein subunit DNA sequence.

(D) Combinatorial Mutagenesis

Combinatorial mutagenesis can also be used to generate mutants (Ladner et al., WO 88/06630). In this method, the amino acid sequences for a group of homologs or other related proteins are aligned, preferably to promote the highest homology
35 possible. All of the amino acids which appear at a given position of the aligned sequences can be selected to create a degenerate set of combinatorial sequences. The

variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level, and is encoded by a variegated gene library. For example, a mixture of synthetic oligonucleotides can be enzymatically ligated into gene sequences such that the degenerate set of potential sequences are expressible as individual peptides, or
5 alternatively, as a set of larger fusion proteins containing the set of degenerate sequences.

Other Modifications of *H. pylori* Nucleic Acids and Polypeptides

It is possible to modify the structure of an *H. pylori* polypeptide for such purposes as increasing solubility, enhancing stability (e.g., shelf life *ex vivo* and
10 resistance to proteolytic degradation *in vivo*). A modified *H. pylori* protein or peptide can be produced in which the amino acid sequence has been altered, such as by amino acid substitution, deletion, or addition as described herein.

An *H. pylori* peptide can also be modified by substitution of cysteine residues preferably with alanine, serine, threonine, leucine or glutamic acid residues to minimize
15 dimerization via disulfide linkages. In addition, amino acid side chains of fragments of the protein of the invention can be chemically modified. Another modification is cyclization of the peptide.

In order to enhance stability and/or reactivity, an *H. pylori* polypeptide can be modified to incorporate one or more polymorphisms in the amino acid sequence of the
20 protein resulting from any natural allelic variation. Additionally, D-amino acids, non-natural amino acids, or non-amino acid analogs can be substituted or added to produce a modified protein within the scope of this invention. Furthermore, an *H. pylori* polypeptide can be modified using polyethylene glycol (PEG) according to the method of A. Schon and co-workers (Wie et al., *supra*) to produce a protein conjugated with
25 PEG. In addition, PEG can be added during chemical synthesis of the protein. Other modifications of *H. pylori* proteins include reduction/alkylation (Tarr, *Methods of Protein Microcharacterization*, J. E. Silver ed., Humana Press, Clifton NJ 155-194 (1986)); acylation (Tarr, *supra*); chemical coupling to an appropriate carrier (Mishell and Shiigi, eds, *Selected Methods in Cellular Immunology*, WH Freeman, San Francisco, CA
30 (1980), U.S. Patent 4,939,239; or mild formalin treatment (Marsh, (1971) *Int. Arch. of Allergy and Appl. Immunol.*, 41: 199 - 215).

To facilitate purification and potentially increase solubility of an *H. pylori* protein or peptide, it is possible to add an amino acid fusion moiety to the peptide backbone. For example, hexa-histidine can be added to the protein for purification by
35 immobilized metal ion affinity chromatography (Hochuli, E. et al., (1988) *Bio/Technology*, 6: 1321 - 1325). In addition, to facilitate isolation of peptides free of

- 64 -

irrelevant sequences, specific endoprotease cleavage sites can be introduced between the sequences of the fusion moiety and the peptide.

To potentially aid proper antigen processing of epitopes within an *H. pylori* polypeptide, canonical protease sensitive sites can be engineered between regions, each comprising at least one epitope via recombinant or synthetic methods. For example, charged amino acid pairs, such as KK or RR, can be introduced between regions within a protein or fragment during recombinant construction thereof. The resulting peptide can be rendered sensitive to cleavage by cathepsin and/or other trypsin-like enzymes which would generate portions of the protein containing one or more epitopes. In addition, such charged amino acid residues can result in an increase in the solubility of the peptide.

Primary Methods for Screening Polypeptides and Analogs

Various techniques are known in the art for screening generated mutant gene products. Techniques for screening large gene libraries often include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the genes under conditions in which detection of a desired activity, e.g., in this case, binding to *H. pylori* polypeptide or an interacting protein, facilitates relatively easy isolation of the vector encoding the gene whose product was detected. Each of the techniques described below is amenable to high through-put analysis for screening large numbers of sequences created, e.g., by random mutagenesis techniques.

(A) Two Hybrid Systems

Two hybrid assays such as the system described above (as with the other screening methods described herein), can be used to identify polypeptides, e.g., fragments or analogs of a naturally-occurring *H. pylori* polypeptide, e.g., of cellular proteins, or of randomly generated polypeptides which bind to an *H. pylori* protein. (The *H. pylori* domain is used as the bait protein and the library of variants are expressed as fish fusion proteins.) In an analogous fashion, a two hybrid assay (as with the other screening methods described herein), can be used to find polypeptides which bind a *H. pylori* polypeptide.

(B) Display Libraries

In one approach to screening assays, the candidate peptides are displayed on the surface of a cell or viral particle, and the ability of particular cells or viral particles to bind an appropriate receptor protein via the displayed product is detected in a "panning assay". For example, the gene library can be cloned into the gene for a surface membrane protein of a bacterial cell, and the resulting fusion protein detected by

panning (Ladner et al., WO 88/06630; Fuchs et al. (1991) *Bio/Technology* 9:1370-1371; and Goward et al. (1992) *TIBS* 18:136-140). In a similar fashion, a detectably labeled ligand can be used to score for potentially functional peptide homologs. Fluorescently labeled ligands, e.g., receptors, can be used to detect homolog which retain ligand-binding activity. The use of fluorescently labeled ligands, allows cells to be visually inspected and separated under a fluorescence microscope, or, where the morphology of the cell permits, to be separated by a fluorescence-activated cell sorter.

A gene library can be expressed as a fusion protein on the surface of a viral particle. For instance, in the filamentous phage system, foreign peptide sequences can be expressed on the surface of infectious phage, thereby conferring two significant benefits. First, since these phage can be applied to affinity matrices at concentrations well over 10^{13} phage per milliliter, a large number of phage can be screened at one time. Second, since each infectious phage displays a gene product on its surface, if a particular phage is recovered from an affinity matrix in low yield, the phage can be amplified by another round of infection. The group of almost identical *E. coli* filamentous phages M13, fd., and f1 are most often used in phage display libraries. Either of the phage gIII or gVIII coat proteins can be used to generate fusion proteins without disrupting the ultimate packaging of the viral particle. Foreign epitopes can be expressed at the NH₂-terminal end of pIII and phage bearing such epitopes recovered from a large excess of phage lacking this epitope (Ladner et al. PCT publication WO 90/02909; Garrard et al., PCT publication WO 92/09690; Marks et al. (1992) *J. Biol. Chem.* 267:16007-16010; Griffiths et al. (1993) *EMBO J* 12:725-734; Clackson et al. (1991) *Nature* 352:624-628; and Barbas et al. (1992) *PNAS* 89:4457-4461).

A common approach uses the maltose receptor of *E. coli* (the outer membrane protein, LamB) as a peptide fusion partner (Charbit et al. (1986) *EMBO* 5, 3029-3037). Oligonucleotides have been inserted into plasmids encoding the LamB gene to produce peptides fused into one of the extracellular loops of the protein. These peptides are available for binding to ligands, e.g., to antibodies, and can elicit an immune response when the cells are administered to animals. Other cell surface proteins, e.g., OmpA (Schorr et al. (1991) *Vaccines* 91, pp. 387-392), PhoE (Agterberg, et al. (1990) *Gene* 88, 37-45), and PAL (Fuchs et al. (1991) *Bio/Tech* 9, 1369-1372), as well as large bacterial surface structures have served as vehicles for peptide display. Peptides can be fused to pilin, a protein which polymerizes to form the pilus-a conduit for interbacterial exchange of genetic information (Thiry et al. (1989) *Appl. Environ. Microbiol.* 55, 984-993). Because of its role in interacting with other cells, the pilus provides a useful support for the presentation of peptides to the extracellular environment. Another large surface

structure used for peptide display is the bacterial motive organ, the flagellum. Fusion of peptides to the subunit protein flagellin offers a dense array of many peptides copies on the host cells (Kuwajima et al. (1988) *Bio/Tech.* 6, 1080-1083). Surface proteins of other bacterial species have also served as peptide fusion partners. Examples include the

5 *Staphylococcus* protein A and the outer membrane protease IgA of *Neisseria* (Hansson et al. (1992) *J. Bacteriol.* 174, 4239-4245 and Klauser et al. (1990) *EMBO J.* 9, 1991-1999).

In the filamentous phage systems and the LamB system described above, the physical link between the peptide and its encoding DNA occurs by the containment of

10 the DNA within a particle (cell or phage) that carries the peptide on its surface. Capturing the peptide captures the particle and the DNA within. An alternative scheme uses the DNA-binding protein LacI to form a link between peptide and DNA (Cull et al. (1992) *PNAS USA* 89:1865-1869). This system uses a plasmid containing the LacI gene with an oligonucleotide cloning site at its 3'-end. Under the controlled induction by

15 arabinose, a LacI-peptide fusion protein is produced. This fusion retains the natural ability of LacI to bind to a short DNA sequence known as LacO operator (LacO). By installing two copies of LacO on the expression plasmid, the LacI-peptide fusion binds tightly to the plasmid that encoded it. Because the plasmids in each cell contain only a single oligonucleotide sequence and each cell expresses only a single peptide sequence,

20 the peptides become specifically and stably associated with the DNA sequence that directed its synthesis. The cells of the library are gently lysed and the peptide-DNA complexes are exposed to a matrix of immobilized receptor to recover the complexes containing active peptides. The associated plasmid DNA is then reintroduced into cells for amplification and DNA sequencing to determine the identity of the peptide ligands.

25 As a demonstration of the practical utility of the method, a large random library of dodecapeptides was made and selected on a monoclonal antibody raised against the opioid peptide dynorphin B. A cohort of peptides was recovered, all related by a consensus sequence corresponding to a six-residue portion of dynorphin B. (Cull et al. (1992) *Proc. Natl. Acad. Sci. U.S.A.* 89-1869)

30 This scheme, sometimes referred to as peptides-on-plasmids, differs in two important ways from the phage display methods. First, the peptides are attached to the C-terminus of the fusion protein, resulting in the display of the library members as peptides having free carboxy termini. Both of the filamentous phage coat proteins, pIII and pVIII, are anchored to the phage through their C-termini, and the guest peptides are

35 placed into the outward-extending N-terminal domains. In some designs, the phage-displayed peptides are presented right at the amino terminus of the fusion protein.

(Cwirla, et al. (1990) *Proc. Natl. Acad. Sci. U.S.A.* 87, 6378-6382) A second difference is the set of biological biases affecting the population of peptides actually present in the libraries. The LacI fusion molecules are confined to the cytoplasm of the host cells.

The phage coat fusions are exposed briefly to the cytoplasm during translation but are rapidly secreted through the inner membrane into the periplasmic compartment, remaining anchored in the membrane by their C-terminal hydrophobic domains, with the N-termini, containing the peptides, protruding into the periplasm while awaiting assembly into phage particles. The peptides in the LacI and phage libraries may differ significantly as a result of their exposure to different proteolytic activities. The phage coat proteins require transport across the inner membrane and signal peptidase processing as a prelude to incorporation into phage. Certain peptides exert a deleterious effect on these processes and are underrepresented in the libraries (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251). These particular biases are not a factor in the LacI display system.

The number of small peptides available in recombinant random libraries is enormous. Libraries of 10^7 - 10^9 independent clones are routinely prepared. Libraries as large as 10^{11} recombinants have been created, but this size approaches the practical limit for clone libraries. This limitation in library size occurs at the step of transforming the DNA containing randomized segments into the host bacterial cells. To circumvent this limitation, an *in vitro* system based on the display of nascent peptides in polysome complexes has recently been developed. This display library method has the potential of producing libraries 3-6 orders of magnitude larger than the currently available phage/phagemid or plasmid libraries. Furthermore, the construction of the libraries, expression of the peptides, and screening, is done in an entirely cell-free format.

In one application of this method (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251), a molecular DNA library encoding 10^{12} decapeptides was constructed and the library expressed in an *E. coli* S30 *in vitro* coupled transcription/translation system. Conditions were chosen to stall the ribosomes on the mRNA, causing the accumulation of a substantial proportion of the RNA in polysomes and yielding complexes containing nascent peptides still linked to their encoding RNA. The polysomes are sufficiently robust to be affinity purified on immobilized receptors in much the same way as the more conventional recombinant peptide display libraries are screened. RNA from the bound complexes is recovered, converted to cDNA, and amplified by PCR to produce a template for the next round of synthesis and screening. The polysome display method can be coupled to the phage display system. Following several rounds of screening, cDNA from the enriched pool of polysomes was cloned into

a phagemid vector. This vector serves as both a peptide expression vector, displaying peptides fused to the coat proteins, and as a DNA sequencing vector for peptide identification. By expressing the polysome-derived peptides on phage, one can either continue the affinity selection procedure in this format or assay the peptides on individual clones for binding activity in a phage ELISA, or for binding specificity in a completion phage ELISA (Barret, et al. (1992) *Anal. Biochem* 204,357-364). To identify the sequences of the active peptides one sequences the DNA produced by the phagemid host.

Secondary Screening of Polypeptides and Analogs

The high through-put assays described above can be followed by secondary screens in order to identify further biological activities which will, e.g., allow one skilled in the art to differentiate agonists from antagonists. The type of a secondary screen used will depend on the desired activity that needs to be tested. For example, an assay can be developed in which the ability to inhibit an interaction between a protein of interest and its respective ligand can be used to identify antagonists from a group of peptide fragments isolated through one of the primary screens described above.

Therefore, methods for generating fragments and analogs and testing them for activity are known in the art. Once the core sequence of interest is identified, it is routine to perform for one skilled in the art to obtain analogs and fragments.

Peptide Mimetics of *H. pylori* Polypeptides

The invention also provides for reduction of the protein binding domains of the subject *H. pylori* polypeptides to generate mimetics, e.g. peptide or non-peptide agents. The peptide mimetics are able to disrupt binding of a polypeptide to its counter ligand, e.g., in the case of an *H. pylori* polypeptide binding to a naturally occurring ligand. The critical residues of a subject *H. pylori* polypeptide which are involved in molecular recognition of a polypeptide can be determined and used to generate *H. pylori*-derived peptidomimetics which competitively or noncompetitively inhibit binding of the *H. pylori* polypeptide with an interacting polypeptide (see, for example, European patent applications EP-412,762A and EP-B31,080A).

For example, scanning mutagenesis can be used to map the amino acid residues of a particular *H. pylori* polypeptide involved in binding an interacting polypeptide, peptidomimetic compounds (e.g. diazepam or isoquinoline derivatives) can be generated which mimic those residues in binding to an interacting polypeptide, and which therefore can inhibit binding of an *H. pylori* polypeptide to an interacting polypeptide and thereby interfere with the function of *H. pylori* polypeptide. For instance, non-hydrolyzable peptide analogs of such residues can be generated using benzodiazepine

(e.g., see Freidinger et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), azepine (e.g., see Huffman et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), substituted gamma lactam rings (Garvey et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), keto-methylene pseudopeptides (Ewenson et al. (1986) *J Med Chem* 29:295; and Ewenson et al. in *Peptides: Structure and Function* (Proceedings of the 9th American Peptide Symposium) Pierce Chemical Co. Rockland, IL, 1985), β -turn dipeptide cores (Nagai et al. (1985) *Tetrahedron Lett* 26:647; and Sato et al. (1986) *J Chem Soc Perkin Trans* 1:1231), and β -aminoalcohols (Gordon et al. (1985) *Biochem Biophys Res Commun* 126:419; and Dann et al. (1986) *Biochem Biophys Res Commun* 134:71).

VI. Vaccine Formulations for *H. pylori* Nucleic Acids and Polypeptides

This invention also features vaccine compositions for protection against infection by *H. pylori* or for treatment of *H. pylori* infection, a gram-negative spiral microaerophilic bacterium. In one embodiment, the vaccine compositions contain one or more immunogenic components such as a surface protein from *H. pylori*, or portion thereof, and a pharmaceutically acceptable carrier. Nucleic acids within the scope of the invention are exemplified by the nucleic acids shown in the Sequence Listing which encode *H. pylori* surface proteins. However, any nucleic acid encoding an immunogenic *H. pylori* protein, or portion thereof, which is capable of expression in a cell, can be used in the present invention. These vaccines have therapeutic and prophylactic utilities.

One aspect of the invention provides a vaccine composition for protection against infection by *H. pylori* which contains at least one immunogenic fragment of an *H. pylori* protein and a pharmaceutically acceptable carrier. Preferred fragments include peptides of at least about 10 amino acid residues in length, preferably about 10-20 amino acid residues in length, and more preferably about 12-16 amino acid residues in length.

Immunogenic components of the invention can be obtained, for example, by screening polypeptides recombinantly produced from the corresponding fragment of the nucleic acid encoding the full-length *H. pylori* protein. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry.

In one embodiment, immunogenic components are identified by the ability of the peptide to stimulate T cells. Peptides which stimulate T cells, as determined by, for example, T cell proliferation or cytokine secretion are defined herein as comprising at least one T cell epitope. T cell epitopes are believed to be involved in initiation and

- 70 -

perpetuation of the immune response to the protein allergen which is responsible for the clinical symptoms of allergy. These T cell epitopes are thought to trigger early events at the level of the T helper cell by binding to an appropriate HLA molecule on the surface of an antigen presenting cell, thereby stimulating the T cell subpopulation with the relevant T cell receptor for the epitope. These events lead to T cell proliferation, lymphokine secretion, local inflammatory reactions, recruitment of additional immune cells to the site of antigen/T cell interaction, and activation of the B cell cascade, leading to the production of antibodies. A T cell epitope is the basic element, or smallest unit of recognition by a T cell receptor, where the epitope comprises amino acids essential to receptor recognition (e.g., approximately 6 or 7 amino acid residues). Amino acid sequences which mimic those of the T cell epitopes are within the scope of this invention.

In another embodiment, immunogenic components of the invention are identified through genomic vaccination. The basic protocol is based on the idea that expression libraries consisting of all or parts of a pathogen genome, e.g., an *H. pylori* genome, can confer protection when used to genetically immunize a host. This expression library immunization (ELI) is analogous to expression cloning and involves reducing a genomic expression library of a pathogen, e.g., *H. pylori*, into plasmids that can act as genetic vaccines. The plasmids can also be designed to encode genetic adjuvants which can dramatically stimulate the humoral response. These genetic adjuvants can be introduced at remote sites and act as well extracellularly as intracellularly.

This is a new approach to vaccine production that has many of the advantages of live/attenuated pathogens but no risk of infection. An expression library of pathogen DNA is used to immunize a host thereby producing the effects of antigen presentation of a live vaccine without the risk. For example, in the present invention, random fragments from the *H. pylori* genome or from cosmid or plasmid clones, as well as PCR products from genes identified by genomic sequencing, can be used to immunize a host. The feasibility of this approach has been demonstrated with *Mycoplasma pulmonis* (Barry et al., *Nature* 377:632-635, 1995), where even partial expression libraries of *Mycoplasma pulmonis*, a natural pathogen in rodents, provided protection against challenge from the pathogen.

ELI is a technique that allows for production of a non-infectious multipartite vaccine, even when little is known about pathogen's biology, because ELI uses the immune system to screen candidate genes. Once isolated, these genes can be used as genetic vaccines or for development of recombinant protein vaccines. Thus, ELI allows for production of vaccines in a systematic, largely mechanized fashion.

Screening immunogenic components can be accomplished using one or more of several different assays. For example, *in vitro*, peptide T cell stimulatory activity is assayed by contacting a peptide known or suspected of being immunogenic with an antigen presenting cell which presents appropriate MHC molecules in a T cell culture.

5 Presentation of an immunogenic *H. pylori* peptide in association with appropriate MHC molecules to T cells in conjunction with the necessary costimulation has the effect of transmitting a signal to the T cell that induces the production of increased levels of cytokines, particularly of interleukin-2 and interleukin-4. The culture supernatant can be obtained and assayed for interleukin-2 or other known cytokines. For example, any one
10 of several conventional assays for interleukin-2 can be employed, such as the assay described in *Proc. Natl. Acad. Sci USA*, 86: 1333 (1989) the pertinent portions of which are incorporated herein by reference. A kit for an assay for the production of interferon is also available from Genzyme Corporation (Cambridge, MA).

Alternatively, a common assay for T cell proliferation entails measuring tritiated
15 thymidine incorporation. The proliferation of T cells can be measured *in vitro* by determining the amount of ³H-labeled thymidine incorporated into the replicating DNA of cultured cells. Therefore, the rate of DNA synthesis and, in turn, the rate of cell division can be quantified.

Vaccine compositions of the invention containing immunogenic components
20 (e.g., *H. pylori* polypeptide or fragment thereof or nucleic acid encoding an *H. pylori* polypeptide or fragment thereof) preferably include a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier that does not cause an allergic reaction or other untoward effect in patients to whom it is administered. Suitable pharmaceutically acceptable carriers include, for example, one or more of
25 water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like, as well as combinations thereof. Pharmaceutically acceptable carriers may further comprise minor amounts of auxiliary substances such as wetting or emulsifying agents, preservatives or buffers, which enhance the shelf life or effectiveness of the antibody. For vaccines of the invention containing *H. pylori* polypeptides, the polypeptide is
30 coadministered with a suitable adjuvant.

It will be apparent to those of skill in the art that the therapeutically effective amount of DNA or protein of this invention will depend, *inter alia*, upon the administration schedule, the unit dose of antibody administered, whether the protein or DNA is administered in combination with other therapeutic agents, the immune status
35 and health of the patient, and the therapeutic activity of the particular protein or DNA.

- 72 -

Vaccine compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Methods for intramuscular immunization are described by Wolff et al. (1990) *Science* 247: 1465-1468 and by Sedegah et al. (1994) *Immunology* 91: 9866-9870. Other modes of administration
5 include oral and pulmonary formulations, suppositories, and transdermal applications. Oral immunization is preferred over parenteral methods for inducing protection against infection by *H. pylori*. Czinn et. al. (1993) *Vaccine* 11: 637-642. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium
10 carbonate, and the like.

The vaccine compositions of the invention can include an adjuvant, including, but not limited to aluminum hydroxide; N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP); N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP); N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-
15 sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE); RIBI, which contains three components from bacteria; monophosphoryl lipid A; trehalose dimycolate; cell wall skeleton (MPL + TDM + CWS) in a 2% squalene/Tween 80 emulsion; and cholera toxin. Others which may be used are non-toxic derivatives of cholera toxin, including its B subunit, and/or conjugates or
20 genetically engineered fusions of the *H. pylori* polypeptide with cholera toxin or its B subunit, procholera genoid, fungal polysaccharides, including schizophyllan, muramyl dipeptide, muramyl dipeptide derivatives, phorbol esters, labile toxin of *E. coli*, non-*H. pylori* bacterial lysates, block polymers or saponins.

Other suitable delivery methods include biodegradable microcapsules or
25 immuno-stimulating complexes (ISCOMs) or liposomes, genetically engineered attenuated live vectors such as viruses or bacteria, and recombinant (chimeric) virus-like particles, e.g., bluetongue. The amount of adjuvant employed will depend on the type of adjuvant used. For example, when the mucosal adjuvant is cholera toxin, it is suitably used in an amount of 5 µg to 50 µg, for example 10 µg to 35 µg. When used in the form
30 of microcapsules, the amount used will depend on the amount employed in the matrix of the microcapsule to achieve the desired dosage. The determination of this amount is within the skill of a person of ordinary skill in the art.

Carrier systems in humans may include enteric release capsules protecting the antigen from the acidic environment of the stomach, and including *H. pylori* polypeptide
35 in an insoluble form as fusion proteins. Suitable carriers for the vaccines of the

- 73 -

invention are enteric coated capsules and polylactide-glycolide microspheres. Suitable diluents are 0.2 N NaHCO₃ and/or saline.

Vaccines of the invention can be administered as a primary prophylactic agent in adults or in children, as a secondary prevention, after successful eradication of *H. pylori* in an infected host, or as a therapeutic agent in the aim to induce an immune response in a susceptible host to prevent infection by *H. pylori*. The vaccines of the invention are administered in amounts readily determined by persons of ordinary skill in the art. Thus, for adults a suitable dosage will be in the range of 10 µg to 10 g, preferably 10 µg to 100 mg, for example 50 µg to 50 mg. A suitable dosage for adults will also be in the range of 5 µg to 500 mg. Similar dosage ranges will be applicable for children. Those skilled in the art will recognize that the optimal dose may be more or less depending upon the patient's body weight, disease, the route of administration, and other factors. Those skilled in the art will also recognize that appropriate dosage levels can be obtained based on results with known oral vaccines such as, for example, a vaccine based on an *E. coli* lysate (6 mg dose daily up to total of 540 mg) and with an enterotoxigenic *E. coli* purified antigen (4 doses of 1 mg) (Schulman et al., *J. Urol.* 150:917-921 (1993); Boedecker et al., *American Gastroenterological Assoc.* 999:A-222 (1993)). The number of doses will depend upon the disease, the formulation, and efficacy data from clinical trials. Without intending any limitation as to the course of treatment, the treatment can be administered over 3 to 8 doses for a primary immunization schedule over 1 month (Boedeker, *American Gastroenterological Assoc.* 888:A-222 (1993)).

It will be apparent to those skilled in the art that some of the vaccine compositions of the invention are useful only for preventing *H. pylori* infection, some are useful only for treating *H. pylori* infection, and some are useful for both preventing and treating *H. pylori* infection. In a preferred embodiment, the vaccine composition of the invention provides protection against *H. pylori* infection by stimulating humoral and/or cell-mediated immunity against *H. pylori*. It should be understood that amelioration of any of the symptoms of *H. pylori* infection is a desirable clinical goal, including a lessening of the dosage of medication used to treat *H. pylori*-caused disease.

VII. Antibodies Reactive With *H. pylori* Polypeptides

The invention also includes antibodies specifically reactive with the subject *H. pylori* polypeptide. Anti-protein/anti-peptide antisera or monoclonal antibodies can be made by standard protocols (See, for example, *Antibodies: A Laboratory Manual* ed. by Harlow and Lane (Cold Spring Harbor Press: 1988)). A mammal such as a mouse, a

hamster or rabbit can be immunized with an immunogenic form of the peptide.

Techniques for conferring immunogenicity on a protein or peptide include conjugation to carriers or other techniques well known in the art. An immunogenic portion of the subject *H. pylori* polypeptide can be administered in the presence of adjuvant. The progress of immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassays can be used with the immunogen as antigen to assess the levels of antibodies.

In a preferred embodiment, the subject antibodies are immunospecific for antigenic determinants of the *H. pylori* polypeptides of the invention, e.g. antigenic determinants of a polypeptide shown in the Sequence Listing, or a closely related human or non-human mammalian homolog (e.g., 90% homologous, more preferably at least 95% homologous). In yet a further preferred embodiment of the invention, the anti-*H. pylori* antibodies do not substantially cross react (i.e., react specifically) with a protein which is for example, less than 80% percent homologous to a sequence shown in the Sequence Listing. By "not substantially cross react", it is meant that the antibody has a binding affinity for a non-homologous protein which is less than 10 percent, more preferably less than 5 percent, and even more preferably less than 1 percent, of the binding affinity for a protein contained in the Sequence Listing. In a most preferred embodiment, there is no crossreactivity between bacterial and mammalian antigens.

The term antibody as used herein is intended to include fragments thereof which are also specifically reactive with *H. pylori* polypeptides. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. For example, F(ab')₂ fragments can be generated by treating antibody with pepsin. The resulting F(ab')₂ fragment can be treated to reduce disulfide bridges to produce Fab' fragments. The antibody of the invention is further intended to include bispecific and chimeric molecules having an anti-*H. pylori* portion.

Both monoclonal and polyclonal antibodies (Ab) directed against *H. pylori* polypeptides or *H. pylori* polypeptide variants, and antibody fragments such as Fab' and F(ab')₂, can be used to block the action of *H. pylori* polypeptide and allow the study of the role of a particular *H. pylori* polypeptide of the invention in aberrant or unwanted intracellular signaling, as well as the normal cellular function of the *H. pylori* and by microinjection of anti-*H. pylori* polypeptide antibodies of the present invention.

Antibodies which specifically bind *H. pylori* epitopes can also be used in immunohistochemical staining of tissue samples in order to evaluate the abundance and pattern of expression of *H. pylori* antigens. Anti *H. pylori* polypeptide antibodies can be

used diagnostically in immuno-precipitation and immuno-blotting to detect and evaluate *H. pylori* levels in tissue or bodily fluid as part of a clinical testing procedure. Likewise, the ability to monitor *H. pylori* polypeptide levels in an individual can allow determination of the efficacy of a given treatment regimen for an individual afflicted with such a disorder. The level of an *H. pylori* polypeptide can be measured in cells found in bodily fluid, such as in urine samples or can be measured in tissue, such as produced by gastric biopsy. Diagnostic assays using anti-*H. pylori* antibodies can include, for example, immunoassays designed to aid in early diagnosis of *H. pylori* infections. The present invention can also be used as a method of detecting antibodies contained in samples from individuals infected by this bacterium using specific *H. pylori* antigens.

Another application of anti-*H. pylori* polypeptide antibodies of the invention is in the immunological screening of cDNA libraries constructed in expression vectors such as λ gt11, λ gt18-23, λ ZAP, and λ ORF8. Messenger libraries of this type, having coding sequences inserted in the correct reading frame and orientation, can produce fusion proteins. For instance, λ gt11 will produce fusion proteins whose amino termini consist of β -galactosidase amino acid sequences and whose carboxy termini consist of a foreign polypeptide. Antigenic epitopes of a subject *H. pylori* polypeptide can then be detected with antibodies, as, for example, reacting nitrocellulose filters lifted from infected plates with anti-*H. pylori* polypeptide antibodies. Phage, scored by this assay, can then be isolated from the infected plate. Thus, the presence of *H. pylori* gene homologs can be detected and cloned from other species, and alternate isoforms (including splicing variants) can be detected and cloned.

VIII. Kits Containing Nucleic Acids, Polypeptides or Antibodies of the Invention

The nucleic acid, polypeptides and antibodies of the invention can be combined with other reagents and articles to form kits. Kits for diagnostic purposes typically comprise the nucleic acid, polypeptides or antibodies in vials or other suitable vessels. Kits typically comprise other reagents for performing hybridization reactions, polymerase chain reactions (PCR), or for reconstitution of lyophilized components, such as aqueous media, salts, buffers, and the like. Kits may also comprise reagents for sample processing such as detergents, chaotropic salts and the like. Kits may also comprise immobilization means such as particles, supports, wells, dipsticks and the like. Kits may also comprise labeling means such as dyes, developing reagents, radioisotopes, fluorescent agents, luminescent or chemiluminescent agents, enzymes, intercalating agents and the like. With the nucleic acid and amino acid sequence information provided

herein, individuals skilled in art can readily assemble kits to serve their particular purpose. Kits further can include instructions for use.

IX. Drug Screening Assays Using *H. pylori* Polypeptides

5 By making available purified and recombinant *H. pylori* polypeptides, the present invention provides assays which can be used to screen for drugs which are either agonists or antagonists of the normal cellular function, in this case, of the subject *H. pylori* polypeptides, or of their role in intracellular signaling. Such inhibitors or potentiators may be useful as new therapeutic agents to combat *H. pylori* infections in
10 humans. A variety of assay formats will suffice and, in light of the present inventions, will be comprehended by the skilled artisan.

In many drug screening programs which test libraries of compounds and natural extracts, high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays which are performed in cell-free
15 systems, such as may be derived with purified or semi-purified proteins, are often preferred as "primary" screens in that they can be generated to permit rapid development and relatively easy detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test compound can be generally ignored in the *in vitro* system, the assay instead being
20 focused primarily on the effect of the drug on the molecular target as may be manifest in an alteration of binding affinity with other proteins or change in enzymatic properties of the molecular target. Accordingly, in an exemplary screening assay of the present invention, the compound of interest is contacted with an isolated and purified *H. pylori* polypeptide.

25 Screening assays can be constructed *in vitro* with a purified *H. pylori* polypeptide or fragment thereof, such as an *H. pylori* polypeptide having enzymatic activity, such that the activity of the polypeptide produces a detectable reaction product. The efficacy of the compound can be assessed by generating dose response curves from data obtained using various concentrations of the test compound. Moreover, a control
30 assay can also be performed to provide a baseline for comparison. Suitable products include those with distinctive absorption, fluorescence, or chemi-luminescence properties, for example, because detection may be easily automated. A variety of synthetic or naturally occurring compounds can be tested in the assay to identify those which inhibit or potentiate the activity of the *H. pylori* polypeptide. Some of these
35 active compounds may directly, or with chemical alterations to promote membrane

- 77 -

permeability or solubility, also inhibit or potentiate the same activity (e.g., enzymatic activity) in whole, live *H. pylori* cells.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references and published patent applications cited throughout this application are hereby incorporated by reference.

Other Embodiments

Many of the nucleic acids and corresponding polypeptides of the invention were disclosed previously in the parent applications, U.S.S.N. 08/761,318, filed December 6, 1996 (Attorney Docket No.: GTN-009CP2), U.S.S.N. 08/736,905, filed October 25, 1996 (Attorney Docket No.: GTN-010CP) and U.S.S.N. 08/738,859, filed October 28, 1996 (Attorney Docket No.: GTN-009CP), which are a continuation-in-part of U.S.S.N. 08/625,811, filed March 29, 1996 (Attorney Docket No.: GTN-009), and U.S.S.N. 08/758,731, filed April 2, 1996 (Attorney Docket No.: GTN-010). The correlation between sequence identification numbers in the above-identified parent applications and sequence identification numbers provided herein is outlined in Table 7 below.

TABLE 7

ORF Name	Source	Parent nt Seq ID#	Parent aa Seq ID#	CIP1 nt Seq ID#	CIP1 aa Seq ID#	Current nt Seq ID#	Current aa Seq ID#
01ae12021orf5	009CP1	5	867	3	1095	1	492
01ce10516orf15	009CP1	15	877	10	1102	2	493
01ce10516orf19	009CP1	18	880	13	1105	3	494
01ce10516orf20	009CP1	19	881	14	1106	4	495
01ce10516orf21	009CP1	20	882	15	1107	5	496
01ce10516orf24	009CP1	21	883	16	1108	6	497
01ce11618orf24	009CP1	36	898	30	1122	7	498
01ce11618orf3	009CP1	37	899	31	1123	8	499
01ce11513orf17	010CP1	44	1957	35	1554	9	500
01cp11414orf2	009CP1	44	906	36	1128	10	501
01cp11710orf1	009CP1	46	908	37	1129	11	502
01ce11618orf1	010CP1	51	1964	38	1557	12	503
01ce11618orf13	010CP1	54	1967	40	1559	13	504
01ep11504orf5	009CP1	65	927	52	1144	14	505
01ep30520orf24	009CP1	67	929	54	1146	15	506
01cp11108orf6	010CP1	74	1987	54	1573	16	507
01gp11016orf13	009CP1	78	940	63	1155	17	508
02ae11612orf1	009CP1	97	959	79	1171	18	509
02ae11612orf15	009CP1	99	961	80	1172	19	510
01ep30520orf8	010CP1	121	2034	86	1605	20	511
02ap21113orf2	009CP1	112	974	88	1180	21	512
02ap71220orf2	009CP1	114	976	90	1182	22	513
01ge10801orf2	010CP1	133	2046	91	1610	23	514

02ce10213orf19	009CP1	116	978	92	1184	24	515
02ce10216orf6	009CP1	123	985	96	1188	25	516
02ce10216orf7	009CP1	124	986	97	1189	26	517
02ce10809orf6	009CP1	130	992	103	1195	27	518
04ce11617orf27	001CP7	1087	1538	119	372	28	519
02ep30607orf27	009CP1	158	1020	120	1212	29	520
02ge20116orf25	009CP1	164	1026	125	1217	30	521
02ae21214orf1	010CP1	193	2106	129	1648	31	522
03ap21820orf4	009CP1	181	1043	139	1231	32	523
03ap21820orf8	009CP1	183	1045	141	1233	33	524
02ce10114orf3	010CP1	206	2119	142	1661	34	525
03ce21717orf1	009CP1	186	1048	144	1236	35	526
03gp20123orf3	009CP1	196	1058	152	1244	36	527
02ce10216orf4	010CP1	225	2138	152	1671	37	528
03xe11215orf7	009CP1	199	1061	154	1246	38	529
02ce11022orf2	010CP1	232	2145	159	1678	39	530
04ce11617orf16	009CP1	207	1069	161	1253	40	531
04ce11617orf26	009CP1	211	1073	162	1254	41	532
14ce21516orf1	001CP7	1306	1757	163	416	42	533
04ce11617orf4	009CP1	214	1076	164	1256	43	534
04ee70114orf10	001CP7	220	1082	169	1261	44	535
hp4e14535orf3	009CP1	1414	1865	181	434	45	536
04ge11713orf9	009CP1	246	1108	185	1277	46	537
04gp11213orf11	009CP1	247	1109	186	1278	47	538
04gp11213orf14	009CP1	248	1110	187	1279	48	539
04gp11213orf22	009CP1	249	1111	188	1280	49	540
04gp11803orf13	009CP1	254	1116	191	1283	50	541
05ae20220orf119	009CP1	263	1125	195	1287	51	542
05ae20220orf56	009CP1	270	1132	197	1289	52	543
05ae20220orf58	009CP1	271	1133	198	1290	53	544
05ae20220orf95	010CP1	280	1142	201	1293	54	545
02ep30607orf32	009CP1	297	2210	204	1723	55	546
05ap21216orf4	009CP1	290	1152	206	1298	56	547
05ce10420orf1	009CP1	291	1153	207	1299	57	548
05cp11911orf35	009CP1	297	1159	209	1301	58	549
05cp20518orf39	009CP1	305	1167	212	1304	59	550
05ee10411orf5	009CP1	308	1170	213	1305	60	551
05ep11717orf2	009CP1	314	1176	219	1311	61	552
05gp11901orf19	009CP1	324	1186	225	1317	62	553
05gp20111orf12	009CP1	326	1188	227	1319	63	554
05gp20111orf4	009CP1	328	1190	229	1321	64	555
05gp20111orf6	009CP1	329	1191	230	1322	65	556
06ce10808orf2	009CP1	343	1205	243	1335	66	557
06cp11118orf7	009CP1	352	1214	251	1343	67	558
06cp30603orf15	009CP1	364	1226	262	1354	68	559
06cp30603orf16	009CP1	365	1227	263	1355	69	560
06ep10306orf5	009CP1	373	1235	266	1358	70	561
06ep11108orf17	009CP1	378	1240	270	1362	71	562
06ge10115orf17	009CP1	386	1248	277	1369	72	563
06ge10115orf19	009CP1	387	1249	278	1370	73	564
06ge10115orf4	009CP1	388	1250	279	1371	74	565
07ap11111orf13	009CP1	408	1270	297	1389	75	566

07ee11519orf1	009CP1	422	1284	304	1396	76	567
07gp11807orf17	009CP1	448	1310	323	1415	77	568
07gp31516orf9	009CP1	453	1315	326	1418	78	569
09ap20802orf14	010CP1	465	1327	337	1429	79	570
05ap10914orf3	010CP1	569	2482	345	1864	80	571
05ce10613orf1	010CP1	586	2499	349	1868	81	572
05ce10613orf2	009CP1	587	2500	350	1869	82	573
09ge70821orf2	009CP1	491	1353	354	1446	83	574
11ap11902orf3	009CP1	497	1359	357	1449	84	575
11cp12006orf13	009CP1	521	1383	381	1473	85	576
11ee10423orf1	009CP1	530	1392	390	1482	86	577
11ee10423orf4	009CP1	531	1393	391	1483	87	578
11ge10309orf12	009CP1	534	1396	394	1486	88	579
11ge10309orf7	009CP1	551	1413	395	1487	89	580
12ap10324orf6	009CP1	565	1427	398	1490	90	581
12ge10305orf5	009CP1	573	1435	403	1495	91	582
13ae10511orf3	009CP1	587	1449	410	1502	92	583
13ae10712orf15	009CP1	592	1454	413	1505	93	584
13ap11517orf15	009CP1	599	1461	418	1510	94	585
13ee10216orf7	009CP1	610	1472	422	1514	95	586
13ep12003orf21	009CP1	625	1487	435	1527	96	587
14ae21813orf2	009CP1	630	1492	438	1530	97	588
14ce10720orf12	001CP6	631	1493	439	1531	98	589
02ep30607orf19	009CP1	1065	1516	440	1372	99	590
14ce10720orf3	009CP1	632	1494	440	1532	100	591
14cp10705orf4	009CP1	645	1507	447	1539	101	592
14ee10308orf1	009CP1	649	1511	451	1543	102	593
14ee10308orf4	010CP1	651	1513	452	1544	103	594
06cp11722orf11	009CP1	739	2652	454	1973	104	595
14ee11217orf2	009CP1	655	1517	456	1548	105	596
14ee11217orf3	010CP1	656	1518	457	1549	106	597
06cp11722orf5	009CP1	745	2658	460	1979	107	598
14ge10705orf14	009CP1	660	1522	461	1553	108	599
14gp11820orf1	001CP6	663	1525	464	1556	109	600
04ge11713orf35	010CP1	1098	1549	466	1398	110	601
06cp20302orf3	010CP1	751	2664	466	1985	111	602
06cp20302orf5	010CP1	752	2665	467	1986	112	603
06cp20302orf6	010CP1	753	2666	468	1987	113	604
06cp20302orf7	010CP1	754	2667	469	1988	114	605
06ee10207orf1	009CP1	763	2676	471	1990	115	606
29ge10307orf3	010CP1	679	1541	475	1567	116	607
06ee11611orf1	009CP1	770	2683	475	1994	117	608
29ge10307orf4	010CP1	680	1542	476	1568	118	609
06ep10306orf10	010CP1	773	2686	477	1996	119	610
06ep10306orf11	009CP1	774	2687	478	1997	120	611
hpl10523orf3	009CP1	687	1549	481	1573	121	612
hplp13852orf4	009CP1	700	1562	494	1586	122	613
hplp13852orf6	009CP1	701	1563	495	1587	123	614
hplp13852orf7	009CP1	702	1564	496	1588	124	615
hplp13947orf11	009CP1	708	1570	502	1594	125	616
hplp14013orf17	009CP1	715	1577	508	1600	126	617
hp2e10229orf2	009CP1	716	1578	509	1601	127	618

hp2e10229orf4	009CP1	717	1579	510	1602	128	619
hp2e10911orf24	010CP1	722	1584	515	1607	129	620
06gp10108orf2	001CP6	816	2729	516	2035	130	621
07ap11015orf2	009CP1	1167	1618	520	1452	131	622
hp2e11858orf6	001CP6	730	1592	520	1612	132	623
07ap11015orf4	009CP1	1168	1619	521	1453	133	624
hp2p10272orf1	009CP1	733	1595	522	1614	134	625
hp2p10625orf5	009CP1	742	1604	525	1617	135	626
hp2p10625orf6	009CP1	743	1605	526	1618	136	627
hp3e10349orf27	009CP1	751	1613	530	1622	137	628
hp3e11024orf34	009CP1	763	1625	539	1631	138	629
hp3e11024orf49	009CP1	767	1629	543	1635	139	630
hp3e11024orf5	009CP1	768	1630	544	1636	140	631
hp3e11075orf3	010CP1	773	1635	546	1638	141	632
07ap80601orf2	010CP1	863	2776	548	2067	142	633
07ce10203orf11	010CP1	871	2784	554	2073	143	634
07ce10203orf17	009CP1	873	2786	556	2075	144	635
hp3p11086orf1	010CP1	796	1658	561	1653	145	636
07ce11206orf1	009CP1	884	2797	567	2086	146	637
hp4p13446orf13	009CP1	808	1670	571	1663	147	638
11ce10917orf10	009CP1	498	1360	572	1504	148	639
hp4p13446orf3	009CP1	809	1671	572	1664	149	640
hp5e15211orf23	010CP1	827	1689	581	1673	150	641
07cp11213orf1	009CP1	905	2818	584	2103	151	642
hp5p15612orf2	009CP1	848	1710	594	1686	152	643
hp5p15641orf23	001CP6	851	1713	596	1688	153	644
12ap10324orf5	010CP1	1265	1716	598	1530	154	645
07ep30818orf4	009CP1	932	2845	600	2119	155	646
01ce11618orf11	009CP1	52	1965	607	1699	156	647
01ce11618orf22	009CP1	61	1974	608	1700	157	648
01ce11618orf27	009CP1	62	1975	609	1701	158	649
01ce11618orf7	009CP1	67	1980	610	1702	159	650
01ce11618orf9	009CP1	68	1981	611	1703	160	651
01cp11710orf16	009CP1	84	1997	612	1704	161	652
01cp11710orf18	009CP1	86	1999	613	1705	162	653
01cp11710orf5	009CP1	90	2003	615	1707	163	654
01cp11710orf6	009CP1	91	2004	616	1708	164	655
01cp11710orf9	009CP1	93	2006	617	1709	165	656
01ge10203orf14	009CP1	125	2038	618	1710	166	657
01ge10203orf6	009CP1	128	2041	619	1711	167	658
01ge10203orf7	009CP1	129	2042	620	1712	168	659
03ge10505orf2	009CP1	376	2289	644	1736	169	660
04ce11617orf10	001CP6	404	2317	645	1737	170	661
14gp12015orf13	001CP6	1330	1781	648	1580	171	662
14gp12015orf16	009CP1	1332	1783	650	1582	172	663
04ge11210orf1	009CP1	449	2362	651	1743	173	664
04ge11713orf10	009CP1	455	2368	653	1745	174	665
04ge11713orf28	009CP1	462	2375	655	1747	175	666
04ge11713orf36	010CP1	464	2377	656	1748	176	667
09ap11406orf2	009CP1	1014	2927	657	2176	177	668
04gp11213orf5	001CP6	487	2400	661	1753	178	669
29ge10111orf1	009CP1	1353	1804	669	1601	179	670

05ae20220orf37	001CP6	548	2461	675	1767	180	671
hp2e10911orf25	009CP1	1377	1828	686	1618	181	672
06ap10209orf1	009CP1	697	2610	690	1782	182	673
06ap10209orf4	009CP1	699	2612	691	1783	183	674
06ee10709orf2	009CP1	767	2680	695	1787	184	675
06ep10306orf1	009CP1	772	2685	696	1788	185	676
07cp10312orf5	009CP1	898	2811	703	1795	186	677
07cp21714orf1	009CP1	908	2821	706	1798	187	678
07cp21714orf3	009CP1	910	2823	708	1800	188	679
09ap20802orf13	009CP1	1025	2938	713	1805	189	680
09ap20802orf21	010CP1	1031	2944	714	1806	190	681
11ce10908orf1	001CP6	1100	3013	716	2235	191	682
hp4p11352orf9	009CP1	1419	1870	718	1650	192	683
11ge10309orf24	009CP1	1155	3068	725	1817	193	684
11ge10309orf28	009CP1	1157	3070	727	1819	194	685
11ge10309orf39	009CP1	1164	3077	731	1823	195	686
11ge10309orf4	009CP1	1165	3078	732	1824	196	687
11ge10309orf5	010CP1	1166	3079	733	1825	197	688
11cp12002orf3	009CP1	1129	3042	745	2264	198	689
13ae10610orf1	010CP1	1245	3158	747	1839	199	690
11ee10423orf2	009CP1	1137	3050	753	2272	200	691
14cp10119orf1	010CP1	1349	3262	758	1850	201	692
11ge10308orf1	009CP1	1145	3058	761	2280	202	693
14ee10308orf7	009CP1	1375	3288	762	1854	203	694
14ge10705orf3	009CP1	1411	3324	763	1855	204	695
hpl1e10506orf5	009CP1	1495	3408	766	1858	205	696
hp3p10807orf4	009CP1	1746	3659	775	1867	206	697
hp3p10807orf7	009CP1	1749	3662	776	1868	207	698
hp4e12063orf1	010CP1	1754	3667	777	1869	208	699
12ap10324orf8	009CP1	1200	3113	778	2297	209	700
hp4p11352orf5	010CP1	1783	3696	782	1874	210	701
12ge10610orf2	010CP1	1217	3130	784	2303	211	702
13ee12016orf7	010CP1	1312	3225	844	2363	212	703
14ee10419orf5	010CP1	1384	3297	898	2417	213	704
14ee11217orf4	010CP1	1390	3303	904	2423	214	705
14ee21118orf1	010CP1	1391	3304	905	2424	215	706
14ee21118orf2	010CP1	1392	3305	906	2425	216	707
14ep11115orf3	010CP1	1397	3310	911	2430	217	708
14ep11905orf13	010CP1	1400	3313	914	2433	218	709
14ep11905orf9	010CP1	1408	3321	922	2441	219	710
29ap10306orf3	010CP1	1462	3375	957	2476	220	711
29ap11902orf1	010CP1	1463	3376	958	2477	221	712
29ep20112orf2	010CP1	1469	3382	964	2483	222	713
29ge10111orf3	010CP1	1471	3384	966	2485	223	714
hpl1e10554orf1	010CP1	1500	3413	982	2501	224	715
hpl1p10543orf4	010CP1	1506	3419	988	2507	225	716
hpl1p13947orf10	010CP1	1552	3465	1025	2544	226	717
hp2e10911orf35	010CP1	1592	3505	1047	2566	227	718
hp3e10057orf3	010CP1	1617	3530	1062	2581	228	719
hp3e10128orf1	010CP1	1619	3532	1064	2583	229	720
hp3e10302orf17	010CP1	1627	3540	1072	2591	230	721
hp3e10302orf26	010CP1	1633	3546	1078	2597	231	722

hp3e11122orf3	010CP1	1693	3606	1127	2646	232	723
hp3p10156orf2	010CP1	1715	3628	1141	2660	233	724
hp3p10156orf3	010CP1	1716	3629	1142	2661	234	725
hp3p10156orf7	010CP1	1718	3631	1144	2663	235	726
hp3p10304orf2	010CP1	1724	3637	1148	2667	236	727
hp3p10807orf6	010CP1	1748	3661	1160	2679	237	728
hp3p11086orf2	010CP1	1753	3666	1164	2683	238	729
hp4e14535orf7	010CP1	1776	3689	1178	2697	239	730
hp4e14535orf8	010CP1	1777	3690	1179	2698	240	731
hp4p11393orf1	010CP1	1785	3698	1182	2701	241	732
hp4p11393orf2	010CP1	1786	3699	1183	2702	242	733
hp4p11393orf6	010CP1	1790	3703	1187	2706	243	734
hp4p12005orf2	010CP1	1792	3705	1189	2708	244	735
hp4p13446orf5	010CP1	1806	3719	1203	2722	245	736
hp5p15580orf1	010CP1	1889	3802	1258	2777	246	737
hp5p15653orf1	010CP1	1898	3811	1264	2783	247	738
hp5p15653orf2	010CP1	1899	3812	1265	2784	248	739
04ap20904orf3	010CP1	205	1067	1281	2800	249	740
06gp11920orf11	010CP1	398	1260	1288	2807	250	741
12ge20305orf26	010CP1	581	1443	1301	2820	251	742
13ee10216orf57	009CP1	609	1471	1303	2822	252	743
04cp11202_24256567_c3_117	009CP1			783	1715	253	744
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01ae12001_24218781_f2_18	009CP1			791	1883	255	746
01ge11619_23711062_c3_14	009CP1			795	1887	256	747
01gp11016_4103403_c2_13	009CP1			799	1891	257	748
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02ae11612_22477267_f2_27	009CP1			802	1894	259	750
02ae11612_23598175_f1_2	009CP1			803	1895	260	751
02ae11612_33203250_c1_51	009CP1			804	1896	261	752
02ge10116_36367936_c1_19	009CP1			807	1899	262	753
02ge11622_875260_f3_36	009CP1			809	1901	263	754
02gp20706_1203402_c3_58	009CP1			810	1902	264	755
02gp20706_15781452_c2_51	009CP1			813	1905	265	756
02gp20706_23632775_f3_32	009CP1			815	1907	266	757
02gp20706_23866562_c2_53	009CP1			816	1908	267	758
02gp20706_4892558_f3_19	009CP1			821	1913	268	759
02gp20814_24415958_f3_9	009CP1			824	1916	269	760
04cp11202_24261588_f2_23	010CP1			827	1919	270	761
07ap11015_23938312_f3_2	009CP1			831	1763	271	762
05ae30220_21619067_f3_56	009CP1			835	1927	272	763
07ap11213_35401528_c1_21	009CP1			835	1767	273	764
05ae30220_24882812_c3_103	009CP1			837	1929	274	765
05ae30220_25953163_c3_98	009CP1			839	1931	275	766
05ee10816_14649077_f3_18	009CP1			841	1933	276	767
05ee10816_4103408_f2_11	009CP1			843	1935	277	768
05ee10816_4687651_c1_22	009CP1			844	1936	278	769
06ap11119_16594193_f1_9	009CP1			845	1937	279	770
06ap20306_23437632_f3_9	009CP1			851	1943	280	771
06cp30603_23452_c3_80	009CP1			854	1946	281	772
06cp30603_23476568_c1_44	009CP1			855	1947	282	773
06cp30603_4689068_c3_79	009CP1			857	1949	283	774

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07ap20216_7227202_f3_10	009CP1		865	1957	285	776
07ep11916_5273452_c3_31	009CP1		866	1958	286	777
09cp11003_19532625_c3_17	009CP1		869	1961	287	778
09cp20502_24001388_c1_31	009CP1		871	1963	288	779
12gp31106_3024126_f2_25	009CP1		876	1968	289	780
13ae10712_14100018_f2_12	009CP1		879	1971	290	781
13ae10712_29569208_c2_27	009CP1		880	1972	291	782
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29ge30321_34157812_f3_10	009CP1		886	1978	293	784
hplp14013_11726503_c2_20	009CP1		888	1980	294	785
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hp2p10272_26829136_f1_1	009CP1		894	1986	296	787
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hp5p15641_21698387_c2_20	009CP1		904	1996	299	790
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hp6e10967_24882750_f2_7	009CP1		909	2001	301	792
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hp6e20339_1190660_c2_46	009CP1		913	2005	303	794
hp6e20339_21492187_c1_40	009CP1		914	2006	304	795
hp6e20339_34024187_c1_37	009CP1		916	2008	305	796
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01ge10203_860166_f3_9	009CP1		931	2023	307	798
01ge11619_13788141_c2_11	009CP1		932	2024	308	799
01ge11619_24415880_c2_12	009CP1		934	2026	309	800
01ge11619_24417813_c1_8	009CP1		935	2027	310	801
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02gp20706_20365905_f2_8	009CP1		947	2039	312	803
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04cp11202_19797128_f1_5	009CP1		956	2048	315	806
04cp11202_23553177_c1_75	009CP1		957	2049	316	807
04cp11202_23553177_c3_109	009CP1		958	2050	317	808
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04ge10816_33726080_c2_29	009CP1		964	2056	319	810
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05ae30220_9882767_f2_34	009CP1		978	2070	321	812
05cp21223_4725443_f3_14	009CP1		981	2073	322	813
05ee10816_259703_f2_7	009CP1		982	2074	323	814
06ap11119_24426508_f3_26	009CP1		984	2076	324	815
06ee10709_21675012_f1_2	009CP1		993	2085	325	816
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07ep11916_5913592_f3_18	009CP1		1006	2098	327	818
09cp11003_5945252_f2_4	009CP1		1013	2105	328	819
09ze10333_22460750_f2_6	009CP1		1014	2106	329	820
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14ap10221_13689381_c3_4	009CP1		1035	2127	331	822
29ep10720_24220926_f2_8	009CP1		1046	2138	332	823
29ep10720_24432762_c3_39	009CP1		1047	2139	333	824
29ge30321_12913562_f1_1	009CP1		1050	2142	334	825
29ge30321_135253_f2_6	009CP1		1051	2143	335	826

29ge30321_21673965_f2_7	009CP1		1052	2144	336	827
29ge30321_24336712_f1_5	009CP1		1053	2145	337	828
hp2p10272_22692325_f3_21	009CP1		1059	2151	338	829
hp2p10272_24406280_c1_26	009CP1		1060	2152	339	830
hp3p10807_29343768_f1_1	009CP1		1061	2153	340	831
hp3p10807_29352212_f2_5	009CP1		1062	2154	341	832
hp6e20339_24317062_c3_57	009CP1		1078	2170	342	833
hp6p10233_12273302_f1_1	009CP1		1087	2179	343	834
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07ap11213_35156577_c1_24	010CP1		1410	2929	345	836
07ap80601_976413_f3_9	010CP1		1414	2933	346	837
hp3p10807_189075_f2_4	010CP1		1464	2983	347	838
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06ep11917_24803153_c3_24					357	848
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02ae31010_35270000_f3_33					361	852
02ae31010_36132785_f2_29					362	853
02gel0116_15781452_c1_87					363	854
02gel0116_16803513_f2_34					364	855
02gel0116_16803513_f2_34					365	856
02gel0116_36367936_c1_92					366	857
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06ae11016_30579712_f2_21					369	860
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06ce20610_3913967_c3_36					371	862
06ce20610_4331338_f3_18					372	863
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06cp11217_19720300_f3_11					374	865
06cp11217_4881263_f2_9					375	866
06cp11217_4897077_f1_6					376	867
06cp30603_21492187_f2_41					377	868
06cp30603_34024187_f1_20					378	869
06cp30603_34024187_f1_20					379	870
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06ep10615_9842_f3_46					381	872
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06ep30223_4698838_f2_55					385	876
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06ep30223_5109443_c1_109					387	878

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09ce10413_5865665_f1_4						395	886
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09cp21607_7224187_c2_12						401	892
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09cp61003_19532625_c1_78						403	894
09cp61003_24063587_c1_74						404	895
09cp61003_24335762_c3_111						405	896
09cp61003_5945252_f1_5						406	897
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11ae80818_783127_c3_63						408	899
11ae80818_7952_c1_49						409	900
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11ap20714_5271967_c1_60						411	902
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14ee41924_23527267_c3_107						415	906
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hp5p15575_6140713_f2_18						426	917
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hp5p15641_24304527_c3_35						428	919
hp5p15641_25635452_c3_34						429	920
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hp3el1188_47327_f2_5						475	966
hp3el1188_5082842_f3_12						476	967
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hp5pl5641_30273312_c2_28						479	970
hp5pl5641_5211687_c2_29						480	971
hp6pl0590_30521093_f2_14						481	972
hp6pl0904_7089062_c1_16						482	973
hp6pl12129_16603417_f3_14						483	974
hp6pl12244_3948467_c1_52						484	975
hp6p22217_23470967_f1_4						485	976
hp7el10192_4412568_f2_5						486	977
hp7pl0287_24611325_c2_24						487	978
hp7pl0290_25548812_f3_14						488	979
hp7pl0290_25585941_f3_12						489	980
hp7pl0290_35156558_f3_15						490	981
hp7pl0290_4351718_f1_6						491	982

11ae11922_12586675_f2_1						983	1037
02ge10116_23866562_c3_146						984	1038
07ee11402_2458267_c3_108						985	1039
07ee50709_10213593_f3_77						986	1040
06ep10615_14649077_f2_30						987	1041
09cp10713_23452_c3_195						988	1042
11ap20714_7227202_f3_40						989	1043
01ce61016_23609580_c3_139						990	1044
06gp71906_3024126_c1_128						991	1045
06ge20501_14100018_c1_34						992	1046
09cp10713_34024187_f1_31						993	1047
hp4p62853_5914693_c3_52						994	1048
13ae10610_859692_c2_32						995	1049
13ae10610_35912_f2_3						996	1050
06ap11119_24426508_f3_27						997	1051
14gp11423_26803801_f3_7						998	1052
06ap10609_12586675_f2_19						999	1053
07ee50709_4818967_f2_43						1000	1054
02ap11117_23495187_c3_81						1001	1055
09cp10713_34024187_f1_31						1002	1056
07ee50709_35156577_f3_80						1003	1057
05ae30220_976413_c3_204						1004	1058
hp3e11188_47327_f2_9						1005	1059
12ap10324_4805318_f2_6						1006	1060
hp1e80523_23485968_c2_49						1007	1061
hp7e10192_25598277_c2_15						1008	1062
hp4e53394_26209843_c3_98						1009	1063
06ep10615_9842_f1_5						1010	1064
06ep30223_34409437_f2_64						1011	1065
06gp10409_3398427_f2_12						1012	1066
09ce10413_5865665_f1_4						1013	1067
09cp10224_1062966_c1_44						1014	1068
01ce61016_12931513_c2_106						1015	1069
01ce61016_23609580_c3_139						1016	1070
14cp11908_25593768_c3_97						1017	1071
14cp11908_783127_c1_72						1018	1072
07ee11402_10759567_c2_86						1019	1073
07ee50709_4818967_f2_43						1020	1074
hp4e13394_5088562_f3_54						1021	1075
hp4e13394_15828963_c2_90						1022	1076
hp4e53394_19720300_c3_98						1023	1077
07ce10312_4554652_f3_2						1024	1078
05ae30220_14350428_f3_91						1025	1079
hp8e10080_19546933_c2_88						1026	1080
01ce10320_30273587_f3_38						1027	1081
07ee50709_26438968_f2_36						1028	1082
05ep10815_4719175_c1_115						1029	1083
06ep30223_23476067_c1_115						1030	1084
hp7e10590_26172564_c1_68						1031	1085
05ae30220_4977193_c3_198						1032	1086
hp7e10557_21698387_f1_1						1033	1087
07ee11402_19565702_c2_88						1034	1088

07ee50709_960952_f2_47						1035	1089
hp6p12244_3948467_c3_88						1036	1090
hp7e10590_13073577_c3_107						1293	1296
01ce61016_492187_c3_120						1294	1297
06ep10615_961562_f1_15						1295	1298

EXEMPLIFICATION

5 I. Cloning and Sequencing of *H. pylori* DNA

H. pylori chromosomal DNA was isolated according to a basic DNA protocol outlined in Schleif R.F. and Wensink P.C., *Practical Methods in Molecular Biology*, p.98, Springer-Verlag, NY., 1981, with minor modifications. Briefly, cells were pelleted, resuspended in TE (10 mM Tris, 1 mM EDTA, pH 7.6) and GES lysis buffer (5.1 M guanidium thiocyanate, 0.1 M EDTA, pH 8.0, 0.5% N-laurylsarcosine) was added. Suspension was chilled and ammonium acetate (NH₄Ac) was added to final concentration of 2.0 M. DNA was extracted, first with chloroform, then with phenol-chloroform, and reextracted with chloroform. DNA was precipitated with isopropanol, washed twice with 70% EtOH, dried and resuspended in TE.

15 Following isolation whole genomic *H. pylori* DNA was nebulized (Bodenteich et al., *Automated DNA Sequencing and Analysis* (J.C. Venter, ed.), Academic Press, 1994) to a median size of 2000 bp. After nebulization, the DNA was concentrated and separated on a standard 1% agarose gel. Several fractions, corresponding to approximate sizes 900-1300 bp, 1300-1700 bp, 1700-2200 bp, 2200-2700 bp, were excised from the gel and purified by the GeneClean procedure (Bio101, Inc.).

20 The purified DNA fragments were then blunt-ended using T4 DNA polymerase. The healed DNA was then ligated to unique BstXI-linker adopters in 100-1000 fold molar excess. These linkers are complimentary to the BstXI-cut pMPX vectors, while the overhang is not self-complimentary. Therefore, the linkers will not concatemerize nor will the cut-vector religate itself easily. The linker-adopted inserts were separated from the unincorporated linkers on a 1% agarose gel and purified using GeneClean. The linker-adopted inserts were then ligated to each of the 20 pMPX vectors to construct a series of "shotgun" subclone libraries. The vectors contain an out-of-frame lacZ gene at the cloning site which becomes in-frame in the event that an adapter-dimer is cloned, allowing these to be avoided by their blue-color.

30 All subsequent steps were based on the multiplex DNA sequencing protocols outlined in Church G.M. and Kieffer-Higgins S., *Science* 240:185-188, 1988. Only major modifications to the protocols are highlighted. Briefly, each of the 20 vectors was

then transformed into DH5 α competent cells (Gibco/BRL, DH5 α transformation protocol). The libraries were assessed by plating onto antibiotic plates containing ampicillin, methicillin and IPTG/Xgal. The plates were incubated overnight at 37°C. Successful transformants were then used for plating of clones and pooling into the
5 multiplex pools. The clones were picked and pooled into 40 ml growth medium cultures. The cultures were grown overnight at 37°C. DNA was purified using the Qiagen Midi-prep kits and Tip-100 columns (Qiagen, Inc.). In this manner, 100 μ g of DNA was obtained per pool. 15 96-well plates of DNA were generated to obtain a 5-10 fold sequence redundancy with 250-300 base average read-lengths.

10 These purified DNA samples were then sequenced using the multiplex DNA sequencing based on chemical degradation methods (Church G.M. and Kieffer-Higgins S., *Science* 240:185-188, 1988) or by Sequithrem (Epicenter Technologies) dideoxy sequencing protocols. The sequencing reactions were electrophoresed and transferred onto nylon membranes by direct transfer electrophoresis from 40 cm gels (Richterich P.
15 and Church G.M., *Methods in Enzymology* 218:187-222, 1993) or by electroblotting (Church, *supra*). 24 samples were run per gel. 45 successful membranes were produced by chemical sequencing and 8 were produced by dideoxy sequencing. The DNA was covalently bound to the membranes by exposure to ultraviolet light, and hybridized with labeled oligonucleotides complimentary to tag sequences on the vectors (Church, *supra*).
20 The membranes were washed to rinse off non-specifically bound probe, and exposed to X-ray film to visualize individual sequence ladders. After autoradiography, the hybridized probe was removed by incubation at 65° C, and the hybridization cycle repeated with another tag sequence until the membrane has been probed 38 times for chemical sequencing membranes and 10 times for the dideoxy sequencing membranes.
25 Thus, each gel produced a large number of films, each containing new sequencing information. Whenever a new blot was processed, it was initially probed for an internal standard sequence added to each of the pools.

Digital images of the films were generated using a laser-scanning densitometer (Molecular Dynamics, Sunnyvale, CA). The digitized images were processed on
30 computer workstations (VaxStation 4000's) using the program REPLICATM (Church et al., *Automated DNA Sequencing and Analysis* (J.C. Venter, ed.), Academic Press, 1994). Image processing included lane straightening, contrast adjustment to smooth out intensity differences, and resolution enhancement by iterative gaussian deconvolution. The sequences were then automatically picked in REPLICATM and displayed for
35 interactive proofreading before being stored in a project database. The proofreading was accomplished by a quick visual scan of the film image followed by mouse clicks on the

bands of the displayed image to modify the base calls. For typical sequences derived by chemical sequencing, the error rate of the REPLICA™ base calling software was 2-5% with most errors occurring near the end of a sequence read. Many of the sequence errors could be detected and corrected because multiple sequence reads covering the same
5 portion of the genomic DNA provide adequate sequence redundancy for editing. Each sequence automatically received a number correspond to (microtiter plate and probe information) and lane set number (corresponding to microtiter plate columns). This number serves as a permanent identifier of the sequence so it is always possible to identify the original of any particular sequence without recourse to a specialized
10 database.

Routine assembly of *H. pylori* sequences was done using the program FALCON (Church, Church et al., *Automated DNA Sequencing and Analysis* (J.C. Venter, ed.), Academic Press, 1994). This program has proven to be fast and reliable for most sequences. The assembled contigs were displayed using a modified version of
15 GelAssemble, developed by the Genetics Computer Group (GCG) (Devereux et al., *Nucleic Acid Res.* 12:387-95, 1984) that interacts with REPLICA™. This provided for an integrated editor that allows multiple sequence gel images to be instantaneously called up from the REPLICA™ database and displayed to allow rapid scanning of contigs and proofreading of gel traces where discrepancies occurred between different
20 sequence reads in the assembly.

II. Identification, Cloning and Expression of *H. pylori* Nucleic Acids

Expression and purification of the *H. pylori* polypeptides of the invention can be performed essentially as outlined below.

25 To facilitate the cloning, expression and purification of membrane and secreted proteins from *H. pylori*, a gene expression system, such as the pET System (Novagen), for cloning and expression of recombinant proteins in *E. coli*, is selected. Also, a DNA sequence encoding a peptide tag, the His-Tag, is fused to the 3' end of DNA sequences of interest in order to facilitate purification of the recombinant protein products. The 3'
30 end is selected for fusion in order to avoid alteration of any 5' terminal signal sequence. The exception to the above is ppiB, a gene cloned for use as a control in the expression studies. The sequence for *H. pylori* ppiB contains a DNA sequence encoding a His-Tag fused to the 5' end of the full length gene, because the protein product of this gene does not contain a signal sequence and is expressed as a cytosolic protein.

*PCR Amplification and Cloning of Nucleic Acids Containing ORF's for
Membrane and Secreted Polypeptides from H. pylori*

- Nucleic acids chosen (for example, from the nucleic acids set forth in the Sequence Listing) for cloning from the J99 strain of *H. pylori* are prepared for
- 5 amplification cloning by polymerase chain reaction (PCR). Synthetic oligonucleotide primers specific for the 5' and 3' ends of open reading frames (ORFs) are designed and purchased from GibcoBRL Life Technologies (Gaithersburg, MD, USA). All forward primers (specific for the 5' end of the sequence) are designed to include an NcoI cloning site at the extreme 5' terminus. These primers are designed to permit initiation of
- 10 protein translation at a methionine residue followed by a valine residue and the coding sequence for the remainder of the native *H. pylori* DNA sequence. All reverse primers (specific for the 3' end of any *H. pylori* ORF) include a EcoRI site at the extreme 5' terminus to permit cloning of each *H. pylori* sequence into the reading frame of the pET-28b. The pET-28b vector provides sequence encoding an additional 20 carboxy-
- 15 terminal amino acids including six histidine residues (at the extreme C-terminus), which comprise the His-Tag. An exception to the above, as noted earlier, is the vector construction for the ppiB gene. A synthetic oligonucleotide primer specific for the 5' end of ppiB gene encodes a BamHI site at its extreme 5' terminus and the primer for the 3' end of the ppiB gene encodes a XhoI site at its extreme 5' terminus.
- 20 Genomic DNA prepared from the J99 strain of *H. pylori* is used as the source of template DNA for PCR amplification reactions (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). To amplify a DNA sequence containing an *H. pylori* ORF, genomic DNA (50 nanograms) is introduced into a reaction vial containing 2 mM MgCl₂, 1 micromolar synthetic oligonucleotide primers
- 25 (forward and reverse primers) complementary to and flanking a defined *H. pylori* ORF, 0.2 mM of each deoxynucleotide triphosphate; dATP, dGTP, dCTP, dTTP and 2.5 units of heat stable DNA polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume of 100 microliters.
- 30 Upon completion of thermal cycling reactions, each sample of amplified DNA is washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA). All amplified DNA samples are subjected to digestion with the restriction endonucleases, e.g., NcoI and EcoRI (New England BioLabs, Beverly, MA, USA)(Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). DNA samples are then subjected to electrophoresis on 1.0 %
- 35 NuSeive (FMC BioProducts, Rockland, ME USA) agarose gels. DNA is visualized by exposure to ethidium bromide and long wave uv irradiation. DNA contained in slices

isolated from the agarose gel is purified using the Bio 101 GeneClean Kit protocol (Bio 101 Vista, CA, USA)

Cloning of H. pylori Nucleic Acids Into an Expression Vector

The pET-28b vector is prepared for cloning by digestion with endonucleases, e.g., NcoI and EcoRI (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). In the case of cloning ppiB, the pET-28a vector, which encodes a His-Tag that can be fused to the 5' end of an inserted gene, is used and the cloning site prepared for cloning with the ppiB gene by digestion with BamHI and XhoI restriction endonucleases.

Following digestion, DNA inserts are cloned (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) into the previously digested pET-28b expression vector, except for the amplified insert for ppiB, which is cloned into the pET-28a expression vector. Products of the ligation reaction are then used to transform the BL21 strain of *E. coli* (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) as described below.

Transformation Of Competent Bacteria With Recombinant Plasmids

Competent bacteria, *E. coli* strain BL21 or *E. coli* strain BL21(DE3), are transformed with recombinant pET expression plasmids carrying the cloned *H. pylori* sequences according to standard methods (Current Protocols in Molecular, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). Briefly, 1 microliter of ligation reaction is mixed with 50 microliters of electrocompetent cells and subjected to a high voltage pulse, after which, samples are incubated in 0.45 milliliters SOC medium (0.5% yeast extract, 2.0 % tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄ and 20, mM glucose) at 37°C with shaking for 1 hour. Samples are then spread on LB agar plates containing 25 microgram/ml kanamycin sulfate for growth overnight. Transformed colonies of BL21 are then picked and analyzed to evaluate cloned inserts as described below.

Identification Of Recombinant Expression Vectors With H. Pylori Nucleic Acids

Individual BL21 clones transformed with recombinant pET-28b-H.pylori ORFs are analyzed by PCR amplification of the cloned inserts using the same forward and reverse primers, specific for each *H. pylori* sequence, that were used in the original PCR amplification cloning reactions. Successful amplification verifies the integration of the *H. pylori* sequences in the expression vector (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994).

Isolation and Preparation of Nucleic Acids From Transformants

Individual clones of recombinant pET-28b vectors carrying properly cloned *H. pylori* ORFs are picked and incubated in 5 mls of LB broth plus 25 microgram/ml kanamycin sulfate overnight. The following day plasmid DNA is isolated and purified
5 using the Qiagen plasmid purification protocol (Qiagen Inc., Chatsworth, CA, USA).

Expression Of Recombinant H. Pylori Sequences In E. coli

The pET vector can be propagated in any *E. coli* K-12 strain e.g. HMS174, HB101, JM109, DH5, etc. for the purpose of cloning or plasmid preparation. Hosts for expression include *E. coli* strains containing a chromosomal copy of the gene for T7
10 RNA polymerase. These hosts are lysogens of bacteriophage DE3, a lambda derivative that carries the lacI gene, the lacUV5 promoter and the gene for T7 RNA polymerase. T7 RNA polymerase is induced by addition of isopropyl-B-D-thiogalactoside (IPTG), and the T7 RNA polymerase transcribes any target plasmid, such as pET-28b, carrying its gene of interest. Strains used include: BL21(DE3) (Studier, F.W., Rosenberg, A.H.,
15 Dunn, J.J., and Dubendorff, J.W. (1990) Meth. Enzymol. 185, 60-89).

To express recombinant *H. pylori* sequences, 50 nanograms of plasmid DNA isolated as described above is used to transform competent BL21(DE3) bacteria as described above (provided by Novagen as part of the pET expression system kit). The lacZ gene (beta-galactosidase) is expressed in the pET-System as described for the *H.*
20 *pylori* recombinant constructions. Transformed cells are cultured in SOC medium for 1 hour, and the culture is then plated on LB plates containing 25 micrograms/ml kanamycin sulfate. The following day, bacterial colonies are pooled and grown in LB medium containing kanamycin sulfate (25 micrograms/ml) to an optical density at 600 nM of 0.5 to 1.0 O.D. units, at which point, 1 millimolar IPTG was added to the culture
25 for 3 hours to induce gene expression of the *H. pylori* recombinant DNA constructions.

After induction of gene expression with IPTG, bacteria are pelleted by centrifugation in a Sorvall RC-3B centrifuge at 3500 x g for 15 minutes at 4°C. Pellets are resuspended in 50 milliliters of cold 10 mM Tris-HCl, pH 8.0, 0.1 M NaCl and 0.1 mM EDTA (STE buffer). Cells are then centrifuged at 2000 x g for 20 min at 4°C. Wet
30 pellets are weighed and frozen at -80°C until ready for protein purification.

III. Purification Of Recombinant Proteins From E. Coli

Analytical Methods

The concentrations of purified protein preparations are quantified
35 spectrophotometrically using absorbance coefficients calculated from amino acid content (Perkins, S.J. 1986 Eur. J. Biochem. 157, 169-180). Protein concentrations are

also measured by the method of Bradford, M.M. (1976) Anal. Biochem. 72, 248-254, and Lowry, O.H., Rosebrough, N., Farr, A.L. & Randall, R.J. (1951) J. Biol. Chem. 193, pages 265-275, using bovine serum albumin as a standard.

SDS-polyacrylamide gels (12% or 4.0 to 25 % acrylamide gradient gels) are purchased from BioRad (Hercules, CA, USA), and stained with Coomassie blue. Molecular weight markers include rabbit skeletal muscle myosin (200 kDa), *E. coli* (-galactosidase (116 kDa), rabbit muscle phosphorylase B (97.4 kDa), bovine serum albumin (66.2 kDa), ovalbumin (45 kDa), bovine carbonic anhydrase (31 kDa), soybean trypsin inhibitor (21.5 kDa), egg white lysozyme (14.4 kDa) and bovine aprotinin (6.5 kDa).

1. Purification of soluble proteins

All steps are carried out at 4°C. Frozen cells are thawed, resuspended in 5 volumes of lysis buffer (20 mM Tris, pH 7.9, 0.5 M NaCl, 5 mM imidazole with 10% glycerol, 0.1 % -mercaptoethanol, 200 (g/ ml lysozyme, 1 mM phenylmethylsulfonyl fluoride (PMSF), and 10 ug/ml each of leupeptin, aprotinin, pepstatin, L-1-chloro-3-[4-tosylamido]-7-amino-2-heptanone (TLCK), L-1-chloro-3-[4-tosylamido]-4-phenyl-2-butanone (TPCK), and soybean trypsin inhibitor, and ruptured by several passages through a small volume microfluidizer (Model M-110S, Microfluidics International Corporation, Newton, MA). The resultant homogenate is made 0.1 % Brij 35, and centrifuged at 100,000 x g for 1 hour to yield a clear supernatant (crude extract).

Following filtration through a 0.8 (m Supor filter (Gelman Sciences, FRG) the crude extract is loaded directly onto a Ni²⁺- nitrotriacetate-agarose (NTA) with a 5 milliliter bed volume (Hochuli, E., Dbeli, H., and Schacheer, A. (1987) J. Chromatography 411, 177-184) pre-equilibrated in lysis buffer containing 10 % glycerol, 0.1 % Brij 35 and 1 mM PMSF. The column is washed with 250 ml (50 bed volumes) of lysis buffer containing 10 % glycerol, 0.1 % Brij 35, and are eluted with sequential steps of lysis buffer containing 10 % glycerol, 0.05 % Brij 35, 1 mM PMSF, and: either 20, 100, 200, or 500 mM imidazole. Fractions are monitored by absorbance at OD₂₈₀ nm, and peak fractions are analyzed by SDS-PAGE.

2. Purification of insoluble proteins from inclusion bodies

The following steps are carried out at 4°C. Cell pellets are resuspended in lysis buffer with 10% glycerol 200 (g/ ml lysozyme, 5 mM EDTA, 1mM PMSF and 0.1 % -mercaptoethanol. After passage through the cell disrupter, the resulting homogenate is made 0.2 % deoxycholate, stirred 10 minutes, then centrifuged at 20,000 x g, for 30 min. The pellets are washed with lysis buffer containing 10 % glycerol, 10 mM EDTA, 1% Triton X-100, 1 mM PMSF and 0.1% -mercaptoethanol, followed by several washes

with lysis buffer containing 1 M urea, 1 mM PMSF and 0.1 % -mercaptoethanol. The resulting white pellet is composed primarily of inclusion bodies, free of unbroken cells and membranous materials.

Dialysis and concentration of protein samples

5 Urea is removed slowly from the protein samples by dialysis against Tris-buffered saline (TBS; 10 mM Tris pH 8.0, 150 mM NaCl) containing 0.5 % deoxycholate (DOC) with sequential reduction in urea as follows; 6M, 4M, 3M, 2M, 1M, 0.5 M and finally TBS without any urea. Each dialysis step is conducted for a minimum of 4 hours at room temperature.

10 After dialysis, samples are concentrated by pressure filtration using Amicon stirred-cells. Protein concentrations are measured using the methods of Perkins (1986 Eur. J. Biochem. 157, 169-180), Bradford ((1976) Anal. Biochem. 72, 248-254) and Lowry ((1951) J. Biol. Chem. 193, pages 265-275).

15 IV. Assessment Of The Antigenicity Of Outer Membrane Localized Antigens Of *H. pylori*

Purification of outer membranes from *H. pylori* can be performed by essentially following the protocol outlined below.

20 *H. pylori* strains J99 (ATCC# 55679) and Ah244 are grown on chocolate blood agar containing 5% (vol/vol) horse blood, at 37°C in an atmosphere containing 10% CO₂ for 48 h. Bacteria were harvested by suspension in 20 mM Tris, pH 7.5. The cells are collected by centrifugation at 12,000 Xg, for 20 min at 4°C and washed 3 times with 20 mM Tris, pH 7.5. Cells are suspended in 20 mM Tris, pH 7.5 and broken by sonication on ice (eight bursts of 30 s at 60 watts with 60 s pauses between bursts).

25 DNase (0.1 mg) and RNase (0.5 mg) are added to the cell suspension, and the mixture is incubated for 30 minutes at room temperature. The cell suspension is centrifuged at 12,000 Xg for 20 min, at 4°C. The supernatant was retained and centrifuged again. Total membranes are collected from the supernatant by centrifugation at 40,000 Xg for 30 minute, at 4°C. The pellet are washed twice in 20 mM Tris, pH 7.5. The protein

30 content is assayed using the Bradford protein assay, with bovine serum albumin (BSA) as a standard. The suspension is then adjusted to 1 mg protein /ml. The solubilization of the membranes is realized by adding N-lauryl-sarcosine to this suspension in a ratio of 6 mg of N-lauryl-sarcosine per mg of protein. The suspension is incubated for 30 minutes at room temperature in presence of N-lauryl-sarcosine. Outer membranes are

35 collected by centrifugation at 40,000 Xg for 30 minutes at 4°C. The pellet is washed 3 times with Milli Q quality water, aliquoted and stored at -20°C until use.

Identification Of Outer Membrane Antigens of H. pylori

Outer membrane antigens can be identified using a protocol outlined below.

Proteins are separated on sodium dodecylsulfate polyacrylamide gels (SDS-PAGE) according to the method described by Laemmli, U.K. (1970) Nature (London) Volume 227, 680-685. Samples are prepared by suspension in standard treatment buffer and heated at 100°C for 10 min. Approximately 1-5 mg of protein is loaded per well on 8X10 cm minigels (0.75 mm). The separated proteins are then transferred to PVDF membranes as described below.

Electroblotting of separated proteins to PVDF membranes is performed in a Bio Rad Mini-Trans Blot Electrophoretic Transfer cell. The PVDF membrane Immobilon-PSQ is employed. Electroblotting is carried out for 60 min at 50V using CAPS transfer buffer (10mM 3-[Cyclohexylamino]-1-propanesulfonic acid, 10% methanol). The membrane is stained with 0.2% Ponceau S and destained with Milli Q quality water.

Antigens within the preparation are then identified using western immunoblotting. After electroblotting, non specific binding sites of the PVDF membrane are blocked with 5% non fat dry milk in 10 mM Tris-HCl-0.9% NaCl, pH 7.5. The membrane is incubated with a appropriate dilution of normal mouse serum in 10 mM Tris-HCl-0.9% NaCl-0.5% Tween 20-0.5% BSA, pH 7.5, for 2 h at 37°C and then washed three times with 10 mM Tris-HCl-0.9% NaCl-0.5% Tween 20, pH 7.5 (TTBS). Alkaline phosphatase conjugated anti-mouse Ig, from goat is then added in 10 mM Tris-HCl-0.9% NaCl-0.5% Tween 20-0.5% BSA, pH 7.5 and incubated for 1h at room temperature. After this incubation, the membrane is washed three times in TTBS. The reactive bands are revealed using 5-bromo-4-chloro-3-indolyl phosphate (Bio-Rad) as the Alkaline phosphatase substrate and Nitro Blue Tetrazolium (Bio-Rad) as the color development reagent.

For amino acid microsequencing, proteins that are identified as immunoreactive are cut from a fresh unreacted immobilon membranes and microsequenced at the Worcester Foundation microsequencing facility. Membranes from which the protein bands are cut are then subjected to western immunoblot as described above to confirm that the appropriate band had been excised.

V. Analysis Of *H. Pylori* Proteins As Vaccine Candidates

To investigate the immunomodulatory effect of *H. pylori* proteins, a mouse/*H. pylori* model was used. This model mimics the human *H. pylori* infection in many respects. The focus is on the effect of oral immunization in *H. pylori* infected animals in order to test the concept of therapeutic oral immunotherapy.

Animals

Female SPF BALB/c mice were purchased from Bomholt Breeding center (Denmark). They were kept in ordinary makrolon cages with free supply of water and food. The animals were 4-6 weeks old at arrival.

5 *Infection*

After a minimum of one week of acclimatization, the animals were infected with a type 2 strain (VacA negative) of *H. pylori* (strain 244, originally isolated from an ulcer patient). In our hands, this strain has earlier proven to be a good colonizer of the mouse stomach. The bacteria were grown overnight in Brucella broth supplemented with 10 % fetal calf serum, at 37°C in a microaerophilic atmosphere (10% CO₂, 5% O₂). The animals were given an oral dose of omeprazole (400 µmol/kg) and 3-5 h after this an oral inoculation of *H. pylori* in broth (approximately 10⁸ cfu/animal). Positive take of the infection was checked in some animals 2-3 weeks after the inoculation.

Antigens

15 Recombinant *H. pylori* antigens were chosen based on their association with externally exposed *H. pylori* cell membrane. These antigens were selected from the following groups: (1.) Outer Membrane Proteins; (2.) Periplastic/Secreted proteins; (3.) Outer Surface proteins; and (4.) Inner Membrane proteins. All recombinant proteins were constructed with a hexa-HIS tag for purification reasons and the non-*Helicobacter* *pylori* control protein (β-galactosidase from *E. coli*; LacZ), was constructed in the same way.

All antigens were given in a soluble form, i.e. dissolved in either a HEPES buffer or in a buffer containing 0.5% Deoxycholate (DOC).

The antigens are listed in Table 8 below.

25

Table 8

Helicobacter pylori proteins

Outer membrane Proteins

30

Protein 1

Protein 2

Protein 3

Protein 4

Protein 5

35

Periplastic/Secreted proteins

Protein 6

Other cell envelope proteins

40

Protein 7

Protein 8

Flagella-associated proteins

Protein 9

Control proteins

5 β -galactosidase (LacZ)

Immunizations

Ten animals in each group were immunized 4 times over a 34 day period (day 1, 15, 25 and 35). Purified antigens in solution or suspension were given at a dose of 100 μ g/mouse. As an adjuvant, the animals were also given 10 μ g/mouse of Cholera toxin (CT) with each immunization. Omeprazole (400 μ mol/kg) was given orally to the animals 3-5 h prior to immunization as a way of protecting the antigens from acid degradation. Infected control animals received HEPES buffer + CT or DOC buffer + CT. Animals were sacrificed 2-4 weeks after final immunization. A general outline of the study is shown in Table 9 below.

Table 9

Study outline, therapeutic immunization:

20 Mice were all infected with *H. pylori* strain Ah244 at day 30.

<u>Substance</u>		<u>Mouse strain</u> n=10	<u>Dose/mouse</u>	<u>Dates for dosing</u>
25	1. Controls, PBS	Balb/c	0.3 ml	0, 14, 24, 34
	2. Cholera toxin, 10 μ g	Balb/c	0.3 ml	0, 14, 24, 34
	3. Protein 1, 100 μ g + CT 10 μ g	Balb/c	0.3 ml	0, 14, 24, 34
	4. Protein 5, 100 μ g + CT 10 μ g	Balb/c	0.3 ml	0, 14, 24, 34
	5. Protein 10, 100 μ g + CT 10 μ g	Balb/c	0.3 ml	0, 14, 24, 34
30	6. Protein 9, 100 μ g + CT 10 μ g	Balb/c	0.3 ml	0, 14, 24, 34
	7. Protein 2, 100 μ g + CT 10 μ g	Balb/c	0.3 ml	0, 14, 24, 34
	8. Protein 6, 100 μ g + CT 10 μ g	Balb/c	0.3 ml	0, 14, 24, 34
	9. Protein 4, 100 μ g + CT 10 μ g	Balb/c	0.3 ml	0, 14, 24, 34
	10. Protein 7, 100 μ g + CT 10 μ g	Balb/c	0.3 ml	0, 14, 24, 34
35	11. Protein 8, 100 μ g + CT 10 μ g	Balb/c	0.3 ml	0, 14, 24, 34
	12. Protein 3, 100 μ g + CT 10 μ g	Balb/c	0.3 ml	0, 14, 24, 34

Analysis of infection

Mucosal infection: The mice were sacrificed by CO₂ and cervical dislocation. The abdomen was opened and the stomach removed. After cutting the stomach along the greater curvature, it was rinsed in saline. The mucosa from the antrum and corpus of an area of 25mm² was scraped separately with a surgical scalpel. The mucosa scraping was suspended in Brucella broth and plated onto Blood Skirrow selective plates. The

plates were incubated under microaerophilic conditions for 3-5 days and the number of colonies was counted. The identity of *H. pylori* was ascertained by urease and catalase test and by direct microscopy or Gram staining.

The urease test was performed essentially as follows. The reagent, Urea Agar
5 Base Concentrate, was purchased from DIFCO Laboratories, Detroit, MI (Catalog # 0284-61-3). Urea agar base concentrate was diluted 1:10 with water. 1 ml of if the diluted concentrate was mixed with 100-200 μ l of actively growing *H. pylori* cells. Color change to magenta indicated that cells were urease positive.

The catalase test was performed essentially as follows. The reagent, N,N,N',N'-
10 Tetramethyl-p-Phenylenediamine, was purchased from Sigma, St. Louis, MO (Catalog # T3134). A solution of the reagent (1% w/v in water) was prepared. *H. pylori* cells were swabbed onto Whatman filter paper and overlaid with the 1% solution. Color change to dark blue indicated that the cells were catalase positive.

Serum antibodies: From all mice serum was prepared from blood drawn by heart
15 puncture. Serum antibodies were identified by regular ELISA techniques, where the specific antigens of *Helicobacter pylori* were plated.

Mucosal antibodies: Gentle scrapings of a defined part of the corpus and of 4 cm
of duodenum were performed in 50% of the mice in order to detect the presence of antibodies in the mucous. The antibody titers were determined by regular ELISA
20 technique as for serum antibodies.

Statistical analysis: Wilcoxon-Mann-Whitney sign rank test was used for
determination of significant effects of the antigens on *Helicobacter pylori* colonization. $P < 0.05$ was considered significant. Because the antrum is the major colonization site for
25 *Helicobacter* most emphasis was put upon changes in the antral colonization.

Results

Antibodies in sera: All antigens tested given together with CT gave rise to a
measurable specific titer in serum. The highest responses were seen with Proteins 3, 4,
9, 1, and 7 (see Figure 1).

30 Antibodies in mucus: In the mucus scrapings, specific antibodies against all antigens tested were seen. By far the strongest response was seen with Protein 6, followed by 1, 3, and 9 (see Figure 2).

Therapeutic immunization effects:

All control animals (BALB/c mice) were well colonized with *H. pylori* (strain
35 AH244) in both antrum and corpus of the stomach. Of the antigens tested 3 proteins (Proteins 4, 7, and 1) gave a good and significant reduction and/or eradication of the *H.*

pylori infection. The degree of colonization of the antrum was lower following immunization with Proteins 8, 9, and 3 compared to control. The effect of Proteins 5, 2, and 6 did not differ from control. The control protein lacZ, i.e. the non-*H. pylori* protein, had no eradication effect and in fact had higher *Helicobacter* colonization compared to the HEPES + CT control. All data are shown in Figures 3 and 4 for proteins dissolved in HEPES and DOC respectively. Data is shown as geometric mean values. n=8-10 Wilcoxon-Mann-Whitney sign rank test * = p<0.05; x/10 = number of mice showing eradication of *H. pylori* over the total number of mice examined.

The data presented indicate that all of the *H. pylori* associated proteins included in this study, when used as oral immunogens in conjunction with the oral adjuvant CT, resulted in stimulation of an immune response as measured by specific serum and mucosal antibodies. A majority of the proteins led to a reduction, and in some cases complete clearance of the colonization of *H. pylori* in this animal model. It should be noted that the reduction or clearance was due to heterologous protection rather than homologous protection (the polypeptides were based on the *H. pylori* J99 strain sequence and used in the therapeutic immunization studies against a different (AH244) challenge strain), indicating the vaccine potential against a wide variety of *H. pylori* strains.

The highest colonization in the antrum was seen in animals treated with the non-*Helicobacter* protein LacZ, indicating that the effects seen with the *Helicobacter pylori* antigens were specific.

Taken together these data strongly support the use of these *H. pylori* proteins in a pharmaceutical formulation for the use in humans to treat and/or prevent *H. pylori* infections.

VI. Sequence Variance Analysis of genes in *Helicobacter pylori* strains

Four genes were cloned and sequenced from several strains of *H. pylori* to compare the DNA and deduced amino acid sequences. This information was used to determine the sequence variation between the *H. pylori* strain, J99, and other *H. pylori* strains isolated from human patients.

Preparation of Chromosomal DNA.

Cultures of *H. pylori* strains (as listed in Table 12) were grown in BLBB (1% Tryptone, 1% Peptamin 0.1% Glucose, 0.2% Yeast Extract 0.5% Sodium Chloride, 5% Fetal Bovine Serum) to an OD₆₀₀ of 0.2. Cells were centrifuged in a Sorvall RC-3B at 3500 x g at 4°C for 15 minutes and the pellet resuspended in 0.95 mls of 10 mM Tris-HCl, 0.1 mM EDTA (TE). Lysozyme was added to a final concentration of 1mg/ml

- 101 -

along with, SDS to 1% and RNase A + T1 to 0.5mg/ml and 5 units/ml respectively, and incubated at 37°C for one hour. Proteinase K was then added to a final concentration of 0.4mg/ml and the sample was incubated at 55 C for more than one hour. NaCl was added to the sample to a concentration of 0.65 M, mixed carefully, and 0.15 ml of 10% CTAB in 0.7M NaCL (final is 1% CTAB/70mM NaCL) was added followed by incubation at 65°C for 20 minutes. At this point, the samples were extracted with chloroform:isoamyl alcohol, extracted with phenol, and extracted again with chloroform:isoamyl alcohol. DNA was precipitated with either EtOH (1.5 x volumes) or isopropanol (0.6 x volumes) at -70°C for 10minutes, washed in 70% EtOH and resuspended in TE.

PCR Amplification and cloning.

Genomic DNA prepared from twelve strains of *Helicobacter pylori* was used as the source of template DNA for PCR amplification reactions (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). To amplify a DNA sequence containing an *H. pylori* ORF, genomic DNA (10 nanograms) was introduced into a reaction vial containing 2 mM MgCl₂, 1 micromolar synthetic oligonucleotide primers (forward and reverse primers, see Table 10) complementary to and flanking a defined *H. pylori* ORF, 0.2 mM of each deoxynucleotide triphosphate; dATP, dGTP, dCTP, dTTP and 0.5 units of heat stable DNA polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume of 20 microliters in duplicate reactions.

Table 10

Oligonucleotide primers used for PCR amplification of *H. pylori* DNA sequences.

Outer membrane Proteins	Forward primer 5' to 3'	Reverse Primer 5' to 3'
Protein 11 (for strains AH4, AH15, AH61, 5294, 5640, AH18, and AH244)	5'-TTAACCATGGTGAAAAGC GATA-3' (SEQ ID NO:1091)	5'-TAGAATTCGCCTCTAAAA CTTTAG-3' (SEQ ID NO:1092)
Protein 11 (for strains AH5, 5155, 7958, AH24, and J99)	5'-TTAACCATGGTGAAAAGC GATA-3' (SEQ ID NO:1093)	5'-TAGAATTCGCATAACGAT CAATC-3' (SEQ ID NO:1094)
Protein 12	5'-ATATCCATGGTGAGTTTG ATGA-3' (SEQ ID NO:1095)	5'-ATGAATTCAATTTTTTATT TTGCCA-3' (SEQ ID NO:1096)
Protein 13	5'-AATTCCATGGCTATCCAA ATCCG-3' (SEQ ID NO:1097)	5'-ATGAATTCGCCAAAATC GTAGTATT-3' (SEQ ID NO:1098)
Protein 14	5'-GATACCATGGAATTTATGA AAAAG-3' (SEQ ID NO:1099)	5'-TGAATTCGAAAAAGTGT AGTTATAC-3' (SEQ ID NO:1100)

The following thermal cycling conditions were used to obtain amplified DNA products for each ORF using a Perkin Elmer Cetus/ GeneAmp PCR System 9600 thermal cycler:

- 5 Sequences for Proteins 12 and 14;
 Denaturation at 94°C for 2 min,
 2 cycles at 94°C for 15 sec, 30°C for 15 sec and 72°C for 1.5 min
 23 cycles at 94°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min
 Reactions were concluded at 72°C for 6 minutes.
- 10 Sequence for Protein 11 for strains AH5, 5155, 7958, AH24, and J99;
 Denaturation at 94°C for 2 min,
 2 cycles at 94°C for 15 sec, 30°C for 15 sec and 72°C for 1.5 min
 25 cycles at 94°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min
- 15 Reaction was concluded at 72°C for 6 minutes.
- Sequences for Protein 11 and Protein 13 for strains AH4, AH15, AH61, 5294, 5640, AH18, and Hp244 ;
 Denaturation at 94°C for 2 min,
 20 2 cycles at 94°C for 15 sec, 30°C for 20 sec and 72°C for 2 min
 25 cycles at 94°C for 15 sec, 55°C for 20 sec and 72°C for 2 min
 Reactions were concluded at 72°C for 8 minutes.

Upon completion of thermal cycling reactions, each pair of samples were
 25 combined and used directly for cloning into the pCR cloning vector as described below.
Cloning of H. pylori DNA sequences into the pCR TA cloning vector.

All amplified inserts were cloned into the pCR 2.1 vector by the method described in the Original TA cloning kit (Invitrogen, San Diego, CA). Products of the ligation reaction were then used to transform the TOP10F' (INVaF' in the case of *H.*
 30 *pylori* sequence 350) strain of *E. coli* as described below.

Transformation of competent bacteria with recombinant plasmids

Competent bacteria, *E. coli* strain TOP10F' or *E. coli* strain INVaF' were transformed with recombinant pCR expression plasmids carrying the cloned *H. pylori* sequences according to standard methods (Current Protocols in Molecular Biology, John
 35 Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). Briefly, 2 microliters of 0.5 micromolar BME was added to each vial of 50 microliters of competent cells. Subsequently, 2 microliters of ligation reaction was mixed with the competent cells and incubated on ice for 30 minutes. The cells and ligation mixture were then subjected to a
 40 "heat shock" at 42°C for 30 seconds, and were subsequently placed on ice for an additional 2 minutes, after which, samples were incubated in 0.45 milliliters SOC medium (0.5% yeast extract, 2.0 % tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄ and 20, mM glucose) at 37°C with shaking for 1 hour. Samples

were then spread on LB agar plates containing 25 microgram/ml kanamycin sulfate or 100 micrograms/ml ampicillin for growth overnight. Transformed colonies of TOP10F' or INVaF' were then picked and analyzed to evaluate cloned inserts as described below.

Identification of recombinant PCR plasmids carrying H. pylori sequences

- 5 Individual TOP10F' or INVaF' clones transformed with recombinant pCR-*H. pylori* ORFs were analyzed by PCR amplification of the cloned inserts using the same forward and reverse primers, specific for each *H. pylori* sequence, that were used in the original PCR amplification cloning reactions. Successful amplification verified the integration of the *H. pylori* sequences in the cloning vector (Current Protocols in
10 Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994).

- Individual clones of recombinant pCR vectors carrying properly cloned *H. pylori* ORFs were picked for sequence analysis. Sequence analysis was performed on ABI Sequencers using standard protocols (Perkin Elmer) using vector-specific primers (as found in PCR2.1, Invitrogen, San Diego, CA) and sequencing primers specific
15 to the ORF as listed in Table 11 below.

Table 11

Oligonucleotide primers used for sequencing of *H. pylori* DNA sequences.

Outer membrane Proteins	Forward primers 5' to 3'	Reverse Primers 5' to 3'
Protein 11	5'-CCCTTCATTTTAGAAATCG-3' (SEQ ID NO:1101) 5'-ATTTCAACCAATTCAATGCG-3' (SEQ ID NO:1102) 5'-GCCCCCTTTTGATTGAAGCT-3' (SEQ ID NO:1103) 5'-TCGCTCCAAGATACCAAG AAGT-3' (SEQ ID NO:1104) 5'-CTTGAATTAGGGGCAAAG ATCG-3' (SEQ ID NO:1105) 5'-ATGCGTTTTTACCCAAAGA AGT-3' (SEQ ID NO:1106) 5'-ATAACGCCACTTCCTTATTG GT-3' (SEQ ID NO:1107)	5'-CTTTGGGTAAAAACGCATC-3' (SEQ ID NO:1108) 5'-CGATCTTTGATCCTAATTCA-3' (SEQ ID NO:1109) 5'-ATCAAGTTGCCTATGCTGA-3' (SEQ ID NO:1110)
Protein 12	5'-TTGAACACTTTTGATTATG CGG-3' (SEQ ID NO:1111) 5'-GGATTATGCGATTGTTTA CAAG-3' (SEQ ID NO:1112)	5'-GTCTTTAGCAAAAATGGCGTC- 3' (SEQ ID NO:1113) 5'-AATGAGCGTAAGAGAGCCTTC- 3' (SEQ ID NO:1114)
Protein 13	5'-CTTATGGGGGTATTGTCA-3' (SEQ ID NO:1115) 5'-AGCATGTGGGTATCCAGC-3' (SEQ ID NO:1116)	5'-AGGTTGTTGCCTAAAGACT-3' (SEQ ID NO:1117) 5'-CTGCCTCCACCTTTGATC-3' (SEQ ID NO:1118)

Protein 14	5'-ACCAATATCAATTGGCACT-3' (SEQ ID NO:1119) 5'-ACTTGGAAAAGCTCTGCA-3' (SEQ ID NO:1120)	5'-CTTGCTTGTCATATCTAGC-3' (SEQ ID NO:1121) 5'-GTTGAAGTGTGGTGCTA-3' (SEQ ID NO:1122)
	5'-CAAGCAAGTGGTTTGGTTTT AG-3' (SEQ ID NO:1123) 5'-TGGAAAGAGCAAATCATTG AAG-3' (SEQ ID NO:1124)	5'-GCCCATAATCAAAAAGCCCAT- 3' (SEQ ID NO:1125) 5'-CTAAAACCAAACCACTTGC TTGTC-3' (SEQ ID NO:1126)
Vector Primers	5'-GTAAAACGACGGCCAG-3' (SEQ ID NO:1127)	5'-CAGGAAACAGCTATGAC-3' (SEQ ID NO:1128)

Results

To establish the PCR error rate in these experiments, five individual clones of Protein 11, prepared from five separate PCR reaction mixtures from *H. pylori* strain J99, were sequenced over a total length of 897 nucleotides for a cumulative total of 4485 bases of DNA sequence. DNA sequence for the five clones was compared to the DNA sequence of Protein 11 obtained previously by a different method, i.e., random shotgun cloning and sequencing. The PCR error rate for the experiments described herein was determined to be 2 base changes out of 4485 bases, which is equivalent to an estimated error rate of less than or equal to 0.04%.

DNA sequence analysis was performed on four different open reading frames identified as genes and amplified by PCR methods from a dozen different strains of the bacterium *Helicobacter pylori*. The deduced amino acid sequences of three of the four open reading frames that were selected for this study showed statistically significant BLAST homology to defined proteins present in other bacterial species. Those ORFs included: Protein 11, homologous to the val A & B genes encoding an ABC transporter in *F. novicida*; Protein 12, homologous to lipoprotein e (P4) present in the outer membrane of *H. influenzae*; Protein 13, homologous to fecA, an outer membrane receptor in iron (III) dicitrate transport in *E. coli*. Protein 14 was identified as an unknown open reading frame, because it showed low homology with sequences in the public databases.

To assess the extent of conservation or variance in the ORFs across various strains of *H. pylori*, changes in DNA sequence and the deduced protein sequence were compared to the DNA and deduced protein sequences found in the J99 strain of *H. pylori* (see Table 12 below). Results are presented as percent identity to the J99 strain of *H. pylori* sequenced by random shotgun cloning. To control for any variations in the J99 sequence each of the four open reading frames were cloned and sequenced again from the J99 bacterial strain and that sequence information was compared to the sequence information that had been collected from inserts cloned by random shotgun sequencing of the J99 strain. The data demonstrate that there is variation in the DNA

sequence ranging from as little as 0.12 % difference (Protein 14, J99 strain) to approximately 7% change (Protein 11, strain AH5). The deduced protein sequences show either no variation (Protein 14, strains AH18 and AH24) or up to as much as 7.66% amino acid changes (Protein 11, Strain AH5).

5

TABLE 12

Multiple Strain DNA Sequence analysis of *H. pylori* Vaccine Candidates

J99 Protein #:	11	11	12	12	13	13	14	14
Length of Region Sequenced:	248 a.a.	746 nt.	232 a.a.	696 nt.	182 a.a.	548 nt.	273 a.a.	819 nt.
Strain Tested	AA identity	Nuc. identity	AA identity	Nuc. identity	AA identity	Nuc. identity	AA identity	Nuc. identity
J99	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	99.63%	99.88%
AH244	95.16%	95.04%	n.d.	n.d.	99.09%	96.71%	98.90%	96.45%
AH4	95.97%	95.98%	97.84%	95.83%	n.d.	n.d.	97.80%	95.73%
AH5	92.34%	93.03%	98.28%	96.12%	98.91%	96.90%	98.53%	95.73%
AH15	95.16%	94.91%	97.41%	95.98%	99.82%	97.99%	99.63%	96.09%
AH61	n.d.	n.d.	97.84%	95.98%	99.27%	97.44%	n.d.	n.d.
5155	n.d.	n.d.	n.d.	n.d.	99.45%	97.08%	98.53%	95.60%
5294	94.35%	94.37%	98.28%	95.40%	99.64%	97.26%	97.07%	95.48%
7958	94.35%	94.10%	97.84%	95.40%	n.d.	n.d.	99.63%	96.46%
5640	95.16%	94.37%	97.41%	95.69%	99.09%	97.63%	98.53%	95.48%
AH18	n.d.	n.d.	98.71%	95.69%	99.64%	97.44%	100.00%	95.97%
AH24	94.75%	95.04%	97.84%	95.40%	99.27%	96.71%	100.00%	96.46%

10

n.d. = not done

VII. Experimental Knock-Out Protocol for the Determination of Essential *H. pylori* Genes as Potential Therapeutic Targets

15 Therapeutic targets were chosen from genes whose protein products appear to play key roles in essential cell pathways such as cell envelope synthesis, DNA synthesis, transcription, translation, regulation and colonization/virulence.

20 The protocol for the deletion of portions of *H. pylori* genes/ORFs and the insertional mutagenesis of a kanamycin-resistance cassette was modified from previously published methods (Labigne-Roussel et al., 1988, J. Bacteriology 170, pp. 1704-1708; Cover et al., 1994, J. Biological Chemistry 269, pp. 10566-10573; Reyrat et al., 1995, Proc. Natl. Acad. Sci. 92, pp 8768-8772).

*Identification and Cloning of *H. pylori* Gene Sequences*

25 The sequences of the genes or ORFs (open reading frames) selected as knock-out targets were identified from the *H. pylori* genomic sequence and used to design primers to specifically amplify the genes/ORFs. All synthetic oligonucleotide primers (Table

- 106 -

13) were designed with the aid of the OLIGO program (National Biosciences, Inc., Plymouth, MN 55447, USA), and were purchased from Gibco/BRL Life Technologies (Gaithersburg, MD, USA). Specific primers (F1 and R1) were chosen which flanked most or all of the ORF, depending on its size. If the ORF was smaller than 800 to 1000
5 base pairs, flanking primers were chosen outside of the open reading frame.

TABLE 13
Oligonucleotide Sequences for Knock-Out Gene/ORFs

Gene Name	Accession Number	Cloning Primers		Deletion-creating Primers		Targeting Primers	
		F1	R1	F2	R2	F3	R3
rnh	P23329	TTGCCCCATCGTA TTGATAGA (SEQ ID NO:1129)	AGAGCGTATTTCA CCCGAAAG (SEQ ID NO:1130)	TCTTGCATCTTAAT CCACTCC (SEQ ID NO:1131)	CGGGTCAAAACGA CCACTTAA (SEQ ID NO:1132)	AATCCGTTTCGCT AATTTAGT (SEQ ID NO:1133)	AACACTTCAATTT CCTCTATA (SEQ ID NO:1134)
ppiB	P29820	TGGTATAAGGATT TGAATGGA (SEQ ID NO:1135)	TTGACTAAACACA TGCGAGAA (SEQ ID NO:1136)	ATAGAGAGCGTTG TGTTTAGC (SEQ ID NO:1137)	CCTTTATTGGTTTT GATCGTG (SEQ ID NO:1138)	ATGTCCGTTGTCT GTATGGAA (SEQ ID NO:1139)	TAGGGTGTCTAG GGATTTGAT (SEQ ID NO:1140)
tsf	P34828	GCGTTTGGCTTCTT CGTTGTC (SEQ ID NO:1141)	GAAATGGAAAATA GCGGTCAA (SEQ ID NO:1142)	GCAAATCCCCAGC CACTTCC (SEQ ID NO:1143)	GTGGCTAAAAATG AGGGCTT (SEQ ID NO:1144)	GTTAGGAAATTAG AAATCATTG (SEQ ID NO:1145)	GCTAAAACTTCAT CGCTCAAT (SEQ ID NO:1146)
MurD	P14900	GTTGGGCAGAAAA TAAGGTGA (SEQ ID NO:1147)	CAAACAAACCTGA CAAGAAAC (SEQ ID NO:1148)	CATTGATGCCTAA AACTTCG (SEQ ID NO:1149)	CGTGGTGGTTTTT CCGTTAG (SEQ ID NO:1150)	GGGCGATTGTGTT TGTTTTT (SEQ ID NO:1151)	TGGTCTATCATGC GAATTAT (SEQ ID NO:1152)
MurE	P22188	GCGTTTGGGGATT TGATGTTT (SEQ ID NO:1153)	CGCGCTAGAGGCT TGTAATA (SEQ ID NO:1154)	GCCCTGATCCATT CCCCCT (SEQ ID NO:1155)	CTGTTTTTAGCGTC CCTGTA (SEQ ID NO:1156)	GGCGTTATTAAGC GACATCG (SEQ ID NO:1157)	TTTCACCGGCAAT TTAGGC (SEQ ID NO:1158)
AlgA	P07874	GCGTTTTGATTCT GTCTGTTA (SEQ ID NO:1159)	GTAAAAACACCGC TAACGCAT (SEQ ID NO:1160)	GCGTGTTTTCTAA GGGTTC (SEQ ID NO:1161)	GGAATTTTAACGC TCTTTTT (SEQ ID NO:1162)	AAATCTCTGTGGG CTTAGTG (SEQ ID NO:1163)	AATCAAAAACAA GAGCGTGG (SEQ ID NO:1164)
metL	P19358	GCCCCAGCCCCAT AATACAAA (SEQ ID NO:1165)	GGAGGGCGCAATT AAACATCG (SEQ ID NO:1166)	TCACGCTTTCTAA ATCATCA (SEQ ID NO:1167)	CGCTAATCACATC CTTTCTT (SEQ ID NO:1168)	TGCCCAAAAATCC ACTAACG (SEQ ID NO:1169)	AACGGGTTTGAC ACTGATGA (SEQ ID NO:1170)

TABLE 13 (continued)

fusA	X16278	GAATGCGGTGGTT TTAGAGAG (SEQ ID NO:1171)	GCGTTTTTAAGAC TGAATACA (SEQ ID NO:1172)	GGGCGATGTGATT GGCGATT (SEQ ID NO:1173)	GGATAGCCTGCCA AAACGCC (SEQ ID NO:1174)	AAGTTTATGCGGG CGAGATT (SEQ ID NO:1175)	GGAGCAATCAGC CATTTTTC (SEQ ID NO:1176)
FlgE	U09549	CTAGCGATTCAAG GCGATGG (SEQ ID NO:1177)	CGGCCTCCTTCAA ACACATT (SEQ ID NO:1178)	AGCGGGCAGTTTA GGACCAC (SEQ ID NO:1179)	GCATTGATCGCAT TTTTAGCC (SEQ ID NO:1180)	ACGGGTTAGCAGG GCAGAAT (SEQ ID NO:1181)	CAAAAGAGGCCG GTTCATGC (SEQ ID NO:1182)
FliM- set A	M37691	TTTAGAAGTCGTT GATGAGA (SEQ ID NO:1183)	CATACACGCTCAC TTCATCG (SEQ ID NO:1184)	AGTGTGGTCGCCT GTGGTGGAG (SEQ ID NO:1185)	CCCCTAATAGTCT GTCAATCAT (SEQ ID NO:1186)	CAAAAGATTGAAG CAGAAGAGT (SEQ ID NO:1187)	AATGGTTTTCTA TACCCTTGA (SEQ ID NO:1188)
FliM- set B	M37691	GAGAGCAAATCCT TATCCAG (SEQ ID NO:1189)	CATACACGCTCAC TTCATCG (SEQ ID NO:1190)	AGTGTGGTCGCCT GTGGTGGAG (SEQ ID NO:1191)	CCCCTAATAGTCT GTCAATCAT (SEQ ID NO:1192)	CAAAAGATTGAAG CAGAAGAGT (SEQ ID NO:1193)	AATGGTTTTCTA TACCCTTGA (SEQ ID NO:1194)
MurC	U32794	TTGAAACCCCAA AGTTTTAC (SEQ ID NO:1195)	TCAACTGATAGGT AATATCCC (SEQ ID NO:1196)	GCTAGGATTTATG CCAATTTA (SEQ ID NO:1197)	TACGAGACAAAAT AGGGATT (SEQ ID NO:1198)	ATAGGCATGCAGA ATTTTTCC (SEQ ID NO:1199)	CCATTACATTTCC CCTC (SEQ ID NO:1200)
dnaE	M10040	CGATAGATATTGT AGAAGTCA (SEQ ID NO:1201)	GGGCTTGATTCA TTTTGTAA (SEQ ID NO:1202)	GTTTTAAAAACGC CATAGCCA (SEQ ID NO:1203)	TTCTAAAAGGTGG TAATCTTC (SEQ ID NO:1204)	TAAGTCAAGCCAT AAAACCAA (SEQ ID NO:1205)	TTTTGGGGTAAAA AGGCTGAA (SEQ ID NO:1206)
SerS	X05017	ATCTTTTTGCCCTT GCTCATA (SEQ ID NO:1207)	AGACAGCACCAGT TTGATAAA (SEQ ID NO:1208)	CAGCCACACTTCA ATGTCTAT (SEQ ID NO:1209)	GTAAGGCGTTAGA AAAATACC (SEQ ID NO:1210)	GCCCCATTAAAAT CCTTTTCT (SEQ ID NO:1211)	AAAGGATACAAG GGGGA (SEQ ID NO:1212)
gly	P00960	CTCGCTCCATTTTA TCTTTTA (SEQ ID NO:1213)	TTTTTTAGGGAGG ATTGAGAT (SEQ ID NO:1214)	TGTTTGGAATGC TGGTGATC (SEQ ID NO:1215)	CTTTTGGGGGAGT TTGACAAG (SEQ ID NO:1216)	TTTGATAAACGCC CACTTTTT (SEQ ID NO:1217)	TTTCAAAACGCTC ACCTTTTG (SEQ ID NO:1218)
Gltx	L14580	TCTATTCTTTTGAT GCTCTCT (SEQ ID NO:1219)	ATAATGAGTTTGA TCGTTACG (SEQ ID NO:1220)	ACAATAATAGGCT TTGTCTTC (SEQ ID NO:1221)	AATTAGCCCTTAA AATAGATG (SEQ ID NO:1222)	AACAACCGCTAAA ATCAAAC (SEQ ID NO:1223)	CTTCAGCGATACT AAAAGAT (SEQ ID NO:1224)
Sig28 (fliA)	M37691	TAGGGGCGATTGA AAACAGC (SEQ ID NO:1225)	GCTGGATAAGGAT TTGCTCT (SEQ ID NO:1226)	TTTTTGGGGGTAT GCTAAAA (SEQ ID NO:1227)	GGCTGGTAAATAC TGGATAG (SEQ ID NO:1228)	AGGCTATTCAAGG TGGCTAAA (SEQ ID NO:1229)	ATTCTCATCAACG ACTTCTAAA (SEQ ID NO:1230)

TABLE 13 (continued)

Sig54	M73443	GCAGTTGGCGGTA TTTGGTG (SEQ ID NO:1231)	GAGAGCGAAGTTT ATGAGAA (SEQ ID NO:1232)	TGATTGTTGGGTA GCTCTCA (SEQ ID NO:1233)	AAAATCGGTCTGA TGCTCTTA (SEQ ID NO:1234)	CTTTTCCTTTCGCT TGAAGA (SEQ ID NO:1235)	AAAACAAACGCA TCAAAAAT (SEQ ID NO:1236)
MurI	U12405	TTTCAAGGCGAGG AGGCAGAT (SEQ ID NO:1237)	GCACAAAGACCCC ACCACGAT (SEQ ID NO:1238)	CGCCCGAATGGAT GAGTAGG (SEQ ID NO:1239)	TGCAACAAAAATA CGCCCTT (SEQ ID NO:1240)	TTTTTAAGGGCGT ATTTTGT (SEQ ID NO:1241)	TGGGTTTTAAGGA ATGTGATG (SEQ ID NO:1242)
dnaB	D26185	CGCGCTCAAAATC CCTAAAT (SEQ ID NO:1243)	GGCCCATTCCTTC GGATATT (SEQ ID NO:1244)	GCCCCATTCCTGTT TTTAGC (SEQ ID NO:1245)	CGCTTTAACGCTC CTTTCAC (SEQ ID NO:1246)	AGCGTTTTTGTA GGGGGTAT (SEQ ID NO:1247)	TCCCTATCATAGC GTTAGTGC (SEQ ID NO:1248)
MurG	D10602	CTTAGGGGTTTTT AGCATGAA (SEQ ID NO:1249)	GCACAATTCCCAC ACGCTGC (SEQ ID NO:1250)	CCAAAGCTAAAGC GGTGT (SEQ ID NO:1251)	GCTCATGGATATA AAGGGGTATT (SEQ ID NO:1252)	CTTAGCCCCTTTA GTGTTTA (SEQ ID NO:1253)	CGCAAAAGGGTA GGGGATAA (SEQ ID NO:1254)
IpxC	U32794	TTTTATTTTAGAA ACGAATC (SEQ ID NO:1255)	CAAACCTATCGCC CTCTCTA (SEQ ID NO:1256)	AAAGATAACGCTA GGATTTCTAC (SEQ ID NO:1257)	TAATTCTACAGAG TGGTTAATGG (SEQ ID NO:1258)	GCGGTCATGGAAT TTTTAGA (SEQ ID NO:1259)	ATTCAAAGAAAG CTGGCTGTCT (SEQ ID NO:1260)
kdtA	M86305	GCTTGTGGGGGTT GTTTTAT (SEQ ID NO:1261)	GAACCCCTAAAA TGACAAT (SEQ ID NO:1262)	ACCATGCTCATTA ACGCTAGG (SEQ ID NO:1263)	GTAAGTTTGAGCG GCTAATTC (SEQ ID NO:1264)	AAAAAGAAAGAA GAACCTCGTG (SEQ ID NO:1265)	AAAGATACTCCC CTGTGATTA (SEQ ID NO:1266)
IpxB	U09549	CAAAGAAACGCAA AATACAG (SEQ ID NO:1267)	GCATGGTATTTCAG CGTTTTTC (SEQ ID NO:1268)	GCAGCGGCACAGC GACTTTAG (SEQ ID NO:1269)	CGCCCCCAAAAAG TCGCAGTA (SEQ ID NO:1270)	AAAGGTTTGAAAC AAGAAATCT (SEQ ID NO:1271)	CACTTGAGCGTTA GCAACAAT (SEQ ID NO:1272)
KO 24		GGGGTGTTTGAAA TTGATAGA (SEQ ID NO:1273)	CGCTAGGAGAAAG GAAGGAAA (SEQ ID NO:1274)	CAAGGGCGTTTTT TGGGGTAT (SEQ ID NO:1275)	GGGATTGTTACAG GAAAAGAT (SEQ ID NO:1276)	GGAATACAATAAC GCATAAAT (SEQ ID NO:1277)	GCCTTTTTAGACA ACCCTACT (SEQ ID NO:1278)
KO 26		CCCCTAAACTCAA ATCTCAAT (SEQ ID NO:1279)	GCTAGAAATGCCA TGAGAAAAG (SEQ ID NO:1280)	GCGATTATGGGGT ATTTATTG (SEQ ID NO:1281)	TTATTGTGGAGTT GCTTGTC (SEQ ID NO:1282)	TATGCGGCTCATC CTATTA (SEQ ID NO:1283)	CCCTAAATCCAA ATCAAGCAG (SEQ ID NO:1284)

Genomic DNA prepared from the *Helicobacter pylori* HpJ99 strain (ATCC 55679) was used as the source of template DNA for amplification of the ORFs by PCR (polymerase chain reaction) (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). For the preparation of genomic DNA from *H. pylori*, see

5 Example I. PCR amplification was carried out by introducing 10 nanograms of genomic HpJ99 DNA into a reaction vial containing 10 mM Tris pH 8.3, 50 mM KCl, 2 mM MgCl₂, 2 microMolar synthetic oligonucleotide primers (forward=F1 and reverse=R1), 0.2 mM of each deoxynucleotide triphosphate (dATP, dGTP, dCTP, dTTP), and 1.25 units of heat stable DNA polymerase (Amplitaq, Roche Molecular Systems, Inc.,

10 Branchburg, NJ, USA) in a final volume of 40 microliters. The PCR was carried out with Perkin Elmer Cetus/GeneAmp PCR System 9600 thermal cyclers. The thermal cycling conditions used to obtain amplified DNA products for each knock-out target are shown in Table 14.

TABLE 14
PCR Conditions

15	<u>MurC</u>
	Denaturation at 94°C for 2 min.,
	25 cycles of 94°C for 15 sec, 48°C for 15 sec, 72°C for 1 min, 30 sec,
20	Final Extension of 72°C for 20 minutes.
	<u>Sig54</u>
	Denaturation at 94°C for 2 min.,
	25 cycles of 94°C for 15 sec, 50°C for 15 sec, 72°C for 1 min, 30 sec,
25	Final Extension of 72°C for 20 minutes.
	<u>lpxC</u>
	Denaturation at 94°C for 2 min.,
	32 cycles of 94°C for 15 sec, 50°C for 15 sec, 72°C for 1 min, 30 sec,
	Final Extension of 72°C for 20 minutes.
30	<u>KO24, KO26, KO27</u>
	Denaturation at 94°C for 2 min.,
	25 cycles of 94°C for 15 sec, 50.5°C for 20 sec, 72°C for 2 min,
	Final Extension of 72°C for 20 minutes.
35	<u>KO29, 26kDa Protein</u>
	Denaturation at 94°C for 2 min.,
	28 cycles of 94°C for 15 sec, 50.5°C for 20 sec, 72°C for 2 min,
	Final Extension of 72°C for 20 minutes.
40	<u>DnaE, Glycyl</u>
	Denaturation at 94°C for 2 min.,
	20 cycles of 94°C for 15 sec, 51°C for 15 sec, 72°C for 1 min, 30 sec,
	Final Extension of 72°C for 20 minutes.
45	

- 111 -

Gltx

Denaturation at 94°C for 2 min.,
25 cycles of 94°C for 15 sec, 51°C for 15 sec, 72°C for 1 min, 30 sec,
Final Extension of 72°C for 20 minutes.

KO28

Denaturation at 94°C for 2 min.,
25 cycles of 94°C for 15 sec, 51°C for 15 sec, 72°C for 2min,
Final Extension of 72°C for 20 minutes.

KO30

Denaturation at 94°C for 2 min.,
25 cycles of 94°C for 15 sec, 51.5°C for 15 sec, 72°C for 1min, 45 sec,
Final Extension of 72°C for 20 minutes.

MurI, MurG

Denaturation at 94°C for 2 min.,
25 cycles of 94°C for 15 sec, 52°C for 15 sec, 72°C for 1 min, 30 sec,
Final Extension of 72°C for 20 minutes.

DnaB, KdtA, LpxB

Denaturation at 94°C for 2 min.,
27 cycles of 94°C for 15 sec, 52°C for 15 sec, 72°C for 1 min, 30 sec,
Final Extension of 72°C for 20 minutes.

Tsf, FlgE, FliM, Sig28, MurB

Denaturation at 94°C for 2 min.,
30 cycles of 94°C for 15 sec, 52°C for 15 sec, 72°C for 1 min, 30 sec,
Final Extension of 72°C for 20 minutes.

PpiB

Denaturation at 94°C for 2 min.,
30 cycles of 94°C for 15 sec, 52°C for 15 sec, 72°C for 2 min, 30 sec,
Final Extension of 72°C for 20 minutes.

MurD, MurE, AlgA, MetL, FusA, SerS, Rnh

Denaturation at 94°C for 2 min.,
30 cycles of 94°C for 15 sec, 55°C for 15 sec, 72°C for 1 min, 30 sec,
Final Extension of 72°C for 20 minutes.

Upon completion of thermal cycling reactions, each sample of amplified DNA was visualized on a 2% TAE agarose gel stained with Ethidium Bromide (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994) to determine that a single product of the expected size had resulted from the reaction. Amplified DNA was then washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA).

PCR products were cloned into the pT7Blue T-Vector (catalog#69820-1, Novagen, Inc., Madison, WI, USA) using the TA cloning strategy (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). The

- 112 -

ligation of the PCR product into the vector was accomplished by mixing a 6 fold molar excess of the PCR product, 10 ng of pT7Blue-T vector (Novagen), 1 microliter of T4 DNA Ligase Buffer (New England Biolabs, Beverly, MA, USA), and 200 units of T4 DNA Ligase (New England Biolabs) into a final reaction volume of 10 microliters.

- 5 Ligation was allowed to proceed for 16 hours at 16°C.

Ligation products were electroporated (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994) into electroporation-competent XL-1 Blue or DH5- α *E. coli* cells (Clontech Lab., Inc. Palo Alto, CA, USA). Briefly, 1 microliter of ligation reaction was mixed with 40 microliters of
10 electrocompetent cells and subjected to a high voltage pulse (25 microFarads, 2.5 kV, 200 ohms) after which the samples were incubated in 0.45 ml SOC medium (0.5% yeast extract, 2% tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄ and 20 mM glucose) at 37°C with shaking for 1 hour. Samples were then spread onto LB (10 g/l bacto tryptone, 5 g/l bacto yeast extract, 10 g/l sodium chloride) plates containing
15 100 microgram/ml of Ampicillin, 0.3% X-gal, and 100 microgram/ml IPTG. These plates were incubated overnight at 37°C. Ampicillin-resistant colonies with white color were selected, grown in 5 ml of liquid LB containing 100 microgram/ml of Ampicillin, and plasmid DNA was isolated using the Qiagen miniprep protocol (Qiagen, Gaithersburg, MD, USA).

20 To verify that the correct *H. pylori* DNA inserts had been cloned, these pT7Blue plasmid DNAs were used as templates for PCR amplification of the cloned inserts, using the same forward and reverse primers (F1 and R1) used for the initial amplification of the J99 *H. pylori* sequence. Recognition of the primers and a PCR product of the correct size as visualized on a 2% TAE, ethidium bromide stained agarose gel were
25 confirmation that the correct inserts had been cloned. Two to six such verified clones were obtained for each knock-out target, and frozen at -70°C for storage. To minimize errors due to PCR, plasmid DNA from these verified clones were pooled, and used in subsequent cloning steps.

The sequences of the genes/ORFs were again used to design a second pair of
30 primers (F2 and R2) which flanked the region of *H. pylori* DNA to be either interrupted or deleted (up to 250 basepairs) within the ORFs but were oriented away from each other. The pool of circular plasmid DNAs of the previously isolated clones were used as templates for this round of PCR. Since the orientation of amplification of this pair of deletion primers was away from each other, the portion of the ORF between the primer
35 would not be included in the resultant PCR product. The PCR product was a linear piece of DNA with *H. pylori* DNA at each end and the pT7Blue vector backbone

between them which, in essence, resulted in the deletion of a portion of the ORFs. The PCR product was visualized on a 1% TAE, ethidium bromide stained agarose gel to confirm that only a single product of the correct size had been amplified.

A Kanamycin-resistance cassette (Labigne-Roussel et al., 1988 J. Bacteriology 170, 1704-1708) was ligated to this PCR product by the TA cloning method used previously (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). The Kanamycin cassette containing a *Campylobacter* kanamycin resistance gene was obtained by carrying out an EcoRI digestion of the recombinant plasmid pCTB8:*kan* (Cover et al., 1994, J. Biological Chemistry 269, pp. 10566-10573). The proper fragment (1.4 kb) was isolated on a 1% TAE gel, and isolated using the QIAquick gel extraction kit (Qiagen, Gaithersburg, MD, USA). The fragment was end repaired using the Klenow fill-in protocol, which involved mixing 4ug of the DNA fragment, 1 microliter of dATP, dGTP, dCTP, dTTP at 0.5 mM, 2 microliter of Klenow Buffer (New England Biolabs) and 5 units of Klenow DNA Polymerase I Large (Klenow) Fragment (New England Biolabs) into a 20 microliter reaction, incubating at 30°C for 15 min, and inactivating the enzyme by heating to 75°C for 10 minutes. This blunt-ended Kanamycin cassette was then purified through a Qiaquick column (Qiagen, Gaithersburg, MD, USA) to eliminate nucleotides. The 5' overhang was then generated by mixing 5 micrograms of the blunt-ended kanamycin cassette, 10 mM Tris pH 8.3, 50 mM KCl, 2 mM MgCl₂, 5 units of DNA Polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA), 20 microliters of 5 mM dTTP, in a 100 microliter reaction and incubating the reaction for 2 hours at 37°C. The "Kan-T" cassette was purified using a QIAquick column (Qiagen, Gaithersburg, MD, USA). The PCR product of the deletion primers (F2 and R2) was ligated to the Kan-T cassette by mixing 10 to 25 ng of deletion primer PCR product, 50 - 75 ng Kan-T cassette DNA, 1 microliter 10x T4 DNA Ligase reaction mixture, 0.5 microliter T4 DNA Ligase (New England Biolabs, Beverly, MA, USA) in a 10 microliter reaction reaction and incubating for 16 hours at 16°C.

The ligation products were transformed into XL-1 Blue or DH5- α *E. coli* cells by electroporation as described previously. After recovery in SOC, cells were plated onto LB plates containing 100 microgram/ml Ampicillin and grown overnight at 37°C. These plates were then replica plated onto plates containing 25 microgram/ml Kanamycin and allowed to grow overnight. Resultant colonies had both the Ampicillin resistance gene present in the pT7Blue vector, and the newly introduced Kanamycin resistance gene. Colonies were picked into LB containing 25 microgram/ml Kanamycin and plasmid

DNA was isolated using the Qiagen miniprep protocol (Qiagen, Gaithersburg, MD, USA).

Several tests by PCR amplification were conducted on these plasmids to verify that the Kanamycin was inserted in the *H. pylori* gene/ORF, and to determine the orientation of the insertion of the Kanamycin-resistance gene relative to the *H. pylori* gene/ORF. To verify that the Kanamycin cassette was inserted into the *H. pylori* sequence, the plasmid DNAs were used as templates for PCR amplification with the set of primers (F1 and R1) originally used to clone the *H. pylori* gene/ORFs. The correct PCR product was the size of the deleted gene/ORF but increased in size by the addition of a 1.4 kilobase Kanamycin cassette. To avoid potential polar effects of the kanamycin resistance cassette on *H. pylori* gene expression, the orientation of the Kanamycin resistance gene with respect to the knock-out gene/ORF was determined and both orientations were eventually used in *H. pylori* transformations (see below). To determine the orientation of insertion of the kanamycin resistance gene, primers were designed from the ends of the kanamycin resistance gene ("Kan-1" 5'-ATCTTACCTATCACCTCAAAT-3' (SEQ ID NO:1285), and "Kan-2" 5'-AGACAGCAACATCTTTGTGAA-3' (SEQ ID NO:1286)). By using each of the cloning primers (F1 and R1) in conjunction with each of the Kan primers (4 combinations of primers), the orientation of the Kanamycin cassette relative to the *H. pylori* sequence was determined. Positive clones were classified as either in the "A" orientation (the same direction of transcription was present for both the *H. pylori* gene and the Kanamycin resistance gene), or in the "B" orientation (the direction of transcription for the *H. pylori* gene was opposite to that of the Kanamycin resistance gene). Clones which shared the same orientation (A or B) were pooled for subsequent experiments and independently transformed into *H. pylori*.

Transformation of Plasmid DNA into H. pylori cells

Two strains of *H. pylori* were used for transformation: ATCC 55679, the clinical isolate which provided the DNA from which *H. pylori* sequence database was obtained, and AH244, an isolate which had been passaged in, and had the ability to colonize the mouse stomach. Cells for transformation were grown at 37°C, 10% CO₂, 100% humidity, either on Sheep-Blood agar plates or in Brucella Broth liquid. Cells were grown to exponential phase, and examined microscopically to determine that the cells were "healthy" (actively moving cells) and not contaminated. If grown on plates, cells were harvested by scraping cells from the plate with a sterile loop, suspended in 1 ml of Brucella Broth, spun down (1 minute, top speed in eppendorf microfuge) and

resuspended in 200 microliters Brucella Broth. If grown in Brucella Broth liquid, cells were centrifuged (15 minutes at 3000 rpm in a Beckman TJ6 centrifuge) and the cell pellet resuspended in 200 microliters of Brucella broth. An aliquot of cells was taken to determine the optical density at 600 nm, in order to calculate the concentration of cells.

5 An aliquot (1 to 5 OD₆₀₀ units/25 microliter) of the resuspended cells was placed onto a prewarmed Sheep-Blood agar plate, and the plate was further incubated at 37°C, 6% CO₂, 100% humidity for 4 hours. After this incubation, 10 microliters of plasmid DNA (100 micrograms per microliter), was spotted onto these cells. A positive control (plasmid DNA with the ribonuclease H gene disrupted by kanamycin resistance gene)

10 and a negative control (no plasmid DNA) were done in parallel. The plates were returned to 37°C, 6% CO₂ for an additional 4 hours of incubation. Cells were then spread onto that plate using a swab wetted in Brucella broth, and grown for 20 hours at 37°C, 6% CO₂. Cells were then transferred to a Sheep-Blood agar plate containing 25 micrograms/ml Kanamycin, and allowed to grow for 3 to 5 days at 37°C, 6% CO₂,

15 100% humidity. If colonies appeared, they were picked and regrown as patches on a fresh Sheep-Blood agar plate containing 25 micrograms/ml Kanamycin.

Three sets of PCR (three tests) were done to verify that the colonies of transformants have arose from homologous recombination at the proper chromosomal location. The template for PCR (DNA from the colony) was obtained by a rapid boiling

20 DNA preparation method. An aliquot of the colony (stab of the colony with a toothpick) was introduced into 100 microliters of 1% Triton X-100, 20 mM Tris, pH 8.5, and boiled for 6 minutes. An equal volume of phenol : chloroform (1:1) was added and vortexed. The mixture was microfuged for 5 minutes and the supernatant was used as DNA template for PCR with combinations of the following primers to verify

25 homologous recombination at the proper chromosomal location.

TEST 1 PCR with F1 and R1 primers (cloning primers originally used to amplify the gene/ORF). A positive result of homologous recombination at the correct chromosomal location should show a single PCR product whose size is expected to be the size of the deleted gene/ORF but increased in size by the addition of a 1.4 kilobase

30 Kanamycin cassette. A PCR product of just the size of the gene/ORF was proof that the gene had not been knocked out and that the transformant was not the result of homologous recombination at the correct chromosome location.

TEST 2 PCR with F3 (primer designed from sequences upstream of the gene/ORF), and either primer Kan-1 or Kan-2 (primers designed from the ends of the

35 kanamycin resistance gene), depending on whether the plasmid DNA used was of "A" or "B" orientation. A positive result of homologous recombination at the correct

chromosomal location of the sequences of the gene/ORFs upstream from the kanamycin resistance gene should show a single PCR product, the expected size to be from the location of F3 to the insertion site of kanamycin resistance gene. No PCR product or PCR product(s) of incorrect size(s) would prove that the plasmid had not been integrated at the correct site and that the gene had not been knocked out.

TEST 3 PCR with R3 (primer designed from sequences downstream of the gene/ORF) and either primer Kan-1 or Kan-2, depending on whether the plasmid DNA used was of "A" or "B" orientation. A positive result of homologous recombination at the correct chromosomal location downstream from the kanamycin resistance gene would show a single PCR product, the expected size to be from the insertion site of kanamycin resistance gene to the downstream location of R3. Again, no PCR product or PCR product(s) of incorrect size(s) would prove that the plasmid had not been integrated at the correct site and that the gene had not been knocked out.

Genes that are not essential for survival *in vitro* normally resulted in many transformants as observed for the positive control of ribonuclease H gene. Any transformants showing positive results for all three tests above would result in the conclusion that the gene was not essential for survival *in vitro*.

Genes that are essential for survival *in vitro* normally showed very few transformants. All transformants would be screened. A negative result of any of the three above tests for each transformant would lead to the conclusion that the gene had not been disrupted, and that the gene was essential for survival *in vitro*.

In the event that no colonies resulted from two independent transformations while the positive control with the disrupted ribonuclease H plasmid DNA produced transformants, the plasmid DNA was further analyzed by PCR on DNA from transformant populations prior to plating for colony formation, to verify that it can enter the cells and undergo homologous recombination at the correct site. Briefly, plasmid DNA was incubated according to the transformation protocol described above. DNA was extracted from the *H. pylori* cells immediately after incubation with the plasmid DNA and the DNA was used as templates for the above TEST 2 and TEST 3. Positive results of TEST 2 and TEST 3 would verify that the plasmid DNA could enter the cells and undergo homologous recombination at the correct chromosomal location. If TEST 2 and TEST 3 are positive, then failure to obtain viable transformants indicates that the gene is essential and cells suffering a disruption in that gene are incapable of colony formation.

Genes used in these experiments have been found to be essential, non-essential, or are still in progress, as indicated in Table 15.

TABLE 15

Summary of knock-out genes/ORFs			
Gene	Accession Number	Pathway	Status
rnh	P23329	Transcription	Not essential
ppiB	P29820	Translation	Not essential
tsf	P34828	Translation	Essential
MurD	P14900	Cell envelope	Essential
MurE	P22188	Cell envelope	Essential
AlgA	P07874	Virulence/Colonization	Not essential
metL	P19358	Amino acid biosynthesis - aspartate family	Not essential
fusA	X16278	Translation	Essential
FlgE	U09549	Virulence/Colonization	Not essential-motility impaired
FliM	M37691	Virulence/Colonization	Not essential-motility impaired
MurC	U32794	Cell envelope	Essential
dnaE	M10040	DNA replication	Essential
serS	X05017	Translation	Essential
gly	P00960	Translation	Essential
gltX	L14580	Translation	Essential
sig28 (fliA)	M37691	Regulatory functions	Not essential-motility impaired
sig54		Regulatory functions	Not essential-motility impaired
MurI	U12405	Cell envelope	Essential
dnaB	D26185	DNA replication	In progress
MurG	D10602	Cell envelope	In progress
lpxC/envA	U32794	Cell envelope	In progress
kdtA	M86305	Cell envelope	In progress
lpxB	U09549	Cell envelope	In progress
KO 24		thiolase-like	In progress
KO 26		histone-like	In progress
KO 27		respiratory chain NADH dehydrogenase-like	In progress

VIII. Cloning, purification and characterization of the gene encoding the peptidyl-propyl *cis-trans* isomerase of *H. pylori*

The *Helicobacter pylori* genome contains an open reading frame (ORF) of 170 amino acids was found to have homology with the *Synechococcus sp.* (strain PCC 7942).ppi gene (NCBI Accession number P29820). Therefore, to evaluate whether this ORF encoded a protein with PPIase activity, the gene was isolated by polymerase chain reaction (PCR) amplification cloning, overexpressed in *E. coli*, and the protein purified to homogeneity. To facilitate purification, a polyhistidine tag was added to the N-terminus of this ORF. A simple assay using PPIase to evaluate protein folding function was developed for future use as a high-throughput drug screen.

Currently, the class of PPIases is divided into three unrelated families: the cyclophilins, the FK506-binding (FKBPs) and the parvulins. Although PPIase mutants have been reported from yeast and fruit fly, attempts to isolate disruption mutants in *Escherichia coli* were unsuccessful (Shieh, B.H., et.al. (1989) *Nature* 338:67-70). This suggests that this activity is essential for viability in bacteria.

Cloning, expression and protein purification

To facilitate the cloning, expression and purification of ppi from *H. pylori*, a powerful gene expression system, the pET System, for cloning and expression of recombinant ppi in *E. coli*. In this study, the sequence for *H. pylori* ppi contains a DNA sequence encoding a His-Tag fused to the 5' end of the full length gene, because the protein product of this gene does not contain a signal sequence and is expressed as a cytosolic protein.

A synthetic oligonucleotide primer (5'-TTATGGATCCAAACCAATTAAAA CT-3' (SEQ ID NO:1287)) specific for the 5' end of ppi gene encoded a BamHI site at its extreme 5' terminus and a primer (5'-TATCTCGAGTTATAGAGAAGGGC-3' (SEQ ID NO:1288)) specific for the 3' end of the ppi gene encoded a XhoI site at its extreme 5' terminus. Genomic DNA prepared from the J99 strain of *Helicobacter pylori* was used as the source of template DNA for PCR amplification reactions (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). To amplify a DNA sequence containing the *H. pylori* ppi gene, genomic DNA (50 nanograms) was introduced into a reaction vial containing 2 mM MgCl₂, 1 micromolar synthetic oligonucleotide primers (forward and reverse primers) complementary to and flanking a defined *H. pylori* ORF, 0.2 mM of each deoxynucleotide triphosphate; dATP, dGTP, dCTP, dTTP and 2.5 units of heat stable DNA polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume of 100 microliters.

The following thermal cycling conditions were used to obtain amplified DNA products for each ORF using a Perkin Elmer Cetus/ GeneAmp PCR System 9600 thermal cycler:

Conditions for amplification of H. pylori ppiB;

Denaturation at 94°C for 2 min,
2 cycles at 94°C for 15 sec, 32°C for 15 sec and 72°C for 1.5 min
25 cycles at 94°C for 15 sec, 56°C for 15 sec and 72°C for 1.5 min
Reactions were concluded at 72°C for 6 minutes.

Upon completion of thermal cycling reactions, the amplified DNA was washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA). The amplified DNA sample was subjected to digestion with the restriction endonucleases, BamHI and XhoI (New England BioLabs, Beverly, MA, USA) (Current Protocols in Molecular Biology, Ibid). The DNA as subjected to electrophoresis on a 1.0 % NuSeive (FMC BioProducts, Rockland, ME USA) agarose gel. DNA was visualized by exposure to ethidium bromide and long wave uv irradiation. DNA contained in slices isolated from the agarose gel was purified using the Bio 101 GeneClean Kit protocol (Bio 101 Vista, CA, USA)

Cloning, transformation, expression and purification of the PPI gene was carried out essentially as described in Examples II and III above.

Assay for PPIase activity

The assay for PPIase was essentially as described by Fisher (Fischer, G., et.al. (1984) *Biomed. Biochim. Acta* 43:1101-1111). The assay measures the *cis-trans* isomerization of the Ala-Pro bond in the test peptide N-succinyl-Ala-Ala-Pro-Phe-p-nitroanilide (Sigma # S-7388, lot # 84H5805). The assay is coupled with α -chymotrypsin, where the ability of the protease to cleave the test peptide occurs only when the Ala-Pro bond is in *trans*. The conversion of the test peptide to the *trans* isomer in the assay is followed at 390 nm on a Beckman Model DU-650 spectrophotometer. The data were collected every second with an average scanning of time of 0.5 second. Assays were carried out in 35 mM Hepes, pH 8.0, in a final volume of 400 μ l, with 10 μ M α -chymotrypsin (type 1-5 from bovine Pancreas, Sigma # C-7762, lot 23H7020) and 10 nM PPIase. To initiate the reaction, 10 μ l of the substrate (2 mM N-Succinyl-Ala-Ala-Pro-Phe-p-nitroanilide in DMSO) was added to 390 μ l of reaction mixture at room temperature.

PPIase assay in crude bacterial extract.

A 50 ml culture of *Helicobacter pylori* (strain J99) in Brucella broth was harvested at mid-log phase ($OD_{600\text{ nm}} \sim 1$) and resuspended in lysis buffer with the following protease inhibitors: 1 mM PMSF, and 10 $\mu\text{g/ml}$ of each of aprotinin, leupeptin, pepstatine, TLCK, TPCK, and soybean trypsin inhibitor. The suspension was subjected to 3 cycles of freeze-thaw (15 minutes at -70°C , then 30 minutes at room temperature), followed by sonication (three 20 second bursts). The lysate was centrifuged ($12,000\text{ g} \times 30\text{ minutes}$) and the supernatant was assayed for PPIase activity.

10 *Results*

PPI from *H. pylori* was expressed in *E. coli* using the pET-28b expression vector from Novagen (cat # 69868-1). The expressed recombinant protein was isolated from the soluble fraction of bacterial cells that had been disrupted by cavitation in a Microfluidics Cell disruption chamber. The expression levels of recombinant PPI produced 100 mg of protein. The recombinant protein could be purified to homogeneity by Ni^{2+} chelate chromatography and gel filtration. On sodium dodecyl sulfate polyacrylamide gels, the recombinant protein migrates as a single band at 21 kDa, in accordance with the predicted molecular weight of 20,975 deduced from the gene sequence.

20 The PPIase activity was assayed using the chromogenic tetrapeptide substrate succinyl-Ala-Ala-Pro-Phe-p-nitroanilide. An initial velocity of $4.9\text{ }\mu\text{mole/min/mg}$ protein was measured with the purified enzyme (Figure 5). This corresponds to a k_{cat} of 1.6 sec^{-1} which is similar to the one obtained for the *E. coli* PPIase (Liu, J. and Walsh, C.T. (1990) *Proc.Natl. Acad. Sci. USA* 87:4028-4032) and the one from porcine kidney (Fischer, G. (1989) *Nature* 337:476-478).

25 The recombinant protein has a high catalytic efficiency of $2.06 \times 10^9\text{ M}^{-1}\text{ s}^{-1}$ when the assay is measured at 25°C . These values are one to two orders of magnitude higher than that observed for other characterized PPIases. However, in those studies, the ppiase assay was conducted at 10°C , which may account for the discrepancy. The catalytic efficiency is very close to the 1×10^8 to $1 \times 10^9\text{ M}^{-1}\text{ s}^{-1}$ upper diffusional limit for "kinetically perfect" enzymes (Albery, W.J. and Knowles, J.R. (1976) *Biochemistry* 15:5631-5640) and suggests that by at least one measure, the *H. pylori* PPIase is a highly effective catalyst in the *cis-trans* isomerisation of the Ala-Pro bond in the oligopeptide substrate.

The presence of PPIase was also determined in an *H. pylori* extract. As with the assay for the recombinant protein, PPIase activity was detected, and was dependent on the concentration of extract added (Figure 6).

These results show that PPIase activity can be measured on either *H. pylori* extracts or on the recombinant protein in *E. coli*. The high catalytic efficiency also demonstrates that *H. pylori* enzymes, such as PPIase, can be expressed at high levels and in an active form in *E. coli*. Such high yields of purified proteins provide for the design of various high throughput drug screening assays.

10 IX. Cloning, purification, and characterization of the gene encoding the glutamate racemase of *H. pylori*.

The *Helicobacter pylori* genome contains an open reading frame (ORF) of 255 amino acids that was found to have homology to the *Staphylococcus haemolyticus* glutamate racemase gene (*dga*) (NCBI Accession number U12405) and to the *E. coli* *murI* gene which encodes glutamate racemase activity in that organism. To evaluate whether this *H. pylori* ORF encodes a protein with glutamate racemase activity, the gene was isolated by polymerase chain reaction (PCR) amplification cloning, overexpressed in *E. coli*, and the protein purified to apparent homogeneity. A simple assay for glutamate racemase activity resulting in the isomerization of D-glutamic acid to L-glutamic acid was developed to facilitate purification and for future use as a high-throughput drug screen.

The ORF in *H. pylori* has been found by gene disruption studies to be essential for viability of *H. pylori* cells in laboratory culture (see Example VII above). Therefore, inhibition of the enzymatic activity would be expected to be lethal for the organism, and such inhibitors may have utility in antimicrobial therapy of human infectious diseases.

Cloning of H. pylori murI gene encoding glutamate racemase

A 765 base pair DNA sequence encoding the *murI* gene of *H. pylori* was isolated by polymerase chain reaction (PCR) amplification cloning. A synthetic oligonucleotide primer (5'-AAATAGTCATATGAAAATAGGCGTTTTTG-3' (SEQ ID NO:1289)) encoding an *NdeI* restriction site and the 5' terminus of the *murI* gene and a primer (5'-AGAATTCTATTACAATTGAGCCATTCT-3' (SEQ ID NO:1290)) encoding an *EcoRI* restriction site and the 3' end of the *murI* gene were used to amplify the *murI* gene of *H. pylori* using genomic DNA prepared from the J99 strain of *H. pylori* as the template DNA for the PCR amplification reactions (Current Protocols in Molecular Biology, John Wiley and Sons, Inc. F. Ausubel et al., editors, 1994). To amplify a DNA sequence containing the *murI* gene, genomic DNA (25 nanograms) was introduced into

each of two reaction vials containing 1.0 micromole of each synthetic oligonucleotide primer, 2.0 mM MgCl₂, 0.2 mM of each deoxynucleotide triphosphate (dATP, dGTP, dCTP & dTTP), and 1.25 units of heat stable DNA polymerases (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume of 50 microliters.

- 5 The following thermal cycling conditions were used to obtain amplified DNA products for the *murI* gene using a Perkin Elmer Cetus/ GeneAmp PCR System 9600 thermal cycler:

Conditions for amplification of H. pylori murI;

10

Denaturation at 94°C for 2 min.
2 cycles at 94°C for 15 sec, 30°C for 30 sec and 72°C for 15 sec
23 cycles at 94°C for 15 sec, 53°C for 30 sec and 72°C for 15 sec
Reactions were concluded at 72°C for 20 minutes

15

- Upon completion of thermal cycling reactions, the amplified DNA was washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA). The amplified DNA sample was subjected to digestion with the restriction endonucleases, *NdeI* and *EcoRI* (New England Biolabs, Beverly, MA USA) (Current
20 Protocols in Molecular Biology, Ibid). The DNA samples from each of two reaction mixtures were pooled and subjected to electrophoresis on a 1.0% SeaPlaque (FMC BioProducts, Rockland, ME, USA) agarose gel. DNA was visualized by exposure to ethidium bromide and long wave uv irradiation. Amplified DNA encoding the *H. pylori murI* gene was isolated from agarose gel slices and purified using the Bio 101
25 GeneClean Kit protocol (Bio 101 Vista, CA, USA).

Cloning of H. pylori DNA sequences into the pET-23 prokaryotic expression vector.

- The pET-23b vector can be propagated in any *E. coli* K-12 strain, e.g., HMS174,
30 HB101, JM109, DH5α, etc., for the purpose of cloning or plasmid preparation. Hosts for expression include *E. coli* strains containing a chromosomal copy of the gene for T7 RNA polymerase. These hosts are lysogens of bacteriophage DE3, a lambda derivative that carries the *lacI* gene, the lacUV5 promoter and the gene for T7 RNA polymerase. T7 RNA polymerase is induced by addition of isopropyl-B-D-thiogalactoside (IPTG),
35 and the T7 RNA polymerase transcribes any target plasmid, such as pET-28b, carrying its gene of interest. Strains used in our laboratory include: BL21(DE3) (Studier, F.W., Rosenberg, A.H., Dunn, J.J., and Dubendorff, J.W. (1990) Meth. Enzymol. 185, 60-89).

The pET-23b vector (Novagen, Inc., Madison, WI, USA) was prepared for cloning by digestion with *NdeI* and *EcoRI* (Current Protocols in Molecular Biology,

Ibid). Following digestion, the amplified, agarose gel-purified DNA fragment carrying the *murI* gene was cloned (Current Protocols in Molecular Biology, Ibid) into the previously digested pET-23b expression vector. Products of the ligation reaction were then used to transform the BL21(DE3) strain of *E. coli*.

5

Transformation of competent bacteria with recombinant plasmids

Competent bacteria, *E. coli* strain BL21 or *E. coli* strain BL21(DE3), were transformed with recombinant pET23-*murI* expression plasmid carrying the cloned *H. pylori* sequence according to standard methods (Current Protocols in Molecular, Ibid).
10 Briefly, 1 microliter of ligation reaction was mixed with 50 microliters of electrocompetent cells and subjected to a high voltage pulse, after which, samples were incubated in 0.45 milliliters SOC medium (0.5% yeast extract, 2.0 % tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄ and 20 mM glucose) at 37°C with shaking for 1 hour. Samples were then spread on LB agar plates containing 100
15 microgram/ml ampicillin for growth overnight. Transformed colonies of BL21 were then picked and analyzed to evaluate cloned inserts as described below.

Identification of recombinant pET expression plasmids carrying H. pylori sequences

20 Individual BL21 clones transformed with recombinant pET-23-*murI* were analyzed by PCR amplification of the cloned inserts using the same forward and reverse primers, specific for each *H. pylori* sequence, that were used in the original PCR amplification cloning reactions. Successful amplification verified the integration of the *H. pylori* sequences in the expression vector (Current Protocols in Molecular Biology,
25 Ibid).

Isolation and Preparation of plasmid DNA from BL21 transformants

Colonies carrying pET-23-*murI* vectors were picked and incubated in 5 mls of LB broth plus 100 microgram/ml ampicillin overnight. The following day plasmid
30 DNA was isolated and purified using the Qiagen plasmid purification protocol (Qiagen Inc., Chatsworth, CA, USA).

Cloning and expression of the E. coli groE operon

It has been demonstrated that coexpression of the *E. coli murI* gene with the
35 genes in the *E. coli groE* operon reduces the formation of insoluble inclusion bodies containing recombinant glutamate racemase (Ashiuchi, M., Yoshimura, T., Kitamura, T., Kawata, Y., Nagai, J., Gorlatov, S., Esaki, N. and Soda, K., 1995, *J. Biochem.* 117,

495-498). The *groE* operon encodes two proteins, GroES (97 amino acids) and GroEL (548 amino acids), which are molecular chaperones. Molecular chaperones cooperate to assist the folding of new polypeptide chains (F. Ulrich Hartl, 1996, *Nature London* 381, pp. 571-580).

5 The 2210 bp DNA sequence encoding the *groE* operon of *E. coli* (NCBI Accession number X07850) was isolated by polymerase chain reaction (PCR) amplification cloning. A synthetic oligonucleotide primer (5'-GCGAATTTCGATCAG AATTTTTTTTCT-3' (SEQ ID NO:1291)) encoding an *EcoRI* restriction site and the 5' terminus of the *groE* operon containing the endogenous promoter region of the *groE*
10 operon and a primer (5'-ATAAGTACTTGTGAATCTTATACTAG -3' (SEQ ID NO:1292)) encoding a *ScaI* restriction site and the 3' end of the *groEL* gene contained in the *groE* operon were used to amplify the *groE* operon of *E. coli* using genomic DNA prepared from *E. coli* strain MG1655 as the template DNA for the PCR amplification reactions (Current Protocols in Molecular Biology, *Ibid*). To amplify a DNA sequence
15 containing the *E. coli groE* operon, genomic DNA (12.5 nanograms) was introduced into each of two reaction vials containing 0.5 micromoles of each synthetic oligonucleotide primer, 1.5 mM MgCl₂, 0.2 mM each deoxynucleotide triphosphate (dATP, dGTP, dCTP & dTTP) and 2.6 units heat stable DNA polymerases (Expanded High Fidelity PCR System, Boehringer Mannheim, Indianapolis, Indiana) in a final
20 volume of 50 microliters. The following thermal cycling conditions were used to obtain amplified DNA products for the *groE* operon using a Perkin Elmer Cetus/ GeneAmp PCR System 9600 thermal cycler:

25 *Conditions for amplification and cloning of the E. coli groE operon;*

25 Denaturation at 94°C for 2 min,
2 cycles at 94°C for 15 sec, 30°C for 30 sec and 72°C for 2 min
23 cycles at 94°C for 15 sec, 55°C for 30 sec and 72°C for 2 min
Reactions were concluded at 72°C for 8 minutes

30 Upon completion of thermal cycling reactions, the amplified DNA was washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA). The amplified DNA sample was subjected to digestion with the restriction endonucleases, *EcoRI* and *ScaI* (New England Biolabs, Beverly, MA USA) (Current
35 Protocols in Molecular Biology, *Ibid*). The DNAs from each of two reaction mixtures were pooled and subjected to electrophoresis in a 1.0% SeaPlaque (FMC BioProducts, Rockland, ME, USA) agarose gel. DNA was visualized by exposure to ethidium bromide and long wave uv irradiation. DNA contained in slices isolated from the

agarose gel was purified using the Bio 101 GeneClean Kit protocol (Bio 101 Vista, CA, USA).

A DNA fragment, *EcoRI* to *ScaI*, containing the *E. coli groE* operon was cloned into the corresponding sites of the pACYC184 expression vector (New England Biolabs, Beverly, MA, USA) to make pACYC184-*groE*. The BL21(DE3) strain of *E. coli* was transformed with pACYC-*groE*. A tetracycline-resistant transformant overexpressing proteins of $M_r \sim 14,000$ (GroES) and $M_r \sim 60,000$ (GroEL) was isolated.

10 *Transformation of E. coli strain BL21(DE3) carrying the pACYC-groE plasmid of E. coli.*

Competent bacteria derived from a clone of strain BL21(DE3) carrying the pACYC-*groE* plasmid were transformed with 50 nanograms of pET23-*murI* plasmid DNA, isolated as described above (Current Protocols in Molecular Biology, Ibid). A clone of BL21(DE3) carrying both the pACYC-*groE* expression plasmid and the pET-23-*murI* plasmid was isolated and used for expression of recombinant glutamate racemase as described below.

Expression of recombinant H. pylori murI

A bacterial clone of BL21(DE3) carrying both the pACYC-*groE* expression plasmid and the pET-23-*murI* plasmid was cultured in LB broth supplemented with 1.0 mM D,L-glutamic acid and 100 microgram/ml ampicillin and 10 micrograms/ml tetracycline at 30°C until an optical density at 600 nm of 0.5 to 1.0 O.D. units was reached, at which point, isopropyl-beta-D-thiogalactoside (IPTG) was added to the culture at a final concentration of 1.0 mM. Cells were cultured overnight to induce gene expression of the *H. pylori* recombinant DNA constructions .

After induction of gene expression with IPTG, bacteria were pelleted by centrifugation in a Sorvall RC-3B centrifuge at 3000 x g for 20 minutes at 4°C. Pellets were resuspended in 50 milliliters of cold 10 mM Tris-HCl, pH 8.0, 0.1 M NaCl and 0.1 mM EDTA (STE buffer). Cells were then centrifuged at 2000 x g for 20 min at 4°C. Pellets were weighed (average wet weight = 6 grams/liter) and processed to purify recombinant protein as described below.

Purification of soluble glutamate racemase

All steps were carried out at 4°C. Cells were suspended in 4 volumes of lysis buffer (50 mM Potassium phosphate, pH 7.0, 100 mM NaCl, 2 mM EDTA, 2 mM EGTA, 10% glycerol, 10 mM D,L-glutamic acid, 0.1 % β -mercaptoethanol, 200 μ g/ml lysozyme, 1 mM PMSF, and 10 ug/ml each of leupeptin, aprotinin, pepstatin, L-1-

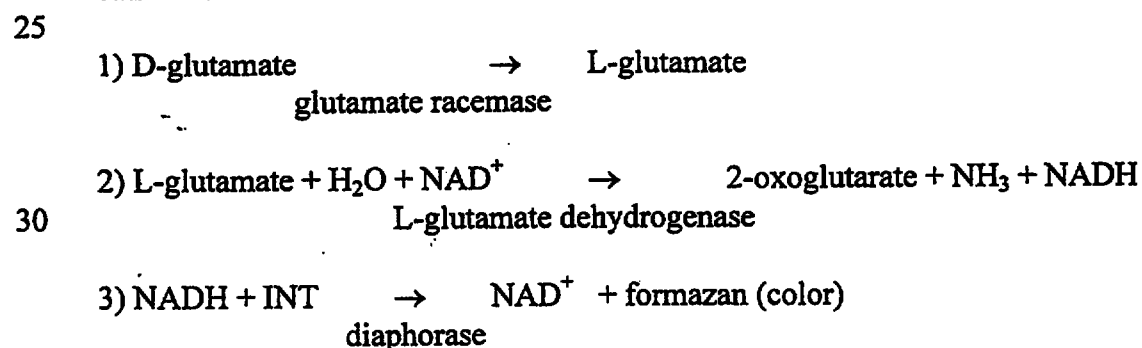
chloro-3-[4-tosylamido]-7-amino-2-heptanone (TLCK), L-1-chloro-3-[4-tosylamido]-4-phenyl-2-butanone (TPCK), and soybean trypsin inhibitor, and ruptured by three passages through a small volume microfluidizer (Model M-110S, Microfluidics International Corporation, Newton, MA). The resultant homogenate was diluted with 1 volume of buffer A (10 mM Tris-HCl pH 7.0, 0.1 mM EGTA, 10 % glycerol, 1 mM DL-Glutamic acid, 1 mM PMSF, 0.1% beta-mercaptoethanol), made 0.1 % Brij-35, and centrifuged (100,000 x g, 1 h) to yield a clear supernatant (crude extract).

After filtration through a 0.80-um filter, the extract was loaded directly onto a 20 ml Q-Sepharose column pre-equilibrated in buffer A containing 100 mM NaCl and 0.02 % Brij-35. The column was washed with 100 ml (5 bed volumes) of Buffer A containing 100 mM NaCl and 0.02 % Brij-35, then developed with a 100-ml linear gradient of increasing NaCl (from 100 to 500 mM) in Buffer A. A band of $M_r = 28,000$ corresponding to glutamate racemase, the product of the recombinant *H. pylori murI* gene, eluted at a gradient concentration of approximately 200-280 mM NaCl. Individual column fractions were then characterized for glutamate racemase activity (see below for description of assay) and the protein profile of the fractions were analyzed on 12 % acrylamide SDS-PAGE gels.

Fractions containing glutamate racemase were pooled, brought to 70% saturation with solid $(\text{NH}_4)_2\text{SO}_4$, stirred for 20 min, and then centrifuged at 27,000 x g for 20 min. The resulting pellet was resuspended in lysis buffer to a final volume of 8 ml and loaded directly onto a 350-ml column (2.2 x 92 cm) of Sephacryl S-100HR gel filtration medium equilibrated in buffer B (10 mM Hepes pH 7.5, 150 mM NaCl, 0.1 mM EGTA, 10% glycerol, 1 mM D,L-glutamic acid, 0.1 mM PMSF, 0.1 % beta-mercaptoethanol) and run at 30 ml/h. Fractions found to contain a glutamate racemase activity were pooled, and 0.5 volume of buffer C (10 mM Tris pH 7.5, 0.1 mM EGTA, 10% glycerol, 1 mM D,L-glutamic acid, 0.1 mM PMSF, 0.1 % B-mercaptoethanol) was added (to reduce the NaCl concentration to 100 mM), and loaded onto a MonoQ 10/10 high-pressure liquid chromatography column equilibrated in buffer C containing 100 mM NaCl. The column was washed with 5 bed volumes of this buffer and developed with a 40 ml linear gradient of increasing NaCl (from 100 to 500). Glutamate racemase eluted as a sharp peak at 310 mM NaCl. Fractions containing a glutamate racemase activity were pooled, concentrated by dialysis against storage buffer [50% glycerol, 10 mM 3-(N-morpholino)propanesulfonic acid (MOPS) pH 7.0, 150 mM NaCl, 0.1 mM EGTA, 0.02 % Brij-35, 1 mM dithiothreitol (DTT)], and stored at -20°C.

*Assays for glutamate racemase activity.*Conversion of D-glutamate to L-glutamate (two enzyme coupled assay)

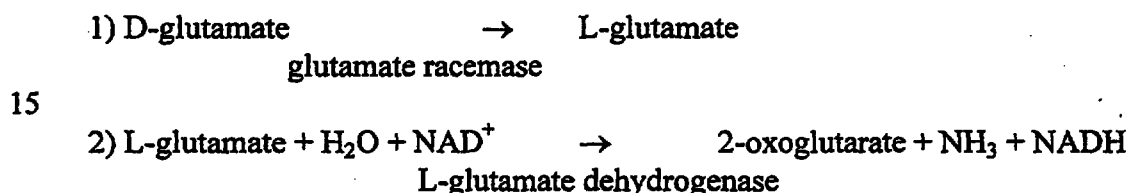
The activity of glutamate racemase, interconversion of the enantiomers of glutamic acid, was measured using D-glutamic acid as substrate. The method of Gallo and Knowles (Gallo, K.A. and Knowles, J.R., 1993, Biochemistry 32, 3981-3990) that was used to measure the glutamate racemase activity of *Lactobacillus fermenti* was adapted for the measurement of glutamate racemase activity of the *H. pylori murI* gene product isolated as a recombinant protein from *E. coli*. In this assay, the measurement of the activity of glutamate racemase is linked to an OD change in the visible range in a series of coupled reactions to the activities of L-glutamate dehydrogenase (reduction of NAD to NADH) and diaphorase (reduction of the dye p-iodonitrotetrazolium violet, INT). Initial rates were determined by following the increase in absorbance at 500 nm in a reaction volume of 200 μ l containing 50 mM Tris-HCl, pH 7.8, 4% v/v glycerol, 10 mM NAD, 2 mM INT, 60 Units/ml L-glutamate dehydrogenase, 5 Units/ml diaphorase, and varying concentrations of either substrate (from 0.063 mM to 250 mM D-glutamic acid) or purified enzyme (from 1 μ g to 50 μ g). After a preincubation of all reagents except either the substrate (D-glutamic acid) or the enzyme (*murI* gene product) for a period of 5 minutes, reactions were initiated by adding the missing ingredient (i.e., the enzyme or the substrate, as required), and the increase in optical density at 500 nm was measured in a Microplate Spectrophotometer System (Molecular Devices, Spectra MAX 250). Measurements were followed for 20 minutes, and initial velocities were derived by calculating the maximum slope for the absorbance increases. The coupled reaction can be summarized as shown below:

Conversion of D-glutamate to L-glutamate (single enzyme coupled assay)

In this assay, the conversion of D-glutamic acid to L-glutamic acid is coupled to the conversion of L-glutamic acid and NAD^+ by L-glutamate dehydrogenase to 2-oxoglutarate, ammonia. The production of NADH is measured as an increase of

- 128 -

absorbance at 340 nm (the reduction of NAD^+ to NADH) at 37°C. The standard assay mixture (adapted from Choi, S-Y., Esaki, N., Yoshimura, T., and Soda, K., 1991, Protein Expression and Purification 2, 90-93) contained 10 mM Tris-HCl, pH 7.5, 5 mM NAD^+ , 5 Units/ml L-glutamate dehydrogenase, varying concentrations of the substrate D-Glutamic Acid (0.063 mM to 250 mM), and the purified recombinant *H. pylori* enzyme glutamate racemase (1 μg to 50 μg). The reaction was started by the addition of either the substrate D-glutamic acid or the recombinant glutamate racemase after a preincubation at 37°C for 5 minutes with all of the other assay ingredients. The change in absorbance at 340 nm was measured in a Spectra MAX 250. Initial velocities were derived from the initial slopes. The coupled reactions can be summarized as shown below:



Results

1) Expression of the *H. pylori murI* gene in *E. coli* cells

To examine its biochemical properties, the *H. pylori* glutamate racemase was overexpressed in *E. coli* and purified. In the presence of the *E. coli* chaperones GroES and GroEL, the glutamate racemase was expressed as a soluble protein. About 20 mg of soluble MurI was produced per liter of culture as judged by intensity of the protein band after SDS-PAGE. No band corresponding to the molecular weight of *murI* protein was seen in control gel lanes containing extracts from cells transformed with the pET vector lacking a *murI* insert. Addition of 1 mM DL-glutamic acid during cultivation of the expressing cells increased the apparent expression level by about five-fold.

2) Purification of recombinant *H. pylori murI* protein

MurI was purified by cation exchange chromatography and gel filtration. Upon SDS-PAGE analysis, the purified protein migrated as a single polypeptide species with an apparent mass 29 kDa which is consistent with the predicted mass of 28,858.

3) Kinetic properties of recombinant *H. pylori* murI enzyme

Kinetic constant for recombinant glutamate racemase were estimated by assaying its activity at various concentrations of protein and D-glutamic acid as described above.

Purified recombinant *H. pylori* glutamate racemase exhibits a $V_{\max}$ of ~ 300

5 nmoles/min/mg protein ($k_{\text{cat}} = 8.6 \text{ min}^{-1}$) and a K_m of ~100 μM for D-glutamate.

Although the $V_{\max}$ value is lower than that observed for highly purified glutamate racemase from some other bacterial species, its K_m for D-glutamic acid is higher than that observed for the enzyme from most other species, resulting in a catalytic efficiency (k_{cat}/K_m) which is typical of purified preparation from *E. coli* and *P. Pentococcus*.

10

4) Characterization of MurI: Inhibition by L-serine-O sulfate

The *H. pylori* glutamate racemase was tested for inactivation with a suicide inhibitor, L-serine-O sulfate, which is known to inhibit *murI* from *E. coli*. The enzyme was incubated in the presence of 20 mM L-serine-O sulfate, and at different times

15 interval, aliquots were removed to determine residual activity. The initial velocity of purified recombinant *H. pylori* murI protein was determined in the single enzyme

coupled assay following incubation with the inhibitor L-serine-O-sulfate (LSOS) at 20 mM for the times indicated on the x-axis. The control was incubated in an identical manner but without LSOS. As shown in Figure 7, the *H. pylori* glutamate racemase can

20 be readily inactivated by the inhibitor.

Future application of the glutamate racemase activity in high throughput drug screening assays.

The assays for measurement of *H. pylori* glutamate racemase activity described
25 above have been carried out in 96-well plates in which multiple reactions were conducted simultaneously. Measurements of activity in a multi-well format are readily amenable to scale-up to permit rapid analysis of numerous compounds for inhibition of the glutamate racemase activity. Compounds which inhibit the activity of glutamate racemase may have application as novel antibiotics and may be suitable for the treatment
30 and eradication of bacterial (e.g., *H. pylori*) infections in humans. Known inhibitors of glutamate racemase, such as L-serine-O-sulfate, can be used to calibrate high throughput screens of new compound libraries to facilitate identification of new compounds with properties suitable for *in vivo* human therapeutics.

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments and methods described herein. Such equivalents are intended to be encompassed by the scope of the

5 following claims.

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- (ii) TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI AND
VACCINE COMPOSITIONS THEREOF

- (iii) NUMBER OF SEQUENCES: 1298

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- (A) MEDIUM TYPE: CD/ROM ISO9660
- (B) COMPUTER:
- (C) OPERATING SYSTEM:
- (D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/625,811
- (B) FILING DATE: 29-MAR-1996

(viii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/758,731
- (B) FILING DATE: 02-APR-1996

(ix) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/736,905
- (B) FILING DATE: 25-OCT-1996

(x) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/738,859
- (B) FILING DATE: 28-OCT-1996

(xi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/761,318
- (B) FILING DATE: 06-DEC-1996

(xii) ATTORNEY/AGENT INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GAAGAGATAA GGGACTTGAA AAAAATCATC AGCGCACAAA ACACGGAGAT TAACCAATTA	180
AGAAAAGTGC AAGAAGTCTT ATCTGGGCAA TTAGGGGACA TGCCTAAGGA TATATTAAGC	240
ACTAGAGATT ACTGTATCAG CTTAAGGCCT TATATTTATA ATTGGCGC	288

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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AAGCTTTTAG AAATCCAAAG GGAAGCGGCG AAAATGACCG CTATTTTGG GGCCAAACAA	180
CCTCACCCAC AAAGCCTAAC GGTGGGGGGT GTTACGAGTG TCATGGATAT ATTGGATCCA	240
ACAAGGTTGG CTGAATGGAA GAGCAAGTTT GAAGTGGTGG CTAATTTTAT CAACCATGCT	300

TACTACCCTG	ATTTGGTGAT	GGCAGGCGAA	ATGTTTCGCTA	ACGAACCATC	TGTTATTAAA	360
GGCTGTGGTT	TAAGGAATTT	TATCGCTTAT	GAAGAAGTGT	TGCTTGGGAA	GGATAAATAC	420
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AGCGTGGGGA	TTGAAAATAA	AATAATCCCT	GCTAAAGTGC	TTGACACTAA	GGATAAATAT	660
TCTTGATAAA	AATCGCCCAG	ATACGATAGT	AAGCCCATGG	AAGTAGGGCC	TTTAAGTTCC	720
GTAGTGGTAG	GTTTAGCGGC	GAAAAACCCT	TATGTTACTG	AAGTGGCTAC	TAAATTTTTA	780
AAAGACACGA	AACTGCCTTT	AGAGGCGTTG	TTTTCAACGC	TTGGGCGCAC	AGCTGCAAGG	840
TGTATTGAAG	CTAAGACTAT	CGCTGATAAT	GGTCTTTTGG	CGTTTGACGC	GTTAGTGGAA	900
ATC						903

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGATTAACA	TGTCAAAAAA	AATCGTAGTC	GATCCTATCA	CTAGGATTGA	GGGGCATTTA	60
AGGATTGAGG	TGATCGTAGA	TGATGATAAT	GTGATCACCG	ATGCGTTTTT	TTCTTCTACG	120
CTTTTTAGGG	GGCTAGAAAC	GATCATTAAAG	GGCAGAGACC	CACGAGATGC	AGGCTTTATC	180
GCTCAAAGGA	TTTGTGGGGT	ATGCACTTAT	TCGCATTATA	AAGCCGGTGT	TACTGCGGTA	240
GAAAACGCTT	TAGGAATCAC	TCCCCCATT	AACGCGCAAT	TGGTGCGATC	TTTGATGAAC	300
ATGGCGTTGC	TTTTTTCACG	TCATGTGGTG	CATTTCATATA	CTTTGCATGG	GCTTGATTGG	360
TGCGATATTT	TGAGCACTTT	AAAAGCTGAT	CCCATTC AAG	CAGCAAAACT	TTCTTTCAAA	420
TACAGCCCTT	ATCCCATTA	TACCGGTGCG	GGGCGAATTA	AAAGCGGTTC	TAAAACGCTT	480
GGAATGATTT	CGTTAAAAGC	GGATCTT				507

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGGCTATGGT TACACCAAAG AATGAGTCAA AAAATCCTAA TTTTAGGCAT TGGCAATATC	60
CTTTTGGCG ATGAAGGGAT TGGGGTGCAT CTAGCCCACT ACCTCAAAAG GAATTTTCT	120
TTTTTCCCTA GCGTGGATAT TGTGGATGGG GGGACTATGG CTCAGCAACT CATTCTTTA	180
ATCACTTCGT ATGAAAAGGT TTTGATTTTA GATTGCGTGA GCGCTAAAGG CGTTGAAATT	240
GGCTCAGTTT ATGCCTTTGA TTTAAGGAC GCTCCTAAAG AAATCACATG GGCTGGGAGT	300
GCGCATGAAG TGGAAATGCT GCACACTTTA AGGCTCACGG AGTTTTTAGG GGATTGCTT	360
AAAACCTTTA TCGTGGGGCT TGTGCCTTTT GTGATAGGGA GCGAGACCAC TTTCAAGCTT	420
TCAAGCGAAA TGTTAAACGC TTTAGAAACA GCCCTAAAAG CCATAGAAAC CCAACTCAAC	480
GCATGGGGAG TAAAATGCA ACGCACCGAT CATATTGCCC TAGATTGTAT CGCTGAACTC	540
TCTTATAAGG GTTTT	555

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TATCAAATCT TAAACCAAAG AAAAACCATG AAAAAAGTCC TCTTACTAAC TCTCTCTCTC	60
TCTCTCTCGT TTTGGCTCCA CGCTGAAAGG AACGGATTTT ATTTAGGTTT AAATTTTGCA	120
GAAGGAAGCT ATATTCAAGG ACAAGGTAGC ATCGGCGAAA AAGCTTCAGC AGAAAACGCC	180
TTAAATCAAG CGATCAATAA CGCACAAAAT TCATTATTCC CTAACACACA AGCCATAAGA	240
GATGTGCAAA ACGCCTTAAA TGCAAGTAAA GATTCAAACA AAATCGCTAA CCGATTGCGA	300
GGAAATGGTG GATCGGGCGG TATT	324

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGCGTTAGTG GAAATCTAAA GAGCGATCAA AGCACTTGTG CTCCTTATCA TATTGATAAA	60
AATCAAGAAT ATAAAGGGCG CTACATTGGT CAAGTGCCAA GGGGCATGTT AAGCCATTGG	120
GTGCGTATTA AAAACGGCGT GGTGGAAAAT TATCAAGCGG TAGTGCCTTC CACTTGAAT	180
GCAGGGCCTA GAGATTCTAA AAATCAAAGG GGGGCTTATG AAATGAGCTT GATTGGCACT	240
AAAAATCGCTG ATTTAACCCA GCCTTTAGAA ATCATTAGGA CTATCCATTC TTTTGATCCA	300
TGCATCGCAT GCTCAGTGCA TGTGATGGAT TTAAAGGGC AGTCTTTGAA CGAGTTCAAA	360
GTAGAGCCTA ATTCGCTAA ATTC	384

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTATACCAGA ACGACAAGGG TTTTAAAACA GAACTGCGCA TTTTGAGCGT GTTTATCGTG	60
GAATTTTTTG TGAATATTCT AGGGTTTATG TTGGCTCATA TGCTTCATTT CTGGTTTTTA	120
AGGTGCGTTA AAGCTTTAGC GTGGCTCATG AAAACTTTTG ATAGGCGCCG TTATTTTGAC	180
GCTAAGGCCA ATTTGGATTT TGTGTTTGA GATTCTAAAA GCGAAGAAGA GAAAAAAGG	240
ATCATTAATAA AAGGGGTA	258

(2) INFORMATION FOR SEQ ID NO:8:

137

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TACAAAAAAG GAAATCAAAT AATGAATATT CAAACAAAGA AAAGATTTTT AGCAAATTTA	60
TTGCTTTTTA GCCTGTTTTT TTGCCTTAAG GCTGAAACCC TTTCAGAAGA CCATCAAATC	120
CTGTTGAGTT CAGACGCTTT CCATAGAGGG GATTTTGCCA CCGCTCAAAA AGGCTATATG	180
AATCTCTATA GAGCAAACCA A	201

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 768 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...768
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTGTGTTTGA AACTCTTAAT TTGGAATTTT AAGGAGCATT CTTTGAAAGT CAATTTCTTT	60
GCCACTTGTC TAGGAGCAGC TATTTATAGC AACGCATCGC TTAACGCTAT CAAATTACTC	120
CGCAAGGAAA ATTTGGAAGT GGTTTTTAAA AAAGACCAGA CATGTTGTGG CCAGCCAAGC	180
TACAACTCAG GATACTATGA AGAGACTAAA AAAGTCGTTT TATACAATAT CAAACTTTAT	240
TCCAATAACG ACTACCCTAT TATTTTGCCT AGCGGTTTCAT GCACAGGGAT GATGCGGCAT	300
GATTATTTGG AATTGTTTGA AGGGCATGCG GAATTTAACA TGGTTAAAGA TTTTGTCTCT	360
AGGGTGTATG AATTGAGCGA GTTTTGGAT AAAAAATTGC AAGTCAAATA CGAAGATAAG	420
GGCGAACCTC TCAAAATCAC ATGGCATTCT AATTGCCATG CCTTAAGGGT GGCTAAAGTG	480

ATTGACTCGG	CGAAAAATCT	CATCAGACAG	CTTAAAAATG	TGGAATCAT	TGAATTGGAA	540
AAAGAAGAAG	AATGCTGCGG	GTTTGGGGGG	ACTTTTTCAG	TTAAAGAGCC	TGAAATTTCA	600
GCGGTTATGG	TCAAAGAAAA	GATTAAAGAC	ATAGAGAGCC	GTCATGTGGA	TGTGATCGTT	660
TCAGCGGATG	CTGGGTGCTT	GATGAATATC	AGCACCGCTA	TGCAAAAAAT	GGGCTCTTTG	720
ACAAAACCCA	TGCATTTTTA	TGACTTTTTA	GCCTCAAGGC	TTGGACTT		768

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGAAAAAGA	TTTTTTTAGG	TATGGCATT	GCCTTTAGTG	TGTCCATGGC	AGAAAAAAGC	60
GGCGCGTTTT	TAGGAGGGGG	GTTTCAATAT	TCTAATTTAG	AAAACCAAAA	CACCACCCGC	120
ACCCCAAGCG	CTAACAATA	CACCCCGATA	AACACTTCAA	TGTTTGCCAA	CAATCAAGCG	180
GCTCCAGCCC	AAGAAACGCC	AAGCGTGATC	AACACCAATA	ATTACGGGCA	AATGTATGGG	240
GTAGATGCGA	TGGCAGGGTA	TAAGTGTTTC	TTTGGCAAAA	CCAAACGCTT	TGGCTTTAGG	300
ACTTATGGAT	ACTACAGCTA	TAACCATGCG	AATTTGAGCT	TTGTAGGCAG	TAAGCTTGGA	360
ATCATGGATG	GCGCATCTCA	AGTGAATAAC	TTCACTTATG	GCGTGGGCTT	TGATGCGCTC	420
TATAACTTCT	ATGAAAGCAA	AGAGGGCTAT	AACACAGCAG	GGTTGTTCGT	GGGCTTTGGA	480
TTAGGAGGGG	ATTCTTTTAT	CGTTCAAGGA	GAGAGCTACT	TGAAATCTCA	GATGCAAATT	540
TGCAACAACA	CCGCCGGCTG	TTCAGCGAGC	ATGAACACGA	GCTACTTCCA	AATGCCTGTG	600
GAATTTGGTT	TTAGGAGCAA	TTTCTCTAAA	CACAGCGGGA	TTGAAGTGGG	CTTTAAATTG	660
CCTTTATTTA	CCAACCAATT	CTATAAAGAA	AGGGGCGTAG	ATGGATCGGT	AGATGTGTTT	720
TATAAAAGGA	ATTTCTCTAT	CTATTTTAAAC	TACATGATCA	ACCTC		765

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

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GCATGTGAAA TTAGAGCATG GCGGTTTGAT AGAATGTTAA GGGTTTTAAG CGTTGGTGTG      60
GTTTTTATTT TACTAGGGTG TCAGTTTTTC AACAAAACGA CTCTGCATTT AAAATATAAG      120
GATTACCCCA AAAACAGCCC TTTAAAAACC GCTTCCACTT TAACCCCCC TAAAATCTTT      180
TTTAACGCTC ATTTGTGCC GCCCTTTTAC CAAAAAGAAT TAAAAAAGC GCTCGCCCAG      240
CAAATCGCTT ATTTTTTAAA GGATAAAAGC GCTCTCACTT TCAATATTTT AGGCAATGTT      300
TTTTTTTCTT TTGAAGAGAG TCCTAAGGAT TTAAAGCCA TTAAAGAAAG GCTTAAAAAG      360
ACGATTGAGC CTAACACTGA CCAAAAGCC GTCATGCGTT TTTTAAACCT TCAAGCGAGC      420
TTGATTTTAG AATGTGTCCC ACAAACCGCT TGCCCATTTG ACACCCTTTT AATCCCCACC      480
GCTCTCAGCG TGCCTATTGA TTACGCCAAT CGTTTGGGCG ATAACCCCTC TCTTTTTCCC      540
CAAGAAGATA AATCCTATCA TAACGCTTTA ATCAAAGCCC TTAATAAGGC TTACTATTCT      600
CTTATGGAGG GTTTAGAAAA GCGTTTGAAC GCTATAGAAA ATGCGGCATG GCTT          654

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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ACGATCCAAG AAAGGCTTTA CCGCCATGAA ATCAGCCGCT TGCAGGTAAA GACTGATGAA      60
ACTTTAAAAC TCATTAAAGA AGCCAAAAG CGTTTGAATT ATAACGATGA TATACGAGAT      120
GTTTTGCAAG GGCTTTTGAA TATTGTGCCG GATCTTATCA CCATTAATAG CATTGAAATA      180
GACCAACAAA GCGTGGTGGT TAGCGGTAAA ACCCCCTCTA AAGAAGCCTT TTACTTTTGT      240
TTTCAAAACA AACTAAACCC CATGTTTGAT TATTCTAGGG CGGAATTTT CCCTTTAAGC      300
GACGGGTGGT TTAATTTTGT CTCCACCAAC TTTTCTAATT CCTTACTGAT AAAAAACCCG      360
GAGTCTATTA AA                                     372

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1134 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATCTCTATAG	AGCAAACCAA	TAAAGTGGTG	TATGCTAAAG	AGGCGGCCAT	TTCAGCGGCG	60
AGTTTAGGGG	ACATTAAAAC	CGCTATGCAT	TTAGCCATGC	TTTATCAAAA	AATCACCAAT	120
AATCGTAACG	ATGTTTCTAT	CAATAAGATT	TTAGTGGATG	GCTATGCACA	AATGGGGCAG	180
ATTGATAAGG	CGATTGAACT	ATTACACAAG	ATTCTGAAGG	AAGAAAAAAC	CATAGCCACA	240
GACAATGTGT	TAGGGACTTT	GTATTTGACT	CAAAAGCGTT	TGGATAAGGC	TTTCCCGTTG	300
TTGAATAAGT	TTTATAACCA	AGTGCATGAT	GAAGACAGCC	TAGAAAAACT	CATTACGATC	360
TATTTTTTAC	AAAACCGCAA	AAAAGAGGGT	TTGGTTCTGT	TGCAATCTCA	TATAGACAGG	420
TATGGTTGCT	CAGAGCAATT	GTGCCAAAAA	GCGCTCAACA	CCTTCACGCA	ATTTAACGAG	480
CTTGATTTGG	CTAAAACGAC	TTTCGCTCGT	TTGTATGAAA	AAAACCCCTAT	TGTTCAAAAC	540
GCCCAATTTT	ACATAGGGGT	ATTAATCTTG	TTAAAAGAGT	TTGATAAGGC	CCAGCAAATC	600
GCAGAATTAT	TCCCCTTTGA	CAGGCGTTTG	TTGCTAGACT	TATACACCGC	GCAAAAAAAA	660
TTTGATCAAG	CTTCCAAACA	GGCTTCTTTA	ATCTATCAAG	AAAGAAAAGA	CCCTAAATTC	720
TTAGGCTTAG	AGGCGATTTA	TCATTATGAA	AGCTTGAGCG	CGAATAAGAA	AAAGCTCACC	780
AAAGAAGAGA	TGTTGCCCAT	CATTCAAAAA	TTAGAGCAAG	CCACCAAAGA	GCGCCAAGCA	840
TGGCTTGCTA	AAACTAAAGA	TAAAGAAGAC	GCGCAAGACG	CTTCTTTTTA	TAATTTTTTTA	900
GGGTATTTCCT	TAATAGATTA	TGACATGGAT	GTTAAAAGGG	GCATGGATCT	TGTGAGGAAA	960
GCCTTAGCGT	TAGATTCTAA	CTCAGTGCTT	TATTTGGATT	CTTTAGCATG	GGGTATTATC	1020
AAATTAGGGA	ATTGTTTGGG	GGCTAAAAAA	ATCTTTTCTA	GCATCGCTAA	AGAGCTTATC	1080
CAAAACGAAC	CCGAATTGAA	AGAACACAAT	AAAATCATTC	AAGAATGCAA	GAAA	1134

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

141

(B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTTACACTG	GCAAAAAGGG	GGCTTGCATG	CGTAAGATCT	TGTTAATGGG	CTTGATTTTA	60
CAAGCGCTCT	TTGGCGAAGA	AACCGCGCAA	GAATTGTTGC	AATGCTCTGC	GATTTTGTAA	120
TCTAAAAAAG	CCGAATTGAA	AGAGGATTTG	CGCCAATTGA	GTGAAAAAGA	GCAGTCTTTG	180
AGGATCTTGC	AAACCGAAAA	CGCCCGCCTT	TTAGATGAAA	AAAGCGATCT	GTAAACAAG	240
AAAGAAAAAG	AAATAGACGA	AAAAC TGAAA	AATTTAGCCG	CTAAAGAAGA	AGCCTTTAAA	300
ACCTTACAAA	CAGAAGAAAA	AAAACGCCTT	AAAAATTTGA	TAGAAGAAAA	TGAAGGCATT	360
TTAAGAGAAA	TCAAGCAGGC	TAAAGACAGC	AAGATTGGCG	AGACTTATTC	TAAAATGAAA	420
GATTCTAAAT	CGGCTCTGAT	TTTAGAAAAT	TTACCCACTC	AAAACGCT		468

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAAAGGCTTT	GTGATAGGCT	TTGGAGCGGG	GGATATTACC	TATCAGTTGA	GAGGCGAAAT	60
GTAATGGGCG	TAGCGGTTGT	TTTATTTTAA	ACGCTAATTT	TATTGTTTTT	AGTTTTAAGG	120
GATTTTGGTT	TAGCTAGCCC	CAAACAAAAG	ATTTTAGCTT	TTTAAATCGT	AGGGATTATA	180
GGAGCGAGCA	TCAGCGTTTA	TACTTATAAA	CAAAACCAAC	AAAACCAACA	AGAAATCGCT	240
TTGCAAAGAG	CGTTTTTAAAG	GGGGGAAACC	TTGTTGTGTA	AAGGCATCAA	AGTCAATAAC	300
CAAACCTTTA	ATTTAGTGAG	CGGGACTTTG	AGCTTTT TAG	GCAAAAAACA	AACCCCTATG	360
AAAGATGTTT	TTGTGGATTT	GGATTCTTGT	CAGACGCTTC	AAAAAGATCC	CTTAATCCAA	420
CCT						423

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCAAAAATA CTATTTTAA TAACGCTAAT TTAAACAACA GCACTTCTTT TAATTTCAAT	60
AATTCTAGCG CGACCACTTC GTTTGTGGGG GATTTCATA ACGCTAATTC AAATTTGCAA	120
ATCGCTGGGA ACGCTGTTT TGGGAACCTCT ACTAATGGCT CTCAAAATAC CGCTAATTTT	180
AATAATACCG GCTCTGTTAA TATTGCAGGG AATGCAACCT TTGATAACGT GGTATTTAAC	240
AGCCCTACGA ACACAGGCGT GAAAGGGAAA GTTACTCTCA ATAACATCAC TTAAAAAACT	300
TGA	303

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TGGGCGATGA ATGTTTGGGT GTATAGGCCT TTGTTGGCTT TTATGGATAA CAGACAGGCA	60
GAGATAAAGG ACAGCTTGGC TAAAATCAAA ACGGATAACA CCCAAAGCGT GGAGATTGGC	120
CATCAAATTG AGACTCTTCT TAAAGAAGCC GCTGAAAAGC GCAGGGAAAT GCTAGCAGAA	180
GCGATTCAAA AAGCTACAGA GTCTTATGAC GCTGTGATCA AGCAAAAGGA GAACGAACTC	240
AATCAAGAGT TTGAAGCGTT CGCAAAGCAA TTACAAAATG AAAACAAAT CTTAAAAGAG	300
CAATTGCAAG CGCAAATGAC GGTATTTGAA GACGAGTTAA ACAAGCGTGT GGCTATGGGT	360
TTAGGGAGT	369

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

143

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AAGGGGGGAT TTATATCGGC AAAGAGTTGT TTAAGCATGG CTAGTGGCCT TTTTGAAAAC	60
GATGAAATCA AAAACAACAA AGCGCGAGAT TTTTTTTATA GCCATAGCTC CCTTATTGTC	120
TTTTTCCTCT TACTGCTTGG GTTTGGGTAT TATTTAGGGA AGTTGCTTTT TGGGGGTTCT	180
TCTTTAGAGG TCTATTTGGA TTTAAGAGAC AAGCATGAAC GATTGCAACA AGAAATCACC	240
GAATTGCAAA GCAAGAATGT GCGCTTGCAA AAGCGTTTGT TTGAGTTGAG GGAATTACGG	300
CCTAGAGAT	309

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 996 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTATACTATA ATAGCCAATT AAATTGGGGT TTTACTGATT TGTCTTTGTG CGAGCTTTGG	60
CTTAGTTTTG TAAGGAATGA GATGATAAAG AGTTGGACTA AAAAGTGGTT TTTGATTTTA	120
TTTTTAATGG CAAGCTGTTT TGGTCATTTG GTGGCTACAA CCGGTGAGAA ATATTTTAAG	180
ATGGCTAATC AAGCCCTTAA GAGAGGGGAT TACCATAGAG CCGTGGCTTT TTATAAGAGG	240
AGCTGTAATT TGAGGATGGG GGTGGTTGTC ACGAGTTTAG GCTCTATGTA TGAATATGGC	300
GATGGCGTGG ATCAGAATAT TTCAAAAGCC GTTTTTTATT ACAGAAGAGG GTGTAATTTG	360
AGGAATTATC TCGCTTGCGC GAGTTTAGGC TCTATGTATG AAGATGGCGA TGGCGTGCAA	420
AAAGACTTTC CAAAGGCTAT CTATTATTAT AGGAGAGGGT GCCACTTAAA AGGTGGGGTG	480
AGCTGCGGTA GTTTGGGTTT TATGTATTTT AATGGTACGG GCGTTAAACA AAATTACGCC	540
AAAGCCCTTT CTTTTTCTAA ATACGCTTGC AGTTTGAATT ATGGCATTAG TTGTAACCTT	600
GTAGGGTATA TGTATAAGAG CGCCAAAGGC GTGGAGAAGG ATTTGAAAAA AGCCCTTGCG	660
AATTTTAAAA GAGGGTGCCA TTAAAAGAC GGGGCGAGCT GTGTGAGCTT GGGATACTTG	720

TATGAAGCCG	GTATGGATGT	CAAACAAAAT	GAAGAGCAGG	CTTTGAATCT	TTATAAAAAG	780
GGTTGCTCTT	TAAAAGAAGG	GAGCGGTTGT	CATAATGTGG	CGGTGATGTA	TTACACGGGT	840
AAGGGAGCTC	CAAAGATTT	GGAGAAAGCC	ACTTCATATT	ATAAGAAAGG	GTGCGCTTTA	900
GGCTTTAGTG	GTAGTTGTAA	GGTGTTAGAA	GTGATTGGCA	AGGAGTCTGA	TAATTTGCAA	960
GATGACGCGC	AAAACGACAC	GCAAGATAGC	GTGCAA			996

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATTAAGGTGA	GGAGCGTCAA	AAAGACTGAG	CGAGGCTTAT	TGATTGAGAA	ATTCACCTTCT	60
CAAGGCGAAT	TAGTGCCCTT	AGAAATTGTG	GTAGAAACGA	TCCTTTCAGA	GATTAAAAGC	120
TCTAGTAAAG	GGATCATTTT	AATTGATGGC	TATCCCAGGA	GCGTGGAGCA	AATGCAAGCT	180
TTGGATAAGG	AATTGAACGC	TCCAAATGAA	GTGATTTTAA	AAAGCGTGAT	TGAAGTAGAA	240
GTGAGCGAAA	ACACCGCTAA	AGAAAGGGTT	TTAGGGCAGT	TT		282

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

145

CACTTTGTTT	TTAGGGGCGA	TTTTTGTTGG	GCTTATCGCT	ATTACTCCAT	AGATAAGGAG	60
AGAGAGACTC	AGAGGCATGA	CAGCTCTTAC	ATTGTGATAG	ACGAATTAGT	GGGCATGTGC	120
CTTGCGATGG	CGATTAACGG	ATTATCGTTA	GTGGGTGTGA	TCTTGAGTTT	TATCTTTTTA	180
GGATGCTATG	ATATTACTAA	ACCCTCACTC	ATTGGCAAAA	TAGACAAAGA	AGTTAAAGGG	240
GGCTTAGGGG	TTGTGGCTGA	TGACGCTTTA	GCCGGGGTTT	TAGCCGGATT	GAGCACGTTA	300
TTAGCCATCA	ATATTTTAGG	ATTTTTTAAC	ATTAAGTTT			339

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGTGGCCTG	TGGCTCTCAA	GCAGCCTAAT	AGGGTGTCCC	ATCATTTTTTA	TATCATGGCC	60
ATGCTTTTTTA	TTTTATTGTA	TGTAGAAATC	GTTTTTCATGT	TCCCTTGGGC	GATTGATTTT	120
AAAAAGTTAG	GCTTGTTTGG	GCTCGTTGAA	ATGCTAGGCT	TTGTCTTCTT	TTTGGCAATC	180
GGTTTTATTT	ACGCTTTAAA	GCGAAACGCT	TTGAGCTGGC	AAAAATTAGA	GGTGAAA	237

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTTGATTG	TGG	GCGTGC	GCAC	CAACTT	TGCA	AAAACCA	AATT	TCAATA	AAGCA	CAGATT	AGAC	60
CAAGGG	ATAG	AATTTG	GGGT	GAAATC	CCCT	GTTATC	GCCTC	ATAAAT	TATTT	TGCAAC	CCCA	120
GGCTCA	AGCG	CGAGCT	TATAT	GAGGA	ATTTT	AGCTTC	ATAT	GTGGG	CTATT	CAGTC	GGTTT	180

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTTG	GTTC	AA	GAGC	TTTT	AG	AAGA	ATTTT	ACAA	AGTGG	GCGA	AAGAG	ATTTAG	AAAA	60			
GGCG	CAGTT	G	TTT	TAAT	GCG	TTT	ATTG	ATC	GCGC	TAGTTT	TGTT	CTT	ATG	GTGG	TAAAT	120	
TTAG	GCG	CTA	AAGA	AGC	GGA	TTT	CATC	TCT	GATT	GGA	AAT	ACGG	ACTGG	C	CTTT	TATAAA	180
AACC	CTAG	GG	GTGT	TG	CGTG	CGCC	AAAT	G	CATG	G	CATTA	AAGG	CGA	ACA	AAGAA	ATC	240
ACCT	TTT	ATT	ATGA	AAA	AGG	CGA	AAAA	AAAA	ATC	CTTT	TACG	CCC	CTAA	AAT	CAAC	CATTG	300
GATT	TTA	AAA	CCTT	TAA	AGA	CGC	CTT	GAGT	TTGG	GTTTTT	GTAT	GAT	GCC	TAC	ATA	CAAC	360
CTGA	ATTT	AG	AAGA	ATCC	A	AGCG	ATTT	AC	CTT	TAC	ATCA	CCT	CTTT	AGG	GCAT	AAAG	420
GAGC	GTA	AGG	ATC	CTT	CCAA	GCCT											444

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAAAATAGGC ATAAACTCTT ATACCTTCTA CTTAAAAACC TTAATTTTTT AAAAACCATT	60
TCCACAATTT TTACACAAAA GAGGGTTATC ATTCGTTTCG AACAGGATT TTCTTGTTAT	120
CTTAATTTAA AGGTCAAAAC GATGAAAAAG TTAGCCGCTT TATTTT TAGT AAGCGCGTTG	180
GGGGTTATGA GTTTGAACGC ATGGGAGCAA ACCCTAAAAG CTAATGATT GGAAGTGAAA	240
ATCAAATCCG TGGGCAACCC CATTAAAGGC GATAACACTT TTGTGCTTAG CCCCACTTTA	300
AAAGGTAAGG CTTTAGAAAA AGCTATCGTT AGGGTGCAGT TTATGATGCC TGAAATGCCC	360
GGCATGCCAG CGATGAAAGA AATGGCGCAA GTGAGTGAAA AAAACGGCCT TTATGAAGCT	420
AAAACCAATC TTTCCATGAA CGGGACATGG CAGGTTAGGG TGGATATTAA ATCCAAAGAA	480
GGCCAAGTTT ATCGCACTAA AACAAGCCTG GATTTA	516

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGCTTATTTG TCCTTACAAA ATCTCAAAGG ATTAGAATGA AACGGCTTTT ATTGTTAGCC	60
TTGGCCCTCT TTTT TAGCCT CTCATGCACT AACGCTCAAG AAATTAAAGA AACTCAAGAG	120
ACTAAAAAAA CTAAAGAAAC TAAAAGCCAA ACCCGTTTTA ACATTTCAC CACTAAGGTC	180
ATAGAAAAAG AATTTTCTCA AAGCCGGCGC TATTACGCGC TT	222

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATAAAGTTTG	CTAAAAAGAT	AGTTTAAATT	TTAAAAAAG	GTGGTTTTAT	GAAAACAAAC	60
GGGCTTTTTA	AAATGTGGGG	GCTATTTTTA	GTTTTAATCG	CTTTAGTCTT	TAACGCATGC	120
TCTGATAGCC	ATAAAGAAAA	GAAGGACGCT	TTAGAAGTCA	TTAAACAAAG	GGGGGTTTTA	180
AAGGTGGGGG	TTTTTAGCGA	TAAGCCTCCT	TTTGGCTCTG	TGGATTCTAA	AGGGAACAT	240
CAAGGCTATG	ATGTAGTCAT	CGCTAAACGC	ATGGCCCTTG	ATTTATTGGG	CGATGAAAAT	300
AAGATTGAGT	TTATCCCTGT	AGAAGCCTCA	GCTAGGGTGG	AATTTTAAA	AGCCAATAAA	360
GTGGATATTA	TCATGGCTAA	TTTCACGCGC	ACTAAAGAAA	GAGAAAAAGT	CGTGGATTTC	420
GCTAATCCGT	ATATGAAAGT	CGCTTTGGGG	GTGATTCTTA	AAGATGGGGT	CATTAAAAAT	480
ATAGAAGAGC	TGAAAGATAA	AGAGTTGATC	GTGAATAAAG	GCACGACAGC	GGATTTTTAT	540
TTCACTAAAA	ATTACCCCAA	TATCAAACCT	TTGAAATTTG	AACAAAACAC	AGAGACTTTT	600
TTAGCCCTTT	TAAACAATAA	GGCCATCGCA	TTAGCCCATG	ATAACACTTT	GTTGCTCGCT	660
TGGGTGAAAC	AACACCCTGA	ATTTAAATTA	GGCATTACAA	GCCTTGCGCA	TAAGGATGTG	720
ATCGCTCCAG	CGATTAAAAA	AGGCAACCCT	AAGCTTTTAG	AGTGGTTGAA	TAACGAGATT	780
GATTCCCTCA	TTTCTAGCGA	CTTTTAAAAA	GAAGCTTATC	AAGAGACTTT	AGAGCCTATT	840
TATGGCGATG	GAATCAAACC	GGAAGAAATT	ATTTTTGAA			879

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2028 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCTTTTGAAG	AATTAGAGCC	TTTGAGTTTT	TCCTTCAATT	CGCCTAAAGG	GGCGTGCGAA	60
AGTTGTTTGG	GTTTAGGGAC	AAAATTTAGC	TTAGATATTA	GTAAGATTTT	AGATCCTAAC	120
ACGCCTTTAA	ATCAAGGAGC	GATTAAAGTG	ATTTTTGGGT	ATAACCGCAG	TTATTACGCT	180
CAAATGTTTG	AAGGCTTTTG	CACTTATAAT	GGCATTGACA	GCGCGCTTTG	TTTCAACGAA	240
TTGAACAAAG	AGCAGCAAGA	CGCTCTTTTG	TATGGGAATG	GCACTGAAAT	CAGCTTTCAT	300
TTTAAAAACA	GCCCCTTGAA	ACGCCCTTGG	AAAGGCATTA	TCCAAATCGC	TTATGACATG	360
TTTAAAGAGC	AAAAGGATT	GAGCGATTAC	ATGAGCGAAA	AAACCTGTTC	TTCGTGTAAT	420
GGGCATCGCT	TGAAAGCCTC	AAGTTTGAGC	GTCCAAGTCG	CTGGCTTGAA	AATGGCGGAT	480
TTTTTAACTA	AGCCCATTGA	AGAAGTCTAT	CATTTTTTTA	ATGATCCAC	GCATTTTAAC	540
TATCTTAACG	AGCAAGAAAA	AAAGATCGCT	GAACCCATTT	TAAAAGAGAT	TTTAGAAAGG	600

GTGTTTTTTT	TATACGATGT	GGGGCTAGGG	TATTTGACTT	TGGGGAGGGA	TGCGCGAACG	660
ATTAGCGGAG	GGGAGAGCCA	AAGGATACGA	ATCGCCAGTC	AAATCGGGAG	CGGTTTGACA	720
GGGGTTTTGT	ATGTTTTAGA	CGAGCCTAGC	ATTGGCTTGC	ATGAAAAAGA	CACGCTCAAA	780
CTCATCAACA	CCCTTAGGAA	TTTACAAAAA	AAGGGGAACA	CGCTCATTGT	CGTAGAGCAT	840
GATAAAGAGA	CGATTAAGCA	TGCGGATTTT	GTTGTGGATA	TTGGGCCAAA	GGCTGGAAGG	900
CATGGGGGTG	AAGTGGTTTT	TAGCGGGAGC	GTAAAAGATT	TATTGCAAAA	TAACCATTCT	960
ACCGCCTTGT	ATCTCAACGG	CACTAAAAAG	ATTGAGCGCC	CCAAATTGTA	ACCCCCTAAA	1020
GAAAAGCATT	TTTtagAAAT	TAAAAATGTC	AATATCAATA	ACATTAAGAA	TTTGAGCGTT	1080
CAAATCCCCT	TAAAACAATT	GGTGTGCATT	ACGGGGGTGA	GCGGGAGCGG	TAAAAGCTCG	1140
CTGATTTTAC	AAACCCTTTT	ACCCACCGCT	CAAACCCTTT	TAAACCATGC	TAAAAAAAAT	1200
CAAAGCTTGA	ATGGGGTGGA	GATTGTAGGG	TTGGAGTATT	TGGATAAAGT	GATTTATTTA	1260
GATCAAGCCC	CCATAGGCAA	AACCCACGCA	AGCAACCCCG	CCACTTACAC	GGGAGTGATG	1320
GATGAAATCA	GGATTTTATT	TGCCGAGCAA	AAAGAAGCTA	AAATTTTAGG	CTATAGCACG	1380
AGCCGTTTCA	GCTTTAATGT	TAAAGGAGGG	CGGTGTGAGA	AATGCCAAGG	CGATGGGGAT	1440
ATTAAAATAG	AAATGCACTT	TTTGCCCTGAT	GTGTTAGTCC	AATGCGATAG	CTGTAAGGGC	1500
GCTAAATACA	ACCCCCAAAC	TTTAGAAATC	AAGGTGAAAG	GCAAATCCAT	TGCTGATGTG	1560
TTGAACATGA	GCGTGGAAGA	AGCTTATGAA	TTTTTTGCTA	AATTCCCTAA	AATCGCTGTG	1620
AAGTTAAAAA	CGCTTATAGA	TGTGGGCTTA	GGCTATATCA	CTTTAGGGCA	AAACGCTACG	1680
ACTTTAAGTG	GGGGGGAGGC	TCAAAGGATC	AAATTGGCTA	AAGAATTGAG	TAAAAAAGAC	1740
ACAGGCAAAA	CCCTTTTATAT	TTTAGATGAG	CCTACCACCG	GTTTGCAATT	TGAAGATGTG	1800
AATCACCTTT	TACAAGTCTT	GCATTCTTTG	GTGGCGTTAG	GCAATTCCAT	GCTAGTGATT	1860
GAGCATAATT	TAGACATCAT	CAAAAACGCT	GACTACATTA	TAGACATGGG	GCCTGATGGG	1920
GGGGATAAGG	GCGGGAAAGT	CATTGCGAGC	GGCACGCCTT	TAGAAGTGGC	GCAAATTTGC	1980
GAAAAAACCC	AAAGCTATAC	GGGAAAATTT	TTAGCTTTGG	AATTGAAA		2028

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATTATTATTG	ACTATTCAAG	CCAGTATTTT	AGCGGGAGGG	CTGCGGCGTT	CTATCAAGCT	60
TTGGATAATT	TCATCTCACG	ATACGCGCAA	CGCTTGATCG	TAACCAATTT	GAGTCAAGCG	120
ATTCGCATTT	ATGGCTATGA	AGTGGGTGGG	ACTTTTAGAT	ACAAGGGCGT	GAGTTTGAAT	180
GTGGGGATCT	CGCGCACTTG	GCCCACCACT	AGGGGGTATT	TAATGGCGGA	CAGCTATGAG	240
CTTGCCGCAA	GCACCGGTAA	TGTTTTTATC	ATTAAATTGG	ATTACACCAT	TTCCAAAAAC	300
AGGGATCAAT	CTTGCA TGCC	TTTAGCCGCT	TTGTTACCGG	TTTGGATTAT	TGCGGGTTTG	360
ATATTTACTT	GCCTGATTAT	GGGACAGCTG	AAAAACCCAA	AACCCCTACC	GATT	414

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 519 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...519
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAAGGAATGG	GCTTGAAAAA	TCTCTCAACA	CTTCTGGTGT	TTTTATTCTT	TTGTTTGGGG	60
TGTGTGAGCA	ATTTTAATGA	AGACACTTAC	ACGCTAGACT	TAGTTTTAGA	AAAAAAGATC	120
CAAGCCAGTA	GGAAAGGCGA	AATCACCCAA	GATAATGTGC	CTATCATCAC	GGCTATCGCT	180
ACGCATTTAA	ACGATGTGGA	TAGCGGCACT	TACTACGATC	ATGAGTATTT	TTTAGTGGAG	240
ATTTTCACGC	AAAATAACGA	CTGGATAGAT	GATGGCTATA	TTTCTTATGA	ACTTTTGGGC	300
ACAAAACCTA	CAGGATCAGA	ACCTTTATGG	GTGCGAGAGA	TTACAAGAGA	TGAATTTGAT	360
GGCATTTTAG	AAACCACGAA	CCGGTGGAGC	CGAGCCTTTT	TGATCGCTTT	TGACAAATTG	420
GATTATTTAG	CGGTGCAAGA	AGCCAAACTA	GAGCTTGATG	CCTATAGTTT	AGGCAAAATT	480
GTTTTTAATT	TCGCTTACCA	AGTCCCCTTA	CCTCAATTT			519

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAAAAAGAAG	TATCTAACTA	TGAGGAATCC	ATTTTAGTCA	ACACTCCTTA	TGCAAGGGTT	60
AATATTCTCG	CGATTGAAAA	AAATGAAAGT	CCTATTGAAT	TACTGGCTCC	GGTAGATTTA	120

GTTACCGCTT	TGAGCGATTT	GATGCTAGGA	GGTGAGGGGG	CGAGCAAGGA	AGAAATGGAT	180
AATGACGATT	TAGACGCTTT	TAAAGAAATG	GCTTCTAATA	TTTTTGGTGC	GATCGCTACA	240
AGCTTGAAAGT	CTCAAGAATT	GCTCCCTAAA	CTCAATTTCA	CCACCACGAA	CGCTGAAATC	300
GCTAAAGAGC	TTCCTAAAAA	AGAAGAT				327

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATTTGTTTAT	TAAAGGAAAA	AATCATGTCA	AATAGCATGT	TGGATAAAAA	TAAAGCGATT	60
CTTACAGGGG	GTGGGGCTTT	ATTGTTAGGG	CTAATCGTGC	TTTTTTATTT	GGCTTATCGC	120
CCTAAGGCTG	AAGTGTTCGA	AGGGTTTTTA	GAGGCTAGGG	AATACAGCGT	GAGCTCTAAA	180
GTCCCTGGCC	GCATTGAAAA	GGTGTTTGTT	AAAAAAGGCG	ATCGCATTAA	AAAGGGCGAT	240
TTAGTTTTTA	GCATTTCTAG	CCCTGAATTA	GAAGCCAAGC	TCGCTCAAGC	TGAAGCCGGG	300
CATAAAGCCG	CTAAAGCCGT	TAGCGATGAA	GTGAAAAGAG	GCTCAAGAGA	TGAAACGATC	360
AATTCTGCGA	GGGACGTTTG	GCAAGCGGCA	AAATCCCAAG	CGAATTTGGC	TAAAGAGACT	420
TATAAGCGCG	TTCAAGATTT	GTATGACAAT	GGCGTGGCGA	GTTTGCAAAA	GCGCGATGAA	480
GCCTATGCGG	CTATGAAAGC	ACCAAATACA	ACGAGAGCGC	GGCTTACCAA	AAGTATAAAA	540
TGGCTT						546

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGGAATTTT	TGAGCGGGTA	TTTTTTATGG	GTTAAAGCTT	TCCATGTGAT	AGCGGTCATT	60
TCGTGGATGG	CAGCGTTATT	TTATTTGCCA	CGCCTTTTTG	TCTATCATGC	AGAGAACGCG	120
CATAAAAAAG	AGTTTGTAGG	CGTGGTTCAA	ATCCAAGAGA	AAAAGCTCTA	TTCCTTTATC	180
GCTTCGCCGG	CGATGGGTTT	CACGCTTATT	ACAGGGATT	TGATGTTGTT	GATCGCCCCCT	240
GAAATGTTTA	AAAGCGGGGG	TTGGTTGCAT	GCTAAATTGG	CTTTAGTGGT	ATTGCTTTTA	300
ATCTATCATT	TTTATTGCAA	AAAATGCATG	CGCGAGCTGG	AAAAAGACCC	TACAGGGAAA	360
AACGCAAGGT	TTTATCGTGT	GTTTAATGAA	ATACCCACGA	TTTTAATGAT	CCTTATTGTG	420
ATCTTAGTGG	TTGTCAAGCC	TTTT				444

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 873 base pairs.
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGATTAACCA	TTAGACAGGC	GTTTAACAAA	ACAAGATCCA	CGCATTCAAG	AACCCTTTTA	60
CTAGACATTG	ATTGCGTTAT	CCCTAATATT	GTTAGGCGTT	TGCTCTCTAA	TAAAACGCTC	120
CCTAAAAGAT	TCGCCACTTA	TAGCTTGCAA	GAAGTGGGCG	TTATTTTCCT	GACCACTCAG	180
ATTTTATCTA	TCATGCGCAA	GACCCGTTGC	TCTAAAACGC	TTTTTTTTAT	CACTAGGGGC	240
AGGGAGAGTT	TCCGCTACCA	GCTGTGCGAT	CATTACAAAC	AAAAACGCCA	CCAATTTGAT	300
GAAGATTTTA	GATCCCTTTT	AAAAGCTCTC	AAAATCGCTT	TAGTGGAAAA	ATACCCCTTA	360
AAAAAAGGGG	CTAAAATCCA	GGGCGAACAT	TGTTTTGAAT	ATGAAGCCGA	TGATATTATC	420
TCTTTTTTACA	AAAAGAAAGA	CCCCAACAAAT	TATGTGATAG	CGAGCATGGA	TAAGGATATT	480
TTGTATTCCA	ATAGAGGCTC	TCATTTCAAT	CTCAAAACGA	ACGCTTTTTT	TAATGTGAGC	540
CAAAAAGAAG	CCCATTTTTT	TGCTTATTAC	CAATGCGTTG	TGGGGGATAA	AGGGGATAAT	600
ATTAAGGGGG	TTAAAGGGAT	TGGCGGCTTC	AACTATAAAG	ATTTTTTAAA	CGAAGACGCT	660
AAAGAGCATG	AACTATGGGA	GCAGATCATT	CAAGCGTTCA	AAATTAAAGA	AGATTTGAGC	720
GATAGCGAAG	CCAAAGAAAA	GGCTCTATTA	AACATGCGTT	TAGTCAATAT	GCACCAGATG	780
ACCCACCATG	GCGTGATCAA	ACTATGGGAG	CCTGAGTTTA	AAAAAGCTTT	TTTCCCTAAA	840
AAACCCCAA	GACCTGATTT	TAAAAGAATT	TCT			873

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGCGTTTATC ATAATAAGGA AATCATTTGTC GCTTATAGGA AGATTGGCAA GGTGCATTCC	60
ACTTTAACCA CAACAAGCAT GATTTTAGCG TTTGGCGTTC AGAAGGTGCT TTTTAGCGGG	120
GTGGCTGGAA GCTTAGTTAA AGATTTAAAA ATCAATGATT TGTTAGTGGC TACTCAATTA	180
GTCCAGCAGC ATGTGGATT T GAGCGCGTTT GATCACCCCTT TAGGGTTTAT CCCCGAAAGC	240
GCGATTTTTA TTGAAACGAG TGGAAGTTTA AACGCTTTAG CTAAAAAGAT CGCTAATGAG	300
CAACATATCG CGCTCAAAGA AGGCGTCATC GCATCAGGCG ATCAGTTTGT GCATAGCAAA	360
GAAAGGAAAG AATTTT TAGT TAGCGAGTTT AAAGCGAGCG CCGTGGAAT GGAGGGGGCG	420
AGCGTGCGCT TTGTGTGCCA AAAATTTGGC GTGCCATGCT GCGTGCTAAG GAGCATTAGC	480
GATAACGCCG ATGAAAAAGC CCGTATGAGT TTTGATGAAT TTTTAGAAAA AAGCGCTCAC	540
ACTTCAGCGA AATTCTTAA AAGCATGGTG GATGAGCTT	579

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAACTCGCCC TTTTCAAACA ACGCCAATC AAACAAATA AAAACGCTCA AGCTAATCCT	60
AAAAGCCCTT TCATACCCA TGTGGTCTTG CCTAAAGAAA CCTTATCTTC TATCGCTAAA	120
CGCTATCAAG TCAGCATTTT CAGTATCCAA TTAGCCAATA ACCTCAAAGA TTCTAATATC	180
TTTATCCACC AGCGCTTAAT CATCCCCACT AACAAAAAT TACTCGCTAC AAGGGAATTT	240

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

GGTCATAGAA AAAGAATTTT CTCAAAGCCG GCGCTATTAC GCGCTTTAGA GCCTAATGAA      60
GCGCTGATTT TTTCTCAAAC CCTGCGTTTT GATGGCTATG TGGAAAAGCT TTATGCGAAT      120
AAAACCTATA CCCCATTAA AAAGGGCGAT AGGCTATTGA GCGTGTATTC CCCTGAATTA      180
GCGGGCGTTC AAAGCGAGCT GTTATCGTCA TTGAAATTCA ACCAGCAAGT GGGAGCGATT      240
AAAGAAAAAT TAAACTACT AGGGCTAGAA AACTTTAGCA TTGAAAAAAT CATCAGCAGC      300
CATAAAGTCC AAAATGAAAT CACTATTTAC TCTCGTTTCA ACGGCGTTAT TTTTAAAAAA      360
AGCCCGGATC TCAATGAGGG GAGTTTCATT AAAAAAGGGC AAGAGCTTTT CAAAATCATA      420
GATTTAAGCC GATTGTGGGC GCTTGTTAAA GTCAATCAAG AGGATTTAGA ATTTTAAAAA      480
AACACGCATC AAGCGATTTT GTTCGTAGAG GGGGTAAAG GCAAGCAAGC AATCACGCTT      540
GAAAACATCA ACCCCATCAT AAATGCGCAA GATAAAATGC TAGAAGCGCG CTTCAATGTG      600
CCTAATCTTA AATTGCTTTA TTACCCTAAC ATGTTTCGCTC AAGTAGAAAT CTTTCACAAA      660
CCCCAAAAAA TGAAGATCTT GCCTAAAGAA GCGGTTTTGA TTAAGGGGGG GAAAGCTATC      720
GTGTTTAAAA AAGAT

```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGTGGAGAAC	ACACAATGAA	AAAATATATC	TTAAATTTAG	CGTTAGTGGG	CGCGTTGAGC	60
GCGTCGTTTT	TGATGGCTAA	GCCGGCTCAT	AATGCGAATA	ACTCTACGCA	TAACACGAAA	120
GAAACGACTG	ATGCTTCAGC	AGGCGTGTTA	GCGACAGTGG	ATGGCAGACC	CATCACCAAA	180
AGCGATTTTG	ATATGATTAA	GCAACGAAAT	CCTAATTTTG	ATTTTGACAA	GCTTAAAGAG	240
AAAGAAAAAG	AAGCCTTGAT	TGAGCAAGCT	ATCCGCACCG	CGCTTGTAGA	AAATGAGGCT	300
AAGGCAGAAA	AGCTTAATCA	GA CTCCAGAA	TTTAAAGCGA	TGATGGAAGC	GGTTAAAAAA	360
CAGGCTTTAG	TGGAATTTTG	GGCTAAAAAA	CAGGCTGAAG	AAGTGAAAAA	AGATCCCAAT	420
CCCAGAAAAA	GAAATGCAGG	ATTTTACAA	CGCCAA			456

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGAGCCTTAA	AAACGCATGG	CGCTCTTGCC	TTTGTTCAAG	CTTTTTTGGA	GTCTTTTAAG	60
GGATTTTTAA	GCCAAGCGAC	CTTAATTAGC	GTTTTAATAG	CGAGCGTTTT	AATCCTTTTT	120
TGCGCGATTT	TGCTCCTTTT	GGCTCTGCTT	TTAAGAAACC	GCTGGGCTAG	TTATATAACA	180
ACAGCAGCTT	TTTTGGGCGC	GTTTTTAAGC	ATGCCTTTTG	TTTTGAACGT	TTTACTCACT	240
CAAGCGATTT	ACCCCATAGA	AACGCGCATC	TGACAGCTA	ATCCCTTAAG	TTATAGCAAC	300
GCCTTTTCTT	TGCAAGTGGG	AGTCAAAAAC	ATTTCCAAAT	TCAGTCTAAA	CAATGCGTT	360
TTACGTCTAG	AAGTCCTTAA	AAACCCTCAC	AATTTTGTGG	AAGAGCGAGC	TTTTAAATGG	420
TTTGTCAAAA	AAAGCTATGA	AAAAACCTTT	AAAGAAAAGA	TTTTGCCTGA	AGAATCCAAG	480
GTCTTTTCAT	TCTTTATTGA	CGACTACCCT	TATTCAAAAA	CGGCCCCCTTA	TCAAGTTTCT	540
TTGTTTTGTT	TG					552

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

156

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCCATGAATA	TCAAAACCCA	TTCTTCAAAT	GAAAAAGAAC	GCTTTGTACG	CATAGAAGAG	60
GACGAAAAGA	AAGAATTATT	CGCCGAAGCT	ACAAATGAAA	ATCCGCACGG	CCTTTCTTTA	120
ATGGCTTTAA	TAGGGGTGTT	GGTTTTTGGG	GGTGCGTTT	TAGCCTTATT	AGTGCCTAAA	180
ATCTATTTAA	GCAATAATAT	CTATTATATT	AGCCGTAAAA	TTAATACCCT	AGAAGATCAA	240
AAACGCCTGC	TTTTAGAAGA	ACAGCAAATC	CTAAAAACG	AATTAGAAAA	AGAGCGTTTT	300
AAATACTACA	TAGAGAATAG	TGAAAATATT	GGCGATATTG	CGTTT		345

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 714 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTCCTTTTAA	TCCACTTTCT	TATTTTAAGG	AAACTCTTGC	AACATAAAAC	CATTATGGAT	60
AAGATCATTA	TTCAAGGGGC	TAGGGAAAAC	AATCTCAAAA	ATATCTTTTT	AGAAATCCCT	120
AAAAACCAAT	TTGTTGTTTT	TACCGGATTA	AGCGGTTCCG	GTAAATCCAC	TCTGGCGTTT	180
GACACTCTAT	ACGCTGAAGG	GCAAAGGCGC	TATTTAGAGA	GTTTGTCTAG	TTATGCGAGG	240
CAATTTTTAG	ACAAAGTGGG	TAAGCCTAAT	GTGGATAAAA	TTGAAGGCCT	AACCCAGCG	300
ATCGCTATTG	ATCAAAAAAC	CACTTCTAAA	AACCCTAGAT	CCACTGTGGG	GACGATCACT	360
GAGATTTATG	ATTATTTAAG	GTTGTTGCTT	GCAAGGGTTG	GGGAGCAATT	TTGCCCCACA	420
TGTTTAGAGC	CTATTAGTTC	TATGAGCGCG	AGCGATATCA	TTTCTCAAAT	CTGTCATTTA	480
GAAGAAAATT	CTAAAATCAT	TATTCTAGCC	CCCATTATTA	AAGATAAAAA	AGGTTCGTTT	540
AACGATAAAT	TAGAGAGTTT	GCGTTTGAAG	GGGTATGTGA	GGGCTTTTGT	TGATGGGGTG	600
ATGGTGCGTT	TAGATGAAGA	AATCCATTG	CACAAAACCA	AAAAACACAC	CATTGAAGCG	660
GTGGTGATA	GGGTGGTTAT	CAATAGCGAA	AATGCTTCAC	GGATCGCTAG	CGCG	714

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1083 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1083
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

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CACCAATCTT TTAAAAGAGC GTTTGAACCA AGAAGAAAAG GGCGAGTTTT TAGAATAATG      60
GGTTTTGAAA AAAGCATTTT AGACAATTTG AACGGAGCGC AAAAAATTGC CGCATGCCAC      120
ATTCAAGGGC CTTTATTGAT TTTAGCGGGA GCTGGGAGCG GTAAGACTAA GACTTTAACG      180
AGCCGTTTAG CGTATTTGAT TGGCGCTTGT GGCGTGCCTA GCGAAAACAC TTTAACGCTC      240
ACTTTCACCA ATAAAGCGAG TAAAGAAATG CAAGAAAGGG CTTTGAAATT GTTGAAAAAC      300
CAAGCCCTTA TCCCCCCTT GCTTTGCACT TTCCATCGTT TTGGTTTGCT GTTTTTAAGG      360
CAACACATGA ATCTTTTAAA AAGGGCGTGC GATTTTTCGG TGCTAGATAG CGATGAAGTG      420
AAAACGCTCT GCAAACAGCT CAAAATTTCA AATTTCAGGG CGAGCATTTT TCAAATCAAA      480
AACGGCATGA TGGATTTGAG CGTGCAAGAT AGCGAATGTT ACAAAGCGTA TGAGCTTTAT      540
CAAAACGCGC TCAAAAAAGA CAATTTAGTG GATTTTGACG ATTTGCTTTG TTTGAGCCTT      600
AAGATTTTAC AAGATAATGA AAAACTCGCC AAAGAGACCA GCGAACGCTA CCATTACATT      660
ATGGTAGATG AGTATCAAGA CACGAACGCC CTGCAACTGG AATTTTAAA ACAATTGAGT      720
TTCACGCACC ATAATTTGTG CGTGGTGGGC GATGACGATC AGAGCATTTA TGGGTTTAGG      780
GGGGCTGATA TTTCTAACAT TTTAAATTTT TCCAAGCATT TTAAAGGGGC TAAATAGTG      840
AAATTAGAGA CCAACTACCG CTCTAGCGCT GAAATCTTAG CGTGCGCTAA TTCCCTGATC      900
AGCCATAACC AACACCGCCA CATTAAAACG CTTCAAAGTT TCAAAGGTTT GCACAAAAGC      960
GTGATTTGTA AAGAATACCC CACGCAAAAA GAAGAGAGCC TGGATGTGGC TTATCAGATT     1020
CAAAGCCCTT TTAAAGAAGG GCGAGAATTT AGAAAATATC GCTATTTTGT ATCGTTTAAA     1080
TGG                                     1083

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(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATGAGAAAAA	CGATTTCAGC	GTTGTTTTTA	TCAGCGTGTA	TAGGGTTATC	GTCTGTTTAT	60
GCGAGTAACG	CTTTGATTTT	ACAAACAGAT	TTTAGCCTAA	AAGATGGGGC	CGTCTCGGCG	120
ATGAAAGGCG	TCGCTTTCAG	CGTTGATTCT	AATCTTAAAA	TCTTTGATTT	AACGCACGAA	180
ATCCCCCCGT	ATAACATTTG	GGAAGGCGCT	TACCGCTTGT	ATCAGACCGC	TAGTTATTGG	240
CCAAAAGGCT	CGGTATTTGT	GAGCGTAGTG	GATCCGGGCG	TAGGCACTAA	TCGTAAATCG	300
GTGGTATTGA	AAACTAAAAA	CGGCCAGTAT	TTCGTCTCTC	CAGATAACGG	CACGCTGACT	360
TTGGTAGCGC	AAACTTTGGG	GATTGATAGC	CGAGCTGAAA	TTGATGAAAA	TTCCATCCGT	420
CTGAAAGGTT	CGAAATTCCT	GTCTTCCCGT	CCGGTG			456

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GACATCTTTA	ATAAGGAAGA	GATCATGGCC	ATTGATTTAG	CAGAAGTTAC	AGGAGCTAAA	60
GCCGCGCAAG	AAAGGAAAAA	AGAACAGCCC	ACCATCGCTA	ACGGGTTGGA	TAAAAACGCT	120
TTCATGAAAC	TCTTTT TAGA	GCAATTGAAA	AATCAAGACC	CCACCGCTCC	TATGGAAACG	180
GATAAAATCA	TCACCCAAAC	CGCGCAACTC	ACGCAAGTGG	AAATGCAAGA	AGAAAACAAA	240
AAGACCATGC	AAGAAGTCGC	CAGTGCGATG	AAATCCAATA	AAGAAACTAA	CGAATCTTTA	300
AAAGACTTTC	AAGGCGCTTT	AAAAGACACC	ATGGAAAACC	TGAACAAAGG	CATGGACGAT	360
AGCTTAAAGG	CTAACACGCG	TTTAAGGGAA	GTAAGCGCCC	TTAATTCTGT	GAGCATGATA	420
GGCAAAATCG	CTGAAACCGA	TGTGAGTGGG	GCGAATTTTG	ACGGCAACAA	CAAGCTTTCT	480
TTTTCGCTCT	TTTTTGATGA	AAAAATTGAC	GCTTCTAAAG	GAGTGCCAGC	GATTCAAATC	540
TTAAACGAAA	ACAATGAATT	GGTCAAAACG	ATTCTTTTAA	AAGATTATAA	CGGGCAAAAG	600
GGGTATATCA	ATTTTGAATG	GGACGGCACA	AACGAAAAGG	GCGAAAAAGT	TCCTAAAGGC	660
AATTACAAAA	TCAAGGCTGA	ATACAATTTA	GGCTCTCCAA	AGCAAGCTGT	ATTTGCAAAC	720
GCGCATTGG						729

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AACGCTCATG CCTTTACCCA TCCATTTAGC GCACCAGCTC GCTTTCGCCT AGCTCAAAAA	60
AGAAAAGACA ACACCTTGCC TTTTTTAAGG CCTGATGGCA AGTCTCAAGT GAGCGTGCCT	120
TATGAAAACA ACAAGCCTGT AAGCGTTGAT ACGATTGTCA TTTCCACCCA ACATTCCCCA	180
GAAGTTTCAC AAAAGCATT T AAAAGAAGCG GTGATTGAAG AGATCGTGTA TAAGGTTTTA	240
CCCAAAGAAT ATTTGCATGA CAATATCAAG TTTTTTATAA ACCCTACAGG AAAATTTCGTC	300
ATCGGTGGGC CTCAAGGCGA TCGGGGTTTG ACAGGTAGAA AAATCATCTG GGATACTTAT	360
GGAGGGTTTT GCCCGCATGG AGGGGGAGCG TTTACCGGGA AAGACCCTTA CAAGGTGGAT	420
ATGAGCGCGG CTTATGCGGC CCGCTATGTG GCTAAAAATT TGGTAGCGAG CGGGGTTTGC	480
GATAAAGCGA CCGTGCAGCT TGCTTATGCG ATTGGGGTGA TAGAGCCTGT GTCTATTTAT	540
GTGAACACGC ATAACACGAG CAAGCATTCA AGCGCGGAGT TGGAAAAATG CGTGAAATCG	600
GTTTTCAAAC TCACGCCAAA AGGCATCATT GAAAGCTTGG ATTTGTTAAG ACCCATTTAT	660
TCGCTCACTT CAGCTTATGG GCATTTTGGG CGCGAGTTAG AAGAATTCAC TTGGGAAAAG	720
ACTAACAAGG TTGAAGAGAT TAAAGCGTTC TTTAAGCGT	759

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GTTATTAGTT ACCATTTTAT TATTCTTAAG GATGTGTTTA TAATGAGAAT TAAGGCTTAT	60
TTTTTGCGTT TATCGCACTG GTTTTATCG TTTGGTTGGG TTTTAGCGCT TGTA AAAACT	120
CTCAAAATC TCAAGATTCT CAAAACAATA CCACCCAACA AGATAGCCCT AAAACCTACA	180
CCGTATGGAT CTGAA	195

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AAAGGAATAA GCATGAAAAA ATCCCTTTGT TTGTCTTCT TTCTGACCTT CTCTAACCCT	60
CTTCAAGCCC TTGTCATTGA GCTTTTAGAA GAGATTAAAA CTTCGCCGCA TAAAGGCACT	120
TTTAAGGCTA AAGTCCTTGA TTCTAAAGAA CCAAGACAAG TTTTAGGCGT TTATAATATC	180
TCCCCACACA AAAAAGTCAC GCTCACTATC ACTCACATAT CCACGGCAAT CGTCTATCAA	240
CCCCTTGATG AAAAAGTTTC TTTAGAAACG ACCTTAAGCC CTAACCGCCC TACTATCCCT	300
AGAAACACCC AAATCGTTTT TTCTTCAAAA GAATTGAAAG AACCGCACTC AAACCCAATA	360
CCTTCT	366

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAAAAATTC	ACACTTTAAT	ACTTCCTGTT	GAGTGGGGAA	CTGAGATTGT	CTTGGTGGTT	60
AGTGGCTCGT	TGCAAAACAT	TGTTTCGTTCT	TTTTTGCGAA	GGATCAGCGT	TTTCTTCATT	120
ATTGATTCA	TCAATTTTAT	TTTCGTTATT	GATCAGATCA	TTCACTTCTT	TGGTGACTTT	180
TTTCATCTCT	TCTTCATGCT	CAATCTTTTT	TATATCCTTA	TTAGGTTGAT	TGATTTGATT	240
GTTTTGAGTG	GTTTTAGTGT	TGTTTTGGTG	CGATTGGGAC	AATTTTTTAG	GCTCATCTTT	300
GCGTGCGCTC	AACACGCTTT	TAACAAGGTA	GATATCGATA	AAATGAGTGA	TTTTAGATTT	360
CATCAATTAA	GTTTCTTTAA	ATCAGTGTAT	AATTGTGTTA	TTTTATCA		408

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TACTTCCTGT	TGAGTGGGGA	ACTGAGATTG	TCTTGGTGGT	TAGTGGCTCG	TTGCAAAACA	60
TTGTTTCGTT	TTTTTTGCGA	AGGATCAGCG	TTTTCTTCAT	TATTGATTTC	ATCAATTTTA	120
TTTTTCGTTAT	TGATCAGATC	ATTCACCTCT	TTGGTGACTT	TTTCATCTTC	TTCTTCATGC	180
TCAATCTTTT	TTATATCCTT	ATTAGGT				207

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ACTCTTTT	TAAGTCAAGCGA	TAAAGTTTGC	AACCTAATGA	GAGTAATAAT	AAAGTTTATG	60
CTGATTTTCAT	TAAAAACATT	CCTAAAAATA	TTATTGGAAA	TATTCCTAAA	AACCTTCCAA	120
AAGATTTGGA	TAGTTTGCGT	GGTTATTG	GGGTTGGGCT	GTAGTTTTTT	AAACGCTAAC	180
AGCGTTCAAT	TAGAAGAAAC	GCTGAGACGA	AATCCTAAAA	ATCTTATTTG	GCAACACTTT	240
AAAAAGAAGT	TTAAAAAGAG	TAACACGATC	CCTTATGCCC	CTAATAGCCG	TTGGAAATAT	300
TTAGGCACAA	GTATAGGGAT	TTTGGGCGTG	TCGTTGGTGA	TAGGGATTGT	GGGGTTGTAT	360
CTCATGCCAG	AGAGCGTAAC	GAATTGGGAT	AAAGAAAAGT	TTGGCGTCAA	AAGTTGGTTT	420
GAAAATGTCC	GCATGGGGCC	AAAAC TAGAC	AATGATAGTT	TTATTTTAA	TGAAATCTTG	480
CACCCTTATT	TTGGGGCTAT	GTATTACATG	CAACCGCGCA	TGGCTGGGTT	TAGCTGGATG	540
ACATCAGCGT	TTTTTCTTT	TATCACTTCT	ACACTTTTTT	GGGAATATGG	CTTGGAACCG	600
TTTGTGGAAG	TGCCTAGCTG	GCAGGATTTG	GTGATCACGC	CCTTACTAGG	TTTCATTTTA	660
GGGGAAGGGT	TTTACCAGCT	CACGCCTATA	TCCAACGCAA	CGAAGGCAAG	CTGTTTGGCT	720
CTTTATTTT						729

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AAAAAAAGGA	AACCAATGTT	TAGAAACTA	GCAACCTCTG	TATCGCTCAT	AAGCCTACTA	60
ATCTCCAACG	CTCTTTATGC	TAAAGAAATA	AGTGAAGCCG	ATAAGGTCAT	TAAGGCCACT	120
AAAGAAACTA	AAGAGACCAA	GAAAGAGGCT	AAACGCCTCA	AAAAAGAAGC	TAAACAGCGC	180
CAACAGATCC	CTGATAATAA	GAAACCTCAA	TATGTCTCTG	TTGATGACAC	AAAAACTCAA	240
GCGCTTTT	ATATATATGA	CACTTTGAAT	GTGAATGACA	AAAGCTTTGG	GGATTGGTTT	300
GGTAATAGCG	CTTTGAAAAA	CAAACTTAT	CTCTACGCTA	TGGATCTATT	GGATTATAAC	360
AACTACTTAT	CCATAGAAAA	CCCTATTATC	AAAACAAGAG	CGATGGGAAC	TTATGCAGAT	420
CTGATTATCA	TCACAGGTTT	GTTAGAACAA	GTCAATGGGT	ATTACAATAT	TCTAAAAGCG	480
CTCAACAAAC	GCAACGCTAA	GTTTGTGTTA	AAAATCAATG	ACAAAATACC	TTATGCCCAA	540
GCGACTTTTT	TGAGAGTGCC	AAAAAGAAGC	GATCCCAACG	CCCACACGCT	TGATAAGGGA	600
GCGTCAATTG	ATGAAAGCAA	GCTTTTGTGA	CAACAAAAGA	AAATGTATTT	CAACTACGCC	660
AACGATGTGA	TCTGCAGACC	CAACGATGAA	GTGTGTTTCG	CCCTAAGAGA	TGAAATGGTA	720
GCTATGCCCA	CTAACGATAG	CGTTACTCAA	AAACCCAATA	TCATTGCTCC	TTATAGCCTG	780
TATAGACTAA	AAGAGACAAA	TAACGCCAAT	GAAGCCCAAC	CATCACCTTA	TGCCACTCAA	840
ACCGCTCCTG	AAAACAGCAA	AGAGAAGCTC	ATAGAAGAGC	TAATCGCCAA	CTCCCAACTC	900
ATAGCCAATG	AAGAAGAGAG	GGAAAAGAAA	CTCTTAGCAG	AAAAAGAAAA	ACAAGAGACT	960

GAATTGGCTA	AATACAAGCT	GAAAGATTTA	GAAAATCAAA	AGAAACTAAA	AGCTTTAGAA	1020
GCAGAGTTGA	AAAAGAAAAA	CAC TAAGAAA	CCTAGAGTAG	TGGAAGTGCC	TATTCCTCCT	1080
AAAACAAGTG	ATTCTGATGA	AACAATGAGA	GTTATCAAAAG	AAAAAGAAAA	CTATAATGGG	1140
TTATTAGTGG	ATAAAGAGAC	CACGATCAAA	AGAAGCTATA	AGGGGACTTT	GATCAGTGAA	1200
AATTCTTACA	GCAAAAAAAC	ACCCATCAAC	CTTGAGGACT	TGAGAAAGCTT	AGAAGAAGAA	1260
ATTAAGAGCT	ACTATGTCAA	GTCTAATGGC	TTGTGTTACG	CTAATGGCAT	TAACCTCTAT	1320
GTAAAAATCA	AAAACGATCC	CTACAAAGAG	GGAATGCTGT	GTGGTTATGA	GAGCGTTCAA	1380
AAACTGCTTT	CACCACTAAG	GGACAAGCTC	AAATACGACA	AGCAGAAGTT	ACAAAAAGCG	1440
TTACTGAAAG	ATTTAAAG					1458

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

G TAGTAGGCA	CAATGGAAGA	CTTTTTGTAT	AACACCTTAT	ATTT CATAGA	GGATTATAAG	60
TTGGTTGTTA	TTTTTAGTTT	CATAGGGTTA	ATAGCGTTAT	TTTTCCTCTA	CAAATTCATA	120
AAA ACTCAA	AAAAGGTTTT	TAAAGATAAA	GCTAACCAGC	CTCAAAAGAA	AAAAAGCTTT	180
AAAGAAATCA	TTATAGATGG	GCTGAAAGAA	AGGGTTAAAA	CCTTTGGCTT	TTGGTTGCCA	240
AGCTATACTA	TTACTATCCT	ATTCTTTTAT	CACATCAGGG	TTATTTTCT	TGATTCTCTT	300
AGG						303

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

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AGAATGGCTC AAATTGTAAA AGGATCTGAC ATGTTTGAAG ATTTTATCG CACTACCCCTC      60
TCTTTTTTAA GGTCTTTATT GCTTTTATTG GGTTTATTGT TGCCGTTTTC GCTTTGTATA      120
GCTGATGAAT ATATTAGCAT AAGTGATGAT TGGGATGAAA GGGCGCGAAA TCAGTGGGAT      180
GAAACTGCGC GAAATCATAA GACATATTAT TTTGAAAATG GTTTAGACCA TTTTAATCAA      240
GGCCAATACA AGCAAGCCTT TAAAGATTTT AAATTGGCGC AAGAATACAG CATCGGGCTT      300
GGCAACGTTT ATTTAGCCAA AATGTATTTG GAGGGAAAGG GCGTGAAAGT GGATTACAAA      360
AAAGCGCAAT TCTATGCACA AAACGCTATC AAAGGGTATG GGAGCGGGTT GTTAGGGGGC      420
GCTCTTATTT TAGGACGCAT GCAAGCAGAA GGCTTAGGGA TGAAAAGGA TTTGAAACAA      480
GCACTCAAGA CTTACAGGCA TGTGGTTCGC ATGTTTTCTA ATAAAAGTGC AAATTTTGCT      540
AACAAATTTG GATCAAACCT TCGGAATTT ACTAGTATGC TTATTGGATC GCGATTCATT      600
GATCTTTCAG GTTTGAGCGC GAATCCTATA AAATTTGGAA ATAAATTTGG AATACTTGTT      660
AAGAAAGCCC TTCAAATCAA AGATAATACA CTTTCTTGGG AAGACATTGC TGAAATTTCA      720
AGCAATATTA TTTTACTCAA ACAACAAATG GGGGAAATCC TTTATAGGAT TGGGATCGCT      780
TATAAAGAAG GGCTTGGCAC TAGAAAGAAA AAGGACAGGG CTAAAAAATT CTTGCAAAAA      840
TCCGCAGAAT TTGGCTATGA AAAAGCCATG GAAGCTCTG      879

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(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

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GACTTTCACG ATTTCTGTGC GAATATCCAT CATCGTATCC GTTGGAGGCA CAGGCATATA      60
GCCTCCTTGC TTTCCCGGTC TATGCCCAA ATTACGCGCG TTTTCAAAGC TTTTATCCCT      120
ATTCCATTGC CCCTCTTCGC TATCCACTTC GTAGTATTGG GAATTGGAAG CGTCTTTAAT      180
CTTAATAGAA TCAAAGATAA AAAATTCATT CTCCGCGCCA AAATAAGCCA CATCGCCCAA      240
GCC

```

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

165

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

AAAGCCATGC TTTCTTCTAC GAATGACATA CGGTATCAAA ACCCTAAAAA CAAGGCTTTG	60
AAAGGCGAAA TATTAGCGAA TCTGAAATTC ATAAAAAAAC TGCTTGGTAT TGGGTGTAAA	120
GACCCTAGCG CGTATGTCCA ATTAGGCGTG AGCAAGAGCG AAAAACAAGA AATTGAAAAC	180
AAGATAGAAG AAAGAAAACG TGCCAAAGAA CAAAAAGATT TTTTAAAAGC CGATAGCATC	240
AGAGAAGAGC TTTTACAACA AAAAATCGCT TTGATGGACA CCCCACAAGG CACGATTGG	300
GAGAAGCTTT TT	312

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1587 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

ATGAGAAAGG TTATCATAAT GAATGGTTAT TTGAGGGTAA AAACCCCGTA TTTTTTAGCG	60
TCGGTCGTTT TGACTTTTTG GACTTTTAAAT TCTTTTATGA GCGCGAAAGA TAAGCACCAT	120
TTTTTAAAAA AAGTTACAAC CACCGAGCAA AAATTCAGTT CTAGTGCCCC AATTTTCATGG	180
CAAAGCGAAG AGGTGCGTAA TTCCACAAGC TCTCGCACGG TGATTTCCAA CAAAGAACTC	240
AAAAAAACGG GGAATTTGAA TATTGAAAAC GCCTTGCAAA ATGTACCAGG GATTCAAATC	300
AGAGACGCTA CAGGCACGGG CGTGCTGCCT AAAATTTTCG TGCGCGGTTT TGGTGGGGGC	360
GGTAACGGGC ATAGCAACAC CAACATGATT TTAGTCAATG GTATCCCCAT TTATGGCGCG	420
CCGTATTCCA ATATTGAACT GGCGATTTTC CCTGTAACTT TCCAGTCAGT GGATAGGATT	480
GATGTGATTA AGGGGGGAAC GAGCGTCCAA TACGGCCCTA AACTTTTGG AGGCGTGGTG	540
AATGTCATCA CTAAAGAAAT CCCCAGAGAG TGGGAAAATC AAGCGGCTGA AAGGATCACT	600

TTTTGGGGGC	GCTCCTCTAA	TGGGAATTTT	GTCGATCCCA	AAGAAAAAGG	CAAGCCCTTA	660
GCCCAAACCTT	TAGGAAACCA	AATGCTGTTT	AACACTTATG	GGCGAACGGC	TGGGATGTTG	720
GGTAAATATA	TAGGCATTAG	CGCTCAAGGC	AATTGGATTA	ATGGGCAAGG	TTTCAGGCAA	780
AATAGCCCTA	CAAAGGTGCA	AAACTACTTG	TTGGATGCGA	TTTATAAGAT	CAATGCGACC	840
AATACTTTTA	AAGCTTATTA	CCAGTATTAT	CAATACAAC	CTTACCATCC	AGGCACTTTG	900
AGCGCGCAAG	ATTACGCCTA	TAACCGCTTC	ATCAATGAGC	GCCCTGACAA	TCAAGATGGA	960
GGGCGAGCCA	AGCGCTTTTG	GATCGTGTAT	CAAACTACT	TTGGCGATCC	GGATAGGAAA	1020
GTGGGGGGCG	ATTTTAAATT	CACTTATTTT	ACGCATGACA	TGAGTAGGGA	TTTTGGGTTT	1080
TCCAACCAAT	ACCAAAGCGT	GTATATGAGC	GGTCAAAATA	AGATTTTACC	CTTTAAAGGC	1140
AAGGGAGAAA	TCAGCGCAAA	AAACCCTAAT	TGCGGTCTGT	ATTCTTATAG	CGACACGAAT	1200
AGCCCTTGCT	GGCAATTTTT	TGACAATATC	CGCCGATCCG	TGGTGAATGC	CTTTGAGCCA	1260
AAACTCAATC	TTATCGTCAA	TACTGGTAAA	GTCAAACAAA	CTTTTAACAT	GGGAATGCGC	1320
TTTTTAACTG	AAGATTTATA	CCGCCGATCC	ACCACCAGGA	AAAACCCTAG	CATGCCTAAT	1380
AATGGGAGTG	GGTTTGATGC	AGGAAC TTCA	CTCAATAATT	TCAACAATTA	TACCGCTGTG	1440
TATGCCAGCG	ATGAAATCAA	TTTCAATAAC	GGCATGCTAA	CGATCACGCC	GGGCTTGAGA	1500
TACACTTTTT	TAAATTACGA	AAAAAAAGAC	GCTCCTCCCT	TTAAGGTGGG	TCAAACCCCA	1560
AAAACCACGA	AAGAGCGTTA	TAACCAA				1587

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CGGGTTGGAT	TTCGCTCCTT	TAGTGGTGGT	CATTGTGCTG	AAATTTTATAG	ATTTAACCCCT	60
CATCCAATGG	CTTTTTCGCG	TCGCCAAAAG	CCTCTAAAGG	AAATCATGCG	TTTTTTTATT	120
TTATTTTTTA	TGGGTATGCT	TGGCGTTGGT	TTTTCTCAAA	CCGAGTTGGA	TTTAAAGGAT	180
TTAGAAAAAA	AGCCCGCCGG	GATCGTTAGG	GATTATTATT	TATGGCGTTA	TATTAGCGAT	240
AAAAAAACGA	GTTTAGAAAA	CGCTAAAAAA	GCCTATGAAT	TGACTCAAAA	TAAAAACAGC	300
GCCCTACAAA	AAGCCATGCA	AGAAAAAGGC	GTAGAAAATT	CAGATAAAAG	CCCTGATGCC	360
AAAATGCCTG	AAGATATTTA	TTGCAAGCAA	ATTACCTTAG	AAAGCATGTT	AGAAACAACA	420
GACGCTTTCC	AAGCGAGTTG	TATCGCTATC	GCTTTAAAAT	CAAAAATCAG	AGATTTTGAT	480
AAAATCCCCA	TTCAAACCTT	TAAACCTTTA	CAAGAAAAAA	TCAAAGAGGC	TTACCCCAT	540
CTTTATGAAG	AATTAGAAAT	CTTGCAAAGT	AAGAACGTGA	GC		582

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CACGCCTTGT ATTCGCCCAT CAAAATCGCT TTTGAAAAAG CCCTTAAAAA CGCTAAAGAA	60
TCCGTTTTTA TCGCTTCATC GTATTTTATT CCAGGTAAAA AGATAATGAA AATCTTTAAA	120
AATCAAATTT CTAAGGGGAT TGAATTGAAT ATTCTTACCA ATTCCCTTTC ATCTACGGAC	180
GCTATCGTGG TCTATGGGGC GTGGGAAAGG TATCGCAATA AATTAGTGGC AATGGGCGCG	240
AATGTCTATG AAATACGAAA CGATTTTTTC AACCGCCAGA TTAAAGGGCG CTTTAGCACC	300
AAACATTCCT TACACGGCAA GACAATTGTT TTTGACGATG CCCTAACGCT TCTAGGGAGT	360
TTTAATATTG ATCCGCGCTC TGCATATATT AACACTGAAA GTGCGGTCTT GTTTGACAAC	420
CCGTCTTTTG CAAAAGGGT GCGTTTGTGC CTAAAGATC ATGCCCAACA ATCATGGCAT	480
TTAGTCTTGT ATCGGCATAG AGTGATTGG GAAGCTACAG AAGAAGGCAT CTTAATCCAT	540
GAAAAAACT CGCCTGATAC CTCTTTCTTT TTGCGTTTGA TTAAAGAATG GTCTAAAGTC	600
CTTCCTGAAA GAGAACTT	618

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1326 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGAAAAATTA AAGGTGTGAT GATGAAATTT TTTCTTTTAA AGAAATTCAG CGAATTTTTTA	60
AACACTCAAA CGCATTTTAA CCTCAAACGC TTGAACGCGT CTAGTTTTTT ATTAGAGACT	120
TTTTCTAAAG AAAAACACGC CTTTGTGTG GATTTGAGCG CGCCTTATAT TGGTTTGTCC	180
AAAAAACCCC CAGAGAGCGT TTAAAAAAC ACTTTAGCGT TAGATTTTTG TTTGAATAAA	240

TTCACCAAAA	ACGCCAAAAT	TTTACAAGCA	AACGTCATTG	ATAACGATCG	GATTTTGTAGAA	300
ATCAAGGGCG	CTAAAGATTT	AGCTTATAAG	AGTGAAACTT	TTATTTTGCG	TTTAGAAATG	360
ATCCCTAAAA	AAGCCAATCT	CATGATTTTA	GATCAAGAAA	AATGCGTGAT	AGAGGCTTTT	420
CGTTTTAATG	ACAGGGTGGC	TAAAAACGAT	ATTTTAGGGG	CATTGCCTCC	TAATATTTAC	480
GAGCATCAAG	AAGAGGATTT	GGATTTTAAG	GGATTGTTGG	ACATTTTAGA	AAAAGATTTT	540
TTATCCTATC	AGCACAAAGA	ATTGGAACAC	AAAAAAATC	AAATCATCAA	GCGATTAAAC	600
GCCCAAAAAG	AACGCTTGAA	AGAAAAATTA	GAAAAACTAG	AAGATCCTAA	AACTTTACAG	660
CTGGAAGCGA	AAGAATTGCA	AACTCAAGCC	TCATTGTTGC	TCACCTACCA	GCATTTAATC	720
AACAGGCGTG	AAAATCGCGT	GATTTTAAAG	GATTTTGAAG	ATAAAGAATG	CATGATTGAA	780
ATTGATAAGA	GCATGCCCTT	AAACGCTTTT	ATCAATAAAA	AATTCACTCT	CAGCAAGAAA	840
AAGAAACAAA	AATCGCAATT	CTTGTATTTA	GAAGAAGAGA	ATCTGAAAGA	AAAAATCGCT	900
TTTAAGGAAA	ATCAATCAA	CTATGTTAGA	GACGCTGCAG	AAGAAAGCGT	TTTAGAAATG	960
TTTATGCCGG	TAAAAAACTC	TAAATCAAAA	CGCCCGATGA	ACGGGTATGA	AGTGCTGTAT	1020
TATAAGGATT	TTAAATCGG	TTTAGGGAAA	AACCAAAAAG	AGAATATCAA	GCTTTTACAA	1080
GACGCAAGAG	CGAATGATTT	GTGGATGCAT	GTGAGAGATA	TTCCTGGATC	GCATTTGATC	1140
GTTTTTTGCC	AAAAGAATAC	GCCTAAAGAT	GAGGTCATTA	TGGAATTAGC	CAAATGTTG	1200
ATTAAAATGC	AAAAAGATGC	GTTTAATGGT	TACGAGATTG	ACTACACGCA	ACGAAAATTT	1260
GTCAAAATCA	TCAAAGGAGC	TCATGTCATT	TACTCAAAAT	ACCGAACTAT	TAGTCTAAAG	1320
GACACT						1326

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GGATTTATGA	TGATTTTCAT	TGACGCATGT	TTTAGAAAGG	AAACGCCTTA	CACACCCATT	60
TGGATGATGA	GGCAAGCGGG	GCGTTACCTT	AGCGAATACC	AAGAGAGCCG	TAAAAAAGCG	120
GGGAGCCTCT	TGGAATTGTG	TAAAAATAGC	GATTTAGCCA	CAGAAGTTAC	CCTACAGCCG	180
GTAGAGATTT	TAGGCGTGGA	TGCGGCTATT	TTGTTTAGCG	ATATTTTAGT	AGTGCCCTTG	240
GAAATGGGCT	TGAATTTGGA	GTTTATCCCC	AAAAAGGGGC	CGCATTTTTT	AGAGACGATT	300
ACGGATTTAA	AAAGCGTGGA	AAGCCTAAAA	GTAGGGGTTT	ATAAACAAC	AACTATGTC	360
TATGATACGA	TTTCTCAAAC	GCGCCAAAAG	CTTTCTAAAG	AGAAAGCGCT	AATCGGTTTT	420
TGCGGATCGC	CTTGACTTTT	AGCGACTTAC	ATGATAGAAG	GCGAGGGGAG	CAAATCGTAT	480
GCCAAAAGCA	AGAAAATGCT	TTATAGCGAG	CCTGAAGTTT	TAAAAGCGCT	TTTAGAAAAG	540
TTAAGCCTTG	AATTGATAGA	GTATTTGAGC	CTTCAAATCC	AAGCAGGGGT	CAATGCAGTG	600
ATGATCTTTG	ACTCATGGGC	TAGCGCTTTA	GAAAAAGAAG	CGTATTTGGA	ATTCAGTTGG	660
GATTATTTGA	AAAAATCTC	TAAAGAGCTT	AAAAAACGCT	ATGCGCACAT	CCCAGTTATC	720
CTTTTCCCTA	AAGGGATTGG	CGCTTATTTG	GATAGCATAG	ATGGGGAATT	TGATTTGTTT	780
GGCTTGATG	GGGGCACGCC	TTTAACTGCG	GCAAAAAAAA	AATTAGCGGT	AATTATTTTT	840

TTGCAAGGAA TTTACAACCC ACCCGCCTTT ATGATAAAA

879

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

AGGGTGTTTT	TGACTAAAAA	ATTCATGTCT	TGGATGGTGG	TTATCGGGGC	TTTAATTTGC	60
GTGCTTTTAG	GGGTGTTTAT	CTTCTTCACT	AGCATGTCGG	TTAAAAAATC	TTTAACCGCT	120
TATCTTAACG	CTTATTTAGA	GCAACGCCCA	AATATCGAGG	GCATGGGGAT	TATAGGAGTT	180
CCTTTTAAAT	GCGAAAGGTT	TTTAAAATC	GCATGCGTTT	CTAAAGAACT	TCGTTTTTTA	240
AATCCTCAAA	ACTCTCCTAT	TATGGATTTT	AAAAATTTAG	AGATCAAGCT	CCATTCTTTA	300
GATAAAAGCT	CTCTTACCCT	TTCTATCCAT	TCTCAAATCC	AATCCCCTAT	TTTAGAACAA	360
TCCATTTCAGC	AAAAAATCAG	CCAAATCCCC	TTAAAAAATC	TGAATGCCTT	ATTGGAAAAA	420
TTCAAACCCA	CGCGCTTGAA	TTGCTCTTTA	ACATTCAACG	CTTTAGATGA	AAAAACCTTA	480
AACGATAATT	TAAAATGCGA	TTTGACTAAT	GCAGAGAATC	TCCTGCTACA	CTTTTTTTCA	540
AGAGGGTTTA	ATGGAGGCGC	AAGAAAATCT	CTCCCT			576

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CAGGATCAAC	CCATGCAATT	TCAAAAAACC	TTACTTTCTT	TATCTTTATT	ATTTTTATCT	60
TATTGTATCG	CTGAAGAAAA	TGGGGCGTAT	GCGAGCGTGG	GTTTTGAATA	TTCCATCAGT	120
CATGCCGTTG	AACACAATAA	CCCTTTTTTG	AATCAAGAAC	GCATCCAAAC	GATTTCTAAC	180
GCTCAAAACA	AAATCTATAA	ACTCAATCAA	GTCAAAAATG	AAATCACAAA	CATGCCCAAC	240
ACCTTTAACT	ACATCAACAA	CGCTTTAAAA	AACAATGCTA	AATTAACCCC	TACTGAAAAG	300
CAAGCCGAAA	CCTACTACCT	GCAATCTACC	CTTCAAAACA	TTGAAAAAAT	AGTCATGCTT	360
AGCGGGGGCG	TTGCGTCTAA	CCCTAAATTA	GCCCAAGCGT	TAGAAAAAAT	GCAAGAACCC	420
ATTACTAACC	CTTTAGAATT	GGTAGAAAAC	TTAAAAAATT	TAGAATTACA	ATTGAGCCAA	480
TCTCAAAACA	GCATGCTTTC	TTCTTTGTCT	TCTCAGATCG	CTCAAATTTT	AAATTCCTTG	540
AACGCGCTTG	ATCCCAGCTC	TTATTCTAAA	AACGTTTCAA	GCATGTATGG	GGTAGGTTTG	600
AGCGTAGGGT	ATAAGCATT	CTTTACCAAG	AAAAAAAATC	AAGGGTTTCG	TTATTACTTA	660
TTCTATGACT	ATGGTTACAC	TAATTTTGGT	TTTGTGGGTA	ATGGCTTTGA	TGGTTTAGGC	720
AAAATGAATA	ACCACCTCTA	TGGGCTTGGC	ATAGATTATC	TTTTCAATTT	CATTGATAAT	780
GCGCAAAAC	ATTCGAGCGT	GGGGTTTTAT	GTAGGCTTTG	CTTTAGCGGG	GAGTTCGTGG	840
GTAGGGAGTG	GTTTAGGCAT	GTGGGTGAGT	CAAATGGATT	TCATCAACAA	CTATTTGACG	900
GATTATCGGG	CTAAAATGCA	CACGAGTTTT	TTCCAAATCC	CTTTGAATTT	TGGGGTTTCG	960
GTGAATGTGG	ATAGGCACAA	TGGTTTTGAA	ATGGGCTTAA	AGATCCCTTT	AGCGGTCAAT	1020
TCCTTTTATG	AAACGCATGG	CAAGGGGTTA	AACGCTTCCC	TCTTTTTCAA	ACGCCTTGTC	1080
ATGTTTAAACG	TGAGTTATGT	TTATAGTTTT				1110

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GAACCCATGC	CTATGGGCAA	AGCGCTCAAA	GAATACCAGA	TCAAAAAAAC	CAGAGATGTG	60
GGCATTGGCG	CTAAAAACAG	CGAAATCATG	ACCTCCGCTC	AAGTGGAATT	AGGCAAAATG	120
CTCTATTTTG	ACCCTAGGAT	TTCCACTTCC	TATCTTGTGT	CTTGCAACAC	ATGCCATAAT	180
TTGGGCTTAG	GCGGGGTGGA	TCTAATCCCA	AGCGCTATAG	GCTCTCAATG	GAAGAAAAAC	240
CCCCACCTTT	TAAGTTCCCC	AACGGTGTAT	AACTCTGTGT	TTAACGATGT	GCAGTTTTTG	300
GATGGTAGGG	TTACGCATTT	AAACGAACAA	GCGCAAGGGC	CAATCCAATC	TTCTTTTGAA	360
ATGGGGGCTG	ATCCTAAAGT	CGTGGTAGAA	AAAATCAATT	CCATACCAGG	CTATGTCAAG	420
CTCTTTAGAA	AAGCTTATGG	CTCTAAAGTC	AAAATTGATT	TTAAATTGAT	CGCTGATAGT	480
ATCGCTATGT	TTGAAGCCAC	GCTCATTACC	CCAAGCCGTT	ACGATGATTT	TTTAAGGGGC	540
AATCCTAAAG	CGCTCAGTAA	AGCCGAAAAA	GAAGGGCTGG	ATTTATTCAT	TTCTAAAGGC	600
TGTGTGGCGT	GTCATAATGG	CATCAATCTT	GGGGGGACGA	TGCAGCCTTT	TGGGGTGGTC	660
AAACCTTATA	AATTCGCTAA	TGTGGGCGAT	TTCAAGGGCG	ATAAAAACGG	GCTTGTGAAA	720

GTGCCTACT

729

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

AACGATTTTT	GGAGAAAGGA	AATAACCATG	AGAGCTACGG	CGATAAAAAT	CTTTTCATTC	60
TCATCAGCGC	TCGCCCTATT	GCTTCAGGGT	TGCTTGAGCA	TTAATTTAAA	ACAAATGCTG	120
CCAGAAATCA	GAACCTTATGA	TTTAAATGCG	AGTTCTTTTG	AAATGACGCA	ATGCCCTAAA	180
CCTTTGACTG	AAGTGAGGCT	CATTATCATT	TTGAGCGCGG	ATTTATTCAA	CACTAAAGAG	240
ATCGTGTTTA	AAGCGCAAGA	CGGGCAGATT	ACGCATGGGA	AGCACCAAAA	ATGGATAGAC	300
TTGCCTCGCA	ACATGTTAAA	AACCATGTTT	ATGCAAGAAG	CGCAAAAAGC	ATGCTTAGGC	360
GTGGCTTTGC	CCCCTTATGG	CGCGGGCGCG	CCCACTTATG	CGGTTTCGTT	TACGATTTTA	420
TCGTTTTTCT	TTTGTAGAAA	AGAAAATTCT	ACTTACAGGG	CGGAATTCGC	GCTAGGCTAT	480
GATATTAGCG	TGAAAGGCGA	TTCGCATTCT	GGAGTGATCA	TTAAGCATGA	AAATATTTCT	540
AGCTTGGA	ATAAACGAC	CAAAACGAGT	AAAAATGGCA	GTCAAGATTT	CCAAGAAAGC	600
GCGATACAAT	CCCTCCAACA	TGTCAGCACG	CAAGCGATGC	AAGAAGCGAT	TTCTTTGATT	660
AAAAAAGCGG	TTGAAGCGCA	AAGCGTAAGC	CCGTAAAAAA	AA		702

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

AGGCAATTTA	TTCAATTCAA	CACGAGGAGA	GAAATTTTGG	AAAGGCATGT	GAATTACACT	60
TTAATCGGCG	GGCTCTTCTT	TTTATGCTTA	GTGTGCATGG	TAGGCTTTAT	TTTATGGCTA	120
GGCCATTTGG	GATTAGATGA	TGGGAAGTAT	TATGAATATG	TGGTCTATAC	GGACAAAGAC	180
TTGGGAGGCA	TTGCGACCAA	CTCGCCCATT	AATTACAAAG	GGATTCAAGT	GGGTAATGTC	240
ATCAAAGTGG	GTTTTGCAAA	GGATAAAGTG	GGGGTGGTCC	GTTTGGATTT	GATGATCAAA	300
TCCAGCGTTA	AGATCCGTAA	AGATTCCAAA	GTGGCGGTTT	CTTCTAGAGG	GTTTATGGGG	360
TTAAAATTTT	TAGCCTTAGA	GCAAAGCCAC	AATGAAGAAT	TTTATGGTAG	CGGCGATAAA	420
GGGGAGCGGA	TTTTAATCTT	TAAAGAAGGG	CTTATGGATC	GCTTGAGCGG	TGATGCTAAT	480
CAAGTGGTGC	AAGAAGTGAT	GAAAGCGATC	AGGAATGTGA	ATAGGATTTT	AGACGATGAA	540
AACGTGGAGA	AATTCAAGCA	CATTCTCGCT	TCAGTGGATG	ATCTCATCGC	TAACTTGGAT	600
TCAAGAAAGA	CTCAATTGTA	TTCTTGTATC	AACAACGCTA	ACAACCTTGT	TTCTAATGTC	660
AATAATGTGG	CTTTGGATGT	GGATAAACGC	GTCAAACAGG	GGCAATACGA	CTTTAAGGCG	720
ATGTTCACTC	CTTTAATCAT	GCAAGCGCAG	TTGAGCTTAA	GAAACATTGA	TAATTTTGTG	780
GAAAAAGGCT	CTGCTTTGAT	AGATAAATTT	GACGCTAACC	CCTATAAAAC	GATTTTGTGA	840
GAAAGGAAA						849

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AGCAGCTCAC	AATCTATAGC	CTTACTCATT	GGCTTGTGGT	TTGGGTTTCA	AAAACGCATC	60
GCTTTGGGGG	TGTGGTTTTT	CTTTAGCATC	TTATTAGGTG	AATTCACCTT	AAAATCCCTT	120
AAGCTTTTAG	TGGCGCGCCC	ACGGCCTGTA	ACCAATGGCG	AATTGGTTTT	TGCGCATGGC	180
TTTAGTTTCC	CTAGCGGGCA	TGCTTTAGCT	TCAGCGCTTT	TTTACGGCTC	TTTGGCGTTG	240
TTGTTATGCT	ATTCTAACGC	AAACAATCGC	ATTAAACTA	TTGGTGCTAT	TATTTTACTT	300
TTTTGGATTT	TTTTAATGGC	GTATGATAGG	GTTTATTTAG	GGGTGCATTA	CCCTAGCGAT	360
GTTTATAGGAG	GGTTTTTATT	AGGGATTGCT	TGGTCGTGCT	GCTCTTTAGC	GCTTTATTTG	420
GGGTTTTTGA	AACGCCCTTA	TAAAGCCGCT	TAA			453

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid

173

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ATGATGGATT TAGAAAGTTT GAGAGGTTTT GCGTATGCGT TTTTACCAT TCTTTTACG	60
CTCTTTTGT ATGCTTATAT TTTTAGCATG TATAGAAAGC AAAAAAGGG CATCGTGGAT	120
TATGAGCGAT ACGGGTATTT AGCGTTAAAT GATGCTTTAG AAGACGAGTT GATTGAACCA	180
CGCCATAAAG AAGTTCATGA TAAAGGCATA AAGGAAAGT	219

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGAAATTTAA TGGGACAAAC TAAAGAAATT ATAACGACGC TTTTACCCCT TTTGGTGTG	60
TTTCTTATTT TTTATTTTTT GATCGTTCGC CCGCAACGCC AACAGCAAAA AAAGCATAAA	120
GAAATGATAG AGGGCTTGAC TAAGGGCGAT AAAATTGTCA CTCAAGGAGG GCTGATCGTT	180
GAAGTGCTTA AAGCGGAAGC GAATTTTTTT AGCGTGAAAC TCAATGATGA CACCACCGCT	240
AAACTTTCTA AAAACTATGT AGCGTTCAAA TTAGACGAAG AAACAACACC CAACAACAAC	300

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs

(B) TYPE: nucleic acid

174

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ATGAACTTT	TTAACCTCG	TTTAATCGTT	TTTATATTCG	CGCTTCTTTT	AGGGGTAGGG	60
TTTTCTGTGC	CTTCTTTGCT	AGAACTAAA	GGCCCTAAAA	TCACTTTAGG	TTTGGATTTA	120
AGGGGGGGGT	TGAACATGCT	TTTAGGGGTG	CAAACCGATG	AGGCTTTAAA	AAACAAGTAT	180
TTAAGCCTAG	CGTCTGCTTT	AGAATACAAC	GCTAAAAAGC	AAAATATCTT	GCTTAAAGAC	240
ATTAAATCCA	GTTTAGAGGG	GATCAGTTTT	GAGCTTTTAG	ATGAAGATGA	GGCGAAAAAA	300
TTAGACGCGC	TTTTATTGGA	ATTGCAAGGT	CATAGCCAGT	TTGAAATCAA	AAAAGAAGCG	360
GAGTTTTATA	GCGTGAACT	CACCCCTTTA	GAGCAAGAGG	AATTGCGTAA	AAACACGATC	420
TTGCAAGTGA	TAGGGATCAT	TCGTATCCGC	TTGGATCATT	TGGCTTGGCA	GAGCCTG	477

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GGGAATGTTA	AAGTGAATAA	AAAGCACCGC	TTGGCTTTTT	TAGGGCTAAT	TGTTGGGGTT	60
CTATTCTTCT	TTAGCGCGTG	CCAACACCGC	CTGCACATGG	GGTATTATTC	AGAAGTTACA	120
GGGGATTATT	TGTTCAATTA	TAATTCCACT	ATCGTGGTGG	CTTATGACAG	AAGCGATGCG	180
ATGACTTCTT	ATTATATCAA	TGTGATTGTT	TATGAATTGC	AAAAATTAGG	CTTTTATAAT	240
GTCTTCACGC	AAGCGAATTC	CCGC				264

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AAAGCGTTGA TGGTAGGAAT GAAAACTGGA GCATGGACCG GTTTAAACT TTTTGCACAG	60
CCTTTGTTGG TGGTTTTAGC GTTCATGTTG TTGTATGCTT TAGCGCATGC TGTGCTTGGT	120
TTTTACGTGA AAAAAGACAG CGCTCCAATG AGTCCAAATG TAGAAAAAAG CGAGACAGAG	180
CGCCAAAACA GCACGTTTTTC GCCTAAAGAA GAAGCCAACG CAACCACAAC CGCCACAGAA	240
CAAAACCCCA CCAAAGACAC AGTGCCACCT TTAGACACAG CCACACAAAA ACAAGAGATT	300
AAACAAGAGA TTAAACAAGA GATTAAACAA GAGATTAAAC AAGAGATTAA ACAAGAGATT	360
AAACAAGAGA TTAAACAAGA AACTAAACAA GAGCAAGAAA AAGAAAATAA GCCTAAACAA	420
AACAGTGTCT CGCCCGTTCA AAACGATCAA AAAACCCCCA CAACCCCTT AATGGGTAAA	480
AAAACCTCTA GAGTA	495

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

ATGCTTTATG CATCAAAGC GCGTTTATTT TTACAAATCA AAGGAAAGTT TATGTTAAGA	60
ATTTTAATCC CCTTACTCAT TATTGTGTGG GTTTTATGGC GTTTGTTTT GAGGCAAAAA	120

CCCCACAAAG ATGACCACAG AGACAACCAC TCTTACACGC AACAAACCCC CAAAGAATTA	180
GAAGATCACA TGATTGTATG CTCTAAATGC CAAACTTATG TCTCTAGTAA AGACGCCATT	240
TATAGTGGGG CGGTAGCCTA TTGCAGTGAA ACTTGTTTGA AGGATAAGGG G	291

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

AAAACAATCA ATAAATTAAG GATTATAATG AAACCAACGA ACGAACCTAA AAAACCTTTT	60
TTTCAAAGTC CCATTGTTCT TCGGGTTCTT GGAGGGATT TACTCATTTT TTTCTACGC	120
TCTTTCAATT CTGATGGCAG TTTTTCGGAC AATTTCCTAG CTTCTAGCAC TAAAAATGTG	180
AGCTACCATG AAATCAAACA ACTCATCAGC AATAATGAAG TGGAAAATGT AAGTATCGGT	240
CAAACCTTAA TC	252

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTCAAAAATA ATAAGACACC CCTAACTTTT GAGCGTGATA AAGGGTCATT GGATGGTTTG	60
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AAAAAAGAAA	GACAAGGATT	TTACAAGCAA	GTGCATTATT	TAAGAATTTT	AATACTGAGT	120
ATGAGTTTTT	TAAATATTTT	AAATGCTGAA	AATTTGAGTT	ACATGTCTTC	TTCTTATCAA	180
ATAGGCACGG	TGTTTATGCG	CCCCTTAAAC	ACCAACAAAC	TTTTACAAGG	GGCTTCAATC	240
CTTCAAGGCT	ATGAAGTGAA	TCCTAAAAAC	GACTGGGCTT	ATTCTAGGTA	TTATTTCTTT	300
ATAGATTATG	GTAATGTGCT	TTTCAATAAC	GATTCCACTT	TGCAAGCGAA	CATGTTCACT	360
TATGGGGTGG	GAGGAGATTT	TATGGTTCGCT	TACGCTAAAA	ACCCTATCAA	CCGCTGGGCT	420
TTTTTCTTTG	GTTTGCAACT	AGCGGCTAAC	ACATGGATAC	TCAATAATAA	AGTCAAAGAT	480
TTGGTGGTGA	ATACTTGGGA	TTCATTGAAA	GATTTCAATT	TTCATAACAC	TTATTTTAGG	540
GCTATCGGGA	AATTTGGGGT	GCAGTTTCGC	ACGATCGTTT	TGTATCATAA	GGTGGATGTG	600
GAAATTGGCA	TGAAAATCTT	TTTAACGCCT	GAAAGGCGCA	GCTTGTTTGA	AAGGAGTTTT	660
TTGTTTTTTG	TTTCGCACTC	GTGGCATTTT				690

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GGAATTTGTT	TGAAGTTTCA	AATTGTGAGT	TTGTTATTGG	CTTTTTTATT	AGCCTCTTGT	60
TTGCCCCCTA	AGGGCCATCA	TTCTGGTTTG	GTGAATATGT	ATATTGCGCA	TCAAGGCCAG	120
AGCGTACGCA	CTTATTGGCG	CAAAGTGGAT	AGAGGAGTTG	TCGCCAAACA	CAATGAAACG	180
CTTAAAGAAA	ACCCCAAAAT	AAAGCTCAAA	GACCCTAAGG	GGCCTTTGTT	CATGCTAGGG	240
AGCAATCGTT	TCATGCTTTT	ATGGAAAAAC	CGCTATACTT	TAGCTAAAGT	CCAATCGTTC	300
AAGCTAGAGG	CTGGGTTTTA	TTACTTGGAT	TCTTTTAGCG	TGGAAACTCA	AAAAGGCATC	360
TTGCAAAGCG	CTCCTGGCTA	TTCATACACC	AAAAATGGCT	ACGATTTTAA	GAACAACCGC	420
CCCTTTTTTC	TAGCCTTTGA	AGTCAAACCT	GACAGCAAGA	TCGTTCTCCC	TAGCGTGGAA	480
TTGAGCTTGA	TTAAAACCCC	TAGAGGCTTT	TTAGGGGTGT	TTTTATTTGA	CAACAACGAA	540
AAGGGGGCTA	ATACCCCATG	GATTGAGGGG	AGCTTGAATT	TAAAGCTTAA	AAACGCTTCT	600
TTTAAAGACG	CATGGGAGTT	GGAACGA				627

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAACCCCTTG	GCTATCTCGG	GCTATTGTAT	AAGCAAGGGA	CGCAAAAAAA	CCCTCACAGC	60
TATGTGGGGG	CTCCAGCGCG	TCTTGGGGTG	GATTTTCTT	ATAGCAATGG	GTGGTCGTTT	120
GGTATTGGGG	CTATTGGGGC	TTGGAATATT	TATAACAAAC	AGCGTTTGGC	TAACCTTTAC	180
ATCAGTCTAG	GGAATTTTTT	TGGTAACCCT	AACAACGTTA	AGCCTTATT	GAGCGCCGGC	240
GATGTTCTG	ATGCGTATCT	TCAATACGCT	AACCAGCGTT	TTAAAATCGC	TTAGGGCGT	300
TTTAATACCG	ATTTTGTGGA	TTTTGATTGG	ATAGGGGGCA	ATATTCAAGG	GGTCTCTGTG	360
GCTTTCAAGC	AAAATCCCAT	GCGTTATTTT	GGGATTTTTA	TGGATAGCAT	GCTTTATAAT	420
GGGCATCAAA	TCAATAAAGA	GCAAGGGAAT	CGGATCGCCA	CTTCCTAAA	CGCTCTAGCT	480
CTTATGATCC	TGTGTCTAAA	CGCTTGATG				510

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 585 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TTAGGATCAC	CCATGCAATT	TCAAAAAACC	TTATCTTCCT	TATCTTTATT	TTTATCTTTA	60
TCTTTATTCT	TATCTTTTAG	TATCGCTGAA	GAAAATGGGG	CGTATGCGAG	CGTGGGTTTT	120
GAATATTCCA	TTAGTCATGC	CGTTGAGCAC	AATAATCCCT	TTTTAAATCA	AGAACGCATC	180
CAACGATTT	CTAACGCTCA	AAACCAAATC	TATAAACTCA	ATCAAATTGA	AAATGAAATC	240
ACAAACATGC	AAAACACCTT	TAACACACC	AACAACGCTT	TGAAAAACAA	TGCTAAATTA	300
ACCCCCACTG	AAATGCAAGC	CGAACAATAC	TACCTCCAAT	CCACCCTTCA	AAACATTGAA	360
AAAATAGTCA	TGCTTAGCGG	TGGCGTTGCG	TCTAACCCTA	AACTAGTCCA	AGCGTTAGAA	420
AAAATGCAAG	AACCCATTAC	TAACCCTTTA	GAATTGGTAG	AAAACCTAAA	AAATTTAGAA	480
TTACAATTCA	GCCAATCTCA	AAACAGCATG	CTTTCTTCTT	TGTCTTCTCA	GATCGCTCAA	540
ATTTCAAATT	CTTTGAACGC	GCTTGATCCC	AGCTCTTATT	CTAAA		585

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

AAAGGCAAGG TCATGAATAG TTCTAACCTC AAAAATTGGC TATCCCCAC TATTTGCTTT	60
TTTTTATTTT GTTATATTTT AATTTTTTTG ATATTTTTTA TGTTTAAAAA CTTGCAATCG	120
CAATCTTTTG GCTCTGTGGC AGAAACCGGA AAAAAACCCA TCACCACCAC CAAGAAATTT	180
GGTAAGGAAT TGCAAAAACA GATTTCAAAA ATCCAT	216

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TTGATGCGTA AGGTTTTATA CGCTCTCATG GGCTTTTTGT TGGTTTTTAG TGCTTTAAAA	60
GCCGATGATT TTTTAGAAGA AGCGAACGAA ACAGCCCCAG CGAATTTAAA CCACCCCATG	120
CAGGATTTAA ACGCCATTCA AGGGAGCTTT TTTGACAAAA ACCGCTCCAA AATGTCCAAC	180
ACTTTGAACA TTGATTACTT TCAAGGGCAA ACTTATAAAA TCCGCTTGCG TTATGCGATG	240
GCGACTTTAT TGTTTTTTTC AAAACCCATT AGCGATTTTG TTTTGGGGGA TAAGGTGGGT	300
TTTGATGCGA AAATTTTAGA AAGCAATGAT CGCATTTTAC TCATCAAACC CTTACAAATC	360

180

GGCGTGGATT	CTAATATCAG	CGTGATTGAT	AGCGAGGGTA	AGATTTTTC	TTTCTATGTG	420
TTTTCTACCA	CTTTCACCAG	CTCCAAACAC	CCTAATTTAC	AGGTTTTTAT	AGAAGATAAA	480
AAC TATTACA	CTAACGCTTT	TATCAAGCCC	CAAAAAGAAA	ATCAAGAAAA	TATGTCTGAA	540
AATGCCCCCTA	AAGATGCCCA	AAAAAATAAT	AAGCCCCTAA	AAGAAGAAAA	AGAAGAAACT	600
AAAGAAAAAG	AAGAAGAGAC	TATAATTATT	GGCGATAACA	CCAACGCGAT	GAAAATTATT	660
AAAAAAGACA	TCCAAAAAGG	CTATAAGGCT	TTAAAAAGCT	CTCAAAGGAA	ATGGTATTGT	720
TTATGGGCTT	GTTCTAAAAA	ATCCAAACTC	TCCTTAATGC	CTAAAGAAAT	CTTTAACGAC	780
AAGCAATTCA	CTTATTTC	CAATTTGACAAA	AGATTAGCAC	TCTCTAAATC	CCGG	834

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TATCGTGAGA	TGGATTATGC	GGTGTTTAGC	ATGACAATCC	ACCCTGATGT	GAGCGCCCGT	60
CCGCAAGTGT	TGCTCATGCA	TGAAAAAATC	ATTGAGCATA	TCAACCAGCA	CGAGGGCGTG	120
GCTTGGGTAA	CGTTCAATGA	AATCGCTGAT	GATTTCTTAA	AACGAAACCC	TAGGAAAAAA	180

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CTTGTGTAC AAGGGGCTGA GGTTTAAATC TATCCTAGTG CGTTTGGCAA AGCTAGGGCT	60
TATAATTGGG ATTTGTTGAG CAAAGCTAGA GCGTTAGAAA ATGGCTGTTT TGTGTGCGCT	120
TGCAATCATA GTGGGGAAGA AACTAACGCT AAATTAAAAC AAACGCTAGA ATTTGCCGGT	180
GATTCAAGGA ATCATCGCAC CCAATGGGAA AATCATCGCC CAAGCCACCA AGCTTAA	237

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AATTTGCCGG TGATTCAAGG AATCATCGCA CCAATGGGA AAATCATCGC CCAAGCCACC	60
AAGCTTAATG AAGTCATTAT CGCCGAAATG GATTTAAACG AAGTGGCACT GCAACGCCAA	120
AAAATCCCTT ATTTACAAGA TTTTGACACC AAATCACCA AAAAGGGGTT TGGAAACTC	180
ACT	183

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ATCATTATGT	TTGGCATGGG	CTTTTTTTGAA	ATCCTTGTGG	TGTTGATTGT	AGCGATTATT	60
TTTTTAGGAC	CAGAAAAATT	CCCTCAAGCT	GTCGTGGATA	TAGTGAAATT	TTTTCGCGCG	120
GTAAAAAA	CGCTCAATGA	CGCTAAGGAC	ACTTTAGATA	AAGAAATCAA	TATTGAAGAA	180
ATCAAAAAAG	AAACCTTAGA	GTATCAAAAA	CTCTTTGAAA	ACAAAGTGA	GAGTCTTAAA	240
GGCGTTAAGA	TTGAAGAATT	AGAAGACGCT	AAAGTAACTG	CAGAAAATGA	GATTAAAAGC	300
ATTCAGGATT	TGATGCAAGA	TTATAAACGC	AGCTTAGAAA	CCAACACGAT	TCCTAACCAT	360
TTAAATGAAG	AAGTTTCCAA	TGAAGAAGCT	TTAAATAAAG	AAGTTTCAAG	CGATGAATCT	420
CCTAAAGAAG	TCCAATTAAC	AACCGATAAC	AACGCCAAAG	AACACGACAA	AGAAAAAGAG	480
CATGTT						486

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CGCTATCGGT	CCTTTAGCCG	CAATCAGTCA	AACTTTAGAA	GATGCGAGCA	GCCCTATGGG	60
AGTACTTTAA	ACTCTGTGCC	GTTGTGGATT	ATGGTAGTAG	GGGCAGCTGG	GATCGCTTTA	120
GGCTTGAGCT	TGTATGGGCC	AAAGCTCATT	AAAACGGTGG	GGTCTGAAAT	CACAGAATTA	180
GACAAAATGC	AAGCTTTTTG	CATCGCGCTT	TCAGCGGTCA	TCACCGTGCT	TTTAGCCTCT	240
CAATTAGGCT	TACCGGTAAG	CTCTACGCAT	ATTGTGGTGG	GCGCGGTGTT	TGGGGTGGGC	300
TTTTTAAGGG	AGCGTTTGAG	GGAGCAATCC	AGAAGGCGTT	TTGCTAGAAT	CAGAGACAAC	360
ATTGTAGCGG	CGCACTTTGG	GGAAGATTTA	GAAGAAATTG	AAGGCTTTTT	AGAGCGCTTT	420
GATAAAGCCA	ATTTGAAAGA	AAAATCGCTC	ATGCTAGAGA	GCTTGAAAAA	AAGCAAGAAC	480
ACCGCTATCG	CTTTGGAATT	GAAAAAGAAA	GACAAAAAGT	CGCTTAAAAA	AGTGTATAAA	540
GAAGAAGTGA	TCAAA					555

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GCGCAAATCT TTGTGCGTTT CAATTATGTT TTAGGCGCGA TCGGTTTTGT GGTGTTACTT	60
TATGAAATCA TTTCGTTTAT CTACTATAAA AGATCGTTAG TGTATTTGAT CCTTGCGCTG	120
GCGATAGGGG CGTTGTGTTT GCTCTTTGTT TTTTATTACA CGCCTTATAT TTTAAACGCT	180
CAAAAGGTGG GTGAAGTTGC GCTTCAAAGT GCTGAATTTG CCCGCTCGCA CGCTCAAAGC	240
GAATGGCTGT TTAAGGAATT GTTGTGCTG GTGTGTGCTT TGTTTTTTTG GCGTTTGTTT	300
GGGAAAATG CGCTT	315

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AAGGCTTGCA AGATGAAGTG CTCAAGCTTT ACCTCTAATA GCGTCTTAAA CTTTTTTGTA	60
GTTTTGTCTT TCATCACGAT AGGGCTAGTG TTTTCTTTT TGCGTTCCCA ACCAACTAGC	120
GTAGTTTCTA AAGAAAATAT CCTTAAATT GAATTAGAAA ATTTTAAAGC GTTTCAAATC	180
AACGATAAAA TCCTTGATCT GTCCATAGAG GGCAAAAAAG CCCTACAATA CGATGATCAT	240
GAAATCTTTT TTGATTCTAA AATCAAGCGC TATGATGAAG ACACCATGA AAGCGTTGAG	300
TCCCCTGAAG CCAAACGGCA GCAGGATTTG TATTTCTTCC CTAACGGG	348

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AATCAAACAA AGCCAGAAAG AAAAGAAAAA ATTCCCCACT TTCAAAGGAG GGTTTTAATG	60
CGTTGGTGGT GTTTTTTGGT GTGTTGTTT AGCGTTTTTAA GCGTGATGGA CGCTAAAAAA	120
TTAGAGAATA AAGGCTTGAA AAAAGAAAGA GAGCTTTTAG AAATTACCGG CAACCAATTT	180
GTAGCGAACG ACAAACCAA AACCGCCGTT ATTCAAGGCA ATGTGCAGAT CAAAAAAGGT	240
AAAGACCGGT TGTTTGCGGA TAAAGTGAGC GTGTTTTTAA ACGATAACG AAAGCCAGAA	300
CGCTATGAAG CAGCA	315

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 957 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AAAGAAAGTA ATTCTATGGA CTTAGACAAA CTCAAAGATT ATAGGGCTTT AAGAAACGCT	60
ATTTTAAGGC TATTGCCTTA TTTAGATAGC GGTATTACAG AGCTAATTAT GAATAAAGAA	120
AAAGAAATTT GGCTCTATAA GCTTAATGGA GTAAGAGAAA AAGTCTTTGA TGAAAATTTA	180
GACAAAGCCT TTATTCTGGG GTTTGGGGAA CAATTAGCGA GTTTTAGAGA TTTGTTTTTT	240
AATGCTAATT ACCCCACCCT TAATACTTCC ATTCCTACTT CTAGATACAG AGTGAGCATG	300
AACCACTTTG CTATTAGTGC GGATAATGAA TTGAGTTTGA ATATTAGAGT GCCAAGTGAT	360
AAAAAGTTTG ATTTAAAAGC TTTCAAGCTT TCTAGTATCT GTCAATACGA TTATGAGTAT	420
TTAAAAAAT TAATGATTGA TGGCAAAAAC TTAATCATTG GTGGAGGCAC AGGCAGTGGA	480
AAAACGAGTT TTTTAAACGC TCTAATTGAG TTTATCCCCA AACACACACG AATAGTAAGC	540
GTTGAAGATA GCGAAGAATT AGATTTAAGA GCGTTTGAAA ATCATAAATC CTTGTTAGTG	600
GATAAAACTG AAAGCTCTAA ATTTACATAT GAAAACGCCT TGAATATGGC AATGAGAATG	660
TCTCCTGATA GGCTTATGGT AGGCGAGATT GACACACGAA ATTCCATGCT CTTTTTAAGA	720
TTTGGAACA CTGGGCATAA AGGCATGGTT TCTACTTTAC ATGCAGATAG TGTGCATGGG	780

GTTATAGAGG CGATTGCTTT AAATTTACAA ATGAATAAAA GTGGTTTAGA TGTCAATGTA	840
GCAAAAAAAT TCTTTAAAAG CAGTGTGGAT GTTGTCGTTT AAATTGTATT AGATAAAGCC	900
ACTAACACCA GATACATTCA AGAAATCTTA CCAGCAAAAG ATTTAAGAGA TAGTCTA	957

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...261
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GGAGTTAAAG CAATGAATTA CGATGTTTTA ATGGGATTTT TAGCACTAAT CTTGCTAATT	60
CTTTGGTATG CCTATGGATT AAGGCAATAT CTTAAATTAA AAGATAAGAA TAAGAGATTA	120
AAAGAGAAAT TACAACGCTG TAATTGTAAT ATTAAAATTC CTAGTATTCT TGAAATGGCG	180
CATAAACCTA TCATTATGGA TATTAAGGGG GAATTGCTAC CACATCTTAC AGAGAGTTAT	240
AGAAAATCAA AATTTAAGGA G	261

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...285
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CTCTCAAGGA ATGGCGTGGT CTCTAGCGTG AGTTCTGATG GCTCTAAAAT TTTAATGTCT	60
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TTAGCCCCTG ATGGCCAACC GGATGTTTAT TTGTATGACA CGCATAAAAA AACTAAAACC	120
AAAATAACGC GCTATCCGGG GATAGATGTT TCAGGCGTGT TTTTAGAAGA TGACAAGTCT	180
ATGGCTTTTG TTTCAGATAG ATCCGGTTAT CCTAACATCT ATATGAAGAA ATTGGGGTTA	240
AAAGAGAGGC GGAGCAACTC CTTTATGAAG GAAGAAGCAA TGAAT	285

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GGGGATAAAA TGCTAAAAAA GTTATTGCTC ATTTCACTAT TTTTAGGGTT TTTAAGAGCA	60
GAGGGCGAAC ATTATGAAAT CATCGCTGAA CTTTCCAAGG CTTTTTTGAA AGCCAAAGAG	120
GTTTTGACTG CGATCAATAA AACCTATAAA ACCTGTATTG AAACCGGGCA TGATCGCACT	180
CAAATACGCC TTCAAACGA TTTTTTAGAG AATTTGTCTC AAACAGAGCA ACAATTTGAT	240
GATTATTTTG AAAAGGATTT TAAAAGCGTA GGGGTTTTAA AAACCTTGCT TAAAGACATC	300
CAATCCTTAG AAAAACTTC CAACAAGCTC GTATGCGTTG CCCCAGAGCA CGCTAAAAAT	360
TTTGAAATAT TAGAGGGAGC GATAACGCAA ATCATAGGAT TAGAAGAGCA GATGAATCAA	420
TTTATCAATG GCGCGAAA	438

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATCCAAAGGC TAAAAGAAAT GCTTAGAAAT CAATTTTCGTA TCGTGTTTGT CACCTGCATT	60
GTCGCTAGCA GTTTGCAAGC TCAAGAAAAT ACCCCCACTT TGGGTAAGGT AACCCTAAG	120
GGTGAAAGGA CTTTTGAATA CAACCATCAA ATGTATACTG ACAGGAAAGA GCTCCAACAA	180
CGCCAAAGTA ACCAAACCCG TGATATTTTT AGGACTAGGG CGGATGTGAA TGCGGCCAGT	240
GGGGGCTTAA TGGCGCAAAA AATCTATGCC AGGGGGATTG AGAGCCGTCT CTTAAGGGTA	300
ACGATAGATG GCGTCGCTCA AAATGGTAAC ATTTTCCACC ATGAC	345

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GCGGTAAGTT GGATAATGGC GTGTTGGCAT AAAAGATTGG CAGTTGGTTG TTGTATCGTT	60
TTATTGTCAT GCGTAATGAG TGCTAATAAT GTTAGTATCG TTAGAGACGA TCCGCCCCTT	120
GATCCAACGC TCCCTGCATG GATTTATTCT GTTGCGTTAT TGAAAGTGTA TTTTAGCGAT	180
GGGACTTATA AAGAAGGCTA TGCGACTTTG CTAGAAAACG GCGGTTATAT CGCTTCTTCT	240
GAAACGCTCT ATTCTAATGG CTTGTATCCT AAAATGATTT TAGCCAAAAT GCAAGACAGC	300
AGTGCTAAAG AGCTGATTTG CATAGCCAGC TTGCACCTTG AAGCGATGGA TAGGGATCAA	360
GGGCTTTCGC TCTTAAAAAC CGCCGATTTT AGAGACGATT ATTGTCATAA AAGAGAAGAG	420
AGCTATTATC ATGCAAGGAT TTATGCCAAA TACGCTCAA CTTTCCATTC AAATCCTTAT	480
ACCAATCAA AAACACCCAC TTCCGATCTC TACTACCCGG CGTTAAATGA GGGGAATTCT	540
TTTTCCATAC AGACAACGGA CATTCTGTG GCTGAACCTT TGAAATCTAA AAAGTTTCTT	600
TCGCTTGATG CTTCTTTTAA AAAGGGGAGC GTGTTGTGGG GAGGGAGACC TTATTTTAGC	660
GAGGTAGGGG AGTTTATGGG AATGACTAGC AGCACTTTAG AAAACCAAGA AAGTTTGGTG	720
ATTATCCCTA AAGAAAAGAT TGCGCGATTT TTAAGCGCTC TAAAAAATCA AAATATTTTT	780
CCAAACATTC CC	792

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CTTGGAGGAC TAGACATGTA TAAATTAGGA ATATTTTTAT TAGCCACCTT ACTATCAGCT	60
AACACGCAAA AAGTGAGCGA TATTGCTAAA GACATCCAAC ATAAAGAAAC CCTTTTGAAA	120
AAAACCCATG AAGAAAAAAA CCAACTGAAC AGTCGTTTGA GTTCTTTAGG CGAAGCGATC	180
CGCTCTAAAG AGCTTCAAAA GGTTGAGATT GAACGCCAAA TGGTCGCCTT AAAAAAGAGT	240
CTTGAAAAAA ATCGTAACGA AAGTTTGGTG CAAGAAAAAG TCCTAACCAA CTACCGCAAG	300
TCTTTAGATC ATTTGCAAAA ACAACGATCG TTTTACAAA AGAGAGTGTT TGATACGCTT	360
TTAGAGGATT TTCTTTTCTC ACAAGCCCTA AAGGGGCAGA ATTTAGCCTC TTCTAATGAT	420
GTGATTTTGC TAAGTGGCGT T	441

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1569 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TATATTCCAT TCAATTTATT TCAAGGACAA ACAAACATGA AAAAATTCTT TTATACCATG	60
CTCGCGCTTC TTTTAATCGG CCTTTTAACG GCCTATCTTA TCCTTTTAC AGAATGGGGG	120
AATAAGATCA TCGCTTCGTA TATAGAGAAA AAAATCAATC CGAACGAGCG TTATTTGAGC	180
GTAAAAACCT TTAAATTGAG ATTCAACTCT TTGGATTTC AAGCTCAAGC CAACGATGAT	240
TCCACGCTCA TTCTTAAGGG GGATTTCTCG CTTTAAACGC AAAGCGTAAA TTTGGATTAC	300
CACATAGACA TTAAAAATTT ACGCTCTTTT AAGGATTTGA TACCCTACCC CTTAAGAGGG	360
GCTATTGTTA CTTCTGGGAA TATCAAAGGG CATAGAAAAG CCCTTGTAAGT TCAAGGCGTC	420
TCCAATGTCG CTCAATCCCA CACTGCCTAC AACGCCCTTT TAGATGATTT CAAGCTTTCT	480
CACTTAAGTT TGAACGCAAA AGACGCCAAT TTAGAAGATT TGCTTTATTT AATCAACCGC	540
CCCGCTTATG CGAACGCAAA AGTGTCTTCA CAAGCGGATT TTAAGCTCTT AAAGCCCTTA	600
GAAGGGCATT TGATCCTAAC AGCTAATAAC GCTTTAATCA ATAACGCCCT AATCAATCAA	660

ATCTTTCATT	TAAACCTTAA	AGACACGCTC	GTTTTCAACC	TCTCGCACTC	AAGCGATTTT	720
AAAGGAAACA	AAGCCATCAG	CGATACCACC	CTAACTAGCC	CTTTAGTTAA	TTTCACAGCC	780
CTAAAAAGCG	AATATTCTTT	CCCTGCTTTA	AAACTCAACG	CCCCCTACAC	TTTAGAAATA	840
CCCCATCTAG	CCAAACTCCA	AAACATTACC	AACCACCCCT	TAAAAGGGAG	CTTGACTTTA	900
AAAGGCGATA	TAGAGCAAAG	CCCTAAACTC	TTAAAAGTCA	GTGGCCATTTC	AAATTTACTA	960
GACGGCGCGC	TAGACTTCAC	GCTTTTAAAT	AAAGATTTGA	AAGCCCGTTT	TTCCAATATT	1020
TCCACTTCAA	AAGCCTTAGA	TTTATTCCAT	TACCCTAAAT	TTTTCCAATC	CATTGCAGAC	1080
GCTAACTTGG	ATTATGACCT	TATCTCTAAG	CAAGGCGTGT	TGAAAGCCAA	TCTCAAGAAC	1140
GCAAGATTCC	TCAAAAATGC	ATTGAGCGAT	TTCCTCTATT	CCATTCTCTG	TTTTGATATT	1200
ACTAAAGAAA	TTTATCACGA	TGCCAATCTA	GTAAGCCAAA	TCAACCAGCA	ACGCCTGCTC	1260
TCTGATTTGA	GTTTAAAAAG	CCCCAAAACC	CAATTGAAAA	TCCATAACGG	CTTGTTGGAT	1320
TTAAACACCA	AGCAAATGGA	CATACTCATG	GATGCGGAAA	TCTTAAAATT	CATCTTTAAA	1380
ATGAAACTTC	AAGGCAGCAT	GCACCAGCCA	AAATTTTCCC	TCATTTTAAA	CGAAAAAGCC	1440
ATTGAGCAAA	ACCTGCAACA	AGGCTTGAAA	GAAATCCTTA	AAAACGACAC	CCTTAAAAAA	1500
GGTTTAGATC	ATTTGCTTAA	AGATGATAAA	CTCAAAGAAA	AGCTTGAAAA	AGGGCTTAAG	1560
GGGCTTTTTT						1569

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GCATTTCTTT	ATATTCATTC	AATAGCGCTT	GCGCGGGTAA	TTCTTCAACT	AAAACCTCTA	60
CTAACAAATTC	ATCTGAATGC	AAAATCTCAA	TCCTCCCTAA	AAAACAAAAT	CACTCTTAAG	120
AATAAGCTAA	ATCATGCTAG	AATTATACTT	GAATTTATTC	CTAGTTTAAT	TTATTTCTTA	180
ATACAAAAGG	TGAGCGTTTT	GAAACATTTA	GCCCCACTCA	TTCATATCCC	TTTTAAAGCC	240
TTATGGCTAG	GCACAGCCTT	AAGCATGTTC	TTAAGTTTGA	ATTTGAACGC	TGAAGAAAAC	300
CCTACTAAAA	CAGAGCCTAA	GCCCGCTAAA	GGGGTTAAAA	ACAAGCCCAA	ATCGCCTGTT	360
ACTAATGTCA	TGATGACCAA	TTGCGATAAC	CTTAAAGACT	TTAACGCTAA	GCAAAAAGAA	420
GTTTTTAAAG	CCGCTTATCA	ATTCCGATCT	ACAGAAAATT	TAGGCTATGA	AATGGCGGGC	480
ATTGCGTGGA	AAGAATCATG	CGCAGGGACT	TATAAAATCA	ATTTTTCGAA	TCCGAGTGCG	540
GGCATTTACC	ATGCGTATAT	CCCTAGCGTT	TTAAAAAGCT	ATGGGCATAA	TAATAGCCCC	600
TTTTTGCGTA	ACGTGATGGG	GAGAATTGCT	ACATTAAAGA	CGATGCGTTT	GCTTCTGAAG	660
TGGCCC						666

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs

190

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TTAGTTATAA TATCGCTACT AACAACTC AAGCTAAAAT CCATTAAGGA AATCAGTATT	60
AAAAAATTTA TTCTATCTTC TCTTGTTTTT GCATGTATCA ATACCGGCGT TGAAGCTTTA	120
GAAAATGACG GCTCTAAACC AAACGATTTG GCTTCTCCAA AAGAAACCCC AAAAGAGGCT	180
CAAAAAAATG AAGCTCAAAA CGAAACCTCT CAATCCAATC AAACGCCTAA AGAAATGAAA	240
GTCAAGTCCA TTTCTTATGT CGGGCTTTCT TACATGCTCG ACATGCTCGC TAATGAAATT	300
GCAAAGATTC GCGTGGGCGA TATGGTGGAT TCTAAAAAAA TAGACACCGC TGTTTTAGCT	360
TTGTTCAACC AAGGGTATTT TAAAGACGTT TATGCCACTT TTGAAAACGG CATTTTAGAG	420
TTTCATTTTG ATGAAAAAGC CAGGATTGCC GGGGTAGAAA TCAAGGGTTA TGGGACTGAA	480
AAGGAAAAAG ACGGCTTAAA ATCCCAAATG GGGATCAAAA AGGGCGACAC CTTTGATGAG	540
CAAAAATTAG AGCATGCTAA AACGGCTTTA AAAACGGCTT TAGAGGGGCA GGGCTATTAT	600
GGGAGCGTGG TGGAGGTGCG CACAGAAAAG GTCAGTGAGG GAGCGTTATT GATCGTGTTT	660
GATGTGAATA GGGGGGACAG TATTTATATC AAACAATCCA TTTATGAGGG AAGCGATAAA	720
TTAAAACGCC GTGTGATTGA ATCTTTGAGC GCGAACAAGC AGCGCGATTT CATGGGCTGG	780
ATGTGGGGCT TGAATGACGG GAAATTGCGC TTAGATCAAT TAGAATACGA TTCTTTGCGT	840
ATCCAAGATG TGTATATGCG TAGGGGTTAC TTAGACGCTC ATATTTCTTC GCCTTTT	897

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 864 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GAGTTTGGTG	TGAAGCGAAT	TTTATTTTTT	TTAGCGGCTA	CGACTTTTTT	GTTGAGAGCA	60
GAAACGGCTT	CTGCTACTAT	TAACACTACA	GTTGATCCCA	ATGTTATGTT	TTCTGAAAGC	120
TCCACAGGGA	ATGTGAAAAA	AGACCGCAAG	AGGGTTTTAA	AGAGCATGGT	TGATTTAGAA	180
AAAGAGCGCG	TGAAGAATTT	TAACCAGTAT	TCTGAAACCA	AGATGAGTAA	GGGCGATTTA	240
TCCGCTTTTG	GAGCTTTCTT	TAAGGGGAGT	TTGGAAGATT	GCGTGGAGCA	AAAGATTTGT	300
TACTATGAGC	ATAGGAATGG	CAAGGTTTCT	TTTGTGGTGA	ATGACAGAGA	AAAGTTTTAT	360
AAGCATGTGC	TTAAAGACTT	AGGGACAGAG	CTTTCCTACTCC	CCTTGTTCAT	CTGGCTTTAC	420
AAAGGCTCAG	ATTTTGGGGC	TTTGCATGAG	CAGTTTGGGG	ACATGTATGA	TGGGTATATC	480
AAATACTTGA	TCAGCATGGT	TAGGGTGAGC	CAAAAAGAAA	AGGCTAGAAA	AGTGGATGCA	540
ATCGTTCTTA	AAAAAATGGA	AGAACAAGCT	GAGAAAGACA	CTAAGGCAGC	ATTCCAAAAG	600
AGGAGCAGTG	GGGAGCTTGA	AAGCCATACT	GATAGCCCTG	AATTTATAAG	CTCTTCTAAG	660
ACACAGAATT	CTTCTAACCC	AGATCTAGAC	CCTATGACTA	ACGCTAACAC	GCTCAAAGAA	720
ACAGCTTCAA	AAGAGCCAGA	GACTTCTTCA	AAAAAGGAAA	AAAAGCCCAA	GAAAAACGA	780
CGCCTTTCAA	AGAAAGAAA	GCAACAACAG	GCCTTACAAC	AAGAGTTTGA	AAAGCAAATT	840
AGCGACTCTA	GTAAGTCTGA	AAAA				864

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

AGTCGCACCC	TTTGTGCAAA	AATCGTTTTA	CAAAAAGAAA	GGAAGAAAAT	GGAAATACAA	60
CAAACACACC	GCAAAATCAA	TCGCCCTTTA	GTTTCTCTCG	TTTTAGCAGG	AGCGTTGATT	120
AGCGCCATAC	CGCAAGAGAG	TCATGCCGCC	TTTTTCACGA	CCGTGATCAT	TCCAGCCATT	180
GTTGGGGGTA	TCGCCACAGG	CACTGCTGTA	GGAACGGTCT	CAGGGCTTCT	TAGTTGGGGA	240
CTCAAAACAAG	CCGAAGAAGC	GAATAAAACC	CCAGATAAAC	CCGATAAAGT	TTGGCGCATT	300
CAAGCAGGAA	AAGGCTTTAA	TGAATTTCTT	AACAAGGAAT	ACGACTTATA	CAAATCCCTT	360
TTATCCAGTA	AGATTGATGG	AGGTTGGGAC	TGGGGGAACG	CCGCTAGGCA	TTATTGGGTC	420
AAAGGCGGGC	AATGGAACAA	GCTTGAAGTG	GATATGAAAG	ACGCTGTAGG	GACTTATAAA	480
CTATCAGGGC	TTAGAAACTT	TACTGGTGGG	GATTTAGACG	TGAATATGCA	AAAAGCCACT	540
TTGCGTTTGG	GCCAATTCAA	TGGCAATTCT	TTCAACAAGCT	ATAAGGATAG	CGCTGATCGC	600
ACCACGAGAG	TGAATTTCAA	CGCTAAAAAT	ATTTCAATTG	ATAATTTTGT	AGAAATCAAT	660
AATCGTGTGG	GTTCTGGAGC	CGGGAGAAAA	GCCAGCTCTA	CGGTTTTGAC	TTTGCAAGCT	720
TCAGAAGGGA	TACTAGCAG	TAAAAATGCG	GAAATTTCTC	TTTATGATGG	CGCCACGCTC	780
AATTTGGCTT	CAAACAGCGT	TAAATTAAAT	GGTAATGTGT	GGATGGGCCG	TTTGCAATAC	840
GTGGGAGCGT	ATTTAGCCCC	TTCATACAGC	ACGATCAACA	CTTCAAAAGT	TCAAGGGGAA	900
GTGGATTTTA	ACCATCTCAC	TGTGGGGGAT	CAAAACGCCG	CTCAAGCGGG	CATTATCGCT	960
AGCAATAAGA	CTCATATTGG	CACACTGGAT	TTGTGGCAAA	GCGCCGGGTT	AAATATCATT	1020

GCCCCCTCCAG AAGGTGGCTA CAAGGATAAA CCTAATAGTA CCACTTCTCA AAGTGGCACT	1080
AAAAACGACA AGAAAAGAGAT CAGTCAAAAT AACAATAGCA ACACAGAGGT CATTAACCCA	1140
CCCAATAACA CGCAAAAAAC AGAAACTGAA CCCACCAAGT CATTGATGGG CCTTTTGCTG	1200
AAGGCAAAGA CTCGGTTGTC A	1221

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CAAATCTTTT GCTCCACGCA ATCTTCCAAA CTCCCCTTAA AGAAAGCTCC AAAAGCGGAT	60
AAATCGCCCT TACTCATCTT GGTTTCAGAA TACTGGTTAA AATTCTTCAC GCGCTCTTTT	120
TCTAAATCAA CCATGCTCTT TAAAACCCTC TTGCGGTCTT TTTTCACATT CCCTGTGGAG	180
CTTTCAGAAA ACATAACATT GGGATCAACT GTAGTGTAA TAGTAGCAGA AGCCGTTTCT	240
GCTCTCAACA AAAAAGTCGT AGCCGCTAAA AAAAATAAAA TTCGCTTCAC ACCAAACTCC	300
TATATCCATA ACCGCAACAA AAACAGACGC TATTCTTCAT TAAGCCCTCT TTTAAAATCT	360
TCTTCTATTT GTAAAAACCC ACCTAGAATT CAAGCTATTT TGATTATCTT AAAATACAGA	420
CTTTCAAAGG GTTTTAATCC TGTGGTGGTG ATACTTAGGA TCCAAAAAAT GCGGACTCTC	480
CAAAAACCTT	489

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGTTTAATCA CAATGGATAA AAACAACAAT AATAATCTCC GCTTGATTTT AGCGATCGCT	60
CTGTCTTTCT TGTTAATCGC TCTTAATAGC TATTTTTTCC AAGAACCAAA CAAAACAACA	120
ACCGAAACCA CAAAGCAAGA AACCAACCAAC AACCACACAG CAACAAGCCC CACCGCGTCC	180
AATACCATCA CCCAAGATTT TAGCGTTACC CAAACCATCC CTCAAGAGAG TTTGTTAAGC	240
ACGATTTCTT TTGAACATGC CAAAATTGAA ATTGATTCTT TAGGGCGCAT CAAACAGGTT	300
TATCTCAAAG ATAAAAAGTA TCTAACCCTT AAAGAAAAGG GCTTTTTAGA GCATGTGAGC	360
CATCTTTTTA GCTCCAAAGA AACTCGCAA CCCTCCCTAA AAGAGCTCCC CCTTTTAGCA	420
GCCGATAAAC TCAAGCCTTT AGAAGTGCCT TTTTGTAGACC CCACGCTCAA TAATAAGCG	480
TTCAACACCC CTTATAGCGC CTCAAAAACC ACCCTTGGGC CTAACGAACA GCTCGTTTTA	540
ACCCAAGATT TAGGCACTCT TAGCATCATT AAAACCCTGA CTTTTTATGA TGATTTCAT	600
TAT	603

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GGAGTTTCTA TCATTATGGT ATTGAAAACA AAATTAAAAA TTATAAGCTC GGTGATTTTG	60
AGTACTTTAT TGTGGGTGGG TTGCTCAAGC GAAATGGCGA CTTATCAAAA TGTGAATGAC	120
GCCACTAAAA ATACGACTGC AAGTATTAAT AGCACGGATT TATTGCTAAC CGCTAACGCG	180
ATGTTAGATT CCATGTTAGG GACC	204

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GCGATGAAAA	ATCAAGTTAA	AAAAATTTTA	GGGATGAGTG	TGGTAGCAGC	GATGGTGATC	60
GTAGGTTGTA	GCCATGCCCC	AAAATCAGGT	ATCAGTAAAA	GCAATAAGGC	ATACAAAGAA	120
GCGACTAAAG	GCGCTCCTGA	TTGGGTTGTA	GGGGATTTGG	AAAAAGTGGC	GAAGTATGAA	180
AAATATTCAG	GGGTCTTTTT	AGGAAGGGCT	GAAGATTTGA	TCACTAATAA	TGATGTGGAT	240
TATTCTACGA	ATCAGGCTAC	AGCCAAAGCT	AGGGCTAATT	TAGCGGCGAA	TCTAAAGTCC	300
ACTTTACAAA	AAGATTTGGA	AAATGAAAAA	ACCAGAACGG	TAGATGCTTC	TGGTAAAAGG	360
TCCATAAGCG	GCACTGATAC	TGAAAAAATT	TCTCAATTAG	TGGATAAGGA	ATTGATCACT	420
TCTAAAATGC	TTGCCCGCTA	TGTCGGTAAA	GATAGGGTTT	TTGTTTTAGT	GGGCTTGGAT	480
AAGCAAATTG	TGGATAAAGT	GCGCGAAGAG	TTAGGCATGG	TTAAAAAG		528

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CCCAAACCTT	ACGCCGTCAG	TATTCTATGT	ATTTGCGTTA	TGTTTATACT	TTTTAAGTTT	60
GGTAGGGTTT	TGGGTAAGGC	TTATAGCTTA	TACTTATATA	TATATGAAAG	CTTGATTTGT	120
CAAGCTTTTG	GGTTGTCATT	GAGTTGCAAT	AACTCTATGC	TGTTTTCTAC	TTTTTTGATA	180
AATCTACCAT	TACCACACAA	TGAGTCCTTA	TGCTGTTGTA	GGGATATTTT	AGCGTATTCT	240
AACTCTTCAT	CGCTAAAGAC	ATATTCATTG	GAGTCAAATT	TTTCTTTCAA	TTCTTTATTT	300

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

195

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...300
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

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ACAGCAAGAA TGAATCGCAT GAAACCAATT TTTTGTGTTA TCTTTTGTGTT GTTAGCGAGC      60
CTTATTGCTA GAGAAAAGGA CGCTTCTTCA AACCTTTTGTG ATTTGATCGA TAAGGGGATT      120
AACAGAGAAC AAGAATTGAA AGAGCAGGAG CAAAAAACGC GCTTGAAACT GGCTCAAAGC      180
CCTTTAGTGG CGTTAGAAAT TGTCCCCCAA GAAACGCCCT ATTTAGAATG GCAAGGGGCT      240
AGGGAGTCGT ATTATTTGAA AGTAGAGCGC TGTAGTGGAG AGCGTGGTTA TTTTAAAGAT      300

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(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 693 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...693
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

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GTTGCTCGCG CTTTTATCGC TCTTTATGCC ATTTACGCGG TCAATAAATC CAAAGTGGAA      60
GCCTTAAAAA CCGAATTTAT TAAGATTTTT AATTACGCCC CAAAGCCAGA GGCGATGCAG      120
CCGGTTGTAG TGATCCCCC TGATTCAGGG AAAGAAGAAG AGCAAATGGC GAGCGAAAGC      180
TCCAAGCCGG CTTGCAAAA TACCGAAACA AAAGCCACTA TCGCTCGCAA GGGCGAAGGC      240
AGTGTTTTAG AGCAAATTGA TCAAGGCTCT GTTTTAAAGC TCCCCTCTAG TTTGCTGTTT      300
GAAAACGCCA CTTGAGACGC TATCAATCAA GACATGATGC TTTATATTGA ACGGATCGCT      360
AAAATCATT CAAAACCTCC TAAAGGGTG CATATTAATG TGAGAGGTTT TACGGATAAC      420
ACGCCTTTAA ATAAACCCG TTTTAAAGC CACTATGAAT TAGCCGCCAA TCGCGCTTAT      480
AGGGTGATGA AAGTCCTTAT ACAATACGGC GTGGATCCTA ACCAATTGTC TTTTCTTCT      540
TACGGCTCTA CCAACCCTAT TGCGCCCAAT GATTCCTTAG AAAACAGAAT GAAAAACAAT      600
CGTGTTGAAA TCTTTTTTTC AACCGATGCG AACGATTGTA GCAAGATCCA TTCTATTTTA      660
GATGAAGAAT TCAATCCCCA TAAACAGCAA GAA                                     693

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(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CAGCGTCTAT ACCTAGGAAA ATTAACGCT AAAGTGAATC ACACGATTTT CCAATTTTTA	60
GTGAATGTGG GCATTAGAAC CAATATTTT GAACACCATG GCATTGAGTT TGGTATCAAA	120
ATCCCCACGC TCCCTAATTA CTTTTTCAAA GGTCTACTA CTATAAGAGC GAAAAACAA	180
GGCCCACTAG AGAATGGGAA CCCGACTACT ATCACCAGGAG CAGAAACCAA TTTCAGCTTA	240
ACCCAAACCT TACGCCGTCA GTATTCTATG TATTGCGTT ATGTTTATAC TTTT	294

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1071 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TTTCATTTTT ACTGCTTGTA TTCCTTAAT GGTGGTTATA ATCGGCTTCA TAAATCATAC	60
GAAAGGATTG TCATGCTAAT CGCTCGCTTT AAAAAAGCTT TAATTCCTA TTCTTTAGGG	120
GTTCTTCTTG TTTCATCGTT ATTAGGCGTG GCTAACGCTT CTAATCAAGA GATCCAAGTC	180
AAGGATTATT TTGGGGAGCA AACCATAAAG CTTCTGTTT CTAAAATAAT CTACTTGGGC	240
AGCTTTGCAG AAGTGCTGC CATGTTCAAT ACTTGGGATA GGGTCGTGGG CATTTCCGAT	300

TACGCTTTTA	AATCTGATAT	TGTTAAAGCC	ACTCTCAAAG	ATCTTGAACG	CATTAAACCC	360
ATGAGCAGTG	ATCATGTGGC	GGCGTTGAAT	GTGGAATTAT	TAAAAAAGCT	TAGCCCTAAT	420
CTTGTGGTAA	CCTTTGTGGG	TAACCCTAAA	GCGGTAGAGC	ATGCGAAAAA	ATTTGGGATT	480
TCATTCCCTT	CTTTCCAAGA	AAAAACCATT	GTAGAGGTCA	TGGAAGATAT	TGACGCTCAA	540
GCTAAGGCCT	TAGAAGTTGA	CGCTTCTAAA	AAATTGGCTA	AAATGCAAGA	AACTTTGGAT	600
TTTATCAAAG	AGCGTTTGAA	AAATGTCAAA	AAGAAAAAGG	GGGTGGAGCT	TTTCCATAAA	660
GCCAATAAAA	TCAGCGGCCA	TCAAGCCCTT	GATTCAGACA	TTTTAGAAAA	AGGGGGTATA	720
GATAATTTTG	GCTTGAAATA	CGTTAAGTTT	GGACGCGCTG	ACATTAGTGT	GGAAAAAATC	780
GTTAAAGAAA	ACCCTGAAAT	CATTTTCATT	TGGTGGGTAA	GCCCACTCAC	TCCTGAAGAC	840
GTGTTGAACA	ACCCTAAATT	TTCCACTATC	AAAGCCATTA	AAAACAAGCA	AGTCTATAAG	900
CTCCCCACAA	TGGATATTGG	CGGACCTAGA	GCCCCACTCA	TTAGTCTTTT	TATCGCTTTA	960
AAAGCCCACC	CTGAAGCGTT	TAAGGGCGTG	GATATTAATG	CGATAATCAA	AGATTACTAT	1020
AAAGTGGTCT	TTGATTTGAA	TGACGCGGAA	GTTGAACCCT	TTTTGTGGCA	C	1071

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GATCATCACA	AGGAGTTTCG	TATGAAAAAG	CAAATCTTGA	CAGGTGTTTT	GTTATCAGTT	60
TTGGCAGTGA	GTTCTGCATA	CGCTCACAAA	GATAAAAAAG	ACGCTAAAAA	ACCTGAGTTA	120
AGCTCTCAAT	TAGTGGCTCA	CAAAGATAAA	AAAGACGCCA	AAAAACCTAA	AAACTCAGTG	180
GCC						183

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AGAATAATAA AAGGAAACAT TATGAGCAGC GGGTTAATTT ACATTTTCATT AGAAGTCTTG	60
GTAGCGTGTT TGATCACCGC TCTAATCATG TATTATGTGA TGAAAAAGAT CTATTACGCT	120
AGAGGGCAAG CCATTTTAAA AGGCGCTTCA GCCAAAGCTA AATTAATGGA ATTTCAAGCG	180
AAATCTTTTCG TGGAAGCTGA AGAAATGCGC ATGAAAAGCC AAGAATGCAA GTTGCAACAG	240
CAATATGAAA ATAAGAATTT GCAACTCCAA ACCCATTTTG ATAAAAAGA AGCGCATTTG	300
AAGCATTTAG AAGCGCAGCA CAAAGAATTT GTAAGAGATG AAAAAACGCTA TTTGGAAAAG	360
GAAAAAAAAG AGCTTGAAAA AGAACGCCAA ATTTTAGAAC AAGAGAGGGA AAATTTTAAA	420
AAACAGCGCG CCATTTGTAA AGAAGCTCAA GCCAAAGCGC TAGATGCGAT GCTCAATTAC	480
ATGGCTTATA CCAAAGATGA AATTAAAGC ATGATCTTAG AGCAATTAGA ACAGGAACTA	540
GAAGCGCAAA AGAGCGCCTT GATCAGGCGT TATGAAGAAG AAGCCTTTAT TATGTGTTA	600

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GGCCGAGCTT TTATGATGCG AGAGATCCTT ACTAACCGCT TTTTCCAAG CCTTTTAAA	60
AAAAGGCTTG ATTTTCTAA CAGAGTGGTT TTAGGGCTGG GATCTAATCT TAAAAACCCT	120
TTAAAAATAT TAAAAAGTTG TTTTATAT TTTAAAAATC ATAGTAAAAAT CGGGAAAATT	180
TTTTCTTCAC CCATTTATAT CAATCCGCCT TTTGGTTACA CTAATCAACC TAACTTTTAT	240
AACGCTACGA TTATCCTTAA AACATCTTTA GGTTTGCGCC ATTTTTTTGC TCTAGTGTTT	300
TATATAGAAA GCGTTTTTGG GCGTGCAAGG AAGCGCGATT TTAAAGATGC TCCAAGAACT	360
TTAGATATTG ATATTATCGC TTTCAATCAA GTCATTTTGA GGCAGAATGA TTTGACTTTA	420
CCTCACCTA AATGGAGTGA AAGAGACTCG GTGTTAGTGC CTTTAACTTT ACAACAAATC	480
CTTTTAAAA GAGAAGAGTG G	501

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

ATAATAGAAA	TTTTAGTGAT	TCAAGGGCCT	AATTTAAACA	TGTTAGGACA	CAGAGACCCA	60
AGACTTTATG	GCATGGTAAC	CTTAGACCAA	ATCCATGAAA	TCATGCAAAC	TTTCGTGAAG	120
CAAGGCAATT	TAGATGTGGA	ATTAGAGTTT	TTTCAAACCA	ATTTTGAGGG	CGAAATCATT	180
GATAAAATCC	AAGAGAGCGT	GGGCAGCGAT	TATGAGGGGA	TTATCATTA	CCCTGGAGCG	240
TTTTTCGCACA	CTTCTATTGC	GATTGCGGAT	GCGATCATGC	TAGCGGGCAA	ACCTGTCATT	300
GAAGTGCATC	TACTAACAT	TCAAGCCAGA	GAAGAATTCA	GGAAAAATTC	TTACACCGGA	360
GCGGCTTG	GAGGCGTGAT	CATGGGATTT	GGCCCGCTTG	GCTACAACAT	GGCTTTAATG	420
GCGATGGTCA	ATATTTTAGC	CGAAATGAAA	GCGTTCCAAG	AAGCCCAAAA	AAACAACCCT	480
AATAACCCCA	ATAACCCGAT	CAACAATCAA	AAA			513

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CCGCGAATCA	TAGCATTCTT	TTGGATATGG	GGATCAAATA	CGAACGCTAT	TGCTCTGATA	60
GGACTCGCAC	GGCTTTTTTT	GAACCCTAAA	GACTTTGTGT	TCAAAGGGA	GCAGAGTTTC	120
AAGGATAAAG	AGCGTCAAAA	GATTTATGAC	ATTGTGAAAG	AAGCGCAAGA	AAAGGCTATT	180
CAGGCATTAG	AGCGGGGA					198

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CGATTATGGC TATGGGCAGT ATTCACCTAC AGCACCGGGC ATGGCATTGA CTTAGACATT	60
CATGAGCTTC CCTATATTTT ATCGCGCAGT GAAACCATTT TAGAAGAGGG CATGGTGTTT	120
TCTGTAGAGC CTGGGATTTA TATCCCTGGG TTTTGTGGG TCGGCATTGA GGATTTAGTG	180
GTGATTAAAA ATTCTAGGGC CGAGCTTTTA	210

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TACCAATACA TCCAACAAGG CGGGGGCTTT GGGGTGAATG TCGGGCGCAC GCTGGGTAAT	60
AGAACCCATG TGAGCTTAGG GTATAACCTG AATGTTACCA AACTCCTTGG TTTCAGCAGC	120
CCCTTATACA ACCGCTACTA TTCCTCTGTT AATGAAGTGG CCTCTCCAAG GCAATGTTCC	180
ACACCCGCAT CGGTGATTAT CAACCGCTTA TCAGGCGGTA GAACTCCATT GGTTCTTGAA	240
AGCTGTTCTA GTCCTGGAGC GATCACCATC TTCACCAGAA ATAAAAGGTA TTTGGGA	297

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ATGGCGTGTG AATTTTGTGAA AAAGCCAAAG TATTACAAGT TTATAGAGGG GGCGAATTAT	60
TTGAGCTTAG GGCTTTCTAT GGTGGTGGCG ATCCTTATGG GCGTGGCTAT AGGCTATGGG	120
CTTAAAAAAC TCACTCACAT TTCGTGGCTT TTTTGGCTTG GGGTTATTTG GGGCGTGTTA	180
GCGAGCTTTC TCAATGTCTA TAAGGCTTAT AAAAACATGC AAAAAGACTA TGAAGAATA	240
GCCAAAGACC CTAAATACAC GCAAATAAA ACAAAA	276

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

AGGAACTTGA TGAAAACGAC AGAAAACACA GATGAACTC ACTTAAGGGA AACTAAAAAT	60
AAACTAGGAC GCAAACCAA AGCAGACGCT AATAAAAAAA CTCGCGCGGT AAGCTTGTAT	120
TTTTCTGATG AGCAATACCA AAAACTAGAG AAAATGGCTA ACGAAGAAGA AGAAAGCGTG	180
GGATCTTATA TCAAACGCTA TATTTTGAAG GCTTTAAGAA AAATAGAACA AGGTGGTGGC	240
TTTATAGCTT TTAAGTTGTT TTTAATT	267

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ATTTTGAAGG GGGGGTTTTT AGGGTTTTTT ATCGTGGCGT TGTCTTCGTA TTACGGCGTT	60
AAAAAGCGTT TGGATTTGAG GAAACAAGAT TCAAAAGAAA AAGAAGAAAA GCAAAAATTC	120
CAAAAATTCG CCCTAGGTTT GGAAATGTCT TTCAATGTGT GGCCTTTAGG GGGGTATGGG	180
GTTTTATTAG GTATTTTAGG AGTGCTTTTA TTCTTGCATC TTTTAAACGG ATTGCCGTTT	240
CTTATCGGCG TGTGTGTGAG CTCGCTCTCT AGCGCGTTAT TACGATTCTT AAACAATAAT	300
GGTAAGTTT	309

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 771 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GCCCTTACAC CAAATCCCAT GAAACTCCCG GTCGTTGAGA GCTTTTTTTC CTTACAGGGT	60
GAAGGAAAAA GGATAGGCAA GCCCAGTCTT TTTTGGCGCT TAGGGGGGTG TAACCTTTCA	120
TGCAAGGGCT TTAATTGTAA AACCTTATTC AATGATGAAA TCCTAACAGG TTGCGATAGT	180
TTGTATGCGG TGCATCCTAA ATTCAAAACA TCTTGGGATT ATTACAATGA GCCTAAGCCC	240

TTGATTGAAC	GATTAGTTAA	TTTAGCCCCCT	AATTATAAGG	ATTTTGATTT	CATTCTTACA	300
GGCGGGGAGC	CAAGCTTGTA	TTTAAATAAC	CCTATTTTAT	TGAGCGTTTT	AGAGCATTTT	360
TACCATAAAA	AAATCCCTTT	ATTTGTAGAG	AGTAATGGCT	CTATTTTTTT	TGAATTTAGC	420
CCTATTTTAA	AAGAATTGCA	TTTCACCCTA	AGCGTCAAAC	TCTCTTTTTC	TTTGAGCAA	480
GAAAGCAAGC	GGATCAACCT	TAAAGCCCTA	CAAAATATCT	TAAATAACGC	TAAAAGCGTG	540
CATTTTAAAT	TCGTATTGGA	GAGTCAAAAC	GCCGCTCATT	CTATCGCAGA	AATTCAAAGC	600
CTTTTGAAAC	AGCTCTCCTT	AAAAAATAAT	GAAATCTTTT	TAATGCCCCCT	AGGCACAACT	660
AACAACGAGC	TAGACAAAAA	TCTAAAAACC	CTAGCCCCCC	TAGCCATAGA	GCATGGTTTT	720
AGGCTGAGCG	ATAGGCTTCA	TATCCGCTTG	TGGGACAATA	AGAAAGGGTT	T	771

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TTCAAGGATC	AAGGCATGAA	TTTAAACTTT	ATGCCCTAT	TGCATGCTTA	TAACCATGTA	60
AGCATTGATT	TTCATTTCAA	TTCTAGCGCT	AGGGATTTTT	GCGTGCATGA	AGTGCCTTTG	120
TATGAATTTA	GCAACACGGG	CGAACATGCC	GTTATTCAAG	TGAGAAAAAG	CGGTTTAAGC	180
ACTTTAGAAA	TGCTTCAAAT	TTTTTCTCAA	ATTTTAGGGG	TAAAAATCGC	TGAATTGGGT	240
TATGCGGGCT	TGAAAGATAA	AAACGCGCTG	ACGACTCAAT	TCATCTCACT	CCCTAAAAAA	300
TACGCCCTT	TATTAGAAAA	AAATACGAGC	AACTTTCAAG	AAAGAAACCT	TAAATCCTG	360
TCTTTGAATT	ACCATCACAA	TAAATCAAA	TTAGGGCATT	TAAAGGGGAA	TCGCTTTTTT	420
ATGCGTTTCA	AAAAAATGAC	CCCCCTAAAC	GCTCAAAAAA	CGGAGCAAGT	TTTAGAACAA	480
ATCGCGCAGT	TTGGCATGCC	TAATTATTTT	GGCTCGCAAC	GCTTCGGGAA	GTTCAATGAC	540
AACCATAAAG	AGGGGTAAA	AATCTTGCAA	AATGAAACGA	AATTCGCCCA	CCAAAAATTA	600
AACGCTTTTT	TAATTTCAAG	CTATCAAAGT	TATTTGTTTA	ATTCGCTTTT	AAGCAAGCGA	660
TTAGAAATCA	GTAAAAATCAT	TAGCGCTTTT	AGCGTCAAAG	AAAGTTTAGA	ATTTTTTAAA	720
CAAAAAAATT	TAAGCGTCCA	TTCAAACGCC	CTAAAAGCCC	TTAAAAACCA	AGCCCACCCC	780
TTTAAATCT	TAGAAGGCGA	TGTGATGCGC	CATTACCCTT	ATGGGAAGTT	TTTTGACGCT	840
TTGGAATTAG	AAAAAGAGAG	CGAAAGGTTT	TTGAACAAAG	AAGCTGTGCC	TACGGGGTTA	900
CTGGACGGTA	AAAAAGCTCT	TTATGCAAAA	AATTTGAGTT	TAGAAATTGA	AAAAGGATTC	960
CAGCATAACC	TTTTAAGTGG	CCATGCTAAA	ACGCTAGGAT	CCAGGCGGTT	TTTTTGGGTG	1020
TTTGTGGAAA	ATATAACTTC	TCAATACATC	AAAGAAAAAG	CGCAATTTGA	ATTGGAATTT	1080
TACTTGCCCTA	AAGGGAGTTA	TGCGAGCGCG	CTGCTCAAAG	AAATCAAGCA	TGAGAAAGGA	1140
GAAAATAATG	ACGAATTT					1158

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

204

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

AAGATTAAAG	GAAAAGAGAT	GAAATTTT	AACGGATTAG	CAGGGAATTT	ACTGATTGTG	60
GTTATCTTAT	TGTGTGTGGT	CGTTTTTTTC	GCGCTCAAAG	CGATCCATAT	CCAAAAAGAG	120
CAAGCCACCA	ATTATTACCG	CTATAAGGAT	ATTAACGCTT	TAGAGGCAAA	AAACACCCAA	180
AACCACGCT						189

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

ATGCTAGAAA	TTGAATTAAA	AAAGAAATTC	ACTAAGGATT	TAAAAAAGCA	TATTTTAAAT	60
CAAAAAATTG	AGTTAGAAGT	TTTTGACTTA	GTGGTTGAAA	ATTTAAGAAA	TCAAATTCCA	120
TTGGACAAAA	GATTTAAAGA	CCATGCTTTA	AGTGGAACAT	ACAAAGGCTG	TAGAGAGCGC	180
CACATTAAGC	CTGATGTTTT	GCTTGTGTAT	AGAGTGAAAG	GCAATGTTTT	AACTTTGGTT	240
AGGCTTGGA	GTCATAGCGA	GCTGTTTTGT	AAACCGCCCA	CACCACTCAT	AACGCTTAAA	300

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1938 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TCGAATTACA	ACAACCTAAA	CACTCTTGTA	TCGCTGTCCT	CCGATCCGAG	TGCTGTCAAC	60
GACGCAAGGG	ATAATCTAGG	CTCAAGCGCT	AGGAATTTGC	TAGATGTCAA	AGCCAATTCC	120
CCCGCCTATC	AAGCGGTGCT	TTTAGCATTG	AACGCTGCAG	TGGGCTTG TG	GCAAGTTACA	180
AGCTATGCCT	TTACCGCTTG	TGGTCCTGGT	AGCAATGAGA	ACGCGAATGG	AGGTATCCAA	240
ACCTTTAATA	ATGTGCCAGG	ACAAAACACG	ACGACCATCA	CTTGTAATTC	GTATTATGAG	300
CCAGGACATG	GCGGGCCAAT	ATCCACTGAA	AATTATGCGA	TCATCAACAA	GGCTTATCAA	360
ATCATTCAAA	AGGCTTTGAC	AGCCAATGGA	GAAGGGATCC	CAGTTTTAAG	CAACACCACT	420
ACAAAACCTG	ATTTCACTAT	CAATGGAGAC	AAAAGAACGG	GTGGCGAACC	AAATAAAAAA	480
TTAGTATAAC	CATGGAGTCA	TGGGAAAGCT	ATTTCAACCT	CGTGGAATGC	AACCATAACA	540
GTACCAACAA	CAGAAAATAT	CAATACAACC	AATAGCGCTC	AAGAGCTTTT	AAAACAAGCG	600
AGCATCATT	TCACTACCCT	GAATAGTGCA	TGCCCAAAC	TCCAAAATGG	TGGTAGCGGT	660
TATTGGGCAG	GGATAAGTGG	CAATGGGACA	ATGTGTGGGA	TGTTTAAGAA	TGAAATCAGC	720
GCTATCCAAG	GCATGATCGC	TAACGCGCAA	GAAGCTGTGC	CGCAAGCCAA	AATCGTTAGT	780
GAAAACACGC	AAAATCAAAA	CAGCCTAGAC	GCTGGAAAAC	CATTCAACCC	CTACACAGAC	840
GCTAGTTTTG	CTGAAAGCAT	GCTCAAAAAC	GCGCAAGCCC	AAGCGGAGAT	TTTAAACCAA	900
GCCGAACAAG	TGGTGAAAAA	CTTTGAAAAA	ATCCCTACAG	CCTTTGTAAA	TGACTCTTTA	960
GGGGTGTGTT	ATGAAGTGCA	AGGAGGTGAG	CGTCGTGGCA	CCAATCCGGG	TCAGACGACT	1020
TCTAACACTT	GGGGGGCAGG	CTGTGCGTAT	GTAGGACAAA	CGATAACAAA	TCTTAAAAAC	1080
AGCATCGCCC	ATTTTGGCAC	TCAAGAGCAG	CAGATACAGC	AAGCCGAAAA	CATCGCTGAC	1140
ACTCTGGTGA	ATTTCAAATC	TAGATACAGC	GAATTGGGCA	ACACTTATAA	CAGCATCACC	1200
ACTGCGCTCT	CTAATATCCC	TAACGCGCAA	AGCTTGCAAA	ATGCGGTGAG	TAAAAAGAAT	1260
AACCCCTATA	GCCC GCAAGG	CATAGACACC	AATTACTACC	TCAATCAAAA	CTCTTACAAC	1320
CAAAATCCAA	CCATCAACCA	AGAACTCGGG	CGTAACCCCT	TTAGGAAAGT	GGGGATTGTT	1380
AGTTCTCAAA	CCAATAATGG	CGCGATGAAT	GGGATCGGTA	TTCAGGTGGG	TTACAAACAA	1440
TTCTTTGGCC	AAAAAAGAAA	ATGGGGCGCT	AGGTATTACG	GCTTTTTTGA	TTACAACCAT	1500
GCGTTCATTA	AATCCAGCTT	CTTCAACTCG	GCTTCTGACG	TGTGGACTTA	TGGCTTTGGA	1560
GCGGACGCTC	TTTATAATTT	CATCAACGAT	AAAGCCACCA	ATTTCTTAGG	CAAAAAACAAC	1620
AAGCTTTCTG	TGGGGCTTTT	TGGGGGTATT	GCATTAGCCG	GGACTTCATG	GCTTAATTCT	1680
GAGTATGTGA	ATTTAGCCAC	CATGAATAAC	GTCTATAACG	CTAAAATGAA	CGTGGCGAAT	1740
TTCCAATTCT	TATTCAACAT	GGGAGTGAGG	ATGAATTTAG	CCAGGCCTAA	GAAAAAAGAC	1800
AGCGATCATG	CGGCTCAGCA	TGGGATTGAG	TTAGGGCTTA	AAATCCCCAC	CATCAACACG	1860
AACTACTATT	CCTTTATGGG	GGCTGAACTC	AAATACCGAA	GGCTCTATAG	CGTGTATTTG	1920
AATTACGTGT	TCGCTTAC					1938

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GATTTAAAAA TGCTGACGAT TGAAACCACT AAAAATTTG ATAAGGATCT TAAAATTCTT	60
GTAAAAAATG GGTTTGATTT AAAGCTTTTG TATAAAGTGG TTGGAAATTT AGCCACAGAG	120
CAACCCCTAG AACCCAAATA CAAAGACCAC CCACTCAAAG GCGCTTTAAA AGACTTTAGG	180
GAATGCCACC TAAAACCGGA TTTATTGCTT GTCTATCAA TAAAAAACA AGAAAACACT	240
CTTTTTTTTAG TAAGGCTAGG CAGTCATAGC GAGCTGTTT	279

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CGCGCATGGA GAATGAAAAG CATGCGTTTT AGTTACATTG AGCCAAGAGC GAAATACTTA	60
ATCAGCAAGC TTTCTAAAAT TTGGGTTTTT TACATTTTTT TATCTTTTGT GCTAATAGGG	120
GGGTAGTGT GGTATTATGCA CAACGCCATT AAACGCGCTC AAGACAACGC GTCTAGTCTG	180
ACGATCCAAG AAGAGCTTTA CCGCTGTTAC ATCACCCGCT TGTCTGTTAA GATGATTATA	240
CTC	243

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...447
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```

GTAAATTTTC CTTATCTGTT AAACATACGG ATAATGTTAT ATCTAAGGAA AGAAAATGGG      60
GTTAGGACAC TAATAAGTTT AGGGATTTTG TTAAGCGTTT TGAATGGCGA TGATCTGAGA      120
TTGTATTCAA AACCTTTGGT CTATTCGGCT GGAAGTGGGA TTATTGGGAT TGATATTGAC      180
AAACGGACAT TCTATAAACG AGCGTTCGCT TTCACGATGA AATCGTTGTT TGGTGAAAAC      240
TTGCTTTTGT TTGTTAAATT GAAGCATTCT GCGTTGATGA GCAAACACAT GAAAGGGCCT      300
TTAGAAAACC GCCACCACCA TTCTTTCGCT AAAAATTATG AAAAAGCGGT TAATGGTTGT      360
CAAAAATATG TCCATATCAA ATTGCCTGAA GGGCCTCCTA GCAACTTCCA ATCAGGCTCA      420
TACATGGCGA CTATGGTGAT GCGTTTTT                                     447

```

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...477
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

```

GTCATCACCA ACCAACAAAA CGAAGTCAAA ACTTTCACGC CCATTGAAAC CAAAAAGATC      60
ACTTCCAAAG AACAAGCTTT TTAAACCCTT TCAGCGCTGA TGGATGCGGT AGAAAACGGC      120
ACAGGGAGTT TGGCTCGCAT TAAAGTTTA GAAATTGCCG GTAAAACCGG AACTTCTAAC      180
AACAATATTG ACGCTTGTTT CATTGGCTTT ACCCCACCT TACAAAGCGT GATCTGGTTT      240

```

GGGAGAGACG ATAACACGCC TATTGGCAAA GGAGCGACAG GAGGCGTTGT GAGCGCGCCT	300
GTGTATTTCGT ATTTTCATGCG CAATATCTTA GCGATTGAAC CTTCTTTAAA AAGAAAGTTT	360
GATGTCCCCA AAGGCTTGCG TAAAGAAATC GTGGATAAAA TCCCGTACTA CTCAAGCCCT	420
AATTCCATCA CCCCCACCCC CAAAAAACA GACGATAGCG AAGAACGCTT GTTGTTT	477

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

TTATTGTAA ATCTTAAGAT TTATGTTACA CTCTGTAAAA TCCAAGGGGA TAGCGTGTTA	60
GAAAAATCTT TTTTAAAAAG CAAGCAATTG GTTTTATGCG GGTGGGTGT TTTTATGTTG	120
CAGGCTTTGC ACTTCGCCCA AACACTTCAC AAAGAAATTC TTTTTTACAA GATGTGCCTT	180
ATTGGATGTT GCAAAATCGC AGCCAGTATC TCACGCAAGG GGTGGATAGC TCGCACATTG	240

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GTCAAGTGTG GCAAAAAGGG GATTTTAGTT TCAACGCGCA AGGCAATGTT TTTGTGCAA	60
--	----

ATTCCACTTT	CTCTAACGCT	AATGGAGGCA	CGCTCAGTTT	TAACGCAGGA	AATTCGCTCA	120
TTTTTGCCGG	AAACAACCAC	ATCGCTTTCA	CTAACCATT	TGGAACGCTC	AATTTGTTGT	180
CTAATCAAGT	TTCTAACATT	AACGTCACCA	TGCTTAACGC	AGCAACGGCC	TAAGATTAAC	240
GCCACTAATA	ACAATGTTTC	CGTGTCTCAA	GGCAATCTGT	TTATCAACGC	TAGCTGCGTG	300
CAACAAAGCG	ATCCAACGAC	AGCTAGCGCC	ACAAACCCTT	GCACCACCGC	TCAAATAAC	360
GCTTCTTCTA	GTAATGCGTC	AAACAACGCG	CCAATCGCCT	TAAATAATAA	CGATGAAAGC	420
TTGGTGTTTA	CGGCGAATGG	TTTCAATTTT	TCAGGCAATA	TTTACGCTAA	CGGGGTGGTT	480
GATTTTTCAA	AAATTAAAGG	CTCTGCAAAC	GTTAAAAACC	TGTATCTTTA	CAATAACGCT	540
CAATTCCAAG	CCAACAACCT	CACGATTTC	AACCAAGCGG	TATTAGAGAA	AAACGCTAGC	600
TTTGTAACGA	ATAACTTAAA	CATTCAAGGA	GCGTTTAAAC	ACAACGCCAC	GCAAAAAATA	660
GAGGTGCTTC	AAAATTTAGT	GATCGCTTCA	AACGCTTCTT	TAAGCACCGG	GATTTATGGG	720
TTAGAAGTAG	GGGGGGCATT	GAATAATTTG	GGAGCGATCC	ATTTTAATTT	AGAAAATTCT	780
CAAACGCCTG	TAAATCCGCT	CATTCAAGTA	GGGGGGATCA	TTAATCTCAA	CACCACCCAA	840
ACGCCTTTTA	TGAATGTCAG	CGTGGCTAAT	GGCGGAACTT	ACACTTTATT	AAAAAGCAGC	900
CGTTATATTG	ATTACAATAT	CAACCCTAAC	AGCTTGCAAT	CGTATTTGAA	GCTCTATACC	960
TTAATCAATA	TCAACGGAAA	CCACATAGAG	GAAAAAAACG	GCGTATTGAC	TTATTTGGGC	1020
CAACGGGTTT	TA					1032

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TTGTTGGCGC	GCACCATACT	TGATTTTAGA	GGCAGCCTTA	GTAATTTAAA	CAACACTTAT	60
AACAGCATCA	CCACGACCGC	TTCAAACACG	CCTAATTCCC	CATTCCCTTA	AAATTTGATA	120
AGCCAATCCA	CTAACCTTAA	TAACCCCGGG	GGCTTACAGG	CCGTTTATCA	AGTCAACCAA	180
AGCGCTTATT	CGCAATTATT	AAGCGCCACG	CAAGAATTAG	GGCATAACCC	TTTCAGACGC	240
GTTGGATTAA	TCAGCTCTCA	AACCAACAAT	GGTGCCATGA	ATGGGATCGG	TGTGCAAGTG	300
GGCTACAAAC	AATTTTTTGG	TGAAAAGAGA	AGGTGGGGGT	TAAGGTATTA	CGGCTTTTTT	360
GACTATAACC	ATGCTTATAT	CAAATCTAGC	TTTTTCAATT	CGGCTTCTGA	TGTGTTCACT	420
TATGGGGTAG	GGACAGATGT	CCTCTATAAC	TTTATCAATG	ATAAAACCAC	CAAAAACAGC	480
AAGATTTCTT	TTGGGGTGTT	TGGGGGGATT	GCGTTAGCTG	GCACTTCATG	GCTGAATTCC	540
CAGTATGTGA	ATTTAGCGAC	CTTCAATAAT	TTCTATAGCG	CTAAAATGAA	TGTGGCGAAT	600
TTCCAATTCT	TGTTCAATTT	AGGCTTGAGA	ATGAACCTCG	CTAAGAATAA	GAAAAAGAGC	660
AGCGATCATG	CGGCTCAGCA	TGGCGTGGA	TTGGGCGTGA	AAATCCCTAC	CATTAACACC	720
AATTATTATT	CTTTTCTAGG	CACTAAGCTA	GAATACAGAA	GACTCTATAG	CGTGTATCTC	780
AATTATGTGT	TTGCGTAT					798

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CGCAACGTGG AAGCGCGTTA TTATTATGGG GACACTTCAT ACTTTTATTT GCATGCGGGA	60
GTTTTACAAG AGTTCGCTCA CTTTGGATCG AATGATGTGG CGTCTTTAAA CACCTTTAAA	120
ATCAATGCCG CTCGCAGTCC TTTAAGCACC TATGCAAGAG CGATGATGGG TGGGGAATTG	180
CAATTGGCTA AAGAAGTGT TTTGAATTTG GCGTGGTTT ATTTGCACAA TTTGATTTC	240
AACGCAAGCC ATTTGCTTC CAATTAGGA ATGAGGTATA GTTTC	285

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

AGACTTCCTA AAAAAGAAGA TTACGCTAAG GCGATGGTGT TTTCTTTTAA AATGGAAGCC	60
ATCAAAGAAA GCCAAATCGT TTTATTGATC ACTTCAGCGT TTGAGGGCCA ATTTGAAAAA	120
ACGCATAAAG AAGAAAAAGA AGAAACGACA AAAAGCGCTA CTGAAGAGAC TAAAACCCAC	180
GACGCGTCTT TAGAAAATAT AGAAATCCGC AATATCAGCA TGCTTTTAGA CGTGAAATTG	240
AACGTTAAGG TCGGTATCGG TCAAAAAAAG ATGATTTTAA AAGATGTGGT CTCTATGGAT	300
ATAGGGAGCG TGGTGGAGTT GGATCAATTG GTGAATGACC CTTTAGAAAT CCTCGTAGAT	360

GACAAGGTGA TCGCTAAGGG CGAAGTGGTG ATCGTGGATG GGAATTTTGG CATTCAAATC 420
ACGGATATTG GCACTAAAAA GGAACGATTA GAGCAACTGA AAAAT 465

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

AAACCTACCA ATGTTTGGGC TAACGCTATT GGGGGAGCGA GCTTGAATAG CGGCTCTAAC 60
GCTTCATTGT ATGGCACAAG CGCCGGCGTA GACGCTTTCC TTAACGGGAA TGTGGAAGCC 120
ATTGTGGGCG GTTTTGGGAAG CTATGGTTAT AGCTCCTTTA GCAATCAAGC GAACTCTCTT 180
AACTCTGGGG CCAATAACGC TAATTTTGGC GTGTATAGCC GTTTTTTTGC CAACCACCCT 240
GAATTTGACT TTGAAGCTCA AGGGGCGCTA GGGAGCGATC AATCAAGCTT GAATTTCAAA 300
AGCACTCTAT TACAAGATTT GAATCAAAGC TATAATTACT TAGCCTATAG CGCCACAGCA 360
AGAGCGAGTT ATGGTTATGA CTTGCGGTTT TTTAGGAACG CTTTAGTGTT AAAACCAAGC 420
GTGGGCGTGA GCTATAACCA TTTAGGTTCA ACCAACTTTA AAAGCAATAG CCAATCACAA 480
GTGGCTTTAA AAAATGGCGC GAGCAGTCAG CATTTATTCA ACGCTAACGC AACGTGGAAG 540
CGCGTTATTA TTATGGGGAC ACTTCATACT TTTATTTGCA TGCGGGAGTT TTACAAGAGT 600
TCGCTCACTT TGGATCGAAT GATGTGGCGT CTT 633

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...1029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

CATGCTAGGG	AATTTTGCCA	AGTTGTGATG	TTTCACAAAG	CCCTTATTAC	CTTTATCGTT	60
CTATGGTTTT	TTTTGAATGG	CTTAGGGGCT	TATGATTTCA	AGCATTGTCA	GGCTTTTTTTT	120
AAAAAAGCGA	GCCTTCAAAA	AGGGGGCGTG	GCTTTAAAGG	AATTGCCTAA	GGGCGTGTAT	180
TTGTATTATT	CTAAAACCTA	CCCCAAACAC	GCTAAAGTCA	TCAAATCCGA	TCCTTTTATA	240
GGGCTGTATT	TGTTGCAAAG	CGCGCCAAGC	GAGTATGTTT	ATACATTAAG	GGATTTAGAC	300
AAAGACGCCC	TTATAAGACC	CATGGCCAGT	ATAGGGGCTA	ATCAAGCCAC	AGAAGCGCGA	360
TTATTGGTAG	GGCAAAAAGG	CTATGACCGC	TACGCTCAAA	TTTCACAAAA	AACCCAAAAA	420
AATGGCGTTA	TCAGCAATAT	TTGTTATCAA	ATGCTAGGGC	TAGGGGTAGG	GGGGAACGGC	480
TTTATAGAAA	CGAAATTCAT	CAAGCGCTTT	TTAAACCAAC	AAGAGCCTTA	TTATGGGGAT	540
ATTGGGGTGC	GTTTAGAAGA	ACGTCATAAG	CGTTTGGTGG	TAGCGCAATT	TGATCCCTTT	600
TTCCCTAAAA	ACCCTTTTTT	AAAAAACGAT	GAAATCCTAG	CGATCAATGA	TTACAAGATC	660
CACTCGTTAG	CGGAGTTTGA	ATGGGTGGTG	AGCAATCTTT	CATACCAAAG	CCTCGCCAAA	720
GTGAAAATCA	AACGAAACCA	TCAAATCAAA	GAAGTAACGC	TCAAAGTCAA	TAAACGCTAT	780
GGGGGGTTTT	TGCTCAAAGA	CACTTTTTTA	GAGCGCTATG	GCATCGCTTT	AGACGAGCGT	840
TTTATCATCA	CTAAAATAGG	CGCTCATTTG	CCCAAAGGCT	TGGATTTTTT	AAAGCTTGGG	900
GATAGGATTT	TATGGGTGAA	TCATAGAAGC	GTTTCGTTCA	ACCCGAAAGC	TTTAAGAGAA	960
GCGTTAAGCA	CGCCTAAAAT	TGAATTATTA	GTCTGGCGTC	AAGGCTTTGA	ATTTTACATT	1020
AAAGTCCGT						1029

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ATTAAATTA	ACATGGTAGA	ATGCCAAAAT	TTGCTGTCGT	CATGCGGCAA	AAATTTAGAC	60
AACAAGGAAT	TGGGAATGAG	AAGGAGTTTG	GCTTTTTGCC	TTTTAGCTTT	GCTTGGATTA	120
CAGGTTTTAG	GTGCTAGAGA	CTTTTCGCAA	CTCAAAAACG	AAGAACTTTT	AAAATTAGCA	180
GGAACTCTGC	CTTCTAATGA	AGCGATTGAT	TATCGCATGG	AAGTGTCTAA	ACGCCTTATA	240
GCCTTAAGTG	CTGAAGACGC	TAAGAATTTT	CGCGCGAATT	TCAGCCGGAT	CGCTAGGAAG	300
AATCTTTCTA	AAATGAGCGA	AGAGGATTTT	AAAAAAATGC	GTGAAGAAGT	GCGTAAAGAA	360
TTAGAAGAAA	AAACCAAAGG	TCTAAGCGCT	GAAGAAATCA	AGGCAAAAGG	ACTTAATGTG	420
AGCGTTTGCA	GCGGCGATAC	GAGAAAAGTT	TGGTGTAGGG	CTGTTAAGAA	AAAAGACGAA	480
CATTGCTCTC	CTAAG					495

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

TTTAAAAGGA AAAACATGAA AAAAGCGTTG AAAATACTTT CTGTTGGCGC GTTGCTATTT	60
GTGGCTTTAA ACGCCAAAGA TTTCAGCAAA ACAAGCGATG AAGATTGGC TAAAATGGCT	120
GGCGTTGTCG CTCCGCAGGA TATTGTGGAT TACACAAAAG AGTTGAAAAA GCGCATGGAA	180
AAGATGCCTG AAGACAAGAG AAAGGCGTTC CATAACAAT TGCATGAATA CGCGACTAAA	240
AACACAGACA AAATGACCGT GGCGGATTTT GAAGCCCGCC AAAAAGCCAT TAAAGAAGCG	300
CTTAAAAAAG GCAATATGGA AGACATGGAT GATGATTTTG GGTGAGATC ATGCAAGCAT	360
GGGAAAAAGC ACAAACACGA TAAGCATGGC AAGAAGCATG GCAAAAAACA TGACAAAGAT	420
CATGACGATA AAGACCATGA CCACCATGAT GAAGATCACA GCGATAAGCA C	471

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2031 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ATCCAAAGAT ATTGGAATGG AGCGTTAATG AAAAATCAAC AAAAAAATCC CCTAACAAAA	60
GCTTTAATGA AAACCTATCC ATATAACCAT TTTTATTTT TCTGCTTTAT TCTAGGAGCG	120
TTTTTATTAG GTTTGCTCAG TCCAGCTTAT GCTTTAAGTA TTATCACCAC TAAAGAAATT	180

GACGCTAATT	TGCTTAATGG	AGCGATAGAA	AGCAGGGTGG	TGTTAGGCAA	GAGGGTGTTT	240
AAAGTAGAAG	CTCATGGGTT	TTATTTTAGA	AACAATGCGA	CTAACAGCAT	AGATATAGAA	300
ATCACCAGTC	TTTTAAGAGA	CAATCAATCG	TTTCCTTTGA	CTAGCAGTGC	TAAAACCAGT	360
TTAAAAATAC	CTCCTAACGC	CAAGATTAAA	AAATCCACTA	TCCTTGTTTT	GAAAGGCGAG	420
AACGCTGAAG	AAGTGGCTAA	GATTTTtaggc	GTTAGCAAAG	AAGAATACCA	AAAGCTAGAA	480
AACATCGCTC	AAACCAAAGC	GGCTAATGAC	CCTATGTATG	CTAACACGCC	TTTTAGTAAT	540
GGTTCTGATA	GTTCTTTTAA	CGATAACAAT	CCTAATAGCC	CTAGCAATAA	CGCTATCAAT	600
GGCAAAGATG	GCGCAAATGG	GAGTAACGGC	TATGGGGCAA	ATGGCAATGA	TGGGGTAAAT	660
GGGATCAGTG	GGAGTAATGG	TGCAAATGGG	AGTCATTCAA	ATAATAATGC	AATAGGCAGT	720
GGTATTGATA	CAGATGGCGT	GTTAGGGGTG	GATGGGGTGA	ATGGCTCTAG	TTCTTCAAGT	780
GGCGGCTCTG	TAGGGGGTTA	TGAGAATAAT	TTCCTAATC	ATGGCTCTAC	TAACAATAAC	840
ACAGGAGGGT	ATGACAATTT	TAATAATGGC	AGCTCAAGTG	GTGGGAGTTT	AGGGAATGGG	900
GGGCTTTTCC	CTATTCCTTT	TGGTAATGGA	GACACAAACA	ATTCCAATAA	TTCCACTAAC	960
ACCACTAGCC	CAACTAATGG	CAGTAGTTCT	AATAACGCCA	CTAATCCTAG	TTCCGAAGAA	1020
AACAATTACT	CCAGCCAGTA	TTGTAAAGTG	CCAGAGTTAA	GCCCCAACAA	CACGATGAAA	1080
CTAGATGTTA	TCGCTAAAGA	TGGCTCTTGT	ATTTCTATGA	ACGCTTTAAG	AGATGACACT	1140
AAATGCGCTT	ATAGATACGA	TTTTGAAGCC	GGTAAAGCCA	TCAAGCAAAC	GCAATACTAC	1200
TATGTAGATA	GGGAAAATAA	AACGCAAAAT	ATCGGTGGTT	GTGTGGATTT	ACAAGGCGCT	1260
CAATACGCCA	TGCAACTTTA	CAAAGATGAC	AGCAAATGCG	CCTTACAAAC	CACGAGCGAT	1320
AAAGGTTATG	GTATGGGGAA	AACGCAAACC	TTTCAAACCTG	AAATCGTGTT	TCGTGGGATG	1380
GACAATTTAA	TCCATGTCGC	TGTGCCTTGC	AGCGATTATG	CAAGGGTGCA	AGACAGGATT	1440
GTTAGGTATG	AAAAAATGA	TAAAACCCAA	ACCTTAACGC	CTATAGTGGA	TCAGTATTAT	1500
AATGATCCTA	ACAACCCTAA	CAAGCAAGAG	ATTTTAAATC	GTGGGATTGC	CACCCAATTA	1560
AGCTCGCAAT	ATCAAGAATT	TGCATGCGGT	CAATGGGAAT	ACAATGACGC	TAAATTAGAA	1620
GCCAAAAGAC	CTACAATGCT	AAAAAGCTAT	AACAAGCTTA	ATGGAGAATG	GGTAGAAGTT	1680
ACGCCCTGTA	ATTTTGAAGC	AGGGATTAAA	AGCGGTGCGG	TTGTTAGCCC	TTATGTGATG	1740
GGCGTGCCCTA	GTTCTAAAGT	CTTAAGCGAT	ATTACTACAA	GCCATTATTT	TAGGATAGAA	1800
AGGAAAAATT	ATGGTGAGAG	AGAACAATGC	CAAAAACCTT	ATGGAGTCAA	TCGTTGCCAA	1860
CCGCAATATT	CCATACTGAT	CCTAGTATCA	CCGATTGGAG	CGCCACTTAC	AAAACCACTA	1920
CCACCCAAAC	CACTCAACCT	TATTTACGCC	CAGCCCAAGA	TAATGAAAAA	CACCCACAAA	1980
CCTATAATCT	TATCACCCT	CAAACCACCA	TCAACAGGAC	TCAAAGCGTT	T	2031

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ATGGCTAAAA	TGAACGCTCC	AGATGGGGTT	GCCGTTTGGG	TGAATGAAGA	CAGGTGTAAG	60
GGTTGTGATA	TTTGCCTGTC	GGTATGCCCC	GCTGGAGTTC	TTGGCATGGG	GATTGAAAAA	120

GAAAGGGTGC	TTGGAAGT	GGCCAAAGTA	GCCTATCCAG	AGAGCTGTAT	TGGTTGCGTG	180
CAATGCGAGT	TGCACTGCCC	GGATTTTGCG	ATTTACGTGG	CTGACAGGAA	GGATTTCAAA	240
TTCGCTAAAG	TTTCTAAAGA	AGCCCAAGAA	AGAAGCGAAA	AGGTTAAGGC	CAATAAATAC	300
ATGCTCTTAG	AAGAGACTAT	TTTAGAAGGG	AGAGGCAAA			339

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 987 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

ATGACGACTA	AAAGAGTGAA	TACTGCCACA	AACAAGATAA	TGACATTAAA	CACTTTCTTG	60
GATACATGTT	TTCTTTTCTT	CATCAGTATT	CTTTTTTACC	TAAGTATACC	AATTTATCCT	120
AACAAAGTGG	TGGTTGTCCC	GCAAGGTTTCG	CTCAAAAAAG	TGTTTTTTTC	TTTGAAAGAG	180
CAAGGCGTGG	ATATTAACGC	TTTAGATTTG	CTTTTGTTGC	GCCTAATGGG	CATGCCTAAA	240
AAAGGCTATA	TTGACATGGG	CGATGGGGCT	TTAAGGAAGG	GGGATTTTTT	AGTCCGTTTG	300
ATCAAAGCGA	AAACGGCGCA	AAAAGCGTT	ACTTTAATCC	CTGGAGAAAC	CCGCTATTTT	360
TTCACGCAAA	TTTTGAGCGA	GACTTACCAA	CTAGAAACAA	GCGATCTCAA	TGAAGCTTAT	420
GAAAGCATCG	CTCCACGATT	AAACGGCGCT	GTGATAGAAG	ATGGGGTGAT	ATGGCCAGAC	480
ACTTATCATT	TACCTTTAGG	GGAGGACGCT	TTTAAAATCA	TGCAAACTTT	GATTGGTCAA	540
TCCATGAAAA	AACACGAAGC	CTTAAGCAAA	CAATGGCTTG	GATACTACCA	TAAAGAAGAG	600
TGGTTTGAAA	AAATCATTCT	CGCTTCCATT	GTGCAAAAAG	AAGCCGCTAA	TGTTGAAGAA	660
ATGCCCTGA	TTGCGAGCGT	GATTTTTAAC	CGCTTGAAAA	AAGGCATGCC	TTTACAAATG	720
GATGGGGCTT	TGAATTATCA	GGAATTTTCA	CACGCTAAAG	TAACCAAAGA	GCGCATTAAA	780
ACCGATAACA	CCCCCTACAA	TACCTATAAA	TTTAAGGGCT	TGCCTAAAAA	TCCTGTAGGG	840
AGCGTGAGCT	TAGAAGCGGT	TAGAGCCGTG	GTTTTCCCTA	AAAAAACGGA	TTTCTTGTAT	900
TTTGTGAAAA	TGCCGGATAA	AAAACATGCT	TTCAGCGCAA	CTTATAAGGA	GCATTTAAAA	960
AACATTAATA	TTTCTAATAA	TCATTTT				987

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

AAATTCATGA	GATTGTTGTT	CTTGTTACTG	AGCGCTACTT	TGATGTTACT	GGCTGAAGAA	60
AAAATACCTT	TAAGCGATGA	CGCCCCCATT	AAATTGGTTC	ATTGGCAAAA	TGCGCTAAAA	120
GAAGTCCAAC	CCGATTCAAA	CGCTCCGGCA	ACGCCACCTA	TAAAGGCCGT	GCAAACCACG	180
CTCACTTTTG	AAACGCCTTT	TAATAAAACG	CCTAAAATCA	TGGAGGTTGA	AGGGCAAAAA	240
GTCATCGTGT	TAAAAAACGC	TCAATTGGAT	TCTAAAAAAA	CGATGGATTT	TAAAGAAGCC	300
TCTTTGAATG	CCTTAGAAAT	GTTTTCCTAC	CAAAATGACA	TCTACCTCTT	GTCTAAAAAA	360
GCTAAAGCGG	GATTAGAAAT	CCAAGCTTCA	AGCAGCAAGG	ATAAAAAGCA	ACTCGCTTTC	420
TTTTTTTACC	CAAAGGTTTT	CATT				444

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GAATTGATTT	TAAAGAAAAA	GAAAGAAAGG	AATTTAATGA	AAAAAGGTAG	TTTAGCAATC	60
GTTTTAGGAT	CGTTACTAGC	AAGTGGGACG	TTTTATACGG	CTCTAGCTGA	TGGAATGCCT	120
ATGAAGCAAC	AGCACAATAA	CATGGGTGAG	TCTGTGGAGT	TGCATTTCCA	CTATCCTATT	180
AAAGGCAAAC	AAGAGCCTAA	AAATAACCAT	TTAGTTGTCT	TAATCGATCC	TAAGATAGAG	240
GCTAATAAAG	TTATCCCTGA	AAATTATCAA	AAAGAATTTG	AGAAGTCTTT	GTTCTCTCAA	300
CTGAGTAATT	TTTTAGAGAG	AAAGGGCTAT	AGCGTTTCGC	AATTTAAAGA	TGTTAGCGAA	360
ATCCCTCAAG	ACATCAAAGA	AAAAGCGTTG	CTCGTTTTAC	GCATGGATGG	GAATGTGGCT	420
ATCTTGGAAG	ATATTGTAGA	AGAGAGCGAT	GCGCTCAGTG	AAGAAAAAGT	GATAGACATG	480
TCTTCAGGGT	ATTTGAATCT	GAATTTTGTT	GAGCCAAAAA	GTGAAGACAT	TATCCATAGT	540
TTTGGTATTG	ATGTTTCAAA	GATTAAGGCT	GTGATTGAAA	GGGTGGAATT	GCGGCGTACC	600
AATTCTGGAG	GTTTTGTCCC	CAAACTTTT	GTGCATAGGA	TCAAGGAAAC	CGACCATGAC	660
AGAGCCATTA	AAAAGATCAT	GAATCAAGCC	TATCACAAAG	TGATGGCGCA	TATCACCAAA	720
GAATTAAGCA	AAAAACACAT	GGAACGTTAT	GAAAAAGTTT	CTAGTGAAAT	GAAAAAGCGA	780

AAG

783

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GACCAAAAAT TCAAGGGGAT TATTTTAGCT ATGAAAATCA GTGTTAGTAA AAACGATTTA	60
GAAAACACTT TGCCTACTT GCAAGCTTTT TTGGATAAAA AGGACGCTTC CTCTATCGCT	120
TCACACATCC ATTTAGAAGT CATTAAAGAA AAGCTCTTTT TAAAAGCCAG CGATTTCAGAT	180
ATTGGACTAA AAAGCTATAT TTCTACGCAA TCTACCGATA AAGAGGGCGT AGGCACGATC	240
AACGGGAAGA AGTTTTTAGA TATTATCTCA TGTTTGAAAG ACTCTAATAT TGTTTTAGAG	300
ACTAAAGATG ACAGCTTGGT GATCAAACAA AATAAAAGCT CTTTCAAACCT CCCCATGTTT	360
GACGCTGATG AGTCCCTGA ATTCCCTGTT ATTGATCCAA AAGTGAGTTT AGAAATCAAT	420
GCCCCCTTTT TGGTGGATGC GTTTAAAAAG ATCGCTCCTG TGATTGAGCA AACTAGCCAT	480
AAAAGGGAAT TAGCCGGTGT TTTAATGCAA TTCAATCAAA AACACCAAAC CCTTTCAGTG	540
GTAGGCACGG ATACCAAGCG GCTCTCTTAC ACGCAGTTAG AAAAAATCTC TATCCATTCC	600
ACCGAAGAAG ACATCTCTTG CATTTTGCCT AAAAGGGGCTT TATTGGAAAT CCTTAAACTT	660
TTTTATGAAA ATTTTCAGTTT TAAAAGCGAC GGCATGTTAG CGGTGGTTGA AAACGAAACG	720
CACGCTTTTT TCACCAAGCT CATTGATGGG AATTACCCTG ATTATCAAAA AATCCTCCCT	780
AAAGAATACA CTTCTCTCTC ACTT	804

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```

AACCCATTGA TTCAAAGAA CAAGAGCTTA TCAATCTTTT TAATCTCAA TTCGGTCGTT      60
TTCCTTGGA AAATTATCTT GCATAAAGTT TTTATCATGG AAGCTTTGGA GTGTTTGAAA      120
AGAATAGAAA AAGAAAGCAT CCAAACAATC TATATAGACC CCCCTTATAA CACCAAGAGT      180
TCTAACTTTG AATATGAAGA CGCTCATGCT GACTATGAAA AATGGATTGA AGAACATTTG      240
ATTTTAGCAA AAGCTGTGTT AAAACAAAGT GGTGTATTTT TTATTTCTAT GGACGATAAT      300
AAAATGGCTG AAGTTAAAT CATTGCCAAT GAAATTTTGT GAACGCGCAA TTTTGTAGGC      360
ACTTTTATCA CCAAACAAGC CACAAGATCT AACGCTAAAC ACATCAATAT TACTCATGAA      420
TATGTTTTAA GCTACGCTAA AAATAAAGCG TTCGCTCCTG GTTTTAAAT CTTACGAACG      480
CTTTTGCCCA TTTATGCTAA AGCATTAATA GATTTAATGC GAACGATTAA GAATGTTTTT      540
AAACAAAAG GACAAGCTCA AGCCCAACTT ATTTTAAAG AACAAATCAA AGAGTTATCC      600
CAAAAAGAAC ATTTTAATTT TTTAAAAAAT TATAATTTAG TGGATGAAAA AGGTGAGATC      660
TATTTGCTA AAGATTTATC CACGCCTTCA AACCCGCGCA GTGTAGCGAT ACAAGAAATC      720
AATCTTTTTT TAGAACCTT AAAAAGCAGA GGGTGGAGCA GCGATGAAAA GCTTAAGGAG      780
TTATATTATC AAAATAGACT TATTTTAAAG AATAATCGCC CTTATGAAAA ATATTACCTA      840
AAAGAATCGC AAGATAATTG TTTGAGCGTG TTAGATTTTT ATAGCCGACA AGGCACAAAA      900
GATTTAGAAA AATTAGGCTT AAAGGGGCTT TTTAAACGC CAAAACCTGT AGCATTGATT      960
AAATATTTAT TATTATGCTC CACCCCTAAA GATTCTATTA TTTTAGATTT TTTTGCAGGC      1020
AGCGGGACAA CAGCGCAAGC GGTATAGAA GTTAATAAGG ATTATTATTT GAATTGGTCT      1080
TTTTATTTGT GCCAAAAAGA AGAAAAAATT AAAAATAACC CGCAAGCTGT TAGCATTTTA      1140
AAAAACAAGG GGTATAAAAA CACGATTTCA GACATCATGC TGTTGCGTTT AGAAAAGATC      1200
ATCAAAAGAA GTGAATACGA AATTTTAAAA ACAAAATCTA TTTTATTT      1248

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(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```

AATTTTAGCG GTGAATCCAA AAAGCGCCTA AAGCACCCAG CCCCATTTCC AAGGGAATTA      60
CCCAGGCGTT GCATCCAATT GTTTTCTTTT TTGGAAGACA CGATTTTGA TCCCTTTAGC      120
GGCTCTGGCA CGACTATTTT AGAGGCCAAC GCTTTAGGGC GTTTTAGCGT GGGTTTAGAG      180
ATTGAAAAAG AATATTGCGA GTTGTTCAAA AAGCGTATTT TAGAGAGT      228

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(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

AGGAGATGTT GTAGGAGGGA AGACACGAAG AGATATGTGA TAGAAGTGGT TATATCTTTA	60
AGCACAATGA CAAGTTTATT GTCAGCAGAG ACCCCTAAGC AAGAAAAGGC TATTAAGACT	120
AGCCCTACCA AAAAAGGTGA AAGAAATGCT GCTTTTATAG GGATTGATTA CCAGTTGGGT	180
ATGCTCAGCA CTACCGCTCA AAATTGTTCC CATGGGAATT GCAATGGTAA TCAAAGTGGG	240
GCTTACGGCT CTAATACGCC TAACATGCCT ACAGCGTCAA ACCCAACAGG AGGCCTTACT	300
CATGGCGCTC TAGGGACTCG TGGGTATAAA GGCTTAAGCA ACCAACAATA CGCTATCAAT	360
GGTTTGGGT TTGTTGTAGG GTATAAGCAT TTTTTAAGA AAGCCCCACA ATTTGGAATG	420
CGTTATTACG GATTCTTTGA TTTTGCAAGC TCTTATTATA AGTACTACAC TTATAATGAT	480
TATGGCATGA GAGACGCTCG CAAGGGTTCT CAAAGTTTCA TGTTTGGCTA TGGGGCTGGC	540
ACAGATGTGT TGTTTAACCC AGCTATTTTC AATCGTGAGA AACTTGCAAT TGGGGTTTTT	600
CTTGGGCGTT GCGATTGGTG GCACCTCTTG GGGTCCAACA AACTATTATT T	651

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GGGGGCGTGT	GCGGCGTATT	ATCGTTACAA	GCGCATTGGA	GCTTTGAAAA	TTGCTCTAAG	60
CCCCTAGACT	GCTCACTATT	CGCTACAAC	TGCACCCCGC	AAAACCCGAT	CGGCAGTTGC	120
ATGGTCAGCT	CTCAAGGGGG	CGTGTGCGGC	GTATTATCGT	TACAAGCGCA	TTTGAGCTTT	180
GAAAATTGCT	CTAAGCCCC	AGACTGCTCA	CTATTGCGCA	CAACTTGCAC	CCCGCAAAAC	240
CCGATCGGCA	GTTACATGGT	CAGCTCTCAA	GGGGGCGTGC	GCGGCGTATT	ATCGTTACAA	300
GCGCGTTTGA	GTTTTAAAA	T				321

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

AACTATAGTA	ATAAAGATAA	CCCCATGAGA	TTTTTTTGCT	TCTTTTATT	TTTTCTAACC	60
TTTTCAAACG	CGCAGATAAT	GATGACTTTT	GATTCCCAAA	CTAACGCCAA	ACTTTCGCGC	120
TCCAACGAAC	AGCTTTCCTGA	CATGCTTTAC	AAACTCAATG	AAAGTTTAAG	AATCTATCAA	180
AACGTGCTTT	CTAACAACCA	GGATCAACTT	AAAGAAATCA	AAAAGGCTAA	CAGCACCTTA	240
ACTAGCCAAA	GGCGTTTTTT	TAACGCTAGC	CAGATCCGCC	TTATGGACAC	TGATGCACTA	300
TTGAAACAAA	GCGCTTTTGA	ATTAGAAAAA	TTACAAGCTT	TAGAAAAACA	CTTAAAGAG	360
AGCATGGAGC	ATGAACGCTT	AATCAAAGAA	TCCCAAGCGC	TTTTTTTGCA	AGAGCATTGC	420
CCTTATTTGA	GCGGCGTTAA	GAATTTAGAA	GAGGCATCAA	ACGCTTTAGA	AGTCCAAGAA	480
AAAAATAACG	CCCTTTTCTT	ACTCAAAGAG	CCTAAACTCT	TTCATTTGCT	CTCACGATTG	540
GATTTGATGA	GCGCTTTTAA	CGCCTTATGC	GATCAGGTTT	TAGAAAATGA	AATACAGGAT	600
CAACAATCCC	ATAACAAAAC	CCTAGAATAC	AACGCCCTTA	TGAACCATGA	TTTTCAAGCC	660
TATAAAGCCA	TGCGTTTGAA	AAAAATTAAA	AACAAGCTTC	AAAGCCAAAT	CCAAGCTAAA	720
GAAGACGCCC	TAAAAACCTT	TTTACCCCTA	GAAAAACGCC	CAGAGACTCT	AGGCTCGAGC	780
GATTGTTGCG	ACAAAGAAAA	TCTCAAATCA	TGCGCTAACC	AATTACAGCA	ACGCTACCAA	840
AACGCCCTAA	TAGAGCGAGA	TAAGGAATTA	AAAAACGCTA	AAAACAACAA	AGAAAAGCAT	900
GCTCTAATCT	TAGCCAATTA	CGAACACACT	TTAAAAACCT	TGAATATAGA	ATTTTTAAGC	960
GAATTGAGTG	AGCAAATGGC	GTTTTTGAAT	GAGACCATGG	CGTTAAACGC	CCAAGTTTTA	1020
GCCCTTTTAG	CCCAACAACA	GACTAAAAAG	CCCTTCAATG	TGAGCGATGG	TTTGAGCGGT	1080
GGGAAAGCCC	TTATTAAAAA	TATCCGCTTA	GATCCGCATG	GATTCCCTAG	CTTTAAAAAT	1140
TTTAAGCAAG	AG					1152

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TTAGTATTCA	AAAAGCCCTT	TTTTAAAAAT	AGGTTACTAA	ACGTTACTAA	TAAGTTAAAA	60
TTCGTGAAAA	TAACCATAAT	GATTAAAGAT	TTTAACCACT	ATTGTAGAAA	AATAACGAGA	120
GGGTTTGTAA	AAATTCCCAC	CAAAAAACAA	GGAGCAAAAA	AGATGAAAAA	AGCGGGTTTT	180
CTTTTTTTGG	CGGCGATGGC	TATCATTTGT	GTGAGTTTAA	ACGCCAAAGA	TCCGAATGTG	240
TTGCGTAAGA	TTGTTTTTGA	GAAATGTTTG	CCTAATTATG	AGAAAAATCA	AAATCCTTCA	300
CCATGCATAG	AAGTCAAACC	CGACGCCGGC	TATGTGGTTT	TAAAAGATAT	TAACGGTCCG	360
TTGCAATATT	TGTTGATGCC	AACGACTCAC	ATTAGTGGCA	TTGAAAACCC	TTTGTGCTT	420
GATCCTTCTA	CGCCTAACTT	TTTTTACTTG	TCATGGCAAG	CGCGCGATTT	TATGAGTAAA	480
AAATACGGAA	AACCCATTCC	TGATTATGCG	ATCTCTTTGA	CGATCAATTC	TAAAAAAGGG	540
CGATCGCAAA	ACCATTTTCA	CATCCATATT	TCTTGCAATTA	GCCTTGATGT	GCGCAAACAG	600
CTGGATAATA	ATCTAAAAAA	TATCAACAGC	CGTTGGTCGC	CATTATCAGG	TGGCTTGAAC	660
GGGCATAAAT	ATTTGGCGCG	TCGGGTAACA	GAGAGCGAAT	TAGCGCAAAA	AAGCCCGTTT	720
GTCATGCTTG	CTAAAGAAGT	GCCTAACGCG	CACAAACGCA	TGGGAGACTA	TGGCTTGGCG	780
GTGGTGCAAC	AGAGCGATAA	CTCCTTTGTC	TTGTTAGCGA	CACAATTTAA	CCCATTGACT	840
TTAAATCGCG	CTTCAGCCGA	AGAGATTCAA	GATCATGAAT	GCGCGATTTT	GCGT	894

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 537 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CTAAGGCGTC TAGCTTTGAA TACAATGAAT AGCGTGTTAG AATGTAAAGA ATTAGCGCTC

TATGGAGGGA	GTTTTGATCC	TTTGCACAAG	GCTCATTTAG	CCATTATTGA	GCAAACCTTA	120
GAATTATTGC	CATTCGTTCA	GCTGATTGTC	TTGCCCCGCTT	ATCAAAACCC	TTTCAAAAAG	180
CCATGTTTTT	TGGACGCAAA	AACCCGTTTT	AAGGAATTAG	AAAGAGCTTT	AAAGGGAATG	240
CCTAGGGTGC	TGTTGAGCGA	TTTTGAAATC	AAGCAAGAAA	GGGCTGTGCC	TACGATAGAA	300
AGCGTTCTTC	ATTTCCAAAA	ACTCTACCGC	CCTAAAACGC	TTTATTTAGT	CATAGGAGCG	360
GATTGTTTGA	GGCATCTTTC	TTCTTGGAAT	AACGCTAAAG	AGCTTTTAAA	AAGGGTGGAA	420
TTAGTGGTTT	TTGAAAGGAT	TGGCTATGAA	AAAATTCAAT	TTAAGGGGCG	TTATCACCCCT	480
TTAAAAGGCA	TTGACGCGCC	GATTTCTTCT	AGCGCGATTA	GGGCTAGTTT	AGGGGTT	537

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

TCGTCAATAT	TTGATTATAA	TTATAAGGGA	TTACATTTCT	CCAATAAGAG	ATATATCATG	60
CTAGGAAGCG	TTAAAAAAC	CCTTTTGGG	GTCTTGTTT	TGGGCGCGTT	GTGTTTGAGA	120
GGGTTAATGG	CAGAGCCAGA	CGCTAAAGAA	CTTGTTAGTT	TAGGTATAGA	GAGCGTGAAG	180
AAACAAGATT	TCGCTCAAGC	TAAAGCGCAT	TTTGAAAAAG	CGTGTGAGTT	AAAAGAAGGT	240
TTTGGGTGTG	TTTTTTTAGG	GGCGTTTAT	GAAGAAGGGA	AAGGAGTGGG	AAAAGACTTG	300
AAAAAAGCCA	TTCAATTTTA	CACTAAAGGT	TGTGAATTAA	ATGATGGTTA	TGGGTGTCGC	360
CTACTAGGAA	ATTTATACTA	TAACGGACAA	GGCGTTTCTA	AAGACGCCAA	AAAAGCCTCA	420
CAATATTACT	CTAAATCTTG	TGAATTGAAC	CATGCTGAAG	GGTGTACGGT	CTTAGGAAGC	480
CTACACCATT	ATGGCGTAGG	CAGCCCTAAG	GATTTAAGAA	AGGCTCTTGA	TTTGTATGAA	540
AAAGCTTGCG	ATTTAAAAGA	CAGCCCTGGG	TGTATTAATG	CAGGATACAT	GTATGGTGTG	600
GCAAAGAATT	TTAAGGAGGC	TATCGTTCGT	TATTCTAAAG	CATGCGAATT	AAAAGATGGT	660
AGGGGGTGCT	ATAATTTAGG	GGTTATGCAA	TACAACGCCC	AAGGCACAGC	AAAGGACGAA	720
AAGCAAGCGG	TAGAAAACCT	TAAAAAAGGC	TGCAAAATCAA	GCGTTAAAGA	AGCATGCGAC	780
GCTCTCAAGG	AATTAAAAAT	AGAGCTT				807

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

CATTTTAACA	TCTTTACAGA	AGATAATCGT	GAAATCAGCG	GGAGCACTGA	CAAGCTCAGT	60
TATAACGCGC	TGAATGGGGA	ATACAAATTA	TTGCAAATG	CGGTGGTTAG	AGAAGTGGGA	120
AAATCTAATG	TCATCACCGG	CGATGAAATC	ATTTTAAACA	AAACCAAGGG	TTATGCTGAT	180
GTGTTGGGGA	GCGCGAAGCG	CCCGCTAAAT	TTGTGTTTGA	TATGGAAGAC	ATTAATGAAG	240
AAAATCGTAA	GGCTAAAT					258

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

CCCAAATCCC	CTAAAAAGAT	CGTAAAAAGA	TACGAAAAAA	GCGCTTGGA	AATGCCAAAA	60
GAAACACCA	CCCACGAAGA	CGCTTTAGCG	AAATGCTTTG	CGCCTGCAAT	TTTTAAAGCC	120
ATCATGCTGA	ATAAATTGAT	ATTGGCGGTT	GTGGCTGCTC	CCATTATAAA	GATGCTTAAA	180
TTGAGTAAAG	AGATTTGGTG	GAAAAAATG	GGCAAAAAAC	ATGCGATAGA	TTTTAAATG	240
AGGATAAAGA	TATTGGCTTC	TTTAGCCCCT	AGCTTT			276

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 555 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

AATAAGGATC	ATTTGATGTT	AAACAAGTTT	AAAAAATCG	TTGGCGTGGG	TGTGTTAGTG	60
GGCTGTTTAG	GGGTTTTGCA	AGCTAAAAAC	AGCTTATTTG	TCTTACCTTA	TGAGCAAAGA	120
GACGCTCTCA	ATTCTTTAAT	TTCTGGGATT	AGCAGCGCTA	GAGAGAACGT	GAAAATCGCT	180
ATTTATAGTT	TCACGCACAG	AGATATTGCA	AGAGCGATTA	AAAGCGTAGC	GAGTAGGGGG	240
ATTAAGGTGC	AAATCATTTA	TGATTATGAA	AGCAATCACA	ATAACAAGCA	ATCCACTATT	300
GGCTATTTAG	ACAAATACCC	TAACACGAAA	GTGTGCTTAT	TAAAGGGGCT	TAAGGCTAAA	360
AACGGGAATT	ATTACGGCAT	CATGCACCAA	AAAGTAGCGA	TCATTGATGA	TAAAATCGTG	420
TTTTTAGGCT	CAGCGAATTG	GAGCAAAAAC	GCTTTTGAAA	ACAATTATGA	AGTGTTTTTA	480
AAACGGGATG	ACACAGAGAC	GATCTTCAAA	GCCAAGAGTT	ATTATCAAAA	GATGCTAGAA	540
GGTTGCGTTG	GGTTT					555

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 645 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

GGAAGAACAA	TGAAATATTT	ATGGCTTTTT	TTAATATACG	CTATAGGGCT	TTTTGCAACA	60
GATAAACGC	TAGATATTAT	TAAAACCAT	CAAAACTTC	CTAAGATTGA	AGTGCGCTAC	120
TCCATAGATA	ACGATGCCAA	TTACGCTTTA	AAATTGCATG	AAGTCTTAGC	GAACGATTTA	180
AAGACTAGCC	AGCATTTTGA	TGTTTCTCAA	AACAAAGAGC	AAGGTGCTAT	CAATTACGCA	240
GAACTCAAGG	ATAAAAAAGT	CCATCTTGTA	GCGCTTGTA	GCGTGGCGGT	AGAAAAACGGC	300
AATAAAATTT	CACGATTAAA	ACTTTATGAT	GTGGATACAG	GAACGCTCAA	AAAGACTTTT	360
GACTACCCCA	TTGTAAGTTT	AGATCTATAC	CCTTTTGCAG	CGCACAACAT	GGCCATTGTG	420
GTGAATGATT	ATTTAAAAGC	CCCTTCTATC	GCTTGGATGA	AGCGCCTGAT	TGTTTTTTCT	480
AAATACATTG	GACCAGGAAT	CACAAACATC	GCACTAGCGG	ATTATACGAT	GCGTTATCAA	540

AAAGAAATCA TCAAAAACAA CCGACTCAAT ATTTTCCCCA AATGGGCGAA CGCTGAGCAA	600
ACGGAGTTTT ATTACACGCA GATGGCGGAA AAACGCCCAT GGTTT	645

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GCAGCTATGA TGTTTAATAA TGATATAGAC AGCGCGACCG GATTTTACAA ACCGCTCATC	60
AAGATTAACA GCGCTCAAGA TCTCATTAAG AATACAGAGC ATGTTTTATT GAAAGCGAAA	120
ATCATTGGTT ATGGTAATGT TTCTACAGGT ACCAATGGCA TTAGTAATGT TAATCTAGAA	180
GAGCAATTCA AAGAGCGCCT AGCCCTTTAT AACAATAATA ACCGCATGGA TACTTGTTG	240
GTGCGAAATA CTGATGACAT TAAAGCATGC GGTATGGCTA TCGGCAATCA AAGCATGGTG	300
AACAACCCTG ACAATTACAA GTATCTTATC GGTAAGGCAT GGAGAAATAT AGGCATCAGT	360
AAAACGGCTA ACGGCTCTAA AATTTCGGTG TATTATTTAG GCAATTCTAC GCCTACTGAG	420
AATGGTGGCA ATACCACCAA CTTACCCACA AACACCACTA ATAATGCGCA TTCTGCTAAC	480
TACGCTCTCG TGAAGAACGC TCCTTTCGCT CACAACACCA CTCCTAAT	528

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ATTTTATAGAG	CTTTTAGAAG	AGGATTTTTT	AGAAAAACAT	TTGCATATCG	CTTTACAGCA	60
CACCATGATT	TCATGCTAGA	GAGAATGAAT	CGAAGAAACC	GCACTAAAAG	CGATAGGGAA	120
TTATTAGAGA	TAATCGCTTC	TAAGAATTTT	GCTATCGGCA	CGGATTTTAT	TGTGGGGCAT	180
CCGGGCGAGA	GTGAAAGCGT	TTTTGAAAAG	GCGTTTAAAA	ATTTAGAAAAG	CTTGCCTTTA	240
ACGCATATCC	ACCCTTTTAT	TTACAGCAAG	CGAAAAGACA	CCCCCTCTAG	TTTGATGCGT	300
GATAGCGTGA	GTTTGGAAGA	TTCTAAAAAG	CGTTTGAATG	CGATTAAAGA	TTTGATTTTT	360
CATAAAAATA	AGGCGTTCAG	GCAATTGCAA	CTCAAACCTCA	ACACGCCCCCT	AAAAGCCCTA	420
GTGGAAGCGC	AAAAAGACGG	CGAATTTTAA	GCCTTAGATC	AATTTTTCAT	CCCCATTAAA	480
ATCAAAAGCG	ATAAGCCTTT	AAGGGCTAGT	TTTTTAGAAA	TCAAAGAGTA	TGAAATTAAG	540
GAGAGGGAAA	ATCATGCCGT	TTTC				564

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

AAAGCACTGC	CACAAGGTCG	AAACAGAATG	CGGTCGGATG	TTGAAGTTTT	ATCGCCTTTG	60
CATAAAATAG	ATGAAAAATA	CCTTTTCCAT	TTAAAGATTG	CGGGGGAATT	GGCGAGCATG	120
GGTAAGATTT	TAAGTGATA	TTAGCCAC	AAGCACAGCG	CGTATTTTAT	TTTAAACGCT	180
TTGAGTTAAG	GCTTTAGCCA	CCAGGATAGG	GCGATCATTT	GCTTATTGGG	CGCAATT	237

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

AAGGGAACAA	AAATGAAAAA	AGTCTATTTT	AAAACCTTTT	GGTGTAGGAC	GAATCTTTTT	60
GACACGCAAG	TGATGGGCGA	AAATTTAAAG	GATTTTAGCG	CGACTTTAGA	AGAACAAGAA	120
GCCGATATTA	TTATTATCAA	TTCTTGCACC	GTAACCAATG	GGACCGATAG	CGCGGTAAGG	180
AGTTACGCTA	GAAAAATGGC	ACGATTGGAT	AAAGAAGTGC	TATTTACTGG	TTGCGGGGTG	240
AAAACCCAAG	GCAAAGAGCT	TTTTGAAAAA	GGGCTTTTAA	AGGGCGTTTT	TGGGCATGAC	300
AATAAGAAA	AGATTAACGC	GCTTTTACAA	GAAAAAAGC	GTTTTTTCAT	AGATGACAAT	360
TTAGAAAACA	AACATTTAGA	CACCACGATG	GTGAGCGAGT	TTGTGGGAAA	AACCAGGGCG	420
TTTATCAAGA	TCCAAGAGGG	CTGTGATTTT	GATTGCAATT	ATTGCATTAT	CCCAAGCGTG	480
AGAGGGAGGG	CTAGGAGTTT	TGAAAAGAGG	AAAATTTTAG	AGCAGGTGGG	CCTTTTATGC	540
TCTCAAGGGG	TTCAAGAAGT	GGTTTAAACC	GGCACTAACG	TGGGGAGCTA	TGGGAAAGAT	600
AGAGGAAGCA	ATATCGCGCG	ATTGATTAAA	AAATTAAGCC	AGATTACTGG	ATTGAAACGC	660
ATTAGGATTG	GGAGTTTAGA	CCTAATCAAA	TCAACGATGA	ATTTT		705

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GTTACGGCTT	TAGCCACCAG	GATAGGGCGA	TCATTTGCTT	ATTGGGCGCA	ATTTAGCCAT	60
AAAAAATCC	TTAAAGACTA	CGTTATCGCC	CACATGAGTG	CGATGATGCC	AAGCCTTTTG	120
ACCTTGCACT	GGCTGAGTTT	TATCCTTTCT	TTAGCCGAAA	ATTTGTGCCT	GACAGACAGC	180
CATCATTTAA	AATACACGCT	AGAAAAAAC	AAGCTTGTGA	TCCATTCTAA	TGATGCGCTT	240
TACTTGGCTA	AAGAAATGCT	CCCCAACTC	ATTAAGCCCA	TTCTTGGAC	GATAGAGTTT	300
GCT						303

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

AGCGATGCGT	TTTTAATCAT	ACAAGATTTT	AAAGAGCAGC	GCATCATCCA	TAAATCATT	60
CAAACCCATT	TCAAACGCAT	GCGTGTGGTT	TTGAGCGTGA	AAAGAGATAG	CGAAAAAACT	120
TTAGAAAACA	ATGAAGAAAA	TAAAGATGAA	AAGCTCATTT	TGATTGATGA	ATTTGAAGTT	180
TTAGCCAATA	AATTCATTTT	TCGTTTGCCT	AATATCCCTA	GCACCCCTAG	AGAGTTTGGG	240
TTAGGCAAGG	GCGAGATCAT	GGAGATTGAT	GTGCCTTTTG	GGAGCATTTT	TGCTTATAGG	300
CATATTGGCT	CTATCAGGCA	AAAAGAATAC	AGGATTGTAG	GGCTTTATCG	CAACGATGTT	360
TTGTTGCTCT	CCACTAAATC	TTTAGTCATC	CAACCACGAG	ACATTCTTTT	AGTGGCAGGC	420
AATCCGGA	TTTTAAACGC	GGTGTACCAT	CAAGTCAAAA	GCAATGTGGG	GCAGTTCCCA	480
GCCCCCTTTG	GTAAGAGCAT	TTATTTATAC	ATTGATATGC	GATTGCAGAG	CCGAAAAGCG	540
ATGATGCGCG	ATGTGTATCA	AGCCTTGTTT	TTGCACAAGC	GTTTAAAGAG	CTACAAGCTC	600
TACATTCAGG	TTTACACCC	CACTAGCCCT	AAGTTTTATC	ATAAATTTTT	ATCGCTAGAA	660
ACCGAAAGCA	TTGAAGTGAA	TTTTGATTTT	TATGGGAAGA	GTTTTATCCA	AAAACCTCCAT	720
GAAGACCACC	AAAAAAAAT	GGGTTTGATT	GTGGTAGGCA	GAGAGCTTTT	TTTCTTGAAA	780
AAACACCGAA	GAGCCTTGCA	CAAAACAGCC	ACACCGGTTT	ATAAAACCAA	CACCTCTGGC	840
CTGTCTAAAA	CCACTCAAAG	CATTGTGGTT	TTGAATGAAA	GTTTAAGCAT	TAATGAAGAC	900
ATGTCTTCAG	TGATTTTTGA	TGTGTCTATG	CAAAATGGATT	TGGGCTTGTT	GCTTTATGAT	960
TTTGACCCTA	ACAAGCACTA	TAAAAACGAG	ATTGTCAATC	ATTACGAAAA	TTTAGCCAAC	1020
ACCTTTAACC	GCAAGATTGA	GATTTTTCAA	ACCGATATTA	AAAACCCTAT	CATGTATCTC	1080
AATTCCTTAA	GAAATCCCAT	TTTGCATTTT	ATGCCTTTTG	AAGAGTGCAT	CACGCAAACG	1140
CGCTATTTGT	GGTTTTTATC	CACTAAAGTG	GAAAAATTAG	CGTTTTTTGAA	CGATGATCAC	1200
CCTCAAATTT	TTATCCCTGT	AGCGGAG				1227

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

CCAAATGAAG CGAGCGCGGC TGTTAATGTG GGCTATAAGA TCAGTAAGAG TTTGACAGCG	60
AGCGTGAAAT TAGAATATTT GGGCGTGATG ACGCATTCAG GCTTTACGGT AGGGAGTTAC	120
AGACCCACGC CCGGCTCTAA AGCACTTTAT TCAGACAGGA GCCATCTAAT GACAACCCTT	180
AGCGCCAAAG TC	192

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

TCCATAGTAT ACGGTAAAAA TAAATTATTC TCAGATGAAT TTTATGAAAA AATCGAGGAT	60
ATTTTAACAA ATAACAACCC AAGATACAAA CAAGTGTGCA TTATTTTGA TGCAGACATA	120
AAAAAAGAGA ACCAAGAAAG CGATGCAGGT TTTGATAACA AGCTTAAGCA TATTCGTGAA	180
AAATTCAAAG AAAAAGGGAC TGATTTTCCC AAAGAACAAA TCTTTTATTC CCTAACAATC	240
AAGATGATGG CGATT	255

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GTGCAAGCGT TTGATTATAA AATTGAAGTT TTGGCAGAGT CCTTTTCTAA AGTTGGCTTT	60
AATAAAAAAA AGATTGACAT AGCTAGGGGG ATTTATCCTA CAGAGACTTT TGTAACCGCT	120
GTGGGTCAGG GCAATATTTA TCGGGATTTT TTATCCAAAA GCCTTAAAGA TCAAGGGCAT	180
GTTTTAGAGG GAAAAGTCGG CGGCACAATC GGTGGGATTG CTTATGACAG CACGAAATTC	240
AATCAAGGCG GATCGGTTAT TTATAATTAT ATCGGTTATT GGGATGGCTA TTTAGGGGGT	300
AAAAGGGCCT TGCTTGATGG CACGAGTATC CATGAGTGCG CGCTTGGCTC TGATGGCAAG	360
GTGATTGATT CTATAGCGTG CGGGAACGCT AGAGCCAATA AAATCCGCCG TAATTACTTG	420
ATGAATACCC CTTTCTCA	438

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

TTCCGCTATA AGGATATATT TCGGGCTAAA GGGGGGCGTT ATCAATCCAA TGCTCCTTAT	60
ATGAGCTCTT ATACGCAAGG CTTTGAAATC AGCGCTAAAA TCAAGGATAA AAATGAGGGG	120
AGCCATAAAT TATGGTGGTT TAGCTCATGG GGTAGGGCGT TCGCTTATGG GGAGTGGATT	180
TATGATTTTT ACTCTCCAAG AACCGTGATT AAAAACGGGC GCACTCTAAA TTATGGTATC	240
CATTTAGTGG ATTACACTTA CGAAAGGAAA GGGGTTAGCG TCAGCCCCCTT TTTCCAGTTT	300
TCGCCCCGGA CTTATTATAG CCCTGGGGTG GCTGTAGGCT ATGATAGTAA CCCTAATTTT	360
AATGGCGTGG GCTTTAGATC CGAAACGAAG GCTTATATTT TGCTCCCTGT CCATGCCCCC	420
CTTAAAAGGG ATACTTATCG TTACGCTGTG AAAGCTGGCA CCGCTGGGCA AAGCCTGCTC	480
ATTAGGCAAC GATTTGATTA CAATGAATTT AACTTTGGGG GAGCGTTTTA TAAAGTATGG	540
AAAAACGCAA ACGCTTACAT AGGCACGACA GGAAACCCTC TAGGCATTGA TTTTGGACC	600
AATAGCGTTT ATGATATAGG GCAAGCCTTA AGCCATGTGG TAACCGCTGA TGCCGTCTCT	660
GGTTGGGTTT TTGGTGGAGG CGTGCATAAA AAATGGCTGT GGGGGACTTT GTGGCGTTGG	720
ACTAGCGGCG CTTTAGCCAA A	741

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

TTTTCCCAA	GAACAAATCT	TTTATTCCT	AACAATCAAG	ATGATGGCGA	TTTAGAAACC	60
CTATTATTAG	AAATTGCTAA	ACACGATGAA	TTTCTTAAAT	GCTTTGAAGG	ATACTTAGAA	120
TGTATTAAAA	GTAAAGAACA	TTATAAACCG	ATTAAAAACA	TAAGAAAAAA	TATGCTGTAT	180
GCCTATTTAG	AAGCGCTTGG	ATTAGAGAAT	TTGACCAAGA	CCAATATAGA	TGTTTTTGAT	240
AGTAAAGGTA	AAATAAGAG	TAGATATGAA	GAAACTACA	AAAAATTAAC	AGAAGAAGTT	300
ATTGATTTC	GCTCGAATTC	TCTCATTCCC	CTTAAAAATT	TTCTAGGGCA	ATTCGCAGAA	360
AATAAACAAA	AAACAAATCC	TAAAATTTTC				390

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ATTTACTTTA	GCGCCAAGCG	ATTCAACACC	AAAAACACGC	ATGGCACGGG	TTGTACTTTG	60
TCTAGCTTGA	TTGTGGGCTT	ACTCGCTCAA	GGGCTGGATT	TAAAAAACGC	TATCACAAAG	120
GCTAAAGAGC	TTTAACTAT	CATCATTCAA	AACCCCTTAA	ACATTGGGCA	TGGGCATGGG	180
CCTTTGAATT	TGTGGAGCAT	CAAAAAGCAT	GTT			213

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 699 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

CGCCCTTCAT	TCCAAAAACG	CTGCGCCCAT	TTTAACGCTA	CTTTACCCAT	TCTTTTAAAA	60
GTGCTAGAAA	AACAAGATAA	AGACCTTTTT	CTTTTGCAAG	TGGGTAACAG	GATTATCCCC	120
ACCAAAGCG	AACAGGAATT	AAAAATCAAT	CAGCCTTATT	TTGCGACTAT	GCAAAGAAAT	180
CAGCTGGGCG	ACATTGTGCT	TAAAAATTTA	GTGCCTGCCC	CAAAAATCTT	AGACGCATTG	240
GACGATTTGC	CCGTTATTGA	AATGAAGAAA	TTAAAAGAAA	TATTGAGCGC	CAAAGACAAC	300
ACCCCCCTAA	AAGAATACAA	AGAACTTTTG	AGCGAAAAAT	TAATCCATGC	TAAAAGCTCG	360
CAAGAGTTTT	TGAATACAGC	CAACATGCCT	TTAAGCTTGC	AATCGCAGGT	TTTAAGCTTT	420
GTGGTTGAAA	ACGAACGCAA	AAAAGCTTTT	TTACAGATGA	AAGCCAAAAA	ACAAAGCGTT	480
GATTTTTACG	CTCTGTACCC	TAACTTGGGC	GAAATTGGCG	GCGTTATTTA	TTTAAAAGAA	540
AAAGAGAAAC	AGCTTTTTTT	AAAAACCACC	CTCCAAAGGA	CCAAAGAGGT	TTTAAAAGAG	600
GCTCAAAACA	CCCTTTTAGG	CTTTTCTTTT	GTGGAAATTG	TGTGCGAAAA	AACCCCCATG	660
CTTTTTGCCT	TTGAAGATCG	CTTATTGGAC	ACGCTAGGG			699

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

CTATTAGAGA	TGATTTTTTCG	ATCAAGGCGT	TCAAAATGGG	GGGCGTTATG	CAACGCTCAA	60
ATCATTGAAT	GCGTAGCGAA	CGCTTTAGAA	ACTTGTGATT	TTGGGTTGTG	CGTTTTAGAT	120
CCGGTGATGG	TGGCAAAGAA	TGGGGCTTTG	CTTTTAGAAG	AGGAGGCGAT	TTTAAGCTTA	180

233

AAAAAACGCC	TTTTACCTAA	AACCAATTTA	CTAACCCCTA	ACCTCCCTGA	AGTCTATGCG	240
CTCACAGGCG	TTCAAGCGCG	AGACGATAAA	AGCGCTTCAA	AAGCGATGGG	TGTTTTAAGG	300
GATTTAGGCG	TTAAAAACGC	TGTGATTAAA	GGGGGGCATA	CAGAACATTT	TCAAGGGGAA	360
TTTAGCAACG	ATTGGGTGTT	TTTAGAAGAC	GCTGAATTTA	CTTTAGCGCC	AAGCGATTCA	420
ACACCAAAAA	CACGCATGGC	ACGGGTGTA	CTTTGTCTAG	CT		462

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

TGGCTTCAAT	CAAGGTGTTT	TAGGGATAGC	GCCTTTTGCC	TTAGTTCCGA	AAAATTGTTC	60
GGTAAAAATT	TGAATAAAGT	GGTCATTTTG	GCATTAAGAG	ACATTATCCA	TGAATATGGG	120
CATACTTTAG	GCTATACCCA	TAACGGGAAC	ATGACTTATC	AAAGGGTGCG	TTTATGCCAA	180
GAAGGAAACG	GGCCAGAGGC	ACGCTGTGAG	GGCGGGCATG	AAGTGGAGAA	AAACGGCAAA	240
GAAGAGCTAG	AATTCAGTAA	TGGGCATGAA	GTGCGAGACC	ATGATGGTTA	CACCTATGAT	300
GTTTGCTCTC	GTTTTGGCGG	CAAAAATCAG	CCCCTTTTCC	CTAGCAATTA	CCCCAATTCC	360
ATCTATACCA	ATTGCGCTCA	AGTCCCCGCT	GGGCTTATAG	GGGTACTAC	CGCTGTTTGG	420
CAACAGCTCA	TCAATCAAAA	CGCCCTGCCC	ATTAATTTTCG	CTAACCTAAA	TAGCCAAACC	480
AGCCATTTAA	ACGCCGGGTT	GAATGCGCAA	AATTTTGCAA	CCTCTATGGT	CAGCGCGATC	540
GCGCAAAATT	TTTCCACCAC	TTCCACTACC	ACTTACCGCT	CTTCAAGTAA	GAATTTTAGA	600
AGCCCTATTT	TAGGGGTTAA	TGTTAAATA	GGCTACCAAC	ATTATTTCAA	TGACTACATC	660
GGGTAGCCCT	ATTACGGCAT	TATCCAATAC	AACTACGCTC	AAGCTAACGA	TGAAAAAATC	720
CAGCAATTAA	GCTATGGTGG	GGGAATGGAT	GTGCTGTTTG	ATTTTCATCAC	CACTTACACC	780
AATAAAAAAGC	AAGACCATCC	AACTAAAAAG	GTTTTTGCTT	CCTCTTTTGG	GGTGTGTTGGG	840
GGGTAAAGGG	GCTTATACAA	TAGCTACTAT	GTCTTCAATC	AAGTCAAAGG	AAGCGGTAAT	900
TTAGATATAG	TAACCGGGTT	TAATTACCGC	TACAAGCATT	CTAAATATTC	CATAGCGTTA	960
GCGTTCCTT						969

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

TATGATTTCC TAGGGGTTTC CTTGCATGCC CTTAGCCCCC TAGAAGAACA AGAATTTTTA	60
ATTTTCGTACC GCTTGAAAAT CGTTGATTCT AGAGTGATGG GTGAAGAGTA TTCTGTTTCT	120
AAACCTATCG TTAGTCGCAT TAAACAGCC CCCTATGTTT TAGACTATCA TTGCTCTATC	180
ATCACTCGCA ACTTGCCCGA TTTGAAAAAC CCCTTGCTCC AAATAAAGCT AGAACGCTTC	240
CTTTTAGAAA TAGCGTTAAA AAAAGAAAAA GAGCGAGTCA TTGACTGCCT TTTAAAAAGC	300
CAAGTCGCTA TCACGCATTA TGATCACAGC TATAAAAACG GCACCACTAC CACAAGCATT	360
CTTAACCTCA AAGCCTTAAG CGTTAAAGCG AGTTTAGATG GGAGATATGC TGTCTTTAGA	420
TATTTT	426

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1032 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GAGTGGTTAA TGCTAAAAAA GATTTTTTAT GGTTTTATCG TTTTATTTTT GATTATCGTA	60
GGGTGTTGG CCGTTCTTGT CGCTCAAGTT TGGGTAAC TA CGGATAAGGA TATTGCTAAA	120
ATTAAAGATT ATCGCCCCAG TGTCGCTTCA CAGATTTTAG ACAGAAAAGG GCGTTTGATC	180
GCTAATATTT ATGATAAGGA ATTCGTTTT TATGCGCGTT TTGAAGAAAT CCCCCACGA	240
TTTGTTGAAA GCCTTCTAGC GGTAGAAGAC ACCCTCTTTT TTGAGCATGG GGGGATCAAT	300
TTAGACGCTG TCATGCGCGC TATGATTAAA AACGCTAAAA GTGGTCGTTA CACTGAAGGG	360
GGTAGCACTC TAACCAACA ACTCGTTAAA AACATGGTGC TCACACGGGA AAAAACCTTA	420
ACCAGAAAAC TCAAAGAAGC TATCATCTCC ATACGCATTG AAAAAGTCTT AAGCAAAGAA	480
GAAATTTTAG AGCGTTATTT GAACCAAAC TTTTTTGGGC ATGGGTATTA TGGCGTGAAA	540
ACCGCAAGTT TAGGGTATTT TAAAAAACC CTTGACAAAC TCACGCTTAA AGAAATCACC	600
ATGTTAGTCG CCTTACCTAG GGCTCCAAGT TTTTATGACC CTACCAAAAA TTTAGAATTT	660
TCACTCTCTA GGGCTAATGA TATTTTAAGG CGGTTGTATT CTTTAGGCTG GATTCTCTCT	720

AACGAGCTCA	AATCCGCTCT	CAATGAAGTG	CCAATCGTCT	ATAACCAAAC	TTCCACGCAA	780
AATATCGCTC	CCTATGTCGT	GGATGAAGTG	TTGAAGCAAT	TGGATCAATT	AGACGGGTTA	840
AAAACCTCAAG	GCTATACCAT	AAAACTCACG	ATAGATTTGG	ATTACCAACG	CTTAGCGTTG	900
GAGTCTTTGC	GTTTTGGGCA	TCAAAAAATC	TTAGAAAAAA	TCGCTAAAGA	GAAGCCAAAA	960
ACTAACGCTT	CTAATGATAA	AGATGAAGAC	AACTTAAACG	CCCAGCATGA	TAGTTACAGA	1020
AACGAGCACC	GG					1032

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

ACGCCCAGCA	TGATAGTTAC	AGAAACGAGC	ACCGGTAAGA	TTTTCAGCCTT	AGTGGGGGGG	60
ATTGATTATA	AAAAAAGCGC	TTTCAATCGC	GCCACGCAAG	CCAAACGGCA	GTTTGGGAGC	120
GCGATCAAGC	CTTTTGTTGA	TCAAATCGCT	TTTGATAATG	GCTATTCCAC	CAC'TTCCAAA	180
ATCCCTGATA	CCGCGCGAAA	TTTGTAAAAT	GGCAATTATA	GTAAAAACAG	CGTGCAAAAC	240
CACGCATGGC	ACCCTAGCAA	TTATACTCGC	AAATTTTTCAG	GGCTTGTAAC	CTTGCAAGAA	300
GCCTTGAGCC	ATTCGTTAAA	TCTGGCTACG	ATTAATTTAG	CGATCGCTTG	G	351

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

CCCAGAGACC	ACACTTATAG	CTTAGAAGAC	AGCACGCCTC	ATGGCTCTTT	GTTAGGGAGG	60
AATGGCGTTA	CTTTAAATAT	CCGCCAGGTT	TTTTGGTGGG	ATAATTTCAA	CTGGTCCATT	120
GGCTTTTATA	ACACCTTTGG	CAATTCAGAC	GCTTTTTTTAG	GCTCTCACAC	CATGCCAAGG	180
GGGAATAACA	CTTCCTATAT	CAGTAATGAA	ATCTCAGTAA	CGACTAGGCA	TGCCGGAATG	240
ATCGGCTATG	ATTTTTGGGA	TAATACGGCT	TATGATGGGC	TGGCTGATGC	GATCACTAAC	300
GCGAACACTT	TCACTTTTTA	CACTTCGGTT	GGAGGGATCC	ATAAGCGTTT	TGCATGGCAT	360
GTTTTTGGGC	GCGTCTCTCA	TGCGAATAAA	AATGCGTTAG	GGCAAGTGGG	GAGGGCTAAT	420
GAATATTCCT	TGCAATTCAA	TGCGAGCTAT	GCGTCCACTG	AATCGGTTCT	CCTTAACTTT	480
AGGATCACTT	ATTATGGGGC	TAGGATCAAT	AAAGGGTATC	AAGCAGGGTA	TTTTGGAGCG	540
CCCAAATTCA	ATAACCCGGA	TGGCGATTTT	AGCGCTAATT	ACCAAGACAG	AAGTTACATG	600
ATGACCAACC	TCACGCTGAA	GTTT				624

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

CCAAGAATAC	ACGATATGGG	CGATTTAGAT	TCTCTAAACA	TCAGCCCCGA	TCCTAACACC	60
CCTACCCTAT	TGATTTTAAG	CGCTTTAGAT	AATTCTTTAA	AAGATTACGC	CCCCACCTTT	120
AACGTCTTAA	AAAAAACTTT	TAAAGATCGT	TTGAGGGTGC	TTATTTTACT	CAATCAACCC	180
TATTCAAGCG	ATGCAATCAA	AGGCTTTATT	GCGCCTTCTC	AAACTGATTT	GATGATTTTA	240
AACCCTAAAG	ATACCGCTCT	TTTTGATCAT	TTAAACCATG	ACGCTTTAAA	CCATTCTTTT	300
AACATGCTCT	TATATGACAA	ACACCAATTG	ATTAAAATGT	ATCAAGGGAT	CGTGCCAGCA	360
GAAATGCTCC	AATTTGATAT	TTCCAATTTA	AAGGAC			396

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

AGAAGAAGCC	TTTATTATGT	GTTTATAAAA	TCGTATGCCA	TTTTAGCGGA	AGCGACAGCC	60
CGTTTTGCGG	GCGATTATGC	GACAGAGAAT	TTAACAAGCC	GTATCGCTTT	GCCTTGCTCA	120
GATTATGTGG	GTCGTGTGAT	AGGCAAAGAC	GGGAAAACA	TTGAAGCGTT	TAAAAAGATT	180
AGTGGGGTGG	ATATAGAATT	TAGCGAAGAC	AGTAGCGAAT	TGTGCTTGTC	CAGTTTCAAT	240
ATTTATCGGC	GTGAAGTGGC	GAGCGAGACG	ATTAAAATTT	TAATAGAAGA	CGGCCGTATC	300
CAGCCTAACA	GGATTGAAGA	GGTTTATCCT	AAAATTCACC	CGCAACATGG	AAAAAGAATT	360
GCTTTC						366

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

AAGACGGCCG	TATCCAGCCT	AACAGGATTG	AAGAGGTTTA	TCCTAAAATT	CACCCGCAAC	60
ATGGA AAAAG	AATTGCTTTC	TGAAGGAGAG	AGCGTGGTGC	TAGAATTAGA	GCTTGGA ACT	120
ATGGAAGATG	AGCTTAAAAT	TTTAATAGGC	AAAATGCGTT	ATCGCTTTAG	TTTTGGGCAA	180
AACGCTTTAC	AGCATTCTAA	AGAGATCGCT	CTTTTATCCG	GCTTGATTGC	AGAACAGCTT	240
GGGGGGGATA	AAAAACTCGC	CAGAAGAGCC	GGTATTTTGC	ATGATATTGG	TAAAGCGCTC	300
ACTCAAGAGC	TTGGGAGAGA	CCATGTGAAT	TTAGGGGTTG	AGGTGTGCAA	GCGCCATAAA	360
GAAGACCCGG	TTGTGATCAA	TGCGATTTAT	GCCCACCATG	GGCATGAAGA	AATCATGAGC	420
GTGGAGTGCG	CGAGCGTGTG	CGCGGCTGAT	GCGCTTTCTG	CAGGGCGTCC	GGGCGCTAGG	480
AGAAAGAGCG	ATGAAGAATA	CGCTAAACGC	ATGCAAGCTT	TAGAAGAGAT	CGCGTTAGAA	540
TTTGATGGGG	TGGA AAAAGGC	GTATGCGATG	GAGAGCGGGC	GAGAACTAAG	AGTGATTGTC	600
AAATCCAACC	AAGTCAGGGA	CAATCAAGTG	CCTATTATTG	CTAGAAAGAT	CGCTAAAAGG	660
ATAGAAGAGA	GCACTCAGTA	TGTGGGCGAA	GTGGGCGTGC	AAGTGGTGCG	AGAAAATCGT	720
TTCAAAACGA	CCGCTACGCT	AAGCAATGAT				750

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2412 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2412
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

AGTTTGTGGC	TTAAGTCAAA	ATTCTTTCTT	TTAATGGGCG	TGGGTTTGCT	CTCCCATTCA	60
CTCAACGCTT	TAAGCCTCAC	GCTCACGCAA	GGCAAAGAAG	AAGGAGAAGA	TTTTTCGGTT	120
TTAACCTTAC	GAAACGATAA	GGCGTTTCT	TGCTCTTATG	CTAATGAAAA	ACCGCCGAGC	180
GGGATTGAAG	CGTCTTTATC	TATTATACAC	GCTAAACGCC	CCATAGAATG	CGTGATAGAT	240
TCTATTCCCTA	AAGAGGGCTT	TACCCCTTTA	GAAAACGCTT	TTTTCAATAT	CACCTATTCC	300
ATGCGCCAGC	AACAATTCAT	TTTACACATC	AAACCCAAAG	TGATGCGAAG	GCTCACCCCTT	360
TTTTCTTTTG	ATAGGGATTA	TAAAAAAGCG	ATCCCCCTTT	TTGTGGAAAA	CGACGCTAAA	420
GCCAAGATGT	GGCAAATCAT	AGGCTATGAT	CAAAAAATCC	CTTTTTTGAG	CGAAAAAGAC	480
AACGCTCAAA	AAGGCTTGAA	TTTCCCCATT	ATCATTAAAG	ACGCTCAAAC	CCCTATCATT	540
CAAGAGCTGG	ATGTGAATAA	CAAACCCCTA	CTCACCACAA	AGGGCTATGA	TTTAAACGCC	600
TATTTAGAAG	CTAAAAACA	AATGGATTCTG	CAAGCCTATT	TTGACGCCTT	ACGCACGATC	660
AGCCGCGCGT	TTAAAAATTA	CCCTCAAACG	ATTTTTTAAA	AAGATCTGTA	TTTATTAGAA	720
ATTATCGCAT	TAGGTAAATT	AGGCATTAAA	AAATCCTTAC	TCATAGATAT	TGGCACCCAA	780
TGGATTAAAA	ATTACCCGAC	TGATCCTAAT	ATCCCTGAAG	CGCTATACTA	TGTCGCCAAA	840
GCTTTAGATG	AAAACAACAA	TTACAAACAA	GCGTGCGCT	ATTACAAACG	AATCCTTTTA	900
GAATACAAAA	ACTCCCGCTA	CGCTCCCTTA	GCCCAAATGC	GTTTAGCCAT	TGAAGCGGCT	960
GAAGGCTCTG	ATTTGAGCAA	CGCTAATATG	CTTTTTTAAAG	AAGCTTTTTTC	TAACGCCAAA	1020
GACAAAGAGA	GCGCGAGTGA	AATCGCGCTT	AATTGGGCTG	AAGCAGAGAT	AAACTATCAA	1080
AACTTTAATA	ACGCTAAATA	TCTCATTGAT	AAGGTGGTTC	AATCCAACCC	TGATTATCTT	1140
TCTATGCACA	GCGAATTAGC	CCTAGAATTG	CTCAAGTTAT	TGAAAAAAAA	CCAAATGAAT	1200
GAAAGTGCGA	TTGAGATCGC	TCACTTGCTC	CTCAATCAAG	ATGATGACTT	GAAAGCTAAA	1260
GAGCAAGCGC	TCTATGATTT	AGGGGCGTTG	TATGCAAGGA	TCAAGGATTT	TAAAAACGCC	1320
CACCTTTACA	ATCTGCAATA	TTTGCAAGAC	CATGCGGAAT	TGGAGCGGGC	TTCTGTCTGTT	1380
AGAGCACGCG	ATGAAAAAGC	CCTTTTTTCA	ATGGAAGGGA	ACACGCAAGA	AAAAATCGCC	1440
CACTACGATA	AAATCATTCA	AAATTTCCCT	AATTCTAATG	AAGCCCCAAA	GGCTTTAGAG	1500
TTGAAAGCCC	AACTCTTGTT	TGACAATAAG	CACTATGCTG	AAGTTTTAGG	CATGCAAAAA	1560
AATTTGCCCA	AAGATTCTCC	CTTGATCCAA	AAAACGCTCA	ATATCCTTGC	TAAAAACCCCA	1620
TTAGAGGATC	ATCGTTGCAA	AGAAGCTTTA	AAATACTTAT	CCCAGATCAC	CGCCTTTGCA	1680
TTCAACCCCC	AAGAAGAAAT	CCAAGCCTTT	GATTGCTTGT	ATTTTCGCATC	GCTCAAGGAA	1740
AAAGCGCAAA	TTATTGCCCT	AAACGCTTTA	AAAGCGGCTA	AAACCCCTAG	CGAGAAATTA	1800
ACATGGCTTT	ATCGTTGGG	GCGCAATTAC	TACCGCTTAG	GGGATTTTAA	AAATTCCACT	1860
CTGGCTTCTA	AAGACGCCTT	AATCCTCGCT	CAAAGCTTAA	ATAAAAAAGA	GTTTTATGAC	1920
ATTGCTTTTG	TGTTATTTTC	AGATTACATG	CAAAACAATG	AAAAAGGATT	GGCCCTCAAT	1980
TTGTATGCGT	TTTTAGAAAA	GCATTTCAAA	GACGATAAAC	GCATGGCGTT	GTTTATTTT	2040

AAATTATTAG	AGAATGAAAA	AGACCCTAAA	AGCGTTAAAA	TTTATGCCAC	AAGCTTACTC	2100
AAACTCCAAG	ACGCTTATAA	GGATTATTCT	TACACGCCCT	TTGGCGAATT	TGCCCTTATT	2160
GACGCTTACA	GAACCACCAA	AGATTATTCA	AAAGCGTTAG	AAACGCTAGA	CAAACCTCTTA	2220
AACCGCAGGC	TTTCTTTAGA	AGATCACCAA	AAAGCCTTAT	ACTTGCAATC	CAGCTTATTG	2280
GATTTAACCA	ATCAAAAAGC	AAAATCTAAA	GCCAGTTTAG	AAAAATGCGT	TCAATTAAAG	2340
CAAAAAGATC	AAACAAACGC	ATGGCAAAAT	TTATGCGAAC	AGGGTTTAAA	TTTATTCAAA	2400
AACAAGGAGT	CA					2412

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

AAACACCCAA	ATCGTTTTTT	CTTCAAAAGA	ATTGAAAGAA	CCGCACTCAA	ACCCAATACC	60
TTCTTAAACG	CGCCCATGCA	AAAACCACAA	AATAAACCCA	GCTCATCGCA	ACAATCTCCT	120
CAAACTTTT	CTTACCCAGA	GTCCAAACTA	GGCTCTAAAA	ACTCTAAAAA	CAGCCTTTTA	180
CAGCCTTTAG	TAACCTCTAG	CAAAGTAAGC	CCCCTAACG	AAGTTAAAC	GCCAACAAAC	240
GACGCTAATC	CCCCTTTAAA	GCATTCTTCA	CAAGATCAAG	AAAACAACCT	CTTTGTAGCG	300
CCACCCACTG	AAAAAACGCT	CCCTAACAA	ACCTCTAGTG	CTGATGCGAG	TGAAAACAAT	360
GAAAGCAACG	AAAATAGGGA	TAATGTGGAA	AAACAAGCGA	TTAGAGATCC	TAATATCAAA	420
GAATTCGCAT	GCGGGAAGTG	GGTTTATGAT	GATGAAAATT	TACAAGCCTA	TCGCCCAGC	480
ATTTTAAAC	GCGTTGATAA	AGACAAAGAG	ATTACAACAG	ACATTACCCC	TTGCGATTAC	540
AGCACCGCTG	AAAATAAAAG	CGGTAAAATC	ATTACCCCCT	ATACTAAAAT	CTCTGTTTCAT	600
AAAACAGAGC	CTTTAGAAGA	CCCTCAAAC	TTTGAAGCTA	AAAATAATTT	CGCCATTCTC	660
CAAGCCAGAA	GCTCTACAGA	AAAGTGTA	AGGGCTAGAG	CGAGAAAAGA	CGGCACGACC	720
AGGCAATGCT	ATCTGATAGA	AGAGCCTTTA	AAACAAGCGT	GGGAGAGCGA	GTATGAAATC	780
ACCACGCAAT	TAGTGAAAGC	CATATATGAA	CGCCCCAAAC	AAGACGATCA	AGTAGAGCCG	840
ACTTTTATG	AAACCAGCGA	ATTGGCTTAT	TCTTCCACAC	GAAAAAGCGA	AATAACGCGT	900
AATGAATTGA	ATTTGAATGA	AAAATTCATG	GAATTTGTGG	AAGTGATGA	GGGTCATTAT	960
TTAAACGATA	TAATCAAAGA	GAGCAGCGAA	TACAAAGAAT	GGGTAAAAAA	CCATGTGCGC	1020
TTTAAAGAAA	GGGTGTGCAT	GGCCTTAAAA	ATAAAAAAGC	AACCACGAGC	CAAAAGCAGC	1080
CCTTTGAGTA	TTGAAAAC	TCGTGTTGTG	TGTGTCAAAA	AGGGGAATTA	TTTATTCAAT	1140
GAAGTT						1146

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid

240

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

ACCAAAAAGT TAAACAATAC TCTATTCAAT AAAGGATTAA TTATTTTAA AATGTTTAAA	60
AAAATCATTT TTTTGTGCGT TTTTGTGATA GGGGGATTG TCATTCCACC CCTTGAAGCC	120
ATGCCTATTT TGCGCAATAA AACCCCCAAA AAAAATTACC AAGAAGCCCA TGAAAAGCTC	180
TATAGAAGCA TCATTAACCG CCAAAGCTC ACGCGTAAAA AAAGCGGGTG GTATTTTAA	240
GGGGGGGTG GCGCTGTAGA AGCCATTAAG GACTATCAAG GCAAGGAAAT GAAAGATTGG	300
ATGCCACGCT CAATT	315

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

AGTAAACTT CCTATTGCAA TTCTTACAAG CGTAAGCTCC TCCCCTACCA CTTTCTACTT	60
TTTCCATTAT GGGCGTGTTT TCACAATGTA AGCAGACCAT TTTCATTGAG CCATTTATTT	120
CTCGTAAAAC GCCCTTACAG TCGCCTTTAT TTACATAATC AGAGCAACCA TAAAATGAGA	180
CACCATTCOA TCCTCTTTGT ATCATTT	207

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1374 base pairs

241

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

CAAGATAAGG	GGTTATTATT	GAGTGTAGCA	CTACCTAACT	CAAACAACGC	CTCTCAAAAC	60
AACATTTTAA	GCCTTTCCTGT	CCTTCACAAC	CAGATTAAAA	TGTCTTATGG	TAATAAAGTG	120
ATGGACTTTA	CCCCTCCCAC	CTTACAGGAT	TACATTGTGG	GCATTCAAGG	ACAAAGCGCA	180
CTCAATCAAA	TTGAAGCTGT	TGGGGGGAAT	AACGCTATCA	AGTGGCTTTC	AACATTGATG	240
ATGGAGACTA	AAGAAAACCC	GCTTTTGTGC	CCGATTTATT	TAGAAAACCA	CTCTTTAAAT	300
GAAATCTTAG	GCGTAACAAA	AGATCTTCAA	AACACCGCAA	GCTTGATTTT	TAACCCTAAT	360
TTTAGAAATA	ACGCTACCAG	CCTTTTAGAA	ATGGCGAGTT	ACACCCAACA	AACCAGCCGT	420
TTGACAAAAC	TCTCTGATTT	TAGGGCTAGA	GAGGGAGAGT	CCAATTTTTC	AGAGCGCTTG	480
TTAGAGCTTA	AAAACAAGCG	TTTTAGCGAT	CCTAACCTTA	GTGAGGTTTT	TGTCAAATAC	540
TCTCAACTCA	GCAAACACCC	CAATAACCTT	TGGATTCAAG	GGGTGGGAGG	AGCGAGCTTT	600
ATTTCTGGGG	GCAATGGCAC	GCTTTATGGC	TTGAATGTGG	GCTATGACCG	ATTGGTTAAA	660
AGCGTGATCC	TTGGGGGTTA	TGTGGCTTAT	GGCTATAGCG	GTTTTAACGG	GAACATCATG	720
CATTCTTTGG	CTAATAATGT	GGATGTGGGG	ATGTATGCGA	GGGCTTTTTT	GAAAAGAAAC	780
GAATTCACCT	TGAGCGCGAA	TGAAACTTAT	GGAGGCAATG	CGAGTCATAT	CAATTCTTCT	840
AATTCCTTGC	TCTCTGTGTT	GAACCAACGC	TACAACTACA	ACACCTGGAC	AACGAGCGTG	900
AATGGGAATT	ACGGCTATGA	TTTCATGTTT	AAACAAAAAA	GCGTGGTGCT	AAAACCTCAA	960
GTGGGCTTGA	GCTATCATTT	CATAGGCTTG	AGCGGGATGA	AAGGTAAAAT	GCAAAATCCA	1020
GCTTACCAAC	AATTCGTCAT	GCATTCAAAC	CCTTCTAACG	AATCGGTTTT	AACGCTCAAC	1080
ATGGGGTTAG	AGAGCCGTAA	ATATTTTGGT	AAAAATTCCT	ATTATTTTGT	AACGGCGAGG	1140
TTGGGTAGGG	ATCTTTTGAT	CAAAGCTAAA	GGCGACAATG	TGGTGCCTTT	TGTGGGTGAA	1200
AACACTTTAT	TGTACCGCAA	GGGGGAAATT	TTTAACACTT	TTGCGAGCGT	GATCACAGGA	1260
GGCGAAATGC	ATTTGTGGCG	TTTGATGTAT	GTGAATGCGG	GGGTGGGGCT	TAAAATGGGC	1320
TTGCAATACC	AAGATCTTAA	TATCACTGGG	AATGTGGGCA	TGCGAGTGGC	GTTT	1374

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

242

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

CCCTTTGAAG CCTTGAATTT TTACTCCAAA AAAGCGTTGA ATGAGATTTT TGCAAACGCT	60
AGGAAAATTT GCGGGAACAA GCCTTTGGGG GCGAATATTT TATACGCTAT CAATGACTAT	120
GGCCGTGTTT TAAGGGACTC TTGTGAGGCG GGGGCGAATA TTATCATTAC AGGGGCTGGT	180
TTGCCCACTA ACATGCCTGA ATTCGCTAAG GATTTTAGCG ATGTGGCGCT CATCCCTATC	240
ATTCCTCAG CGAAGGCTTT AAAAATCCTT TGTAAAAGAT GGAGCGATCG CTATAAAAGA	300
ATCCCGGACG CATTCAATGT GGAAGGGCCT TTGAGTGGGG GGCATCAGGG CTTTAAATAC	360
GAAGATTGTT TCAAAGAAGA ATTCCAATTA GAAACTTAG TGCCTAAAGT CGTGGAAGCT	420
TCTAAAGAAT GGGGGAATAT CCCTATCATC GCCGCGGGGG GAATTTGGGA TAGGAAAGAT	480
ATAGACACCA TGTTAAGCCT TGGAGCGAGT GGGGTGCAA TGGCGATCTC GTTTTTTAGG	540
CACGAAAGAA TGCGACGC	558

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GCTATCCGGC TTAGGCTATC AATACGGGGG TTGATCAAAC GCATTGAAGA AGGTAACGCG	60
CCTAAAATCG CATGCGTGAG CAATTGTGTA ACGCCTTGTA ACAGGGGTGA AGAAACTAAA	120
AAGGTGGGCT ATTGTATCGC TGATGGTTTG GGGCGCAGTT ATTTAGGAAA CAGAGAAGAG	180
GGGCTTTATT TTACCGGGGC TAATGGCTAT AGAGTGGATA AGATTATCAG CGTGCAATGAA	240
TTGATTAAAG AGCTTACAGA GGGT	264

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 852 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...852
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

AATTTCAATC	AAAGGGCTTT	TTTGAAACGA	GCGTTATGGT	TAATTTTAGG	GCTTTTTTAC	60
GCGCTTAATG	CAGAGAGCTT	TAAAGATGTT	TTGACTAAAG	GGGATTACAC	TTTTTTTAAT	120
AAAAAGGTGG	TTTCGCCTAT	CAAACGCTAT	GCGGATAGAT	CGGCGTTTTA	TCTGGGGCTT	180
GGGTATCAAT	TAGGGAGCAT	TCAGCACAAAC	TCTAGCAACT	TGAATTTATC	CCAACGATTT	240
AATAAGAGTC	AGATTATTTT	CAGCGATAGT	CTAAGCCCTG	TTTTTAAAAA	TTCGTATGTG	300
TCTAATGGTC	TTGGCGTTCA	AGTGGGCTAT	AAGTGGGTGG	GTAAGCATGA	AGAGACGAAA	360
TGGTTTGGCT	TCAGGTGGGG	GCTGTTTTAT	GATTTGAGCG	CTTCTCTTTA	TGGCTCTCAA	420
GAATCGCAGT	CTATCATCAT	TTCCACTTAC	GGCACTTATA	TGGATTTATT	GCTTAACGCT	480
TATAATGGGG	ATAAGTTTTT	TGCCGGGTTC	AATCTGGGGA	TCGCTTTTGC	TGGAGTGTAT	540
GACAGATTGA	GCGATGCGTT	ATTGTATCAA	ACTCTTCTTC	AAAACACTTT	TGGCGGGAAA	600
GTGAATTTAA	ACGGCTTCCA	GTTTTTGGTG	GATTTAGGGG	TTCGTTTAGG	GAATGAACAC	660
AACCAATTTG	GCTTTGGGAT	TAAAATCCCT	ACTTATTATT	TTAACCATTA	TTATTCCATG	720
AATAACATTA	GCAATAATAG	TGAAAATGTC	TTAAAAGTTT	TACGATTTTT	AGAATACGGG	780
ATCAACAGCT	TGTTGTATCA	AGTTGATTTT	AGGCGCAATT	ACTCGGTTTA	TTTCAACTAC	840
ACTTATAGTT	TT					852

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...198
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

AAAATGCACA	CGAGTTTTTTT	CCAAATCCCT	TTGAATTTTG	GGGTTTCGTGT	GAATGTGGAT	60
AGGCACAATG	GCTTTGAAAT	GGGCTTAAAG	ATCCCTTTAG	CGGTCAATTC	CTTTTATGAA	120
ACGCATGGCA	AGGGGTAA	CGCTTCCCTC	TTTTTCAAAC	GCCTTGTCAT	GTTTAACGTG	180

AGTTATGTTT ATAGTTTT

198

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

ATCAAACGCA TCATTAAATC AAACGCATCA TTAAATCAAT TAAATACCAC TAGATACAAT	60
ACCCCAAGTC ATCTTTTTTT CAAAAAAGGG GTAGGAATGG CAACCATTCA ACCATTCAAC	120
CATTCAACCA TTCAACCATT CAACCATTCA ACCATTCAAC CATTCAATCA TTCAATCATT	180
CAATCATTCA ATCATTCAAC CATTCAAGCA ACGCTACCTT ATTTTATATA CTATTTATCT	240
TTTACAAAA ACCTATTTAA AAATCCCCTA TTTTATTATTA TTCCCCCTTT TATTAACCCT	300
TTTATTAACC CTTTATTATA CCCTTTTATT AACCTTTTAA TTAACCCTTT TATTAACCCT	360
TTTATTAACC CTTTATTATA CCCTTTTATT AACCTTTTAA TTAACCCTTT CATA	414

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

CGCTACCACC ACTTCTCCGG CCTATCAAGC TGTGGCTTTA GCGCTCAATG CGGCTGTGGG	60
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CATGTGGCAA	GTCATAGCCT	TTGGCATCAG	CTGTGGCCCT	GGCCCAATCT	TGGCCCAGAA	120
CATTTAGAAA	ATGGGGGCGT	TCGATCGTTT	GACAACACGC	CAAACCTACAG	CTACAACACC	180
GGTAGCGGAA	CGACCACCAC	CACTTGTAAT	GGAGCCAGTA	ATGTAGGGCC	CAATGGTATC	240
CTATCTAGCA	GCGAATACCA	GGTTCTCAAT	ACCGCTTATC	AAACTATCCA	AACCGCTTTA	300
AACCAAAACC	AAGGAGGCGG	GATGCCTGCC	TTGAATAGCT	CCAAAAATAT	GGTAGTCAAT	360
ATCAATCAAA	CTTTCACAAA	AAACCCTACC	ACAGAATACA	CTTACCCCGA	TGGGAATGGC	420
AATTATTATT	CAGGCGGTTT	ATCAATCCCA	ATCCAGCTAA	AGATTAGTAG	CGTCAATGAC	480
GCTGAAAACC	TTTTGCAACA	AGCCGCTACT	ATCATCAATG	TCCTTACCAC	CCAAAACCCG	540
CATGTGAATG	GTGGTGGTGG	GGTCATGGGG	GTTTGGCGG			579

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

ATGGTGGTGG	TGGGGTCATG	GGGGTTTGGC	GGTAAGACCG	GGAATGTGAT	GGATATTTTT	60
GGCGATAGTT	TTAACGCTAT	TAACGAAATG	ATCAAAAACG	CTCAAGCCGT	TTTAGAAAAA	120
ACCCAACAGC	TTAACGCTAA	TGAAAACACC	CAAATCACGC	AACCAGACAA	TTTCAACCCC	180
TACACTTCTA	AAGACACGCA	GTTTCGCTCA	GAAATGCTCA	ATAGAGCTAA	CGCTCAAGCA	240
GAGATTTTGA	GCTTAGCCCA	ACAAGTAGCG	GACAATTTCC	ACAGCATTC	AGGGCCTATC	300
CAACAAGATC	TAGAAGAATG	CACCGCAGGA	TCAGCCGGTG	TGATTAACGA	CAACACTTAT	360
GGTTCAGGTT	GCGCGTTTGT	GAAAGAGACT	CTCAATTCCT	TAGAGCAACA	CACCGCTTAT	420
TATGGCAACC	AGGTCAATCA	GGATAGGGCT	TTGTCTCAAA	CCATTTTGAA	TTTTAAAGAA	480
GCCCTTAGCA	CTTTAGGGAA	CGACTCAAAA	GCGATCAATA	GCGGTATCTC	TAAGTTGCCT	540
AACGCTAAGT	CCCTTCAAAA	CATGACGCAT	GCCACTCAAA	ACCCTAATTC	CCCAGAAGGT	600
TTGCTCACTT	ATTCTTTTGA	TACCAGCAAA	TACAACCAGC	TCCAAACTGT	TGCGCAAGAA	660
TTAGGCAAAA	ACCCCTTTAG	GCGCATCGGC	GTGATTAACT	ATCAAAACAA	TAACGGGGCG	720
ATGAACGGCA	TCGGCGTGCA	AGCGGGCTAT	AAGCAATTCT	TTGGCAAAAA	AAGGAATTGG	780
GGGTAAAGGT	ATTATGGTTT	CTTTGATTAT	AACCATGCTT	ATATCAAATC	TAATTTTTTT	840
AACTCGGCTT	CTGATGTGTG	GACTTATGGG	GTGGGTATGG	ACGCGCTTTA	TAAGTTTCATC	900
AACGATAAAA	ACACCAACTT	TTTAGGCAAA	AATAACAAGC	TTTCTGTGGG	GCTTTTTTGGT	960
GGCTTTGCGT	TAGCCGGGAC	TTCGTGGCTT	AATTCCCAAC	AAGTGAATTT	GACCATGATG	1020
AATGGCATT	ATAACGCTAA	TGTCAGCGCT	TCTAACTTCC	AATTTTTTGT	TGATTTAGGC	1080
TTGAGAATGA	ACCTCGCTAG	GCCCAAGAAA	AAAGACAGCG	ATCATGCCGC	TCAGCATGGC	1140
ATGGAATTGG	GCGTGAAAT	CCCCACCATT	AACACGGATT	ATTATTCTTT	CATGGGGGCT	1200
GAAGTCAAAT	ACAGAAGGCT	CTATAGCGTG	TATCTCAATT	ATGTGTTTGC	TTAC	1254

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

GCTTTATCGC	GCTGTCTTAG	CGATCGTTTT	AATCAGTATC	CTGCCCTACA	AAAAACCGAA	60
CACCATTTCG	TGGATTTTTT	AAACCAGGAC	AAGCATTACG	CCATTATCCA	AAGAGCGGAT	120
AAAAGCATTT	CCAGTAATGA	AGCGTTGGCT	CGTTCGCTCA	TTGGGGCGTA	TGTGTTAAAC	180
CGAGAGAGCA	TTAATCGCAT	TGACGATAAA	TCCCGCTATG	AACTGGTGCG	CTTGCAAAGC	240
AGCTCTAAAG	TGTGGCAACG	CTTTGAAGAT	TTGATTAAAG	CCCAAAACAG	CATCTATGTG	300
CAAAGCCATT	TAGAAAGAGA	AGTCCATATC	GTCAATATTG	CGATCTATCA	GCAAGACAAT	360
AACCCCATTTG	CGAGCGTGTC	CATTGCGGCT	AAACTTTTGA	ATGAAAACAA	GCTCGTGTAT	420
GAAAAGCGTT	ATAAAATCGT	ATTGAGCTAT	TTGTTTGACA	CCCCGGATTT	TGATTACGCT	480
TCCATGCCC						489

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TCCTTTAAAA	AAAATGAAAG	GTTATTGTTG	CTTGTTTCTC	GCTTTTTTAA	CGCCATTGAT	60
CCTTTTAATT	TAGGGGTGTT	GTTGAGCCGT	TTCCAAATTA	AAAATGGTTG	TATTTATGGG	120
GTGTGTTCTT	ACAAGGTTTC	AAAATTTACC	CCTGGATATG	AAGAAAGCAA	AGCGCGAGTT	180

TTAAACGCTC	TCAATATTTT	AAGCAAGCAT	CAAATTTGGC	AATCCAATCA	AGAAAGCGTT	240
ACAAAAGTCA	AAGGAACTTT	TGTTTTTCATT	TTAGAAAATG	ACCTGCATTT	AGACGAAAAC	300
TCTTTTTATA	AGAAACTTTT	AAATCTGATT	ATAGACAATG	ACTTTTTTAA	CCGCTCTCAT	360
TTAGTAACTC	CGAGCAATGG	CACCAACTCC	CACCCTGAAT	TGCACCGCTC	TATCACGCCC	420
AGAGAAGCCG	CTAGGATACA	AAGTTTTAGC	GATGATTATA	TCTTTTATGG	CAATAAAACG	480
AGCGTTTGCA	AGCAAATCGG	TAACGCCGTG	CCTCCTCTTC	TAGCCCTAGC	CTTAGGCAAA	540
GCGATCTTAA	AAAGCGCAAG	AAATGATACA	AATCCATCAC	GC		582

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

ATGCAGGATA	ATTTAGTGAG	CGTGATTGAA	AAACAAACCA	ATAAAAAGGT	GCGTATGTTA	60
GAAATCAAAC	CTTTAAAATC	CAGCCAGGAT	TTAAAAATGG	TCGTTATTGA	AGATCCGGAC	120
ACTAAATACA	ATATCCCGCT	TGTAGTGAGT	AAGGATGGTA	ATTCAGTCAT	AGGGCTTAGC	180
AATATCTTTT	TTAGCAATAA	AAGCGATGAT	GTGAAATTAG	TTGCAGAAAC	CAATCAAAAA	240
ATCCAAGCCC	TTAACGCTAC	CCAGCAAAAC	AGCGCGAAAT	TGAACGCTAT	TTTTAATGAA	300
ATACCGGCTG	ATTATGCGAT	AGAGTTGCCC	TCTACTAACG	CTGAAAATAA	GGATAAAATC	360
CTTTACATTG	TTTCTGATCC	CATGTGCCCC	CATTGCCAAA	AAGAGCTCAC	TAAACTCAGG	420
GATCACTTAA	AAGAAAACAC	TGTGAGAATG	GTTGTAGTGG	GGTGGCTTGA	AGCAATTCCG	480
CTAAAAAAGC	GGCTT					495

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

ACGGGAGCAA TCATGTTATC TTCTAATGAT TTGTTTATGG TCGTTTTAGG GGCGATTTTA	60
TTGGTGTGG TGTGCTTGGT GGGGTATTTG TATCTTAAAG AAAAAGAGTT TTACCATAAA	120
ATGAGGCGTT TAGAAAAAAC TTTAGATGAA TCCTATCAAG AAAATTATCT CTATTCTAAG	180
CGTTTGAGAG AATTAGAGGG GCGTTTGGA GGCCTTCTT TAGAAAAAG CGCTAAAGAG	240
GACAGCTCAT TAAAAACGAC TCTTTCGCAC CTTTATAACC AGTTGCAAGA AATCCAAAAA	300
TCCATGGATA AAGAGCGCGA TTAAGTAGAA GAAAAATCA TTACT	345

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

GAAAGGAAAA AAATGAACAC TAATTTAAAG AAAGCCTTGT TTTTAACTAC TCTTGTTAT	60
TTGCAAGCTA ATGAGGGCTT TTTAGCCATT ATGCCTGATG AAAATAAACA AGAAGACATT	120
TCTCAAGAAC AGAAATTAGA ACACAAAATG GAGCAAAAAA TTGCTCCACA AAATACCCCTT	180
AAAAAGCAAC AATCAGCTCC TTTACAAAGT GCTGAGTTGT TACAAAGTCA AGTTAAAAGA	240
GAAGTTAAAG AGCAAAAAAA GTCTCAAAA CACCTAGTAG CTATGCAAAAC TAAAAATGGC	300
TTTTTCTTAG GCTCAGAAAT TGCTATTACA GGCACAAGTT TAAACAAAAG TTTAAGCCTT	360
ATTTCTAATG CTACAGATGA TTTACTCACT TATAGCAAGA CTTCTAAAAA CGCTAATTTT	420
AATATGGGAC TATTAATAGG TTATCAGCAT TATTTTGGAG CTAGTAAAG GCATGGGATT	480
AAAATCTCAA GCCATTTGTA TGGAGGCACA CCTAGTGATG TAAGCACAGA CATAAAAATT	540
TACAAATCTA AAGTTAGCAC CAATTACACG CCTTTAAATT TTGGCATAGA TGTGAAGTAT	600
TTGTTTGATT TTTTAAATGT CATTAAAAAG AACCGCCATA CACTAGGATT AAGTGTGGGC	660
TTTGGCTGGC GTATGCAATA TTATTTTGCA AAAATAGACC CCATAAAAC CAGCCATAGT	720
GAGTTTATCA CTAATAAACC TAAAGATATT TTTAATCATG GTTTTATCC CACTATTGGA	780
CTACATTATT ACTTAAACCA TCATCAATTT GAAGTGAATT ATCGCTTTGG AGGAGCAATT	840
AACTATCAGT CAGTTGTGCC TAGCAAAATT GTCGTTCAA ACGGAATTT TAAGGGCGAG	900
GTCTTGTTTT CTAATTTTCT TACCAAAGCG ACTAATTCTA GCTACATAGC GTTCAACTAC	960
GCTTATTTAT TT	972

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...411
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

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GCTAACGAAA AAATGGAGTT AATTAAGAAA TTGGAAAAAG AAAGCGAAGT TTAAAGAAA      60
GATTTACAAC AACATTCAAA CGAGCTTTTT AAAATGTTGA TTATTGATAA TGAAGATTG      120
TTAAAGAGC AATTTGAGAT TATGTTTAAA GCATGGGTTG AAATCGTAAA AATGATGTTT      180
GAATTAACCA AAAAAACCA ATTTGATGGC GAAATGATTG GCTACACAGA AGAACTTTTA      240
ACCTTTTGTAG TTAGAGATTT TTTTAATGGG ATTTTAAAT CCAAAGTAAT ACCTAAATG      300
CCTATTTTTT GCGGTGATGT TAAATGCGAA GATTTTAATG CCCTAAGAAG TTTAGTTTAT      360
CTTCTGTGC TTGAGTTGGA AGAAACGATA AATCCTAATA AAATCCCATT T              411

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(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 681 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...681
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

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AATAAGGAAA ATAACATAAC CATTTGCGTT GCTAATGAAA AGGGTGGCAG TGGTAAAAGC      60
ACGCTTTGTT TAACTTAGC CGTGCAATTA CTCAAAGACA ATAAAGAAGT GGTGTTTTA      120
GATACAGATA GCCAAAAGTC TATGGAAACT TTTGCTACAA TTCGTGCTGA AAAAGAACGC      180
CCCACTTTTA GCTTATTTAA TCGTAGTAGT GGCTTTAGCG ATACTTTAA GCAAATGGTA      240
TCTAAGTATG AAAATATCCT TATTGATACT AAGGGGGAAT ACAGCAAAGA AACCCAAAAA      300

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GCTATGCTTT TAAGTAATAT TGTGCTAGTG CCAACAACCTC CTAGCCAATT AGACACTGAA	360
GTCTTAGCTA ATATGCTAGA AAGAATTGAG CAACTCCAAG AGCTTAATGA AAATCTAAGA	420
GCCTTAATTG TCATCAATAG AATGCCTACT ATTCTACCC TTAAAGAAAG ACAAGCCTTA	480
ATAGAGTTTA TTAAAGAAAA TAACCCTAGC GATAGGATTA CACTTTTAGA AAGCTCTTTG	540
AGTGAGCGCA TTGTTTATAA GCGCAGTGTA AGCGAAGGCT TAGGGGTCAT AGAATACAGC	600
GATAAAAAGG CTATCAATGA GTGGGTAAAT TTTTATAACG AATTAAAAAG CCATTTAGAA	660
AAAGAGAAAA TACATGCGTT T	681

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

CGTTCAACTA CGCTTATTTA TTTTAATTTT AAGGAGCCAA TGATGTCAGA TGAAATCACG	60
CAAGAAAACG AGTTAGAAAT TAACTCCAAT AATCAAAACC AAGAGCCAAA GGAAGTAGAA	120
AAAATGCCAT TGAATAATAT TCAAAAAGCT AAGAAATTAA AAAACCACGC CAATTTAATT	180
GTTCGACGCA CTGATGAGTT AGATAAGGTT ATCAATAAGC GTGAAAGCTT GCAAAGAGAG	240
TTTAAAGAC GCATTAAGCA CTTGGATAAC AAGATTGAAA CGCTTAGTAA CAATATTGAA	300
GAATTAAAAA GAAAG	315

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TCTATGAAAA	AATATCAAAA	CAAACGAAAG	CTGGGTAAGC	GTATCAATTG	CTTTATTTCA	60
AATGAATGTA	AGGACATTTT	AGAAAATTAT	TTAAAAGTCA	AAAAAATTAG	CGTTACTGAG	120
TGTATAGAAA	GCCTTTTATT	AGCCCTAGAC	CCTAGCAAAG	AAACACTAAG	AGCAAGGGAT	180
TTTTATGAAA	GTTTGTTTAA	AGTCATCAGT	CTTAACCAAC	ATGTCTATAA	AGAACTCATG	240
GCTAATGGTA	ATAACATTAA	CCAAATAGCC	AAGAACACCA	ACATTGCCAT	TAAGTATAAC	300
AAGCCCTTTT	ATTTGCAGAA	TTTAGCATTG	TTAGAAGAGA	TTTTTAAGGT	TATGGATACA	360
CTTAATAAAA	ATGTAGAAGA	ATGTAAAAAA	ATCTCTTTGG	AATTATTACT	TCAAATTTAC	420
AAAGAACAAA	AAAGCCAAAC	AGAATTTAAC	GCCATTTCAA	AAATTCTCAA	CGCTCTTAAT	480
GAAAAACAAT	CTACTACTGA	GCCAAAAAAG	GACAACGCA			519

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

AAATCACCTT	ATCGCCATAG	TATATCTTCA	CAGGTTTCTG	TAGAAAACGA	TGAGGAAATT	60
ATTGAAGTTG	AAAAGGGCGA	AAATCAAGGG	GCGTTTTCTT	ACTTTTTTAGG	CGGCCCCACT	120
TGTTTGCGCG	GGGATTTTAT	GGGGAGTTTT	AGCTTTGAAA	CGCCTTTAAA	AAGGGGCGAT	180
AAAATCGTGT	TTCAAGACAT	GCTCCATTAT	ACGATCGTGA	AAAACAACCTC	GTTTAATGGC	240
GTGCCACTGC	CAAGCCTGGC	TAAAATAGAT	TCGCAAGGTT	TTAAGATCCT	CAAAAGCTTT	300
TCTTATGAAG	ATTATAAAAA	CAGGAAT				327

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

252

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GCTTTAGAGA AGAATGGGAC TGCTACTGCT AATAGCACTA GTAGCACTAG CGGTGCGACT	60
GGTTCAGATG GTCAAACCTTA CTCTCAACAA GCTATTCAAT ACCTTCAAGG CCAACAAAAT	120
ATCTTAAATA ACGCAGCGAA CTTGCTCAAG CAAGATGAAT TGCTCCTAGA AGCTTTCAAC	180
TCTGCCGTAG CTGCTAACAT TGGGAATAAG GAATTCAATT CAGCCGCTTT TACAGGTTTG	240
GTGCAAGGCA TTATTGATCA ATCTCAATTG GTTTATAACG AGCTCACTAA AAACACCATT	300
AGCGGGAGCG CGGTTAATAA CGCTGGGATA AACTCCAACC AAGCTAACGC GTGCAAGGGC	360
GTGCTAGTTA GCTCCCTAAC GCTCTTTACA ACGTGCAAG	399

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CTTATAAAAG AAGCGATGAT TCCAGTTTTT GGGAGTGAAA CAGGGATTTA TAACCATAAG	60
GAGCAAAATT TTAAAGGCAA GGGCCGTTTC ATTCTCACTT CAAAGGACAG CAAGGTTGAA	120
GGGCTTGACA TTTCTTATTC GCATGCATTA GCTATTATTG AAGCTCAAAG CATTCAGCC	180
AATTTGTTTT TAGATGAAAT CAAACAAAGC CAGAAAGAAA AGAAAAAATT CCCCACTTTC	240
AAAGGAGGGT TT	252

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

. 253 .

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CCCTTTCTAA	AAAAGAATAA	ATTTTTACAA	ATTTGTCAAT	ATTTTAGCGC	GCATTTCAAG	60
CAAGTGTTAA	AAAATGAAAA	GCCCTTAGTT	TATTATGGGG	TTTTAAAGGC	TAAAGCCCCT	120
AATTGGGCTT	TATGGGTTTA	TGAAAAACCC	TTAAAAAAG	AAATTTACAT	GAACGATAAG	180
GAAGTGGTGG	TTTATGAGCC	TAATTTATTC	CAAGCGACTA	TCACGCCCTT	AAAAGACAAG	240
ACGGATTTTT	TCACCATCT	CAAGCAATTG	AAAAAGCAGA	CTGACGGCTC	TTTTAAAACG	300
ACTATCAACA	AGACCACTTA	TCGTTTGGTT	TTTAAAGACG	GCAAGCCTTT	TTCGTTGGAA	360
TTTAAAGATG	ACATGAATAA	TCTTGTTACG	ATCACTTTTT	CTCAAGCAGA	AATCAACCCT	420
AAAATTCCTA	ATGAAATCTT	TGTTTTTAAC	CCTAAAGATG	AAAATATTGA	TATTGTACGC	480
CAG						483

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

CCTAGCTTTT	TGAAAGAAAA	ATTTGATTTT	TTTAAAGGCA	AAAATTTTAA	AATTGTCTAT	60
TGTATTGGCG	AAGATTTAAC	GACCAGAGAA	AAGGGTTTTA	GGGCTGTAAA	GGAATTTTAA	120
AGCGAGCAAT	TAGAAAATAT	TGATCTTAAT	TATTCCAATT	TAATTGTGGC	TTATGAGCCT	180
ATTTGGGCGA	TTGGCACTAA	AAAAGCGCGC	TTT			213

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...465
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

CGCGATGTTA GATTCCATGT TAGGGACCTA GTTCGGCAAC TCAAGGGCAA GCATTTGATT	60
GAAGTTTCAG ATGTGATTAA CGACACCACT CAGCCCAATT TGGACATGAA TCTTTTGACG	120
ACCGAAATCG CGCGGCAGTT GCGATTGCGA TCTAATGGGA GGTTC AATAT CACAAGGGCG	180
AGTGGAGGGA GTGGTATTGA AGCAGACAGC AGAATGGTGA AACAGCGCGA AAAAGAACGA	240
GAGAGCGAAG AGTATAATCA AGACACCACT GTAGAAAAAG GCACTTTAAA AGCCGCTGAT	300
TTATCTTTAA GTGGTAAAGT ATCCAGTATC GCAGCCTCTA TTAGTAGTTC TAGGCAACGC	360
TTAGACTACG ACTTCACCCT AAGCCTTACC AATAGGAAAA CGGGTGAAGA GGTATGGAGC	420
GATGTTAAGC CTATTGTGAA AAATGCTAGC AATAAGCGTA TGTTT	465

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 657 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...657
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

ATTAAATCTG TTTTAGGTTT AATTTTGATC CAACAAAATT TTAAACACT TAAGGAGTTG	60
TATATGTTAG TTACAAACT TGCCCCGAT TTTAAAGCGC CTGCCGTTT AGGAAACAAT	120
GAGGTTGATG AACACTTTGA GCTTCTAAA AATTTAGGCA AAAATGGTGT GATCCTTTTC	180
TTTTGGCCAA AAGATTTTAC TTTTGTATGC CCTACAGAAA TCATTGCGTT TGACAAAAGA	240
GTGAAAGACT TCCACGAAAA AGGCTTTAAT GTGATTGGCG TGTCTATTGA CAGCGAACAA	300
GTGCATTTTC CATGGAAAA CACCCCTGTG GAAAAAGGCG GTATCGGTCA AGTGTCTTTC	360
CCTATGGTGG CTGATATCAC TAAGAGCATT TCTAGAGACT ATGATGTGCT GTTTGAAGAA	420
CGCATCGCTT TGAGAGGTGC TTTTGTGATT GATAAAAACA TGAAAGTAAG ACACGCAGTG	480

ATCAATGACT TGCCATTAGG TAGGAATGCA GATGAAATGC TTCGCATGGT AGACGCTCTC	540
TTACACTTTG AAGAACATGG TGAAGTATGC CCAGCAGGTT GGAGAAAAGG CGATAAAGGC	600
ATGAAAGCAA CTCACCAAGG CGTTGCAGAG TATCTTAAAG AAAATTCCAT TAAGCTT	657

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GGAGTAATAA TGGAACACCA TAAAGCGCAC ACAACCATTC AGGCTTTACA AGCCAAACGC	60
AAAAGGTTGC TAACCGAATT AGCCGAGTTA GAAGCAGAAA TAAAGGTGAG CAGCGAACGA	120
AGGAGCAGTT TTAACGTTTC GCTCTCGCCG AGTTTGTTAG CCGAAATAGA AGAGATAGAA	180
TACGAAGAAA AAATGAGCAA AGAGCGAAGA ATCCATCACA ATCTTTTGCT TTCGCCCAGT	240
TTCATGGCTA AAGTGGATGA ATACATGAAA GAGAAAGGTT TTCCTAATCG ATCGCTTCTC	300
TTTGAAAAAG CGTTGGAGTT TTATATGCTA AAACACCCA	339

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 561 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

GGTTTTGTTT	GCGGTAGCGT	TTTATTTCAA	TTAGGAGTTT	TTATGGGGTT	AAAGAATAAA	60
ATCAAGGGTT	TTGTTAAAGA	GAGAATGCCT	TTTGTAATGA	GATGCGTTCG	TGGTTTAAAA	120
GGGGCCAAAG	ACACCCATGA	AAACGCCCAT	GATAGGGACG	CTTATTGTGG	AATCAATCGT	180
GAAATTAAGG	AAATGCTAGA	GGCTAAAAAA	CTTCATTTTC	TTCAAGAAAA	AGCTTTATTC	240
AACCACGACC	ATCAAGAAAG	CGTGTTTTTA	GCTATCGCCT	CTTTAAATAA	TGAAAGTTTC	300
ATTGAATACA	ACAAGAGTAT	TTATAAAAAT	AGTTCTCTTA	ATTATAATTA	TGGGGGGCAT	360
TTAGAAGATA	GGGTCATCCA	TCCCACTTTA	ACTTTACCCA	ATCCCACGCA	TTCGGGTTAT	420
TTTGACTATG	ATAAAAAAAG	TCAAACCCT	AAAAGCCCTC	TAAACCCATG	GGCTTTTATT	480
AGAGTCAAAA	ACGAAATCGT	TACTTTAGAA	GAGAGTTTGT	TTTCTATGCT	TCCTGCCGTT	540
CAAAGGGGGG	GTCATTGGTT	T				561

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

AAGAGAGTTT	GTTTTCTATG	CTTCCTGCCG	TTCAAAGGGG	GGGTCATTGG	TTTTAATGAT	60
TGCGATGATG	GCTCTAAAGA	AGTGGTTTTA	GAGTTTTGCA	AAAAGTTCCC	CTCATTTATC	120
CCTATCAGCT	ATCCTTATGA	AGTCATACTA	AAGGATTGTC	CGAGTTTGTG	GCACCAACTC	180
TATCATTA	CTGTAATTATAC	GCTTTCTTTT	ATCCCTAAAA	ATGAGTGGGT	AGTAAAAATT	240
GATTGCGATC	ATATCTATGA	CGCTAAAAAG	CTTTATAAAA	GTTTTTATAT	TCCTAAGAAT	300
ATTAAAGAGG	TTGTGATGTA	TTCGCGCATT	AATTTTGTGG	TGCGAGATTT	TGAAGTGTTC	360
GTTTCGTAACG	ATGGGGATTT	TGGGTTTTTA	GACGCATGGG	GGGATCATTG	GTTATTGTAT	420
AACGATTGCG	AGCCTTTTGA	AATTTGGCGC	TACAATGATG	AAAGTTATGA	AGTCCTAAAG	480
CTTAAAGATA	AACACCATAT	TAAAGATAAG	GAAATGGTGC	AATGGCACTT	CCCTTTGGCT	540
AAAAAGAGGC	GAAACGCTAT	TGTTTATGAC	GATTTGATCC	CTTTAGAAGA	ATTCAAAAAA	600
CGCCATGCCG	ATTTGATAGG	CACAAGGATT	GAAGAAAGCA	TGCTAGATGA	AAAGAGGATT	660
TTAGAGGTAT	ATCAAAAATT	CCGCTTGCCT				690

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

CTAAGTTTAA ATAAAAAAT GATGTTTGAA TTAACCAAAA AAACCAAATT TGATGGCGAA	60
ATGATTGGCT ACACAGAAGA ACTTTTAACC TTTTGTAGTA GAGATTTTTT TAATGGGATT	120
TTTAAATCCA AAGTAATACC TAAAATGCCT ATTTTTTGCG GTGATGTAA ATGCGAAGAT	180
TTTAATGCCC TAAGAAGTTT AGTTTATCTT TCTGTGCTTG AGTTGGAAGA AACGATAAAT	240
CCTAATAAAA TCCCATTT	258

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 492 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

TTTTCAAGAA AGACAGACAA AAACGCTCAA AAAGACGAGC AAAAAAATGA ACAAGAAGAA	60
CAAAGGCGTT TAAGAGAGCA ACAACGCTTG AAACAAAACC AAGAAAACCA AGAGATGTTG	120
AAAGGTTTGC AACAAAATTT GAATCAATTC ACGCAAAAAT TAGAAAGCGT TAAAAACAAG	180
ACTTTAGATT TGCAAAATCCC TAAACAAGAT GGGGTTGATG AAAAGGCTTA TCAAGAGTGG	240
TACGCTCAAA TCTATCAAAT TTTATATAAA GGCTGGAGGG GCGTTTTTTA TCACAAGGCT	300
TCAGTGAGCG TGCTGATTAT GATCACTAAA GATGGAGAGT TTGATTATAC CATTCTTAGC	360
TACTCTGATT TTAAGGATTA TAACAAGAGC GTGATGACCC TTTTAGATGA TTTAAAGAAA	420
GTGGATTTC CCCCATATCC TGGAGGAAAC ATGATTCTA TTAAAGTTAA TTTTACGACT	480
AAGGAAGAAC AA	492

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

AGAGCGCGAT TACTTAGAAG AAAAAATCAT TACTTAGAAA ACAAATTTAA AGACATGGGG	60
CATTATGCCG CTAGCGATGA AGTCAACGAA AAACAGGTTT TGAATATGTA TCAAGAAGGC	120
TATAGCGTGG ATTCTATTTC TAAAGAATTT AAAGTGAGTA AGGGCGAGGT GGAATTTATA	180
TTGAACATGG CAGGGTTAAA ATGG	204

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ACGAAATTGG ATACAATCAG CTTAAAAAGG ATACAAATGG AAAAAATTACC TAAAAAACGA	60
GTTTCTAAAA CCAAATCACA AAAACTTATC CATAGCCTAA CCACCCAAAA AAACAGAGCC	120
TTTCTCAAAA AAATCAGCGC TAATGAAATG CTTTTAGAGT TAGAAAAAGG GGCGTTTAAA	180
AAAAATGAAG CCTATTTTAT TTCTGATGAA GAAGATAAAA ATTACGTTTT AGTGCCGGAC	240
AATGTGATCT CTCTTTTGGC AGAAAACGCC AGAAAGGCTT TTGAAGCCAG G	291

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

AGGAGTATTA	AAATGAAACA	AAGTTTGCGC	GAACAAAAAT	TATTGAAAAT	TTTGGAAAAT	60
GATGTCTTGA	CGATTTTGGA	TAGTTTTTCT	AATTACCTTT	TTGAACTGAG	AGAAGAATTG	120
GACTTCATAG	AAGAAGAAAT	GGAAGGTGAA	ATCACTGAAC	AAAACCTTAC	CGCTCTTTAT	180
GATTTTTCTA	ATTTCTTAGA	AGACCATGTC	AATGTGTTTT	ATGAGAATGT	TTTGAATATA	240
GATGATGTCA	AAACAGAACA	CCTTTATTCA	GGTCTCATAG	ATAGTCTTAA	CGCTAATCTT	300
CACTTTGTCA	AGTCATTTCT	CAGTAATCAG	GATTTAGACT	TCCGCTTTTT	TAAAGAAATA	360
AACGATGGGC	AAGATCCCCA	AAAAACATTA	TCAAGATTGA	TTCCTCTTCA	AAGTGGGAAG	420
AATGATGCAA	GCTCGTTTAA	AGCCAATAAT	TCTTTTGTTT	CATTAGTTTA	TGTTTATGCT	480
TACTTCATGC	TAGAAACTAT	CAGGCAGTCG	TATAGGATTC	TCAGATTACT	AGAAAAACCT	540
ATCAATAACA	ACATAAGCGA	GGACATGCAG	AGCGATATAG	AGAATTTTTT	TGTTCAAGCA	600
AATTTTTTAG	AATACTATGT	TCAGAACAAA	ATATACCCAA	CCAATCATGC	CTATGACTTC	660
ACGCATTTGA	TCATGGACTC	CATTATTCCCT	AATTGGATTC	AGATTGATAT	GAGCGTTGAA	720
GCTAAAAAGA	AAGAGCTTTT	TGAAAAATAT	TTTCAAAACA	TTGATGAAGT	AACAAACAAA	780
ATGCTCGCTC	AAGAAAATCA	AAACAAAAAC	AGCGAT			816

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 687 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GTGAAAGGCG	AGAAAAACGC	TTGGTATCTG	GGGATTAGCT	ATCAAGTCGG	TCAGGCTTCA	60
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CAAAGTGTTA	AAAACCCCCC	CAAAGTAGT	GAATTTAACT	ATCCTAAGTT	CCCTGTGGGT	120
AAAACCGACT	ATCTGGCCGT	TATGCAAGGC	TTAGGGCTTA	CTGTGGGTTA	TAAGCAGTTT	180
TTCGGGGAGA	AAAGATGGTT	TGGTGC GCGC	TATTACGGCT	TTATGGATTA	TGGGCATGCC	240
GTGTTTGGAG	CGAACGCTTT	GACATCAGAT	AATGGTGGGG	TGTGCAAACT	CAATGAGCCA	300
TGCGCGACCA	AAGTAGGGAC	TATGGGCAAT	CTGTCTGACA	TGTTCACTTA	TGGTGTGGGT	360
ATTGACACTT	TATACAATGT	CATTAATAAG	GAAGACGCGA	GTTTTGGTTT	CTTTTTTGGG	420
GCTCAAATCG	CGGGTAACTC	TTGGGGTAAT	ACGACAGGGG	CCTTTTTTGA	AACTAAAAGC	480
CCTTATAAGC	ACACCTCCTA	TAGCCTTGAT	CCGGCGATTT	TCCAGTTCCT	TTTAAATTTA	540
GGGATTCGCA	CCCATATTGG	TCAGCATCAA	GAATTTGACT	TTGGCGTGAA	GATTCCTACT	600
ATCAATGTTT	ATTATTTTAA	CCATGGGAAC	TTGAGCTTCA	CTTACCGCCG	TCAATACAGC	660
CTTTATGTAG	GGTATCGTTA	CAATTTT				687

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

AGCGCTGTAG	TGGAGAGCGT	GGTTATTTTA	AAGATTGACA	TCAATCAGGG	GCGTTCTTGC	60
TCGCTCTACC	CCACGCCTAA	AAGCGTTTCT	TTAGTGAGGA	ATCAAAGCGT	AGCCTATGAA	120
ATTTTATGCG	AAAACCAGCC	GCTATGGATA	GAAGTTAGCA	CCAATTTAGG	GCAAACGCTA	180
CCTTTCAGTT	TAATT					195

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

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CGCTTTAAAC ACTTTAGGGG TGGGGGTTTT CCCCAACCACA ACCTCAACGC ATGTGGTGCT      60
AAACCCACCG GACAAGTCGT ATTCTATCCA ACTAATTCCC TTTTAGGCTC TACTTCTTCA      120
AACAGCAATA ACCAACAACA ATACAACAAC ACCCTTTTAA TGAACACCTT ACAAGGGGAA      180
TTAAGCACTA ACAATCAAAA TAACCCCAAT GGTTCGCCA ATCAAATCCA GTGTTTAGAG      240
CAATTCATCC AAAATTTAAC CCCTTTAGCC GCAACCCCCA CTTCAACTAA CCAGGCCAAC      300
CAGCAAGTCC AAGCCATCGC TCAAAAACCT CAAAGCGTTG CTATCAACGC TTTAGACAAC      360
AATGCGATCA ACAACACCAC CTATAATTTA AACAACCTTG ACAACGCTTT GAATTTCCAA      420
GCCTATCAAA GCACGATAGA ACAATACAAT AACGCTTTAA AGCAAATTTT GTGGATTAGT      480
TTTAGCGAGC CTAAAACTT GCTCAAAAAC ACTTCCAATA ACTACCAAAT CGGCACGGTT      540
ACCAACGATC AAGGGCAAAA TATCAGCGCC TATGATTGCA CAAGCGCTAC CGGAAGCCTT      600
TCTAGCGATG CTTCTAGTGG GATTTCATGC TCAGCCACAA GCTCCACAAG CAACACAAAT      660
AGTTTTGACA ATTCTTTAGT CGCTACCTCC AAAGTCCAAA CCATCAACGG CAAAGAGCAG      720
ATCGGCGTGA ATTCTTTTAA TCTTGTCTCT CAAGTGTTGA GCGTTTATAA CTCTTTAAAA      780
ACTTCAGAAG AAAATTTGCA AAAAAACGCC AAAATATTAT GCAACAATGG ATCGCAATCT      840
GGGACAAGCC CATGCAATAG CTCTTCAGGG GGTTCGAGCA TCAGCGGGAA CGCCCAATTG      900
CAAAATATTT TAAGCCCTAC TAATGGGACT ACCACTAATA CTCAAGCTAA AAGCAACGCT      960
TCCAAACTAA AAGCGATGGT AATGGTGAAT AATGAAGAAG AAGCCAAAAC GACCAATTTT      1020
AATCAAAGCA GTGGGCCAAC CACACAATCT TCTAACAGCA CGGTGATGGG AGCTTTAAAC      1080
ACCGTATTGC AAAAT                                     1095

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(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

```

AACCCATTCT TCACAATCAC AGCCAAACTC CTTTCCAACA CCCAAAGCGC GTTTGATCAG      60
GGCATCGCTC TAAGCTCTAA TATCATTAGT GCAGTCAATA GCCTAAACCC TAGCAACAAC      120
TCCCAAGAAG TCAAAGCCCA GCTCCAAAAC ACCGCGCAAT CCATGACAGA ATTGTTGCAA      180
CAAATTGAAC ACAGCATCAC TAAAACTACT AGCACCCTT ACGCACAATC CTTACTCTCC      240
AATCTGACCG ATGCGGTGAA TGCATCTAGC AATAATACCA CTTATGTGAG CGCTCTTGTT      300
AACGCTTTAA ACACCTTAGG GGTGGGGGTT TTCCCCACCA CAACCTCAAC GCATGTGGTG      360
CTAAACCCAC CGGACAAGTC GTATTCTATC CAACTAATTC CCTTT                                     405

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(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GGAAGAGGAA TGAAATTAAA AAAACGAAAA GTTGC GGCTA CATTGCTAAA GCGTTTGACC	60
TTGCCACTAT TGTTCACTAC GGGTTCATTA GGGGCGGTTA CTTATGAAGT GCATGGGGAT	120
TTTATCAACT TCTCCAAAGT GGGTTTAAAC CGTTCGCCTA TTAACCCTGT TAAAGGTATC	180
TATCCTACAG AAACCTTTGT TAACCTTACG GGTAAGCTAG AGGGGTCTGT GCATTTAGGT	240
AGGGGATGGA CCGTGAATGT AGGCGGTGTT TTG	273

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ATGGAGCAGC CAGTCATTAA AGAAGGGACT TTAGCTTTAA TTGATACCTT TGC GTATTTG	60
TTTAGAAGCT ATTACATGAG CGCTAAAAAT AAGCCTTTAA CCAACGATAA GGGCTTTCCT	120
ACAGGGCTTT TAACGGGGCT TGTGGGCATG GTTAAAAAAT TTTATAAAGA CAGAAAAAAC	180
ATGCCTTTTA TCGTGTTCGC CCTAGAAAGC CAGACTAAAA CTAAAAGAGC TGAAAAACTG	240
GGCGAATACA AACAAAATCG TAAAGACGCC CCTAAAGAGA TGCTTTTACA AATCCCTATC	300

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GCCTTAGAAT GGTGCAAAA AATGGGTTTT ACTTGCGTGG AGGTGGGAGG GTTTGAAGCC 360
GATGATGTGA TCGCAAGTTT AGCCACGCTA AGCCCTTATA AAACCCGCAT TTATTCTAAA 420
GATAAGGATT TTAACCAGCT TTTGAGCGAT AAAATCGCGC TTTTGTATGG CAAAACGGAG 480
TTTTTGGCGA AAGATTGCGT GGAAAAATAC GGGATTTTGC CGAGTCAATT CACGGATTAT 540
CAGGGCATTG TGGGGGATAG CAGCGATAAT TACAAGGGGG TTAAAGGCAT TGGGAGCAAG 600
AACGCTAAGG AATTGTTGCA GCGATTAGGG AGCTTGGAAG AAATCTATGA AAATTTAGAC 660
TTGGCGAAAA ATTTACTCAG CCCTAAAATG TATCAAGCCT TGATACAAGA CAAAGGAAGC 720
GCCTTTTTTAA GCAAAGAATT AGCCACTTTA GAAAGAGGAT GCATTAAAGA ATTTGATTTT 780
TTAAGTTGCG CTTTTCAGAG CGAAAACCCC TTGTTGAAAA TCAAAGATGA ATTGAAAGAA 840
TATGGTTTCA TTTCTACCTT AAGGGATTTA GAAAAATCCC CTTTCATTGT AGAAAACGTG 900
CCCATATTAA ACAGCACGCC TATATTAGAC AATACCCCCG CCTTAGACAA CGCCCCTAAA 960
AAATCGCGCA TGATTGTTTT AGAAAGCGCT GAGCCTTTGA GCATGTTTTT AGAAAAATTA 1020
GAAAACCTTA ACGCTAGGGT TTTTATGCGT TTGGTTTTGG ATAAAGACAA AAAAATTCTA 1080
GCCCTAGCGT TTTTATTACA AGATCAAGGC TATTTTTTAC CTTTAGAAGA GGCGTTGTTT 1140
TCGCCCTTTT CTTTGGGAATT TTTACAAAAC GCTTTTTTCTC AAATGTTACA GCATGCGTGT 1200
ATCATTGGGC ATGATTTAAA GCCTTTATTA AGCTTTTTTAA AAGCCAAATA TCAGGTGCCT 1260
TTGGAAAATA TCCGCATCCA AGACACTCAG ATTTTAGCGT TTTTAAAGAA TCCGGAAAAA 1320
GTGGGGTTTG ATGAGGTTTT AAAGGAATAT TTTAAAGAAG ATTTAATCCC GCATGAAAAG 1380
ATCAAAGATT TTAAGACAAA AAGTAAGGCG GAAAAATCAG AACTTTTAAG CATGGAATTA 1440
AACGCCTTAA AGCGTTTGTG CGAATACTTT GAAAAAGGGG GGCTAGAAGA GGATTGCTC 1500
ACTTTAGCTA GAGACATTGA AACGCCGTTT GTGAAAGTTT TAATGGGCAT GGAATTTCAA 1560
GGCTTTAAGA TTGATGCCGC CTTGAAAAT ATCGTCATCG CAGGTGTTAC AAACAAACCC 1620
AATGGTGCTG GCGCTATCAC ATCCACTGGT CATGTAACCG ACTATGCGGT GTTTAACAAC 1680
ATCAAGGCGA TGCTACCTAT CTTGCAACAA GCGCTTACGC TTTCTCAAAG TAACCACACC 1740
CTATCCACTC AGTTGCAAGC TCGAGCTATG GGATCTCAA CAAATCGTGA ATTCGCTAAA 1800
GACATCTACG CTTTAGCTCA AAACCAAAAG CAAATCCTTT CTAACGCTTC AAGTATCTTC 1860
AATCTCTTTA ATTCCATTCC TAAAGACCAA CTTAAGTATT TGGAGAACGC TTACTTGAAA 1920
GTGCCACATT TGGGTAAAAC CCCTACTAAC CTTACAGAC AGAATGTGAA TTTGAATAAA 1980
GAAATTAATG CGGTTCAAGA CAATGTAGCT AATTATGGTA ATCGTTTGA TTCGGCTTTA 2040
AGCGTGGCTA AAGATGTTTA TAACCTAAAA TCCAATCAAA CAGAGATCGT AACCATTAT 2100
AACGATGCTA AGAATTTGGG CCCAGGGGTT TCTAACTTC CCTGTCGTTG TTTGGAGAAG 2160
ATT

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(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic).

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

ACTTCCCTGT CGTTGTTTGG AGAAGATTTA GCCAAAGAAA AACGATCCAT CGCTAAAAGC

ATTAATTTTG	GGCTGGTGTA	TGGCATGGGG	AGTAAGAAAT	TGAGCGAAAC	TTTAAGCATC	120
CCTTTAAGTG	AGGCTAAAAG	TTACATAGAA	GCGTATTTC	AGCGATTCCC	TAGCATTAAG	180
GATTATTTGA	ATGGCATGCG	AGAAGAGATT	TTAAAAACTT	CTAAAGCT		228

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

AAAGAAAAGG	ATAACCCCTT	GCAAAACTTT	GTTTTTAATA	AAAAATGGCT	CATCTATTCT	60
AGCCTACTCC	CCTTATTTTT	TCTTAACCCCT	TTAATGGCAG	AAGACGATGG	GTTTTTTATG	120
GGGGTGAGTT	ATCAAACCTC	TTTGGCCGTT	CAAAGGGTGG	ATAACTCAGG	GCTTAACGCC	180
AGTCAAGACG	CATCCACTTA	TATCCGCCAA	AACGCTATCG	CTCTAGAATC	TGCGGCGGTG	240
CCTTTAGCCT	ATTATTTAGA	AGCGATGGGC	CAACAAACGA	GAGTCTTAAT	GCAAATGCTC	300
TGCCCTGATC	CTTCTAAAAG	ATGTTTGCTC	TATGCAGGGG	GCTATCAAAA	CGGACAAAAT	360
AATAACGGCG	ATACAGGCAA	CAACCCCCCA	AGAGGCAATG	TCAATGCCAC	CTTTGATATG	420
CAATCTCTAG	TCAATAATTT	AAACAAGCTC	ACCCAACCTCA	TCGGCGAAAC	TTTAATCCGT	480
AACCCTGAAA	ATCTTCCTAA	CTCCAAAGTC	TTTAACGTCA	AATTTGGCAA	TCAAAGCACT	540
GTTATTGCAT	TGCCTGAGGG	TCTAGCCAAT	ACCATGGACG	CTTTAAACAA	TGACATCACC	600
AACGCTTTAA	CCACGCTCTG	GTATAACCAA	ACCTTAAACGA	ATAAATCTTT	TAGCACCCCT	660
AGTAACACTT	CTGTGAATTT	TAGCCCCCAA	GTCTTGCAAC	ACCTTTTACA	AGACGGCTTA	720
GCCACAGCAA	ATAATAATCA	AACCATTTGC	AGCACTCAAA	ACCAATGCAC	CGCCACTAAT	780
GAAGCTAAAT	CTATCGCTCA	AAACGCCCAA	AACATCTTCC	AGGCTTTAAT	GCAAGCAGGG	840
ATTTTAGGGG	GCTTAGCCAA	TGAAAAGCAA	TTTGGCTTCA	CTTACAACAA	AGCCCCCAAT	900
GGCGGCGATT	CCCAACAAGG	CTATTCAAAG	CTTTGCGGCC	CGGGTATTAC	ACCAAAACGA	960
CAACACCACG	CAAGC					975

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

TATAACCAGA	TGCAAGACGT	GATCAATTAC	GGGGAAAGCT	TGCTTAGTAA	CACCGTAGCG	60
TATGGGGATT	TCATCACCAA	TTGGGTCGCC	CCCTATTTGG	ATTTAAACAA	TAAAGGTTTG	120
AATTTCTTGC	CTAATTATGG	GGGGCAATTG	AATGGCGCTA	ATAATCAAAC	CCCACAATTA	180
ACCCACAAAC	AAGCCCAACA	AGAACAAAAA	GTGATCATGA	ACCAATTAGA	GCAAGCCACA	240
AACGCCCCCA	CCCCCGCGCA	AATAAACAGG	ATTTTAGCCA	ACCCCTATTC	CCCCACGGCA	300
AAAACTTTAA	TGGCTTATGG	GCTCTATCGC	TCTAAAGCAG	TGATTGGCGG	AGTGATTGAT	360
GAAATGCAAA	CTAAAGTGAA	TCAAGTCTAT	CAAATGGGCT	TTGCTAGGAA	TTTTTTGGAG	420
CATACACTCT	ACATTCTAAT	AACACTGAAC	GGCTTTGGCG	TGAAAATGGG	CTATAAGCAA	480
TTTTTCGGCA	AAAAGCGCAT	GTTTGGGCTT	AGGTATTATG	GTTTTTATGA	TTTTGGTTAC	540
GCTCAATTTG	GCACAGAATC	TTCTTTAGTG	AAAGCCACCC	TCTCTAGCTA	TGGAGCGGGC	600
ACAGACTTTC	TTTATAATGT	TTTACCCGA	AAAAGAGGGA	CTGAAGCGAT	AGATATAGGT	660
TTTTTTGCCG	GTATCCAAC	TGCAGGGCAA	ACCTGGAAAA	CGAATTTTTT	AGATCAAGTG	720
GATGGCAACC	ATCTTAAACC	TAAGGACACT	TCTTTCCAAT	TCCTTTTTGA	TTTGGGCATA	780
ATGGACCAAA	TTTTTCCAAA	ATCGCTCATC	TCAAAAAGA	ATCTCGTTTT	TCTCAAGGGA	840

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

CAACCACACA	AACAAAGAAA	CATCGCCCAT	CTACAACACG	CGCAAGCTGT	TATCACTTCA	60
GTATTGGCTT	TTTGAGTCT	TTATGCAGGG	AACGCTCTCA	GTTTTCATGT	GACCGGTTTG	120
AATGATGGAT	CTAATTCTCC	TTTAGGAAGA	ATCCATAGAG	ATGGGAACTG	CACAGGATTA	180
CAACAATGTT	TTATGAGCAA	AGAACTTAT	GATAAAATGA	AGACACTTGC	CGAAAACCTC	240
CAAAAAGCTC	AAGGCAATCT	CTGTGCCTTA	TCAGAATGCT	CTAGCAATCA	AGATAGCGGA	300
TTTCTGTGTT	TGGATAGTGC	AGGAAAACAA	GTAATAATAA	CAATAACAAC	GCAAACTAAT	360
GGAGCTAATA	AAAGTGAAAC	TACTACTACT	ACTACTACTA	CTAAT		405

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...372
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

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GGACTATCAA GGCAAGGAAA TGAAAGATTG GATGCCACGC TCAATTTAAA AACCGGCGTG      60
CAAAAGTTTMTT TAAAAAATA CATCGGGATT AGGGGGGTTT TTGCATGGGA TCTTGGGTCA      120
GGAAAAGTGA ATTATCAAAG CTATAAAGAT CCTACCAACT CTTTTTTTAC CATGCTTGCG      180
GTGGGTTTGG ATGTGATCAT GGAATTTCTT CTAGGGAGTT ATAAGCATT TTTAGGGGCG      240
TTTGGGGGAG CTAGGGGGGC TTTAGTTGTT TATACAGACA AGCAAATTT CAAGTTTTTT      300
AAACATTCTG TGGTTTCAGG GGGATTAGCG ATTAGTGGAG GTTGGTTGAT ATTGTTGCGG      360
ACACCGCACT TC                                     372

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(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...309
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

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CCGGTTGGGC TCTACCCCTT TGAATCCCCT TTAATTTATG AAGAAAACCA TTTGTTACCC      60
ATGGGGTTTA TCCATTTAGC CTTTAGAGGG GGTGGGAGCT TGAGCGATAA AAACCAGTTG      120
GGTTTGCGCA AATTGTTTCG GCAAGTTTTA AACGAAGGCA CTAAAGAGCT TGGCGCGGTG      180

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GGGTTTGCGC AACTTTTAGA GCAAAAAGCG ATCAGTTTGA ATGTGGATAC CAGCGCAGAA	240
GATTTGCAAA TCACTTTAGA ATTTTAAAA GAATACGAAG ATGAAGCCAT AATGCGCTTA	300
AAAGAGCTT	309

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

TATAGCGTGT ATATCCGCTC CAACTTTTCT AAAGTGGCGC ATTTTGCGAG CGGGTATTTG	60
CAAACCAAGC TCAGACTCA AGCTAAAAGC GTTGCCTTAG CCAAAAAAAC AACTAAAGAA	120
TTTATAGAAA AAGGCATGAC GCAACAAGAA TTAGACGACG CTAAAAAGTT TTTACTAGGC	180
TCTGAGCCTT TAAGGAATGA AACGATCTCA AGCCGCTTGA ACACCACTTA CAATTATTTT	240
ATTTGGGTTT GCCTTTAG	258

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

AGACGCGCAT GGATTCTGTT GGGTTTGAAG AATCTCAAAG GGGTTGGGT GCTTAAGGGG	60
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TTAAAAAAG	CGTTTAAGGA	GAGGTTTTGC	TCTCAAGTGT	ATATCTCTTT	TAATGTGGAT	120
CACAATCTTT	TATCCGCTCA	AGTTTTAAGG	GTTAAAAACC	ACCGCATCAA	AGAGAAATTT	180
TTTAAACTT	TTGAGACTAA	AGTGGAACCT	AAAAATGGTG	AAGTCCCCAT	TCAAGCCTTA	240
AAAATCGCCA	GAACCTATAG	CCAAAAATAC	CCCTACACCT	ATTTTAGCGC	GATGAGTAAA	300
GCTAAAGAGG	TTTTATGCGA	AAAGCAGGCG	TTTGAACAAA	TCAAACAAGA	AAATCAAGAT	360
TATCAGGCTT	GTGAAGTCAA	TCAAAAGTAT	TGCGTTTATG	TGGAATCTAA	GGATTTTCTA	420
AAGGATTTCA	AGCGTTTTAA	AATCCAGGAT	GTGGATTTTT	TGTTTTCGCC	CTTTAGCCTT	480
ATTTATGATT	TTGTGCGCGA	TAATTTAGAA	AACAAGCCGT	TGTTGTATCT	GCTTTTAGAG	540
CGTTCAAGGT	TTTATTTTTT	GATTGCGGAT	AAAAAAGAGA	TTTTTTTAGC	CAAATCCGTG	600
TTTTTAGAAG	AGCAACCTGA	AGAGTTTATA	GAGAGCAAAG	AAGAAGATTC	TATGGGAATG	660
GATAATGAAG	CTGTGGATTT	GTTTTTGAGT	GAAATCCAAG	AAGATATTGA	CAGCCTTGAA	720
GAAGCGATAG	GCCTAGACAG	CAGCAAGGAT	AATAGCGAAA	AAATAACAGA	GGACGCTTAT	780
AGTTTGATTG	AAGGCATGAC	GAATATCCCC	TTGATTGCAG	ATGTTTTGCA	AGAGGGATTG	840
CGTGGCGTCT	ATCATCTAG	AGAGATAGAC	TTTGTAGAAA	AAGTGGTTGT	TTTAGACAGC	900
TGTCAAATCC	ACCACAAGGC	GTTAATGCAT	TTGCAAGAAA	CTTTGATGAT	AGAAGTGGAT	960
AGGCTCGATT	TTTCTTTAGT	GGAGCGGTTG	AATGTTTTAG	CGCGCATGGA	GAATGAAAAG	1020
CATGCGTTT						1029

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

ATGATTTTTG	GGGATTTTAA	ATATCAAAAA	AGCGTTAAAA	AACTCACAGC	CACTAACCTT	60
AACGAGCTTA	AAAACGCCCT	GGATTTTATC	TCTCAAAATA	GGGGGAAGGG	GTATTTTGTG	120
GGGTATCTTT	TGTATGAAGC	GCGCTTAGCG	TTTTTAGATG	AAAATTTTCA	AAGCCAAACC	180
CCTTTTTTGT	ATTTTGAACA	ATTTTTAGAA	AGAAAAAAT	ACCTTGTAAG	GCATCTAAAA	240
GAGCATGCGT	TTTACCCTAA	AATCCACAGC	TCTTTAGATC	AAAAAACTTA	TTTCAAGCAG	300
TTTAAGGCCG	TTAAAGAGCA	TCTCAAAAAC	GGCGATACCT	ATCAAGTGAA	TTTGACAATG	360
GATTTATTGT	TAAACACTAA	GGCCAAACCA	AAGCGCGTTT	TTAAGGAAGT	GATACACAAC	420
CAAAACACGC	CTTTTAAGGC	TTTTATAGAA	AATGAGTTTG	GGAGCGTTT	AAGCTTTTCG	480
CCGGAATTGT	TTTTTGAATT	AGAGTTTTTA	GACACAGCGA	TTAAGATTAT	CACAAAACCC	540
ATGAAAGGCA	CGATCGCTCG	CTCAACAAC	CCCTTGATAG	ATGAAAAAAA	CCGATTGTTT	600
TTGCAAAATG	ATGACAAAAA	TAGAAGCGAA	AATGTGATGA	TCGTGGATTT	ATTGCGTAAC	660
GATTTGAGCC	GCTTGGCCTT	AAAAAATAGC	GTGAAAGTCA	ATCAATTGTT	TGAAATCATC	720
AGTTTGCCGA	GCGTGTATCA	AATGATAAGC	GAGATTGAAG	CTCAATTGCC	CCTAAAAACA	780
AGCTTGTTTG	AGATTTTTAA	GGCGTTGTTT	CCTTGCGGCT	CTGTGACCGG	ATGCCCTAAA	840
ATCAAAACCA	TGCAAAATCAT	TGAAAGTTTA	GAAAAACGCC	CTAGGGGGGT	GTATTGTGGG	900
GCGATAGGCA	TGGTTGGAGG	AAAAAAAGCC	CTTTTTAGCG	TGCCTATCCG	CACTTTAGAA	960

AAAAGAGCGC	ATGAAGATTT	TTTGCATTTA	GGGGTAGGGA	GTGGGGTAAC	TTATAAAAGT	1020
AAAGCTTCAA	AGGAATATGA	AGAGAGCTTT	TTAAAATCCT	TTTTTGTGAT	GCCCAAATA	1080
GAATTTGAGA	TCGTGGAAAC	GATGAGAGTT	ATCAAAAGGG	ATCAAAATT	AGAGATTAA	1140
AATAAAACG	CCCATAAGA	ACGCTTAATG	CATAGCGCCC	AATATTTTAA	CTTTAATACA	1200
GATGAAAATC	TTTGTAGACTT	TGAATTAGAA	GGAGAAGGGG	TTTAAAGGGT	TTTAATTCAA	1260

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

AAACAAATAA	GAAAAGAACG	CTTGAACAAA	CTGCTTAAAA	AGGGGTTTTT	AGCGTCTTTT	60
TTAAGCGTGT	ATTTAAGGGC	TGATGATCTG	GTTACTTATA	CGATCGCCAA	AGAAGAAGAT	120
CTAGGGTACC	AGCGGTTTTT	AGCCAAGAAG	TGTTTAAGGG	GTAAAACCCA	CCCCCATGT	180
TTTACGCGT	CTAAAAAGCC	CAAGAGGAAA	CCTTTTAATA	TAGATAAAAG	CTCCCATTAT	240
TATGGCACGA	GCGTGGTGCA	AATGTCATGG	CTACAGAGTA	GGGAAAAATT	TGAAAACCAT	300
TCAAAATACC	GAAACATTCC	TTTGTCTGAA	GTCAGTTTGA	TTTATGGCTA	TAAACAATTT	360
TTTCCTAAAA	AAGAGCACTA	CGGCTTCCGT	TTTTATGTCT	CTTTGGATTA	CGCTTATGGC	420
TTTTTTCTTA	AAAATAAAGG	CGCATTAGGC	GATAGTTTGA	GGGCGAGTTC	GCAGATCCCT	480
AAAAGCTATA	GAGAAAAATT	ACAAAGAAAA	GAGACTTTTA	TTAACGCTAT	TTTTTATGGC	540
GTGGGGGCTG	ACTTTTTTATA	CAAACGCGCT	TTTGGGACGC	TGATTTTAGG	GGTGAATTTT	600
GTGGGAGAAA	CCTGGTTTTTA	TGAAACAAAG	ATTTTCAAAC	AATGGGCTAA	AGACTCTCTA	660
AATACTTACC	GCCCCAACAT	GTTTCAAGTG	ATGTTGAATG	TGGGGTATCG	CTACCGCTTT	720
TCAAGGTATA	AGAATTGGGC	GATAGAATTT	GGCGCGCGCA	TCCCCTTTTT	AATTAATGAT	780
TATTTTAAAA	CCCCTTTATA	CACCCTTCAT	TTCAAACGCA	ATATTTCTGT	CTATCTCACT	840
TCAACTTATG	ATTTT					855

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

AATACTCTTT	TTTATTTCTT	TTTATTACAG	GCGGTTATTG	TGTTAGATAG	TTTTGAGATT	60
TTAAAGGCTT	TAAAGAGCTT	GGATTTATTG	AAAAACGCCC	CTGCTTGGTG	GTGGCCTAAC	120
GCTTTGAAAT	TTGAAGCTCT	ACTAGGAGCG	GTTTTAACGC	AAAATACTAA	ATTTGAAGCC	180
GTTTTGAAAT	CTTTAGAAAA	TCTAAAAAAC	GCTTTCATTT	TAGAAAAATGA	TGATGAGATC	240
AATCTTAAAA	AAATCGCTTA	TATAGAGTTT	TCAAAGCTTG	CAGAGTGTGT	CCGCCCTAGC	300
GGGTTTATA	ACCAAAAAGC	CAAACGACTG	ATTGATTTGA	GCAAGAATAT	TTTAAAAGAC	360
TTTCAAAGTT	TTGAAAATTT	TAAACAAGAA	GTAACCAAAG	AGTGGCTTTT	AGACCAAAG	420
GGCATTGGCA	AAGAAAGCGC	GGATGCGATT	TTATGCTATG	TGTGCGCCAA	AGAAGTGATG	480
GTGGTGGATA	AATACAGCTA	TCTTTTTTTA	AAAAAATTAG	GCATAGAGAT	AGAAGATTAT	540
GATGAATTGC	AGCATTTTTT	TGAAAAAGGC	GTTCAAGAGA	ATTTAAATTC	CGCCTTAGCG	600
CTTTATGAAA	ACACCATTTT	TTTAGCGCAA	CTTTATGCGA	GATTCCATGG	AAAGATCGTG	660
GAATTTTCCA	AACAAAAATT	GGAATTGAAG	CTT			693

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 693 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

ATCAGCTTCA	ATGCGGACTA	CTTTAGGATT	TGGGCGCGCG	ATTTTGCCAC	CGGGCAGTAT	60
TCAGTCTATA	CGAGCGGGCC	CATGAAAGGT	AATGTGCGCC	CCATTAATGG	CTATTCTCAA	120
GGCGTGGAGC	TGGAATTGTA	TTACAGGCCC	ATTAGAGGGT	TGCAATTCCA	TGCCGCTTTC	180
AACTACATTG	ACACTCGTGT	AACTAGCCAT	GGCCCTTTAA	CCGACTTGAA	CGGGGATGTG	240
CTAAAAGGGA	CTAGCTATAA	CAAGCATTTT	CCTTTTGTA	GCCCTTTCCA	ATTCATTTTT	300
GACGCTCGCT	ACAATTGGCG	TAAAACCACC	ATTGGTATTT	CTAGCTATTT	TTATAGCCGT	360
GCTTATAGCG	GGATTAGCAA	CAGCGCAGCA	GGAGGCTATT	ATGGGATGCA	ATACTATAGT	420
GGGGGGAACA	ACTATGAAAG	CGTTCCTAAT	AGCGGTTATC	AATGCGAAGC	TTGGTGTATG	480
ACCCAACATG	AAGGGCTCTT	GCCTTGGTAT	TGGGTGTGGA	ATATCCAAGT	GAGCCAAATT	540
TTCTGGGAAA	ACGGAAGACA	CAGAGTTACA	GGAAGCTTAC	AAATCAATAA	CATCTTCAAC	600

ATGAAGTATT ATTTTACAGG GATTGGCTCT AGCCCTGCAG GCTTGCAACC TGCGCCTGGA	660
AGATCGGTTA CAGCGTATTT GAACTACACT TTC	693

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 804 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

AGCGGTGTTG TGAAAATGAA AGACAAAAG ATTGATGAAG AAACGAACGC CGTTTTAGAG	60
GGGGAAAAAT ACACCGTGTG CGTGTCTTGT CAAATCGGCT GTCAAGTGGG TTGCTCGTTT	120
TGTTTCACTC AAAAAGGCGG TTTTGTAAGG GATCTCAAAG CGAGCGAGAT TATCCAGCAA	180
GCCCTACTCA TTAAAGAGGC CAATAACCTC CCCATTGAAA AAGCGCTCAA CATTGTTTTT	240
ATGGGAATGG GCGAGCCTTT GAACAATTTA GATGAGGTGT GTAAAGCGGT TGAGATTTTT	300
AATACCGGCA TGCAAAATTC ACCTAAAAGA GTCACCATTT CCACGAGCGG CGTGGCCGAT	360
AAAATCCCCA TTTTAGCGGG CAAAACCTTA GGCGTGCAAT TAGCCATATC CTTACACGCC	420
GTAGATGATA AAACGCGCTC GTCTTTAATG CCCTTGAATA AAAAATACAA CATTGAATGC	480
GTTTTGAATG AAGTGAGGAA ATGGCCTTTA GAGCAGCGAA AAAGAGTGAT GTTTGAATAC	540
CTTTTAATCA AAGATTTAAA CGATAGCCTG GATTGCGCTA AAAAATTTT AAAACTTTTA	600
AACGGCATT AATCCAAAGT GAATTTGATC TTATTCAACC CGCATGAAG CTCTAAGTTT	660
GAGCGCCCTA GCTTAGAGAG CGCCAGAATG TTTGCGAATT TTTTAAACGC CAAAGGCTTA	720
TTATGCACCA TTAGAGAATC CAAAGCCTTG GATATTGAAG CGGCTTGCGG GCAATTGAGG	780
GAGAAAAAGC TCCAGCAGAA AATT	804

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 708 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

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AGATTGCTCTG AACCCATAGA TAGATTCACA CGCATAAGGT GGTGTTTAA AAACGATTTT      60
GAAAAAATCC  GCCAACAAAG GGTTTTAATC TGTGGCGTGG GGGGCGTTGG AGGCTTTGCA      120
CTAGATTCTT  TGTATCGTGT GGGGATAGGG CAAATCACTA TCATTGATAA AGACATGTTT      180
GATGTTACCA  ATCAAAACCG CCAGATTGGA TCAGAAAGGA TAGGAGAATC TAAAGTGTG      240
GTGTTGCAAG  ATCTCTATAA AGGCATCCAA GCTTTAAATT GTCGCATAGA TGAAGCGTTT      300
TTAAATTCAT  TTAATTTTAG AGATTATGAT TACATTTTAG ATTGCATGGA CGATTTGCCT      360
ATTAAACAA  GCCTAGCGAT AAAATGTCAA AATTTCGCTT ACGGGAAGTT TATCAGCTCT      420
ATGGGGAGCG  CGAAGCGTTT GAATCCTAAA CACATCCAAG TGGGGAGCGT GTGGGAAAGC      480
TATGGCGATA  AATTCGGGCG TAAATTTAGG GATTTTTTAA AAAAACGCCG TTTTAAGGGG      540
GATTTTAAGG  TGGTTTTTAG CCCTGAAGTC CCGCATTGCA TAGAGCTTGG AAGCTTTAAT      600
GCGGTTACGG  CGAGTTTGG TTTGCAAATA GCGAGTGAAG TCGTGCAAGA TATTATCAAA      660
AATGAAAGGC  AATGGAATGA AAGATTACGA AGACGAATTG GAAGATTT      708

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(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

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GCGAAAGCTA GGGTGCAATT CAACCGCGCG AATGAACGCC AACGCAGGGC TAAAGAATTT      60
TATTATGAGG AAGTGCAAAA AGCCATTAAA GAAATCGATT CTAGCAAAAA GCACAATATT      120
AATATGGAAC GCTCTAGGGC AGAAGTGAGC GAGATTTTAA ACAACACCTA TTCTAATTTA      180
GACAAATACG AAGCTTATCA AGGCTTGCTT AACCCGGCGG TTTCTGTATCT TTCAGGGTTG      240
TTTTACGCTT TAAATGGGGA TAAGAATAAG GGATTAGGCT ATCTTAATGA AGCCTATGGG      300
ATCAGTCAAA GCCCTTTCGT GGCTCAAGAC TTGGTTTTTT TCAAAAACCC TAACAGGAGC      360
CATTTCACTT GGATCATCAT TGAAGATGGT AAAGAGCCGC AAAAAAGCGA ATTTAAAATT      420
GATGTGCCTA TTTTATGAT TGATTGGTT TATAACGTGA GCGTGGCCTT GCCCAAGCTA      480
GAAAAAGGGG AAGCGTTTTA TCAAAATTT ACCCTCAAGG ACGGAGAAAA AGTAACACCC      540
TTTGACACTT TAGCCTCAAT AGATGCGGTG GTCGCTAGCG AATTCAGGAA GCAATTGCCC      600
TACATTATCA CTAGGGCTAT TTTATCGGCC ACTTTTAAAG TGGGCATGCA AGCGGTGGCG      660
AACTATTATT TAGGGTTTGT TGGCGGGTTA GTAACCTCGT TGTATTCAGG TGTGAGCACC      720
TTTGCAGACA CCAGAAACAC GAGCATTTTT GCCCATAAAA TCTACCTCAT GCGCATCAAA      780
AACAAAGCCT TTGAAAGTTA TGAAGTTCGA GCCGATTCCA TTGACGCTTT TTCGTTTTCA      840

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273

TTAAAGCCTT GTAAAAGATC GCTTGAAAGC CCTAAAATCA TTGACGCTAG GGAATTGCTT	900
TCAGGGTTTG TAACAGCCCC ACAAGTCTTT TGCTCTAACC GCCATAATAT TTTATATGTG	960
CGCAGCTTTA AAAACGGGTT TGTTTTGAGT CATTTAAAA	999

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

AGGAATAAAG ATAAAAGAGA GTATTTTGAA AACGCCACCG CGCAAATTGG GGCTAAACTC	60
TTGGTGTGCG ATATTAGAGA GCAGTTCTTT AACGATGTGT TGTTCAGCC CAAATACGGC	120
TATGGGAAGT ATTTCAACCC TTGCATTGAT TGCCATGCCA ACATGTTTAG GAACGCTTTT	180
TATAAAATGC TTGAATTGGA TCGCGATTTT GTTTTGAGCG GGGAAAGTGCT AGGCAACGCC	240
CTAAATCCCA AAGGAAAGAA GCGCTCAATC AGG	273

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GGGGAAGTCA TGGCTGATAG TTTAGCGGGC ATTGATCAAG TTACGAGTTT ACATAAAAAAT	60
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AACGAGTTGC	AATTGTTGTG	TTTCAGGCTG	GGTAAAAACA	AGGATTTGTA	TGCGGTCAAT	120
GTCTTTAAGA	TCCGTGAAGT	GGTGAAATAC	CATGGCAATC	TCACTATCAT	TAGCCACGAA	180
AACAATTCGC	TCGTTGAGGG	CTTGATCATT	ATAAGAGAGC	TCACCATTCC	TTTGATTGAC	240
ATGAAAAAAT	GGTTTTATTA	TGACAGCCAA	AACAAGAGCA	AGGATTTACG	CCCTTACAGG	300
ATACAAAAAG	AAAAAAGCGA	AGACGATATT	GTGATGATTT	GTGAGTTTTT	TCGCTGGACC	360
ATAGGGGTTA	GGATTTATGA	AGCGGATAGG	ATTTTCGAGCA	AGAAATGGAC	TGAGATGGAG	420
CAAAGCGCTG	GGCTACGGGG	ATCTGCTGGG	AATAACAAAC	TCGTGAGCCG	CACGCGCTAT	480
TTTGACGGGC	GCTTGGTGCA	AGTGGTGGAT	ATTGAAAAAA	TGCTTATAGA	CGTGTTCCTT	540
TGGATTGAAG	ATGAAAAACA	CAACGATGTA	GAGACGCTTT	CTAAAATCCA	TTCTAACCAA	600
TGCGTTTTGC	TCGCTGATGA	TTCCCAAGC	GTCTTAAAAA	CCATGCAAAT	GATTTTAGAC	660
AAGCTGGGCG	TCAAGCACAT	TGACTTTATC	AATGGTAAAA	CCTTATTAGA	GCATTTGTTC	720
AACCCAACAA	CCGATGTGAG	TAATATTGAC	CTGATTATTA	CCGATTTAGA	AATGCCAGAA	780
GCGAGCGGTT	TTGAAGTGAT	CAACCAGGTT	AAAAACACTC	CTTTGACTTC	AACAATCCCC	840
ATTGTGGTCA	ATTCTTCTAT	GAGCGGGAGC	TCTTATGAAA	AAAATGGCAA	GAATTTGAAT	900
GGCCAA						906

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

GCAGTAGCGT	TTTGCTTACC	GTATTCAAGC	CCAAAGACTT	CTTTAGCCAC	TGAATTGCAC	60
TATAGCGCTA	ATGAACGCAT	AGAGGCTTTT	TCAAGCAATG	ACGAAAAAAC	AGAGAGTTTT	120
GAAGTGAATG	AGCAAAGTTT	TGAGGCGATT	AAAGAGAATG	CGGCGAAGTA	TTCATACCTT	180
AAGGTTTATT	TGAAGAACGT	AGCCTTAAAA	GATAGTGCGC	CTTTAGTGTT	TGTGGATATG	240
CCCGGGTTTG	ATAGCCCCAT	TTCAAGCCAC	ACCCATGCCA	TTTTGGAATA	TTTGGAAGG	300
GGCGTGCAAT	TTGTCATTCT	CACAAGCGTA	GAAGAGGGTA	ACCTCACTAA	ACGCATGGTT	360
AGGGAGTTAA	AAACCTTT					378

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

CGGCACCCGA	TTGAAAATTC	GATCTGCGAT	CTTAGCGAGT	TGAATAATTT	AAAGCCTTTG	60
GGCGCGGAAA	TGTTTGTGGG	GTTAGACGGC	ATTGATGCGA	TGATAGAGGA	GTGCGTTTCC	120
AATTTAGTCA	TTAACGCCAT	TGTGGGCGTA	CCCGGATTGA	AAGCGAGCTT	TAAAAGCTTA	180
CAAAGGAACA	AAAAACTAGC	CCTAGCGAAT	AAAGAAAGTT	TAGTGAGCGC	GGGGCATTTA	240
TTAGACATTT	CACAAATCAC	GCCCCGTTGAT	AGCGAGCATT	TTGGTTTGTG	GGCGTTGTTG	300
CAAAACAAGA	CTTTAAAGCC	TAAATCTTTA	ATCATTAGCG	CGAGTGGGGG	GGCTTTTAGG	360
GACACGCCCT	TAGATCTTAT	CGCTATTCAA	AATGCGCAAA	ACGCGCTCAA	GCACCCTAAT	420
TGGAGCATGG	GGGATAAAAT	CACCATTTGAT	TCAGCGAGCA	TGGTCAATAA	ACTTTTGTAA	480
ATTTTAGAAA	CCTATTGGCT	TTTGGTGCG	TCTTTAAAGA	TTGACGCGCT	GATTGAAAGA	540
AATTCATCG	TGCATGCTTT	GGTGGAGTTT	GAAGACAAC	CTGTCATTGC	GCATTTAGCG	600
AGTGC GGACA	TGCAATTACC	CATAAGCTAT	GCCATTAAAC	CTAAATTAGC	TTCTTTGAGT	660
GCTTCCATTA	AACCCCTAGA	TTTATACGCT	TTAAGCGCGA	TTAAATTCTGA	ACCCATTAGC	720
GTGGAGCGCT	ACACTTTGTG	GCGTTATAAA	GATTTGTTGT	TGGAAAACCC	AAAGCTTGGC	780
GTGGTGCTGA	ATGCGAGCAA	TGAAGTGGCG	ATGAAGAAGT	TCTTGAATCA	AGAAATCGCT	840
TTTGGTGGCT	TTATCCAAAT	CATCTCTCAA	GCTTTAGAAT	TGTATGCTAA	AAAATCTTTC	900
AAGCTCTCTA	GTTTAGATGA	AGTGCTAGCG	TTAGATAAGG	AAGTTAGGGA	GCGTTTGGGA	960
AGTGTAGCGA	GAGTG					975

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 396 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GAGACGCTCG	CAAGGGTTCT	CAAAGTTTCA	TGTTTGGCTA	TGGGGCTGGC	ACAGATGTGT	60
TGTTTAACCC	AGCTATTTTC	AATCGTGAGA	AACTGCAATT	TGGGGTTTTT	CTTGGGCGTT	120
GCGATTGGTG	GCACCTCTTG	GGGTCCAACA	AACTATTATT	TTAAGGACTT	AGCTGAAGAG	180

276

TATAGAGGGA	GTTTCCACCC	ATCAAATTTT	CAGGTCTTAG	TTAATGGCGG	GATCCGCTTA	240
GGCACTAAAC	ACCAAGGTTT	TGAAATTGGC	TTGAAAATCC	AAACCATTTC	CAATAATTAC	300
TATACCGCTA	GCGCGGATAA	TGTGCCTGAA	GGGACTACTT	ATAGATTAC	TTTCCACCGC	360
CCTTACGCCT	TTTATTGGCG	TTACATTGTA	AGCTTT			396

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GTCTTAAAGA	ATGAAATAAG	CTATAATAAG	CCCATTTTGA	ACACCAACGA	TTATTTGAAT	60
AAAGACAATA	CGATGAAAGA	TAGTTTTCTT	TTCATTCCG	AATCAGTAAC	CGAAGGGCAT	120
CCTGATAAAA	TGGCCGATCA	GATCAGCGAT	GCGGTTTTAG	ATTACATGAT	TGAGCGGGAT	180

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

AAAACCAAAG	TCGCATGCAA	GACTTTAGTT	TCTAATGGTT	TATGCATGAT	CACTGGCGAG	60
TTAGAAACTT	CTGTTTATGC	ACCGATGCTA	GAGATCGCAA	GACATATGGT	TAGAAAAATT	120

GGCTATACAA	ACGCTCTCTA	TTGCTTTGAT	TACAGAAGCG	CGGCGGTTTT	AAATGGCATT	180
GGCGAGCAAA	GTCCTGATAT	TAATCAAGGC	GTGGATAGAG	AAGATGGCGA	GATTGGGGCG	240
GGGGATCAAG	GGCTTATGTT	TGGTTATGCA	TGCAAAGAGA	CTGAAACGCT	CATGCCTTTA	300
CCCATCCATT	TAGCGCACCA	GCTCGCTTTC	GCC			333

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

TCCTTATCAA	CACTTGCGGT	TTTATTGAAA	GCGCTAAACA	AGAGAGTATT	CCAAACCATT	60
CTCAACGCAG	CCAAAGACAA	AAAAGAGGGA	GCGATTTTAA	TTGCGAGCGG	GTGCTTGAGC	120
GAGCGCTATA	AAGATGAAAT	CAAAGAATTG	ATCCCTGAAG	TGGATATTTT	TACCGGCGTG	180
GGGGATTATG	ACAAGATTGA	TATTTTAATC	GCTAAAAAAC	AAAACCAATT	CAGCGAGCAG	240
GTGTTTTTAA	GCGAGCATT	TAACGCGCGC	ATTATCACGG	GATCGAGCGT	GCATGCTTAC	300
GTTAAAATTT	CTGAGGGCTG	TAACCAAAAA	TGCTCTTTTT	GCGCTATCCC	TAGCTTTAAG	360
GGAAAATTAC	AAAGCAGGGA	ATTAGACTCC	ATTTTAAAAG	AAGTAGAAGA	TCTAGCCCTT	420
AAAGGCTATA	AAGATATGAC	TTTATCGCT	CAAGATTCTA	GCTCATTTTT	ATCCGATAGG	480
GCAAAAAGTC	GGCTTGATCC	AGCTCAT				507

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

AATTTAAGGA	CTATAATGCA	TTATTCCTAT	GAAGCCTTTT	TAAAAGACAG	CCTGGAGTTA	60
GCTAAACAAG	TGGAGCGCCT	TTGCGGTATC	CCAGAAGCCC	TTGTGTGCGT	GATGCGAGGG	120
GGCATGACTT	TAGTGCATTT	TTTGAGTTTG	CACTGGAATT	TAAGGGAAGT	TTATGGCATC	180
AATGCGATTT	CTTATGACAC	CACCAAGCGA	CAAAACGCCC	TAAAAATTGA	AAATACCCCC	240
ACGATCAAAG	ATCATTTAAA	AACCATTTTA	GTGGTAGATG	AAATCGTAGA	TAGCGGTAAT	300
TCTTTGGAAG	CGGTACTTAA	AGTGTTGCAA	GACAAACACC	CTGATAAAAA	GTTTTATAGC	360
GCGAGTTTGT	TCCAAAAAAC	AAGCGCGAAA	TACAAAGCCG	ATGCGTTTTT	AAAAGACGCT	420
CCTGAATGGA	TTGATTCTT	TTGGGAAGTG	GATTTGAAAA	ACTTGAAAAG	CCAC	474

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

TCCAGCTCAT	TAGAGCGATT	GCCAGCAAGC	CTTAAAGACG	CGCGTATTTT	ATACCTCTAC	60
CCCTCTAGCA	CCACTTTAGA	GCTGATTGGC	GCGATTGAAG	ACTCGCCTAT	TTTTCAAAAT	120
TATTTTTTACA	TGCCCATTCA	GCATATCAGC	GACTCCATGC	TTAAAAAAAT	GCGGCGCAAC	180
TCCAGCCAAG	CACACCATTT	AAAGCTTTTA	AACGCCATGA	AGCAGGTTAA	AGAAAGCTTT	240
ATAAGAAGCA	CGATCATTGT	AGGGCATCCA	GAAGAAAATG	AGAGCGAATT	TGAAGAATTG	300
AGCGCGTTTT	TAGACGAGTT	CCGGTTTGAC	AGATTGAATA	TTTTTGCTTT	CAGTGCTGAA	360
GAAAACACGC	ATGCCTATTC	TTTAGAGAAA	GTGCCTAAAA	AAATCATCAA	CGCCCGCATT	420
AAAGCCTTGA	ATAAAATCGC	TTTAAACAC	CAAAACCATT	CTTTTAAGGC	TTTGTTGAAT	480
AAGCCCATTA	AGGCGTTAGT	GGAACATAAA	GAGGGCGAAT	ATTTTACAA	AGCAAGGGAT	540
TTGAGATGGG	CGCCTGAAGT	GGATGGGGAA	ATTTTAATCA	ATGACAGCGA	ACTAACCACC	600
CCTTTAAAAC	CCGGGCATTA	CACGATTGTG	CCTAGCGCCT	TTAAAGACAA	TATTTTACTC	660
GCTAAGGTTT	TAAGTCCTTT	T				681

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...324
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

ATAACGAATA CAACTTTCCA ACTCCAAGGC GTTTTATTGG AATACGATT TGAACGGCCT	60
GCTATCTCTT ATACCCCTAA AAAAAGCGTT TTTAATGAGC GCTTGAAGGA TTTGAGGGAA	120
AATTTTAGCG CTCTTTTATA CGCTGATTTG AAAGACAAGA TCCATCATAA CGCCTTGTCT	180
AACGATGATT TAGAACGCAT GATAGCTTTT AGAGAGCAAG AATTTGAAAA GAGTTTAGAG	240
GATTGGATGG GTGCATATTC TTATGATGCA ACCCTGAGGT GTTTTAGTAG CGAGCGTATC	300
TATCTAGACC GGTGGGGTG GGAA	324

(2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1092 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1092
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

AAAAAGGTGG TTATGAATGG TTTTTCGCT AGACTACGAG CCATAACATT TAATGAAAGA	60
CTAAAAATGA AAATAGCGGT ATTACTCAGT GGGGGGGTGG ATAGCTCTTA TAGCGCTTAT	120
AGCTTAAAG AGCAAGGGCA TGAATTAGTG GGGATTTATT TAAAACTCCA TGCGAGTGAA	180
AAAAAGCATG ATTTATACAT TAAAAACGCT CAAAAGCGT GCGAGTTTTT AGGCATTCCCT	240
TTAGAGGTGT TGGATTTTCA AAAGGATTTT AAAAGCGCGG TTTATGATGA ATTTATCAAC	300
GCCTATGAAG AAGGGCAAAC CCCTAACCCA TCGCGTTGT GCAACCCTTT AATGAAGTTT	360
GGGCTAGCTT TAGATCACGC TTAAATTA GGGTGTGAAA AGATCGCTAC CGGGCATTAT	420
GCGAGGTCA AAGAAATTGA CAAGGTAAGT TATATTCAAG AGGCTTTGGA TAAAACTAAA	480
GATCAGAGCT ATTTTTTATA CGCTTTAGAG CATGAAGTTA TCGCTAAATT GGTGTTCCCT	540
TTAGGGGATT TGCTAAAAA GGATATTAAG CCTTTAGCCT TGAATGCGAT GCCCTTTTTA	600
GGCACTTTAG AAACCTATAA GGAATCTCAA GAAATCTGCT TTGTGAAAAA AAGCTACATT	660
GACACTTTAA AAAAGCATGT TGAAGTGAA AAAGAGGGCG TGGTGAAAAA CCTACAAGGC	720

. 280

GAAGTCATTG	GCACGCATAA	AGGCTATATG	CAATACACGA	TTGGCAAACG	CAAAGGCTTT	780
AGTGTTAAAG	GCGCGTTAGA	GCCGCATTTT	GTGGTGGGGA	TTGACGCTAA	AAAGAACGAG	840
TTGATTGTGG	GCAAAAAAGA	AGATCTCGCC	ACGCATTTCG	TTAAGGCTAA	AAACAAATCT	900
TTAACGAAAG	ATTTTAAAGA	TGGCGAATAC	TTCATCAAGG	CCCGTTACAG	GAGCGTGCCT	960
ACTAAAGCGT	TTGTGAGCTT	AAAAGATGGA	ATGATTGAAG	TGGAATTTAA	AGAGCCTTTT	1020
TACGGCGTGG	CTAAAGGGCA	AGCCTTGGTC	GTTTATAAAG	ATGATATTTT	GCTTGGCGGG	1080
GGCGTGATTG	TT					1092

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

TTGTTTAAAA	CCAATGGGAT	AAGTGTGGGG	GAATACACTC	ATTTTAGCGA	AGATATAGGC	60
AGTCAATCGC	GTATCAATAC	CGTGC GTTTG	GAAACTGGCA	CTAGGTCAAT	CTTTTCTGGG	120
GGTGTCAAAT	TTAAAAGCGG	TGAAAACTA	GTTATCAATG	ATTTTACTA	TAGCCCTTGG	180
AATTATTTTG	ACGCTAGGAA	TGTTAAAAAT	GTTGAAATCA	CCAGAAAATT	CGCTTCTTCA	240
ACCCAGAAA	ACCTTGGGG	CACATCAAAG	CTCATGTTTA	ATAATCTAAC	CTTGGGTCAA	300
AATGCGGTCA	TGGACTATAG	TCAATTTTCA	AATTTAACCA	TTCAGGGGAT	TTTATCTACA	360
ATCAAGCGAT	ATCATTTGAC	GAAGGGTTTT	TTTACCCCC			399

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

ATGAAAAAAAA	CCCGTATCCG	GAAGAAGTCA	GCTTTAATGA	ATGGCTGTTG	GGCGGAATTT	60
GATAGCGTTT	TTAGCGCCAT	TGTGCCTTTA	GAAGATTTAA	ATAAAACCGC	ATGCGCTCAT	120
CATGCCCTAA	AGGCTTTACA	AGCTACGCTA	AAGACAACGA	TTTGGGCTTT	GATGCGACAG	180
AGTTGGAACA	GATCGCAAAA	GGATTCATCC	CTAGGGGGTA	TTTGTGGCAT	TTTGACGCGA	240
ATGTTT						246

(2) INFORMATION FOR SEQ ID NO:248:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

TGGACTCTAG	CCAAAATTCG	TTGCGTTAAA	AACTTTAAGG	AAGCTATAGA	AGGTTTACAA	60
GAAAAAATCA	AAGAATCCCC	TAACGATTCA	AACGCTATCA	ATGAAGCCTT	TGATAATTTA	120
GAAACAGAGT	TAGAGCGCGC	TACAGAAAAT	TTGAGTCAAA	AAATCGATCC	CGTTTTAGAA	180
CGGAATGAAA	ATTATACGCA	AAAAGCGTTG	GAGTATAGGG	AGTTTTTAGA	AAGCCGTAAA	240
GAGAGCTTTA	TTGTAGATGA	AAAAAACCCG	TATCCGGAAG	AAGTCAGCTT	TAATGAATGG	300
CTGTTGGGCG	GAATT					315

(2) INFORMATION FOR SEQ ID NO:249:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 852 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

```
AGACCTTTGG CACTCATCAT GTGGTGCGA AATATAGACA ATCGTATCTC TATTAAGCGC      60
GTTGTAAACA AGCCCCCAAG AGGCCTTGCC AAGATCACTC AAGAATGGAT TTTTCTCTT      120
TTAGATGAAG AGGGTTTGAA TTTAGAAGAA GCGCTAAAAA TTGGGGCGTT TAAAGACAAA      180
CTCAACCCTA AAAACGAATA CGCTTTAAAG AAATTCACCG CTATGATAGG GCGTTTGAGG      240
GAGGCTTTTG AAATTTCAAGT AGAGAAGTTT TGCGAGCGGT TTTTAGAAGA GACTAACCTT      300
TTAAAAAGCT ATGAAAAAGA AGACAATTAC GAAGAAAGAG AGGGCTTTGT TAAAGAGCTT      360
TTAAGTTTAG TGAAAGAGCA TTTTAAACT AACCACGCGC ATTCTTTACT GGATTTTTTG      420
AATGAAAGCG CACTGGATGT CCATAATACA GAAAACGCGC AAAAAGTGAG TTGCATGAGC      480
GTGCATATGA GTAAGGGCTT AGAGTTTAAG CATGTGTTTG TGATCGGGTT AGAAGAGGGG      540
TTTTTCCCGC ATAGGGGGTT CAATCAAGAA AGCGATTGGG AAGAAGAAAG GCGCTTGGCT      600
TACGTGGCGA TCACTAGGGC TAAAGAAGAA TTACAACCTT CTTATGTCAA AGAGCGTTCG      660
TATTTTGGGA GGAAATTTT TCGCTCGCCC TCTGTGTTT TAGAAGAAGC CCAGTTGCTC      720
CAACAAGACA AGCCTCCTAA ACAAATCAC CAAAAGATA CGCCATTAA AGTGGGGGAT      780
TTGATCAAAC ATAAGATTTT TGGCACC GGGGAGGTTT GGCCTAGAAA AAGGCTTGCA      840
GCGGTTTGTG CT                                         852
```

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

```
GATGGGTCAA AAAAGATGAA GTCAAATAAA AAGTCCAATC ATTTAAGAGC GATTTATAGG      60
GCTTTAGTGA TCGCTATAGG CTTAGCCGTT ATCATGTGTT TCAATTATTT TAACCGCAAA      120
AACATAACG CCCGCTCCAG CCGTAGGGCT TGTTTCGTGT TTTTCCCCC CACCGGGGTT      180
AATTTAGAAA AAATAGGTTT CTTTGACACG GGCGCTAAAC TCATTGTCTT AAACCACCAA      240
AGCTTACTAG ACATTATTTA TTTAGAAGCC TACCACCCTA GTAATATTTG CTGGATCGCT      300
AAAAAGAGC TGGGCGAAAT CCCTTTTAT GGGCATGCTC TAACGGATAC CGGAATGATC      360
TTAATTGACA GAGAGGATAA AAAGGGGATA GTGAGCCTTT TGAAAGCATG TAAAGAAAAG      420
CTAGATCAAA ACCGCCCTTT AGTGATTTTT CCTGAAGGCA CTAGAGGCAA AGGAGGAGAA      480
AAATTCCTCC CTTTAAAGCA AGGGGCTAAA ATCATCGCTG AAAAATTCCA GCTCAAAATC      540
CAGCCCATGG TGTTAATCAA TTCCATTAAA ATCTTTAATT CCAAGCCCCT AGAAGCTTAT      600
AAAGCGCGCA CCCGTTTGGT CATGCTAGAA AGCTATACGC CTGATTTTAG CTCGCCCACC      660
```


TGGTATGAAG AATTACAAGA ACGCATGCAA AAAGAATATT TAAAACACTA CCACGAACTA 720
AACGCA 726

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

GTCATGAAAA CTTCTAACAC AAAAACCCTT AAACCCGTTT TAATCGCCGG GCCATGCGTC	60
ATTGAGAGTT TAGAAAATCT AAGAAGTATC GCTATTAAAT TACAACCCCT AGCCAACAAC	120
GAGCGGTTGG ATTTTATTTT TAAAGCGAAT TTTGATAATG CTAACCGCAC GAGTTTGGAA	180
AGTTACAAAG AACCTGGTTT AGAAAAAGGC TTAGAAATGT TACAACTAT CAAAGATGAA	240
TTTGGTATA AAATTTTAAC CGATGTGCAT GAGAGCTATC AAGCAAGCGT GGCAGCCAAG	300
GTCAGCGATA TTTTACAAAT CCCGGCGTTT TTGTGCCGCC AAACGGATCT GATTGTAGAA	360
GTGAGCCAAA CTAACGCCAT TGTCAATATC AAAAAAGGGC AATTCATGAA CCCAAAAGAC	420
ATGCAATATT CCGTCTTAAA AGCCCTTAAA ACAAGGGATA GTAGCATTCA AAGCCCCACT	480
TATGAAACAG CGTTAAAAAA TGGCGTGTGG CTGTGTGAAA GGGGGAGCAG CTTTGGGTAT	540
GGGAATTTAG TGGTGGATAT GCGCTCTTTA AAAATCATGC GAGAATTTGC CCCTGTGATT	600
TTTGACGCTA CCCATAGCGT GCAAATGCCA GGGGGAGCGA ACGGGAAAAG TTCAGGAGAC	660
AGCTCTTTTC CCCCTATTTT ACCCAGAGCG GCGGCGGCGG TGGGGATTGA TGGGCTGTTC	720
GCTGAAACGC ATATTGATCC TAAAAACGCC CTAAGCGATG GAGCAAACAT GCTAAAACCT	780
GACGAGCTAG AACACTTAGT AACCAACATG TAAAAATCC AAAATTTATT T	831

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

```

CAAAGAGATC ATGGCGTTTT GTATTGCTT AATAACACTA TAATAAAATT TTTAATAAGG      60
AGATACATCA TGTTAGAAAA TGTCAAAAAA TCCCTTTTTA GGGTTTTGTG CTTGGGCGCG      120
TTGTGTTTAG GGGGGCTAAT AGCAGAGCAA GACCCTAAAG AGCTTGTCAG TTTGGGAACA      180
AAGAGCTACA AAGAGCAGGA TTTCACTCAG GCTAAGAAAT ATTTTGAAAA AGCTTGCGAT      240
TTGAAAGAAA ATAGCGGGTG TTTTAATTTA GGGGTGCTTT ATTATCAAGG GCATGGGGTG      300
GAAAAGAATT TGAAAAAAGC CGCTTCATTT TACTCTAAAG CTTGCGATTT AAATTACAGC      360
AATGGGTGTC ATTTGCTAGG GAATTTATAT TATAGCGGGC AAGGCGTGTC CCAAAACACC      420
AACAAAGCCT GGCAATACTA CTCTAAAGCG TGCGATTGTA AATACGCTGA AGGGTGTGCG      480
AGCTTAGGGG GGATCTATCA TGATGGCAAA GTGTTTACTA GGGATTTTAA AAAAGCGGTG      540
GAATATTTCA CTAAAGCTTG CGATTGTAAC GATGGCGATG GTTGACGATG ATTAGGGAGC      600
TTGTATGATG CAGGCAGAGG CACGCCATAA GATTTGAAAA AAGCGCTCGC TTCGTATGAT      660
AAAGCTTGCG ACTTAAAAAG CAGCCCAGGG TGCTTTAACG CAGGGAACAT GTATCATCAT      720
GGCGAAGGTG CGGCGAAGAA TTTTAAAGAG GCCCTCGCTC GTTATTCTAA GGCATGCGAG      780
TTGGAAGATG GCGGAGGGTG TTTCAATTTA GGGGCTATGC AATACAATGG CGAAGGCGCA      840
ACAAGGAATG AAAAGCAAGC CATAGAAAAC TTTAAAAAAG GCTGTAAATT AGGCGCTAAA      900
GGGGCATGCG ATATTCTCAA GCAGCTCAAA ATCAAAGTT      939

```

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1590 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

```

ATGAGCAGCG GGTTAATTTA CATTTCTTA GAAGTCTTGG TAGCGTGTTT GATCACCGCT      60
CTAATCATGT ATTATGTGAT GAAAAAGATC TATTACGCTA GAGGGCAAGC CATTTTAAAA      120
GGCGCTTCAG CCAAAGCTAA ATTAATGGAA TTTCAAGCGA AATCTTTCGT GGAAGCTGAA      180
GAAATGCGCA TGAAAAGCCA AGAATGCAAG TTGCAACAGC AATATGAAAA TAAGAATTTG      240
CAACTCCAAA CCCATTTTGA TAAAAAAGAA GCGCATTTGA AGCATTTAGA AGCGCAGCAC      300
AAAGAATTTG TAAGAGATGA AAAACGCTAT TTGGAAGAGG AAAAAAAGA GCTTGAAAAA      360
GAACGCCAAA TTTTAGAACA AGAGAGGGAA AATTTTAAAA AACAGCGCGC CATTTGTAAA      420
GAAGCTCAAG CCAAAGCGCT AGATGCGATG CTCAATTACA TGGCTTATAC CAAAGATGAA      480
ATTAAAGCA TGATCTTAGA GCAACTAGAA GAGGAAGTAG AAGCGCAAAA AAGCGCCTTG      540
ATCAGGCGTT ATGAAAAAGA AGCCAAAGAA GAGGGTAAGA AAAAATCGTA TGCCATTTTA      600

```

GCGGAAGCGA	CAGCCCGTTT	TGCGGGCGAT	TATGCGACAG	AGAATTTAAC	AAGCCGTATC	660
GCTTTGCCTT	GCTCAGATTA	TGTGGGTCGT	GTGATAGGCA	AAGACGGGAA	AAACATTGAA	720
GCGTTTAAAA	AGATTAGTGG	GGTGGATATA	GAATTTAGCG	AAGACAGTAG	CGAATTGTGC	780
TTGTCCAGTT	TCAATATTTA	TCGGCGTGAA	GTGGCGAGCG	AGACGATTAA	AATTTTAATA	840
GAAGACGGCC	GTATCCAGCC	TAACAGGATT	GAAGAGGTTT	ATCATAGAGT	CGCGCGCAAC	900
ATGGA AAAAG	AATTGCTTTC	TGAAGGAGAG	AGCGTGGTGC	TAGAATTAGA	GCTTGGA ACT	960
ATGGAAGATG	AGCTTAAAAT	TTTAATAGGC	AAAATGCGTT	ATCGCTTTAG	TTTTGGGCAA	1020
AACGCTTTAC	AGCATTTCTAA	AGAAGTCGCT	CTTTTAGCCG	GCTTGATTGC	AGAACAGCTT	1080
GGGGGGGATA	AAAAACTCGC	CAGAAGAGCC	GGTATTTTGC	ATGATATTGG	TAAAGCGCTC	1140
ACTCAAGAGC	TTGGGAGAGA	CCATGTGAAT	TTAGGGGTTG	AGGTGTGCAA	GCGCCATAAA	1200
GAAGACCCGG	TTGTGATCAA	TGCGATTTAT	GCCCACCATG	GGCATGAAGA	AATCATGAGC	1260
GTGGAGTGCG	CGAGCGTGTG	CGCGGCTGAT	GCGCTTTCTG	CAGGGCGTCC	GGGCGCTAGG	1320
AGAAAGAGCG	ATGAAGAATA	CGCTAAACGC	ATGCAAGCTT	TAGAAGAGAT	CGCGTTAGAA	1380
TTTGATGGGG	TGGAAAAGGC	GTATGCGATG	GAGAGCGGGC	GAGAACTAAG	AGTGATTGTC	1440
AAATCCAACC	AAGTCAGGGA	CAATCAAGTG	CCTATTATTG	CTAGAAAGAT	CGCTAAAAGG	1500
ATAGAAGAGA	GCACTCAGTA	TGTGGGCGAA	GTGGGCGTGC	AAGTGGTGCG	AGAAAATCGT	1560
TTCAAAACGA	CCGCTACGCT	CAAGCAATGA				1590

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

ATGAAAAAAG	GTAGTTTAGC	AATCGTTTTA	GGATCGTTAC	TAGCAAGTGG	GACGTTTTAT	60
ACGGCTCTAG	CTGATGGAAT	GCCTATGAAG	CAACAGCACA	ATAACATGGG	TGAGTCTGTG	120
GAGTTGCATT	TCCACTATCC	TATTAAAGGC	AAACAAGAGC	CTAAAAATAA	CCATTTAGTT	180
GTCTTAATCG	ATCCTAAGAT	AGAGGCTAAT	AAAGTTATCC	CTGAAAATTA	TCAAAAAGAA	240
TTTGAGAAGT	CTTTGTTTCT	CCAACTGAGT	AATTTTTTTAG	AGAGAAAGGG	CTATAGCGTT	300
TCGCAATTTA	AAGATGTTAG	CGAAATCCCT	CAAGACATCA	AAGAAAAAGC	GTTGCTCGTT	360
TTACGCATGG	ATGGGAATGT	GGCTATCTTG	GAAGATATTG	TAGAAGAGAG	CGATGCGCTC	420
AGTGAAGAAA	AAGTGATAGA	CATGTCTTCA	GGGTATTTGA	ATCTGAATTT	TGTTGAGCCA	480
AAAAGTGAAG	ACATTATCCA	TAGTTTTGGT	ATTGATGTTT	CAAAGATTAA	GGCTGTGATT	540
GAAAGGGTGG	AATTGCGGCG	TACCAATTCT	GGAGGTTTTG	TCCCCAAAAC	TTTTGTGCAT	600
AGGATCAAGG	AAACCGACCA	TGACAGAGCC	ATTAAAAAGA	TCATGAATCA	AGCCTATCAC	660
AAAGTGATGG	CGCATATCAC	CAAAGAATTA	AGCAAAAAAC	ACATGGAACG	TTATGAAAAA	720
GTTTCTAGTG	AAATGAAAAA	GCGAAAGTAG				750

(2) INFORMATION FOR SEQ ID NO:255:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...357
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

ATGCAAAACA CCTTTAACTA CACCAACAAC GCTTTGAAAA ACAATGCTAA ATTAACCCCC	60
ACTGAAATGC AAGCCGAACA ATACTACCTC CAATCCACCC TTCAAAACAT TGAAAAAATA	120
GTCATGCTTA GCGGTGGCGT TGCCTCTAAC CCTAAACTAG TCCAAGCGTT AGAAAAAATG	180
CAAGAACCCA TTAATAACCC TTTAGAATTG GTAGAAAACT TAAAAAATTT AGAATTACAA	240
TTCAGCCAAT CTCAAAACAG CATGCTTTCT TCTTTGTCTT CTCAGATCGC TCAAATTTCA	300
AATTCTTTGA ACGCGCTTGA TCCAGCTCT TATTCTAAAA ACGTTTCAAG CATGTAT	357

(2) INFORMATION FOR SEQ ID NO:256:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 945 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...945
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

ATGGACTTAG ACAAACCTCAA AGATTATAGG GCTTTAAGAA ACGCTATTTT AAGGCTATTG	60
CCTTATTTAG ATAGCGGTAT TACAGAGCTA ATTATGAATA AAGAAAAAGA AATTTGGCTC	120
TATAAGCTTA ATGGAGTAAG AGAAAAAGTC TTTGATGAAA ATTTAGACAA AGCCTTTATT	180
CTGGGGTTTG GGGAACAATT AGCGAGTTTT AGAGATTGT TTTTAAATGC TAATTACCCC	240
ACCCTTAATA CTTCCATTCC TACTTCTAGA TACAGAGTGA GCATGAACCA CTTTGCTATT	300
AGTGCGGATA ATGAATTGAG TTTGAATATT AGAGTGCCAA GTGATAAAAA GTTTGATTTA	360

287

AAAGCTTTCA	AGCTTTCTAG	TATCTGTCAA	TACGATTATG	AGTATTTAAA	AAACTTAATG	420
ATTGATGGCA	AAAACCTTACT	CATTAGTGGA	GGCACAGGCA	GTGGAAAAAC	GAGTTTTTTA	480
AACGCTCTAA	TTGAGTTTAT	CCCCAAACAC	ACACGAATAG	TAAGCGTTGA	AGATAGCGAA	540
GAATTAGATT	TAAGAGCGTT	TGAAAATCAT	AAATCCTTGT	TAGTGGATAA	AACTGAAAGC	600
TCTAAATTTA	CATATGAAAA	CGCCTTGAAT	ATGGCAATGA	GAATGTCTCC	TGATAGGCTT	660
ATGGTAGGCG	AGATTGACAC	ACGAAATTCC	ATGCTCTTTT	TAAGATTTGG	AAACACTGGG	720
CATAAAGGCA	TGGTTTCTAC	TTTACATGCA	GATAGTGTGC	ATGGGGTTAT	AGAGGCGATT	780
GCTTTAAATT	TACAAATGAA	TAAAAGTGGT	TTAGATGTCA	ATGTAGCAAA	AAAATTCTTT	840
AAAAGCAGTG	TGGATGTTGT	CGTTCAAATT	GTATTAGATA	AAGCCACTAA	CACCAGATAC	900
ATTCAAGAAA	TCTTACCAGC	AAAAGATTTA	AGAGATAGTC	TATGA		945

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

ATGAATATAT	CGGTTAACCC	CTATTTAATG	GCGGTCGTTT	TTGTAGTGTT	TGTGTTGTTG	60
TTGTGGGCGA	TGAATGTTTG	GGTGATAGG	CCTTTGTTGG	CTTTTATGGA	TAACAGACAG	120
GCAGAGATAA	AGGACAGCTT	GGCTAAAATC	AAAACGGATA	ACACCCAAAG	CGTGGAGATT	180
GGCCATCAAA	TTGAGACTCT	TCTTAAAGAA	GCCGCTGAAA	AGCGCAGGGA	AATGCTAGCA	240
GAAGCGATTC	AAAAAGCTAC	AGAGTCTTAT	GACGCTGTGA	TCAAGCAAAA	GGAGAACGAA	300
CTCAATCAAG	AGTTTGAAGC	GTTGCGAAAG	CAATTACAAA	ATGAAAAACA	AATCTTAAAA	360
GAGCAATTGC	AAGCGCAAAT	GACGGTATTT	GAAGACGAGT	TAAACAAGCG	TGTGGCTATG	420
GGTTTAGGGA	GTTGA					435

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

ATGGCTAGTG GCCTTTTTGA AAACGATGAA ATCAAAAACA ACAAAGCGCG AGATTTTTTTT	60
TATAGCCATA GCTCCCTTAT TGTCTTTTTC CTCTTACTGC TTGGGTTTGG GTATTATTTA	120
GGGAAGTTGC TTTTGGGGG TTCTTCTTTA GAGGTCTATT TGGATTTAAG AGACAAGCAT	180
GAACGATTGC AACAAGAAAT CACCGAATTG CAAAGCAAGA ATGTGCGCTT GCAAAAGCGT	240
TTGTTTGAGT TGAGGGAATT ACGGCCTAGA GATTAG	276

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 900 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

ATGAAAAAAA ATATCTTAAA TTTAGCGTTA GTGGGCGCGT TGAGCGCGTC GTTTTGTATG	60
GCTAAGCCGG CTCATAATGC GAATAACTCT ACGCATAACA CGAAAGAAAC GACTGATGCT	120
TCAGCAGGCG TGTAGCGAC AGTGGATGGC AGACCCATCA CCAAAGCGA TTTTGATATG	180
ATTAAGCAAC GAAATCCTAA TTTTGATTTT GACAAGCTTA AAGAGAAAGA AAAAGAAGCC	240
TTGATTGAGC AAGCTATCCG CACCGCGCTT GTAGAAAATG AGGCTAAGGC AGAAAAGCTT	300
AATCAGACTC CAGAATTTAA AGCGATGATG GAAGCGGTTA AAAACAGGC TTTAGTGGAA	360
TTTTGGGCTA AAAACAGGC TGAAGAAGTG AAAAGATCC AAATCCCAGA AAAAGAAATG	420
CAGGATTTTT ACAACGCCAA TAAAGATCAG CTTTTGTCA AGCAAGAAGC CCATGCTAGG	480
CATATTTTAG TGAACCGA AGATGAAGCC AAAAGGATTA TTTCTGAGAT TGACAAACAG	540
CCAAAGGCTA AAAAAGAAGC CAAATTCATT GAGTTAGCCA ATCGGGATAC GATTGATCCT	600
AACAGCAAGA ACGCGCAAAA TGGCGGTGAT TTGGGGAAAT TCCAAAAGAA CCAATGGCT	660
CCGGATTTTT CTAAAGCCGC TTTCGCTTTA ACTCCTGGGG ATTACACTAA AACCCCTGTT	720
AAAACAGAGT TTGGTTATCA TATTATCTAT TTGATTTCTA AAGATAGCCC TGTAACCTAT	780
ACTTATGAGC AAGCTAAACC TACCATTAAG GGGATGTTAC AAGAAAAGCT TTTCCAAGAA	840
CGCATGAATC AACGCATTGA GGAATTAAGG AAGCACGCTA AAATTGTTAT CAACAAGTAG	900

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

289

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

ATGATAAAGA GTTGGACTAA AAAGTGGTTT TTGATTTTAT TTTAATGGC AAGCTGTTTT	60
GGTCATTTGG TGGCTACAAC CGGTGAGAAA TATTTTAAGA TGGCTAATCA AGCCCTTAAG	120
AGAGGGGATT ACCATAGAGC GGTGGCTTTT TATAAGAGGA GCTGTAATTT GAGGATGGGG	180
GTTGGTTGCA CGAGTTTAGG CTCTATGTAT GAATATGGCG ATGGCGTGGA TCAGAATATT	240
TCAAAGCCG TTTTTTATTA CAGAAGAGGG TGTAATTTGA GGAATCATCT CGCTTGCGCG	300
AGTTTAGGCT CTATGTATGA AGATGGCGAT GGCGTGCAAA AAGACTTTCC AAAGGCTATC	360
TATTATTATA GGAGAGGGTG CCACTTAAAA GGTGGGGTGA GCTGCGGTAG TTTGGGTTTT	420
ATGTATTTCA ATGGTACGGG CGTTAAACAA AATTACGCCA AAGCCCTTTC TTTTCTAAA	480
TACGCTTGCA GTTTGAATTA TGGCATTAGT TGTAACTTTG TAGGGTATAT GTATAAGAGC	540
GCCAAAGGCG TGGAGAAGGA TTTGAAAAAA GCCCTTGCGA ATTTTAAAAG AGGGTGCCAT	600
TTAAAAGACG GGGCGAGCTG TGTGAGCTTG GGATACTTGT ATGAAGCCGG TATGGATGTC	660
AAACAAAATG AAGAGCAGGC TTTGAATCTT TATAAAAAGG GTTGCTCTTT AAAAGAAGGG	720
AGCGGTTGTC ATAATGTGGC GGTGATGTAT TACACGGGTA AGGGAGCTCC AAAAGATTG	780
GAGAAAGCCA CTTCATATTA TAAGAAAGGG TGCGCTTTAG GCTTTAGTGG TAGTTGTAAG	840
GTGTTAGAAG TGATTGGCAA GGAGTCTGAT AATTTGCAAG ATGACGCGCA AAACGACACG	900
CAAGATAGCG TGCAATAA	918

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

TTGAAAATCT	TTTtagTTAT	TCTAAGCGTC	TTTTTTTTTTA	ATGGGTGTTT	TGGGCTAGCC	60
TATAAGACTC	CCATTTCAAA	CCCCCTATC	TCTTATGACC	CCTACACTAC	CACCATTGGG	120
AGCTTGATG	CTAAAAATTT	AAAAGAAAAC	CCTAAACATA	GTGCGGCCAT	TCTTTTAGAA	180
GACGGCTTTG	ATGCCTTGTT	GCACAGAGTG	GGTCTTATTA	GAATGAGCCA	AAAAAGCATT	240
GACATGCAAA	CTTATATCTA	TAAAAACGAC	CTTTCCTTCTC	AAGTGATCGC	TAAAGAACTT	300
TTAAACGCGG	CCAATCGTGG	GGTAAAAGTG	CGCATCCTTT	TAGATGACAA	CGGGTTAGAT	360
TCAGATTTTT	CAGACATCAT	GCTTTTAAAT	TTCCACAAAA	ACATTGAAGT	GAAAATCTTT	420
AACCCCTACT	ATATCCGCAA	TAAAGGCTTG	CGTTATTTTG	AAATGCTTGC	GGATTATGAA	480
CGCATTAATA	AACGCATGCA	CAACAAGCTT	TTCATCGTGG	ATAATTTTCGC	TGTCATTATA	540
GGGGGGCGCA	ACATTGGGGA	CAATTATTTT	GATAACGATT	TAGACACGAA	TTTTTTAGAT	600
TTAGACGCTT	TGTTTTTTTG	GGGGGTGCT	TCAAAGGCCA	AAGAAAGCTT	TGAAAATTAT	660
TGGCGATTCC	ACCGCTCTAT	CCCTGTTTCA	TTATTAAGAA	CCCATAAAAG	ACTCAAAAAC	720
AACGTTAAG	AAATCGCTAA	GCTCCATGAA	AAAATCCCTA	TCAGCGCTGA	AGACGCAAAC	780
GAATTTGAAA	AAAAAGTCAA	TGATTTTATA	GAACGCTTCC	AAAAATACCA	ATACCCCAT	840
TATTATGGGA	ATGCCATTTT	TCTAGCCGAT	TTGCCCGCCA	AAATTGACAC	GCCCTTGAT	900
TCGCCCATCA	AAATCGCTTT	TGAAAAAGCC	CTTAAAAACG	CTAAAGACTC	CGTTTTTATC	960
GCTTCATCGT	ATTTTATTC	AGGTAAAAAG	ATAATGAAA	TCTTTAAAAA	TCAAATTTCT	1020
AAGGGGATTG	AATTGAATAT	TCTTACCAAT	TCCCTTTTCAT	CTACGGACGC	TATCGTGGTC	1080
TATGGGGCGT	GGGAAAGGTA	TCGCAATAAA	TTAGTGCGAA	TGGGCGCGAA	TGTCTATGAA	1140
ATACGAAACG	ATTTTTTCAA	CCGCCAGATT	AAAGGGCGCT	TTAGCACCAA	ACATTCCTTA	1200
CACGGCAAGA	CAATTGTTTT	TGACGATGCC	CTAACGCTTC	TAGGGAGTTT	TAATATTGAT	1260
CCGCGCTCTG	CATATATTAA	CACTGAAAGT	GCGGTCTTGT	TTGACAACCC	GTCTTTTGCC	1320
AAAAGGGTGC	GTTTGTGCT	TAAAGATCAT	GCCCAACAAT	CATGGCATT	AGTCTTGAT	1380
CGGCATAGAG	TGATTGGGA	AGCTACAGAA	GAAGGCATCT	TAATCCATGA	AAAAAACTCG	1440
CCTGATACCT	CTTCTTTTT	GCGTTTGATT	AAAGAATGGT	CTAAAGTCCT	TCCTGAAAGA	1500
GAACCTTAA						1509

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

TTGAAAAATC	TCTCAACACT	TCTGGTGTTT	TTATTCTTTT	GTTTGGGGTG	TGTGAGCAAT	60
TTTAATGAAG	ACACTTACAC	GCTAGACTTA	GTTTTAGAAA	AAAAGATCCA	AGCCAGTAGG	120
AAAGGCGAAA	TCACCCAAGA	TAATGTGCCT	ATCATCACGG	CTATCGCTAC	GCATTTAAAC	180
GATGTGGATA	GCGGCACTTA	CTACGATCAT	GAGTATTTTT	TAGTGGAGAT	TTTCACGCAA	240

AATAACGACT	GGATAGATGA	TGGCTATATT	TCTTATGAAC	TTTTTGGCAC	AAAACCTACA	300
GGATCAGAAC	CTTTATGGGT	GCGAGAGATT	ACAAGAGATG	AATTTGATGG	CATTTTAGAA	360
ACCACGAACC	GGTGGAGCCG	AGCCTTTTTG	ATCGCTTTTG	ACAAATTGGA	TTATTTAGCG	420
GTGCAAGAAG	CCAACTAGA	GCTTGATGCC	TATAGTTTAG	GCAAAATTGT	TTTAAATTC	480
GCTTACCAAG	TCCCCTTACC	TCAATTTTAA				510

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1536

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

ATGAAAAAAC	TTCTTTATAC	CATGCTCGCG	CTTCTTTTAA	TCGGCCTTTT	AACGGCCTAT	60
CTTATCCTTT	TTACAGAATG	GGGGAATAAG	ATCATCGCTT	CGTATATAGA	GAAAAAATC	120
AATCCGAACG	AGCGTTATTT	GAGCGTTAAA	ACCTTTAAAT	TGAGATTCAA	CTCTTTGGAT	180
TTCAAAGCTC	AAGCCAACGA	TGATTCCACG	CTCATTCTTA	AGGGGGATTT	CTCGCTTTTA	240
ACGCAAAGCG	TAAATTTGGA	TTACCACATA	GACATTAAAA	ATTTACGCTC	TTTTAAGGAT	300
TTGATACCCT	ACCCCTTAAG	AGGGGCTATT	GTTACTTCTG	GGAATATCAA	AGGGCATAGA	360
AAAGCCCTTG	TAGTTCAAGG	CGTCTCCAAT	GTCGCTCAAT	CCCACACTGC	CTACAACGCC	420
CTTTTAGATG	ATTTCAGCT	TTCTCACTTA	AGTTTGAACG	CAAAAGACGC	CAATTTAGAA	480
GATTTGCTTT	ATTTAATCAA	CCGCCCCGCT	TATGCGAACG	CAAAAGTGTC	CTTACAAGCG	540
GATTTTAACT	CTCTAAAGCC	CTTAGAAGGG	CATTTGATCC	TAACAGCTAA	TAACGCTTTA	600
ATCAATAACG	CCCTAATCAA	TCAAATCTTT	CATTTAAACC	TTAAAGACAC	GCTCGTTTTT	660
AACCTCTCGC	ACTCAAGCGA	TTTTAAAGGA	AACAAAGCCA	TCAGCGATAC	CACCCTAACT	720
AGCCCTTTAG	TTAATTTTAC	AGCCCTAAAA	AGCGAATATT	CTTTCCCTGC	TTTAAAACTC	780
AACGCCCCCT	ACACTTTAGA	AATACCCCAT	CTAGCCAAAC	TCCAAAACAT	TACCAACCAC	840
CCCTTAAAAG	GGAGCTTGAC	TTTAAAAGGC	GATATAGAGC	AAAGCCCTAA	ACTCTTAAAA	900
GTCAGTGGCC	ATTCAAATTT	ACTAGACGGC	GCGCTAGACT	TCACGCTTTT	AAATAAAGAT	960
TTGAAAGCCC	GTTTTTCCAA	TATTTCCACT	TCAAAAGCCT	TAGATTTATT	CCATTACCCT	1020
AAATTTTTC	AATCCATTGC	AGACGCTAAC	TTGGATTATG	ACCTTATCTC	TAAGCAAGGC	1080
GTGTTGAAAG	CCAATCTCAA	GAACGCAAGA	TTCTCAAAAA	ATGCATTTCAG	CGATTTCTCT	1140
TATTCCATTT	CTCGTTTTGA	TATTACTAAA	GAAATTTATC	ACGATGCCAA	TCTAGTAAGC	1200
CAATCAACC	AGCAACGCCT	GCTCTCTGAT	TTGAGTTTAA	AAAGCCCCAA	AACCCAATTG	1260
AAAATCCATA	ACGGCTTGTT	GGATTTAAAC	ACCAAGCAAA	TGGACATACT	CATGGATGCG	1320
GAAATCTTAA	AATTCATCTT	TAAAATGAAA	CTTCAAGGCA	GCATGCACCA	GCCAAAATTT	1380
TCCCTCATTT	TAAACGAAAA	AGCCATTTCAG	CAAAACCTGC	AACAAGGCTT	GAAAGAAATC	1440
CTTAAAAACG	ACACCCTTAA	AAAAGGTTTA	GATCATTTGC	TTAAAGATGA	TAAACTCAAA	1500
GAAAAGCTTG	AAAAAGGGCT	TAAGGGGCTT	TTTTAA			1536

(2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 483 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...483
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

ATGTTTGGCA TGGGCTTTTT TGAAATCCTT GTGGTGTGTA TTGTAGCGAT TATTTTTTTA	60
GGACCAGAAA AATTCCCTCA AGCTGTCGTG GATATAGTGA AATTTTTTCG CGCGGTTAAA	120
AAAACGCTCA ATGACGCTAA GGACACTTTA GATAAAGAAA TCAATATTGA AGAAATCAAA	180
AAAGAAACCT TAGAGTATCA AAAACTCTTT GAAAACAAAG TGGAGAGTCT TAAAGGCGTT	240
AAGATTGAAG AATTAGAAGA CGCTAAAGTA ACTGCAGAAA ATGAGATTAA AAGCATTCAG	300
GATTTGATGC AAGATTATAA ACGCAGCTTA GAAACCAACA CGATTCCTAA CCATTTAAAT	360
GAAGAAGTTT CCAATGAAGA AGCTTTAAAT AAAGAAGTTT CAAGCGATGA ATCTCCTAAA	420
GAAGTCCAAT TAACAACCGA TAACAACGCC AAAGAACACG ACAAAGAAAA AGAGCATGTT	480
TGA	483

(2) INFORMATION FOR SEQ ID NO:265:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...243
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

ATGTTAAGAA TTTTAATCCC CTTACTCATT ATTGTGTGGG TTTTATGGCG TTTGTTTTTG	60
AGGCAAAAAC CCCACAAAGA TGACCACAGA GACAACCACT CTTACACGCA ACAAACCCCC	120

AAAGAATTAG AAGATCACAT GATTGTATGC TCTAAATGCC AAAC TTATGT CTCTAGTAAA	180
GACGCCATTT ATAGTGGGGC GGTAGCCTAT TGCAGTGAAA CTTGTTTGAA GGATAAGGGG	240
TAA	243

(2) INFORMATION FOR SEQ ID NO:266:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 645 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...645
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

TTGGATGGTT TGAAAAAGA AAGACAAGGA TTTTACAAGC AAGTGCATTA TTTAAGAATT	60
TTAATACTGA GTATGAGTTT TTAAATATT TTAAATGCTG AAAATTTGAG TTACATGTCT	120
TCTTCTTATC AAATAGGCAC GGTGTTTATG CGCCCCTTAA ACACCAACAA ACTTTTACAA	180
GGGGCTTCAA TCCTTCAAGG CTATGAAGTG AATCCTAAAA ACGACTGGGC TTATTCTAGG	240
TATTATTTCT TTATAGATTA TGGTAATGTG CTTTTCAATA ACGATTCCAC TTTGCAAGCG	300
AACATGTTCA CTTATGGGGT GGGAGGAGAT TTTATGGTCG CTTACGCTAA AAACCCTATC	360
AACCGCTGGG CTTTTTCTT TGGTTTGCAA CTAGCGGCTA ACACATGGAT ACTCAATAAT	420
AAAGTCAAAG ATTTGGTGGT GAATACTTGG GATTCATTGA AAGATTTCAA TTTTCATAAC	480
ACTTATTTTA GGGCTATCGG GAAATTTGGG GTGCAGTTTC GCACGATCGT TTTGTATCAT	540
AAGGTGGATG TGGAAATTGG CATGAAAATC TTTTTAACGC CTGAAAGGCG CAGCTTGTTT	600
GAAAGGAGTT TTTTGTTTTT TGTTTCGCAC TCGTGGCATT TTAA	645

(2) INFORMATION FOR SEQ ID NO:267:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

ATGAAACCAA CGAACGAACC TAAAAACCT TTTTTTCAAA GTCCCATTTGT TCTTGCGGTT	60
CTTGGAGGGA TTTTACTCAT TTTTTCCTA CGCTCTTTCA ATTCTGATGG CAGTTTTTCG	120
GACAATTTCT TAGCTTCTAG CACTAAAAAT GTGAGCTACC ATGAAATCAT ACAGCTCATC	180
AGCAATCATG AAGTGGGAAA TGTGAGTATC GGTCAAACCTT TGATCAAAGC CAGCCATAAA	240
GAGGGCAATA ATCGTGTGAT TTATATCGCT AAACGAGTGC TGATCTACCT TAGTGCCTTT	300
GTTAGACGAG AAAAAAATCA ATTATTCTGG TTTTGA	336

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

ATGTTAAGGG TTTTAAGCGT TGGTGTGTGTT TTTATTTTAC TAGGGTGTCA GTTTTTCAAC	60
AAAACGACTC TGCATTTAAA ATATAAGGAT TACCCCAAAA ACAGCCCTTT AAAAACCGCT	120
TCCACTTTAA CCCCCCTAA AATCTTTTTT AACGCTCATT TTGTGCCGCC CTTTTACCAA	180
AAAGAATTTA AAAAAGCGCT CGCCCAGCAA ATCGCTTATT TTTTAAAGGA TAAAAGCGCT	240
CTCACTTTCA ATATTTTCAGG CAATGTTTTT TTTTCTTTTG AAGAGAGTCC TAAGGATTTA	300
AAAGCCATTÀ AAGAAAGGCT TAAAAAGACG ATTGAGCCTA AACTGACCC AAAAGCCGTC	360
ATGCGTTTTT TAAACCTTCA AGCGAGCTTG ATTTTAGAAT GTGTCCCACA AACCGCTTGC	420
CCATTTGACA CCCTTTTAAT CCCACCGCT CTCAGCGTGC CTATTGATTA CGCCAATCGT	480
TTGGGCGATA ACCCCTCTCT TTTTCCCCAA GAAGATAAAT CCTATCATAA CGCTTTAATC	540
AAAGCCCTTA ATAAGGCTTA CTATTCTCTT ATGGAGGGTT TAGAAAAGCG TTTGAACGCT	600
ATAGAAAATG CGGCATGGCT TTAG	624

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

ATGAAAAATC AAGTTAAAAA AATTTTAGGG ATGAGTGTGG TAGCAGCGAT GGTGATCGTA	60
GGTTGTAGCC ATGCCCAAAA ATCAGGTATC AGTAAAAGCA ATAAGGCATA CAAAGAAGCG	120
ACTAAAGGCG CTCCTGATTG GGTTGTAGGG GATTTGGAAA AAGTGGCGAA GTATGAAAAA	180
TATTCAGGGG TCTTTTTAGG AAGGGCTGAA GATTTGATCA CTAATAATGA TGTGGATTAT	240
TCTACGAATC AGGCTACAGC CAAAGCTAGG GCTAATTTAG CGGCGAATCT AAAGTCCACT	300
TTACAAAAAG ATTTGGAAAA TGAAAAAAC AGAACGGTAG ATGCTTCTGG TAAAAGGTCC	360
ATAAGCGGCA CTGATACTGA AAAAATTCT CAATTAGTGG ATAAGGAATT GATCGCTTCT	420
AAAATGCTTG CCCGCTATGT CGGTAAAGAT AGGGTTTTTG TTTTAGTGGG CTTGGATAAG	480
CAAATTGTGG ATAAAGTGCG CGAAGAGTTA GGCATGGTTA AAAAGTAG	528

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

ATGAAAAAAA TCGTTGTGAG TTTATGCGTG GCGTTAGGTT TTTTAAGCGC GGATCCAGCG	60
CAGGCCAATA AAGCGATCAG TGATGCGGAT TTGATTGAAG AGATAAGGGA CTTGAAAAAA	120
ATCATCAGCG CACAAAACAC GGAGATTAAC CAATTGAAG AAGTGCAAGA AGTCTTATCT	180
GGGCAATTAG GGGACATGCG TAAGGATATA TTAAGCACTA GAGATTACTG TATCAGCTTA	240
AGGCCTTATA TTTATAATTG GCGCTAG	267

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 774 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

TTGAATAGCG GCTCTAACGC TTCATTGTAT GGCACAAGCG CCGGCGTAGA CGCTTTCCTT	60
AACGGGAATG TGGAAGCCAT TGTGGGCGGT TTTGGAAGCT ATGGTTATAG CTCCTTTAGC	120
AATCAAGCGA ACTCTCTTAA CTCTGGGGCC AATAACGCTA ATTTTGGCGT GTATAGCCGT	180
TTTTTTGCCA ACCAGCATGA ATTTGACTTT GAAGCTCAAG GGGCGCTAGG GAGCGATCAA	240
TCAAGCTTGA ATTTCAAAAG CACTCTATTA CAAGATTTGA ATCAAAGCTA TAATTACTTA	300
GCCTATAGCG CCACAGCAAG AGCGAGTTAT GGTATGACT TCGCGTTTTT TAGGAACGCT	360
TTAGTGTTAA AACCAAGCGT GGGCGTGAGC TATAACCATT TAGGTTCAAC CAACTTTAAA	420
AGCAATAGCC AATCACAAGT GGCTTTAAAA AATGGCGCGA GCAGTCAGCA TTTATTCAAC	480
GCTAACGCTA ACGTGGAAGC GCGTTATTAT TATGGGGACA CTTCATACTT TTATTTGCAT	540
GCGGGAGTTT TACAAGAGTT CGCTCACTTT GGATCGAATG ATGTGGCGTC TTAAACACC	600
TTTAAATCA ATGCCGCTCG CAGTCCTTTA AGCACCTATG CAAGAGCGAT GATGGGTGGG	660
GAATTGCAAT TGGCTAAAGA AGTGTTTTGG AATTTGGGCG TGGTTTATTT GCACAATTTG	720
ATTTCCAACG CAAGCCATTT CGCTTCCAAT TTAGGAATGA GGTATAGTTT CTAA	774

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

ATGTTTGAAG ATTTTATCG CACTACCTC TCTTTTAA GGTCTTATT GCTTTTATTG	60
GGTTTATTGT TGCCGTTTTC GCTTTGTATA GCTGATGAAT ATATTAGCAT AAGTGATGAT	120

TGGGATGAAA	GGGCGCGAAA	TCAGTGGGAT	GAAACTGCGC	GAAATCATAA	GACATATTAT	180
TTTGAAAATG	GTTTAGACCA	TTTAAATCAA	GGCCAATACA	AGCAAGCCTT	TAAAGATTTT	240
AAATTGGCGC	AAGAATACAG	CATCGGGCTT	GGCAACGTTT	ATTTAGCCAA	AATGTATTTG	300
GAGGGAAAGG	GCGTGAAAGT	GGATTACAAA	AAAGCGCAAT	TCTATGCACA	AAACGCTATC	360
AAAGGGTATG	GGAGCGGGTT	GTTAGGGGGC	GCTCTTATTT	TAGGACGCAT	GCAAGCAGAA	420
GGCTTAGGGA	TGAAAAAGGA	TTTGAAACAA	GCACTCAAGA	CTTACAGGCA	TGTGGTTCGC	480
ATGTTTTCTA	ATAAAAGTGC	AAATTTTGCT	AACAAATTTG	GATCAAACCT	TGCGGAATTT	540
ACTAGTATGC	TTATTGGATC	GCGATTCAAT	GATCTTTCAG	GTTTGAGCGC	GAATCCTATA	600
AAATTTGGAA	ATAAATTTGG	AATACTGT	AAGAAAGCCC	TTCAAATCAA	AGATAATACA	660
CTTCTTGGG	AAGACATTGC	TGAAATTTCA	AGCAATATTA	TTTTACTCAA	ACAACAAATG	720
GGGGAATCC	TTTATAGGAT	TGGGATCGCT	TATAAAGAAG	GGCTTGGCAC	TAGAAAGAAA	780
AAGGACAGG	CTAAAAAATT	CTTGCAAAAA	TCCGCAGAAT	TTGGCTATGA	AAAAGCCATG	840
GAAGCTCTGT	AG					852

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

TTGTGCAAAA	TTCCACTTTC	TCTAACGCTA	ATGGAGGCAC	GCTCAGTTTT	AACGCAGGAA	60
ATTGCTCAT	TTTTGCCGGA	AACAACCACA	TCGCTTTCAC	TAACCATTC	GGAACGCTCA	120
ATTTGTTGTC	TAATCAAGTT	TCTAACATTA	ACGTCACCAT	GCTTAACGCA	GCAACGGCCT	180
AAGATTAAACG	CCACTAATAA	CAATGTTTCC	GTGTCTCAAG	GCAATCTGTT	TATCAACGCT	240
AGCTGCGTGC	AACAAAGCGA	TCCAACGACA	GCTAGCGCCA	CAAACCCCTG	CACCACCGCT	300
CAAAATAACG	CTTCTTCTAG	TAATGCGTCA	AACAACGCGC	CAATCGCCTT	AAATAATAAC	360
GATGAAAGCT	TGGTGGTTAC	GGCGAATGGT	TTCAATTTTT	CAGGCAATAT	TTACGCTAAC	420
GGGGTGGTTG	ATTTTTCAAA	AATTAAAGGC	TCTGCAAACG	TTAAAAACCT	GTATCTTTAC	480
AATAACGCTC	AATTCCAAGC	CAACAACCTC	ACGATTTCCA	ACCAAGCGGT	ATTAGAGAAA	540
AACGCTAGCT	TTGTAACGAA	TAACCTAAAC	ATTCAAGGAG	CGTTTAACAA	CAACGCCACG	600
CAAAAAATAG	AGGTGCTTCA	AAATTTAGTG	ATCGCTTCAA	ACGCTTCTTT	AAGCACCAGG	660
ATTTATGGGT	TAGAAGTAGG	GGGGGCATTG	AATAATTTGG	GAGCGATCCA	TTTTAATTTA	720
GAAAATTCTC	AAACGCCTGT	AAATCCGCTC	ATTCAAGTAG	GGGGGATCAT	TAATCTCAAC	780
ACCACCCAAA	CGCCTTTTAT	GAATGTCAGC	GTGGCTAATG	GCGGAACTTA	CACTTTATTA	840
AAAAGCAGCC	GTTATATTGA	TTACAATATC	AACCCTAACA	GCTTGCAATC	GTATTTGAAG	900
CTCTATACCT	TAATCAATAT	CAACGGAAAC	CACATAGAGG	AAAAAAACGG	CGTATTGACT	960
TATTTGGGCC	AACGGGTTTT	ATTACAAGAT	AAGGGGTTAT	TATTGAGTGT	AGCACTACCT	1020
AACTCAACA	ACGCCTCTCA	AAACAACATT	TTAAGCCTTT	CTGTCCCTCA	CAACCAGATT	1080
AAAATGTCTT	ATGGTAATAA	AGTGATGGAC	TTTACCCCTC	CCACCTTACA	GGATTACATT	1140
GTGGGCATT	AAGGACAAAG	CGCACTCAAT	CAAATTGAAG	CTGTTGGGGG	GAATAACGCT	1200

ATCAAGTGGC	TTTCAACATT	GATGATGGAG	ACTAAAGAAA	ACCCGCTTTT	TGCGCCGATT	1260
TATTTAGAAA	ACCACTCTTT	AAATGAAATC	TTAGGCGTAA	CAAAAGATCT	TCAAAACACC	1320
GCAAGCTTGA	TTTCTAACCC	TAATTTTAGA	AATAACGCTA	CCAGCCTTTT	AGAAATGGCG	1380
AGTTACACCC	AACAAACCAG	CCGTTTGACA	AAACTCTCTG	ATTTTAGGGC	TAGAGAGGGA	1440
GAGTCCAATT	TTTCAGAGCG	CTTGTTAGAG	CTTAAAAACA	AGCGTTTTAG	CGATCCTAAC	1500
CCTAGTGAGG	TTTTTGTCAA	ATACTCTCAA	CTCAGCAAAC	ACCCCAATAA	CCTTTGGATT	1560
CAAGGGGTGG	GAGGAGCGAG	CTTTATTTCT	GGGGGCAATG	GCACGCTTTA	TGGCTTGAAT	1620
GTGGGCTATG	ACCGATTGGT	TAAAAGCGTG	ATCCTTGGGG	GTTATGTGGC	TTATGGCTAT	1680
AGCGGTTTTA	ACGGGAACAT	CATGCATTCT	TTGGCTAATA	ATGTGGATGT	GGGGATGTAT	1740
GCGAGGGCTT	TTTTGAAAAG	AAACGAATTC	ACTTTGAGCG	CGAATGAAAC	TTATGGAGGC	1800
AATGCGAGTC	ATATCAATTC	TTCTAATTCC	TTGCTCTCTG	TGTTGAACCA	ACGCTACAAC	1860
TACAACACCT	GGACAACGAG	CGTGAATGGG	AATTACGGCT	ATGATTTCAT	GTTCAAACAA	1920
AAAAGCGTGG	TGCTAAAACC	TCAAGTGGGC	TTGAGCTATC	ATTTCATAGG	CTTGAGCGGG	1980
ATGAAAGGTA	AAATGCAAAA	TCCAGCTTAC	CAACAATTCG	TCATGCATTC	AAACCCTTCT	2040
AACGAATCGG	TTTTAACGCT	CAACATGGGG	TTAGAGAGCC	GTAAATATTT	TGGTAAAAAT	2100
TCCTATTATT	TTGTAACGGC	GAGGTTGGGT	AGGGATCTTT	TGATCAAAGC	TAAAGGCGAC	2160
AATGTGGTGC	GTTTTGTGGG	TGAAAACACT	TTATTGTACC	GCAAGGGGGA	AATTTTTTAAC	2220
ACTTTTGCGA	GCGTGATCAC	AGGAGGCGAA	ATGCATTTGT	GGCGTTTGAT	GTATGTGAAT	2280
GCGGGGGTGG	GGCTTAAAT	GGGCTTGCAA	TACCAAGATC	TTAATATCAC	TGGGAATGTG	2340
GGCATGCGAG	TGGCGTTTTA	G				2361

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

ATGTTTAGAA	AACTAGCAAC	CTCTGTATCG	CTCATAAGCC	TACTAATCTC	CAACGCTCTT	60
TATGCTAAAG	AAATAAGTGA	AGCCGATAAG	GTCATTAAGG	CCACTAAAGA	AACTAAAGAG	120
ACCAAGAAAG	AGGCTAAACG	CCTCAAAAAA	GAAGCTAAAC	AGCGCCAACA	GATCCCTGAT	180
AATAAGAAAC	CTCAATATGT	CTCTGTTGAT	GACACAAAAA	CTCAAGCGCT	TTTTGATATA	240
TATGACACTT	TGAATGTGAA	TGACAAAAGC	TTTGGGGATT	GGTTTGGTAA	TAGCGCTTTG	300
AAAAACAAAA	CTTATCTCTA	CGCTATGGAT	CTATTGGATT	ATAACAAC TA	CTTATCCATA	360
GAAAACCTTA	TTATCAAAAC	AAGAGCGATG	GGAAC TTATG	CAGATCTGAT	TATCATCACA	420
GTTTCGTTAG	AACAAGTCAA	TGGGTATTAC	AATATTCTAA	AAGCGCTCAA	CAAACGCAAC	480
GCTAAGTTTG	TGTTAAAAAT	CAATGACAAA	ATACCTTATG	CCCAAGCGAC	TTTTTTGAGA	540
GTGCCAAAAA	GAAGCGATCC	CAACGCCCAC	ACGCTTGATA	AGGGAGCGTC	AATTGATGAA	600
AGCAAGCTTT	TTGAACAACA	AAAGAAAATG	TATTTCAACT	ACGCCAACGA	TGTGATCTGC	660
AGACCCAACG	ATGAAGTGTG	TTGCCCCCTA	AGAGATGAAA	TGGTAGCTAT	GCCCACTAAC	720
GATAGCGTTA	CTCAAAAACC	CAATATCATT	GCTCCTTATA	GCCTGTATAG	ACTAAAAGAG	780

ACAAATAACG	CCAATGAAGC	CCAACCATCA	CCTTATGCCA	CTCAAACCGC	TCCTGAAAAC	840
AGCAAAGAGA	AGCTCATAGA	AGAGCTAATC	GCCAACTCCC	AACTCATAGC	CAATGAAGAA	900
GAGAGGGAAA	AGAAACTCTT	AGCAGAAAAA	GAAAAACAAG	AGACTGAATT	GGCTAAATAC	960
AAGCTCAAAG	ATTTAGAAAA	TCAAAAGAAA	CTAAAGCTT	TAGAAGCAGA	GTTGAAAAAG	1020
AAAAACACTA	AGAAACCTAG	AGTAGTGGA	GTGCCTATTC	CTCCTAAAAC	AAGTGATTCT	1080
GATGAAACAA	TGAGAGTTAT	CAAAGAAAAA	GAAAACTATA	ATGGGTTATT	AGTGGATAAA	1140
GAGACCACGA	TCAAAAGAAG	CTATAAGGGG	ACTTTGATCA	GTGAAAATTC	TTACAGCAAA	1200
AAAACACCCA	TCAACCTTGA	GGACTTGAGA	AGCTTAGAAG	AAGAAATTAA	GAGCTACTAT	1260
GTCAAGTCTA	ATGGCTTGTG	TTACGCTAAT	GGCATTAACC	TCTATGTAAA	AATCAAAAAC	1320
GATCCCTACA	AAGAGGGAAT	GCTGTGTGGT	TATGAGAGCG	TTCAAAAAC	GCTTTCACCA	1380
CTAAGGGACA	AGCTCAAATA	CGACAAGCAG	AAGTTACAAA	AAGCGTTACT	GAAAGATTTA	1440
AAGTAA						1446

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

TTGCTTTCCC	GGTCTATGCC	CAAAATTCAC	GCCGTTTTCA	AAGCTTTTAT	CCCTATTCCA	60
TTCGCCCTCT	TCGCTATCCA	CTTCGTAGTA	TTGGGAATTG	GAAGCGTCTT	TAATCTTAAT	120
AGAATCAAAG	ATAAAAAATT	CATTCTCCGC	GCCAAAATAA	GCCACATCGC	CCAAGCCTAA	180

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

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ATGAGAAAAA CGATTTTCAGC GTTGTTTTTA TCAGCGTGTA TAGGGTTATC GTCTGTTCAT      60
GCGAGTAACG CTTTGATTTT ACAAACAGAT TTTAGCCTAA AAGATGGGGC CGTCTCGGCG      120
ATGAAAGGCG TCGCTTTCAG CGTTGATTCT AATCTTAAAA TCTTTGATTT AACGCACGAA      180
ATCCCCCGGT ATAACATTTG GGAAGGCGCT TACCGCTTGT ATCAGACCGC TAGTTATTGG      240
CCAAAAGGCT CGGTATTTGT GAGCGTAGTG GATCCGGGCG TAGGCACTAA TCGTAAATCG      300
GTGGTATTGA AAATAAAAAA CGGCCAGTAT TTCGTCTCTC CAGATAACGG CACGCTGACT      360
TTGGTAGCGC AAACCTTGGG GATTGATAGC GTGCGTGAAA TTGATGAAAA AGCCAACCGC      420
TTGAAAGGTT CTGAAAAATC CTATACTTTC CATGGCCGTG ATGTGTATGC TTACTACTGGG      480
GCGCGCTTGG CTTCTGGGGC GATCACATTC GAGCAGGTCG GGCCAGAGCT TCCTATAAAA      540
GTTGTTGAAA TTCCTTACCA AAAAGCGAAA GCCACAAAAG GGGGAGTGAA AGGCAATATC      600
CCGATTTTGG ATATTCAATA TGGCAATGTT TGGAGCAATA TCAGCGATAA ACTGCTCAAT      660
CAAGCAGGGA TCAAACGAAA CGATACAGTG TGTGTAAC TA TTTAAAAAT TCCAAGAAAC      720
AATACGAAGG GAAAATGCCG TATGTCGCGA GCTTTGGCGA TGTGCCAGAA GGCCAGCCGT      780
TGGTCTATTT AA                                          792

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(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

```

ATGAATATCA AAACCCATTC TTCAAATGAA AAAGAACGCT TTGTACGCAT AGAAGAGGAC      60
GAAAAGAAAG AATTATTCGC CGAAGCTACA AATGAAAATC CGCACGGCCT TTCTTTAATG      120
GCTTTAATAG GGGTGTGGT TTTTGGGGGT GCGTTTTTAG CTTATTAGT GCCTAAAATC      180
TATTTAAGCA ATAATATCTA TTATATTAGC CGTAAAATTA ATACCCTAGA AGATCAAAAA      240
CGCCTGCTTT TAGAAGAACA GCAAATCCTA AAAAACGAAT TAGAAAAAGA GCGTTTTTAA      300
TACTACATAG AGAATAGTGA AAATATTGGC GATATTGCGT TTAA                                          345

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(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2826 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

TTGCAACATA	AAACCATTAT	GGATAAGATC	ATTATTCAAG	GGGCTAGGGA	AAACAATCTC	60
AAAAATATCT	TTTTAGAAAT	CCCTAAAAAC	CAATTTGTTG	TTTTTACCGG	ATTAAGCGGT	120
TCGGGTAAAT	CCACTCTGGC	GTTTGACACT	CTATACGCTG	AAGGGCAAAG	GCGCTATTTA	180
GAGAGTTTGT	CTAGTTATGC	GAGGCAATTT	TTAGACAAAG	TGGGTAAGCC	TAATGTGGAT	240
AAAATTGAAG	GCCTAACCCC	AGCGATCGCT	ATTGATCAAA	AAACCACTTC	TAAAAACCT	300
AGATCCACTG	TGGGGACGAT	CACTGAGATT	TATGATTATT	TAAGGTTGTT	GTTTGCAAGG	360
GTTGGGGAGC	AATTTTGCCC	CACATGTTTA	GAGCCTATTA	GTTCTATGAG	CGCGAGCGAT	420
ATCATTCTCT	AAATCTGTCA	TTTAGAAGAA	AATTCTAAAA	TCATTATTCT	AGCCCCATT	480
ATTAAAGATA	AAAAAGGTTT	GTTTAACGAT	AAATTAGAGA	GTTTGCGTTT	GAAGGGGTAT	540
GTGAGGGCTT	TTGTTGATGG	GGTGATGGTG	CGTTTAGATG	AAGAAATCCA	TTTGCACAAA	600
ACCAAAAAAC	ACACCATTGA	AGCGGTGGTG	GATAGGGTGG	TTATCAATAG	CGAAAATGCT	660
TCACGGATCG	CTAGCGCGGT	AGAAAAAGCC	CTTAAAGAAA	GCTATGGGGA	ATTAGAAGTG	720
GAAATCTTGC	AAGACAACGC	ACCAAGTATT	AGGAAGCATT	ACAGCGAGCA	TAAGGCATGT	780
TTTAAGTGCA	AGATGAGTTT	TGAAGAATTA	GAGCCTTTGA	GTTTTTCCTT	CAATTCGCCT	840
AAAGGGGCGT	GCGAAAGTTG	TTTGGGTTTA	GGGACAAAAT	TTAGCTTAGA	TATTAGTAAG	900
ATTTTAGATC	CTAACACGCC	TTTAAATCAA	GGAGCGATTA	AAGTGATTTT	TGGGTATAAC	960
CGCAGTTATT	ACGCTCAAAT	GTTTGAAGGC	TTTTGCACTT	ATAATGGCAT	TGACAGCGCG	1020
CTTTGTTTCA	ACGAATTGAA	CAAAGAGCAG	CAAGACGCTC	TTTTGTATGG	GAATGGCACT	1080
GAAATCAGCT	TTCATTTTAA	AAACAGCCCC	TTGAAACGCC	CCTGGAAAGG	CATTATCCAA	1140
ATCGCTTATG	ACATGTTTAA	AGAGCAAAAG	GATTTGAGCG	ATTACATGAG	CGAAAAAACC	1200
TGTTCTTCGT	GTAATGGGCA	TCGCTTGAAA	GCCTCAAGTT	TGAGCGTCCA	AGTCGCTGGC	1260
TTGAAAATGG	CGGATTTTTT	AACTAAGCCC	ATTGAAGAAG	TCTATCATTT	TTTTAATGAT	1320
CCCACGCATT	TTAACTATCT	TAACGAGCAA	GAAAAAAGA	TCGCTGAACC	CATTTTAAAA	1380
GAGATTTTAG	AAAGGGTGTT	TTTTTTTATAC	GATGTGGGGC	TAGGGTATTT	GACTTTGGGG	1440
AGGGATGCGC	GAACGATTAG	CGGAGGGGAG	AGCCAAAGGA	TACGAATCGC	CAGTCAAATC	1500
GGGAGCGGTT	TGACAGGGGT	TTTGTATGTT	TTAGACGAGC	CTAGCATTGG	CTTGCATGAA	1560
AAAGACACGC	TCAAACATCAT	CAACACCCTT	AGGAATTTAC	AAAAAAAGGG	GAACACGCTC	1620
ATTGTCGTAG	AGCATGATAA	AGAGACGATT	AAGCATGCGG	ATTTTGTTGT	GGATATTGGG	1680
CCAAAGGCTG	GAAGGCATGG	GGGTGAAGTG	GTTTTTAGCG	GGAGCGTAAA	AGATTTATTG	1740
CAAAATAACC	ATTCTACCGC	CTTGTATCTC	AACGGCACTA	AAAAGATTGA	GCGCCCCAAA	1800
TTTGAACCCC	CTAAAGAAAA	GCATTTTTTA	GAAATTAAAA	ATGTCAATAT	CAATAACATT	1860
AAGAATTTGA	GCGTTCAAAT	CCCCTTAAAA	CAATTGGTGT	GCATTACGGG	GGTGAGCGGG	1920
AGCGGTAAAA	GCTCGCTGAT	TTTACAAACC	CTTTTACCCA	CCGCTCAAAC	CCTTTTAAAC	1980
CATGCTAAAA	AAAATCAAAG	CTTGAATGGG	GTGGAGATTG	TAGGGTTGGA	GTATTTGGAT	2040
AAAGTGATTT	ATTTAGATCA	AGCCCCCATA	GGCAAAACCC	CACGAAGCAA	CCCCGCCACT	2100
TACACGGGAG	TGATGGATGA	AATCAGGATT	TTATTTGCCG	AGCAAAAAGA	AGCTAAAATT	2160
TTAGGCTATA	GCACGAGCCG	TTTCAGCTTT	AATGTTAAAG	GAGGGCGGTG	TGAGAAATGC	2220
CAAGGCGATG	GGGATATTAA	AATAGAAATG	CACTTTTTTG	CTGATGTGTT	AGTCCAATGC	2280
GATAGCTGTA	AGGGCGCTAA	ATACAACCCC	CAAACTTTAG	AAATCAAGGT	GAAAGGCAAA	2340
TCCATTGCTG	ATGTGTTGAA	CATGAGCGTG	GAAGAAGCTT	ATGAATTTTT	TGCTAAATTTC	2400

CCTAAAAATCG	CTGTGAAGTT	AAAAACGCTT	ATAGATGTGG	GCTTAGGCTA	TATCACTTTA	2460
GGGCAAAACG	CTACGACTTT	AAGTGGGGGG	GAGGCTCAAA	GGATCAAATT	GGCTAAAGAA	2520
TTGAGTAAAA	AAGACACAGG	CAAAACCCTT	TATATTTTAG	ATGAGCCTAC	CACCGGTTTG	2580
CATTTTGAAG	ATGTGAATCA	CCTTTTACAA	GTCTTGCAAT	CTTTGGTGGC	GTTAGGCAAT	2640
TCCATGCTAG	TGATTGAGCA	TAATTTAGAC	ATCATCAAAA	ACGCTGACTA	CATTATAGAC	2700
ATGGGGCCTG	ATGGGGGGGA	TAAGGGCGGG	AAAGTCATTG	CGAGCGGCAC	GCCTTTAGAA	2760
GTGGCGCAAA	ATTGCGAAAA	AACCCAAAGC	TATACGGGAA	AATTTTtagC	TTTGGAATTG	2820
AAATAG						2826

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

ATGAATTACG	ATGTTTTAAT	GGGATTTTTA	GCACTAATCT	TGCTAATTCT	TTGGTATGCC	60
TATGGATTAA	GGCAATATCT	TAAATTAAAA	GATAAGAATA	AGAGATTAAA	AGAGAAATTA	120
CAACGCTGTA	ATTGTAATAT	TAAATTCCT	AGTATTCCTG	AAATGGCGCA	TAAACCTATC	180
ATTATGGATA	TTAAGGGGGA	ATTGCTACCA	CATCTTACAG	AGAGTTATAG	AAAATCAAAA	240
TTTAAGGAGT	AA					252

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

ATGAGAGTAA	TAATAAAGTT	TATGCTGATT	TCATTAAAAA	CATTCCTAAA	AATATTATTG	60
AAAATATTCC	TAAAAACCTT	CCAAAAGATT	TGGATAGTTT	GCGTGGTTAT	TTGGGGGTTG	120
GGCTGTAGTT	TTTTAAACGC	TAACAGCGTT	CAATTAGAAG	AAACGCTGAG	ACGAAATCCT	180
AAAAATCTTA	TTTGGCAACA	CTTTAAAAAG	AAGTTTAAAA	AGAGTAACAC	GATCCCTTAT	240
GCCCCTAATA	GCCGTTGGAA	ATATTTAGGC	ACAAGTATAG	GGATTTTGGG	CGTGTCGTTG	300
GTGATAGGGA	TTGTGGGGTT	GTATCTCATG	CCAGAGAGCG	TAACGAATTG	GGATAAAGAA	360
AAGTTTGGCG	TCAAAAGTTG	GTTTGAAAAT	GTCCGCATGG	GGCCAAAAC	AGACAATGAT	420
AGTTTTATTT	TTAATGAAAT	CTTGCACCCT	TATTTTGGGG	CTATGTATTA	CATGCAACCG	480
CGCATGGCTG	GGTTTAGCTG	GATGACATCA	GCGTTTTTTT	CTTTTATCAC	TTCTACGCTT	540
TTTTGGGAAT	ATGGCTTGGA	AGCGTTTGTG	GAAGTGCCTA	GCTGGCAGGA	TTTGGTGATC	600
ACGCCCTTAC	TAGGTTCCAT	TTTAGGGGAA	GGGTTTTACC	AGCTCACGCG	CTATATCCAA	660
CGCAACGAAG	GCAAGCTGTT	TGGCTCTTTA	TTTTTAGGGC	GTTTAGCCAT	CGCCCTTATG	720
GATCCTATCG	GTTTTATCAT	TAGGGATTTA	GGGCTTGGGG	AAGCCTTAGG	GATTTATAAT	780
AAACATGAAA	TCCGTTCTAA	TTTAAGCCCC	AATGGTTTGA	ATTTGACTTA	CAAATTTTAA	840

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 531 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

ATGAAACTTT	TTAACCCTCG	TTTAATCGTT	TTTATATTCTG	CGCTTCTTTT	AGGGGTAGGG	60
TTTTCTGTGC	CTTCTTTGCT	AGAAACTAAA	GGCCCTAAAA	TCACTTTAGG	TTTGGATTTA	120
AGGGGGGGGT	TGAACATGCT	TTTAGGGGTG	CAAACCGATG	AGGCTTTAAA	AAACAAGTAT	180
TTAAGCCTAG	CGTCTGCTTT	AGAATACAAC	GCTAAAAAGC	AAAATATCTT	GCTTAAAGAC	240
ATTAAATCCA	GTTTAGAGGG	GATCAGTTTT	GAGCTTTTAG	ATGAAGATGA	GGCGAAAAAA	300
TTAGACGCGC	TTTTATTGGA	ATTGCAAGGT	CATAGCCAGT	TTGAAATCAA	AAAAGAAGCG	360
GAGTTTTATA	GCGTGAAACT	CACCCCTTTA	GAGCAAGAGG	AATTGCGTAA	AAACACGATC	420
TTGCAAGTGA	TAGGGATCAT	TCGTAACCGC	TTGGATCGAT	TTGGCTTGGC	AGAGCCTGTA	480
GTCATTTCAGC	AAGGCCGAGT	AGAATTTTCG	TGCAATTGCC	CGGCATTAAG	A	531

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1311 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

ATGATGAAAT	TTTTTCTTTT	AAAGAAATTC	AGCGAATTTT	TAAACACTCA	AACGCATTTT	60
AACCTCAAAC	GCTTGAACGC	GTCTAGTTT	TTATTAGAGA	CTTTTTCTAA	AGAAAAACAC	120
GCCTTTGTTG	TGGATTTGAG	CGCGCCTTAT	ATTGGTTTGT	CCAAAAAACC	CCCAGAGAGC	180
GTTTTAAAAA	ACACTTTAGC	GTTAGATTTT	TGTTTGAATA	AATTCACCAA	AAACGCCAAA	240
ATTTTACAAG	CAAACGTCAT	TGATAACGAT	CGGATTTTAG	AAATCAAGGG	CGCTAAAGAT	300
TTAGCTTATA	AGAGTGAAAC	TTTATTTTGT	CGTTTAGAAA	TGATCCCTAA	AAAAGCCAAAT	360
CTCATGATTT	TAGATCAAGA	AAAATGCGTG	ATAGAGGCTT	TTCGTTTTAA	TGACAGGGTG	420
GCTAAAAACG	ATATTTTAGG	GGCATTGCCT	CCTAATATTT	ACGAGCATCA	AGAAGAGGAT	480
TTGGATTTTA	AGGGATTGTT	GGACATTTTA	GAAAAAGATT	TTTTATCCTA	TCAGCACAAA	540
GAATTGGAAC	ACAAAAAAA	TCAAATCATC	AAGCGATTAA	ACGCCCAAAA	AGAACGCTTG	600
AAAGAAAAAT	TAGAAAAACT	AGAAGATCCT	AAAACTTTAC	AGCTGGAAGC	GAAAGAATTG	660
CAAACCTCAAG	CCTCATTGTT	GCTCACTTAC	CAGCATTTAA	TCAACAGGCG	TGAAAATCGC	720
GTGATTTTAA	AGGATTTTGA	AGATAAAGAA	TGCATGATTG	AAATTGATAA	GAGCATGCC	780
TTAAACGCTT	TTATCAATAA	AAAATTCACT	CTCAGCAAGA	AAAAGAAACA	AAAATCGCAA	840
TTCTTGTTAT	TAGAAGAAGA	GAATCTGAAA	GAAAAAATCG	CTTTTAAGGA	AAATCAAATC	900
AACTATGTTA	GAGACGCTGC	AGAAGAAAGC	GTTTTAGAAA	TGTTTATGCC	GGTAAAAAAC	960
TCTAAAATCA	AACGCCCGAT	GAACGGGTAT	GAAGTGCTGT	ATTATAAGGA	TTTTAAAATC	1020
GGTTTAGGGA	AAAACCAAAA	AGAGAATATC	AAGCTTTTAC	AAGACGCAAG	AGCGAATGAT	1080
TTGTGGATGC	ATGTGAGAGA	TATTCCTGGA	TCGCATTTGA	TCGTTTTTTG	CCAAAAGAAT	1140
ACGCCTAAAG	ATGAGGTCAT	TATGGAATTA	GCCAAAATGT	TGATTAAAAT	GCAAAAAGAT	1200
GCGTTTAATG	GTTACGAGAT	TGACTACACG	CAACGAAAAT	TTGTCAAAAT	CATCAAAGGA	1260
GCTCATGTCA	TTTACTCAA	ATACCGAACT	ATTAGTCTAA	AGGACACTTA	A	1311

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

ATGGGACAAA	CTAAAGAAAT	TATAACGACG	CTTTTACCCC	TTTGGTGTT	GTTTCTTATT	60
TTTATTTTT	TGATCGTTCG	CCCGCAACGC	CAACAGCAA	AAAAGCATAA	AGAAATGATA	120
GAGGGCTTGA	CTAAGGGCGA	TAAAATTGTC	ACTCAAGGAG	GGCTGATCGT	TGAAGTGCTT	180
AAAGCGGAAG	CGAATTTTT	TAGCGTGAAA	CTCAATGATG	ACACCACCGC	TAAACTTTCT	240
AAAACTATG	TAGCGTTCAA	ATTAGACGAA	GAAACAACAC	CCAACAACAA	CTAA	294

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

TTGAAGTTTC	AAATTGTGAG	TTTGTATTG	GCTTTTTTAT	TAGCCTCTTG	TTTGCCCCCT	60
AAGGGCCATC	ATTCTGGTTT	GGTGAATATG	TATATTGCGC	ATCAAGGCCA	GAGCGTACGC	120
ACTTATTGGC	GCAAAGTGGA	TAGAGGAGTT	GTGCGCAAAC	ACAATGAAAC	GCTTAAAGAA	180
AACCCCAAAA	TAAAGCTCAA	AGACCCTAAG	GGGCCTTTGT	TCATGCTAGG	GAGCAATCGT	240
TTCATGCTTT	TATGGAAAAA	CCGCTATACT	TTAGCTAAAG	TCCAATCGTT	CAAGCTAGAG	300
CCTGGGTTTT	ATTACTTGGA	TTCTTTTAGC	GTGGAAACTC	AAAAAGGCAT	CTTGCAAAGC	360
GCTCCTGGCT	ATTCATACAC	CAAAAATGGC	TACGATTTTA	AGAACAACCG	CCCCTTTTTC	420
CTAGCCTTTG	AAGTCAAACC	TGACAGCAAG	ATCGTTCTCC	CTAGCGTGGA	ATTGAGCTTG	480
ATTAAAACCC	CTAGAGGCTT	TTTAGGGGTG	TTTTTATTTG	ACAACAACGA	AAAGGGGGCT	540
AATACCCCAT	GGATTGAGGG	GAGCTTGAAT	TTAAAGCTTA	AAAACGCTTC	TTTTAAAGAC	600
GCATGGGAGT	TGGAACGATA	A				621

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

ATGAGAAAGG	TTATCATAAT	GAATGGTTAT	TTGAGGGTAA	AAACCCCGTA	TTTTTTAGCG	60
TCGGTCGTTT	TGACTTTTTG	GACTTTTAAT	TCTTTTATGA	GCGCGAAAGA	TAAGCACCAT	120
TTTTTAAAAA	AAGTTACAAC	CACCGAGCAA	AAATTCAGTT	CTAGTGCCCC	AATTTTCATGG	180
CAAAGCGAAG	AGGTGCGTAA	TTCCACAAGC	TCTCGCACGG	TGATTTCCAA	CAAAGAACTC	240
AAAAAAACGG	GGAATTTGAA	TATTGAAAAC	GCCTTGCAAA	ATGTGCCAGG	GATTCAAATC	300
AGAGACGCTA	CAGGCACGGG	CGTGCTGCCT	AAAATTTTCGG	TGCGCGGTTT	TGGTGGGGGG	360
GGTAACGGGC	ATAGCAACAC	CAACATGATT	TTAGTCAATG	GTATCCCCAT	TTATGGCGCG	420
CCGTATTCCA	ATATTGAACT	GGCGATTTTC	CCTGTAACTT	TCCAGTCAGT	GGATAGGATT	480
GATGTGATTA	AGGGGGGAAC	GAGCGTCCAA	TACGGCCCTA	ACACTTTTGG	AGGCGTGGTG	540
AATGTCATCA	CTAAAGAAAT	CCCCAAAGAG	TGGGAAAATC	AAGCGGCTGA	AAGGATCACT	600
TTTTTGGGGG	GCTCCTCTAA	TGGGAATTTT	GTCGATCCCA	AAGAAAAAGG	CAAGCCCTTA	660
GCCCAAACCT	TAGGAAACCA	AATGCTGTTT	AACACTTATG	GGCGAACGGC	TGGGATGTTG	720
GGTAAATATA	TAGGCATTAG	CGCTCAAGGC	AATTGGATTA	ATGGGCAAGG	TTTCAGGCAA	780
AATAGCCCTA	CAAAGGTGCA	AAACTACTTG	TTGGATGCGA	TTTATAAGAT	CAATGCGACC	840
AATACTTTTA	AAGCTTATTA	CCAGTATTAT	CAATACAAC	CTTACCATCC	AGGCACTTTG	900
AGCGCGCAAG	ATTACGCTTA	TAACCGCTTC	ATCAATGAGC	GCCCTGACAA	TCAAGATGGA	960
GGGCGAGCCA	AGCGCTTTGG	GATCGTGTAT	CAAACTACT	TTGGCGATCC	GGATAGGAAA	1020
GTGGGGGGCG	ATTTTAAATT	CACTTATTTT	ACGCATGACA	TGAGTAGGGA	TTTTGGGTTT	1080
TCCAACCAAT	ACCAAAGCGT	GTATATGAGC	GGTCAAAATA	AGATTTTACC	CTTTAAAGGC	1140
AAGGGAGAAA	TCAGCGCAAA	AAACCCTAAT	TGCGGTCTGT	ATTCTTATAG	CGACACGAAT	1200
AGCCCTTGCT	GGCAATTTTT	TGACAATATC	CGCCGATCCG	TGGTGAATGC	CTTTGAGCCA	1260
AAACTCAATC	TTATCGTCAA	TACTGGTAAA	GTCAAACAAA	CTTTTAACAT	GGGAATGCGC	1320
TTTTTAACTG	AAGATTTATA	CCGCCGATCC	ACCACCAGGA	AAAACCCTAG	CATGCCTAAT	1380
AATGGGAGTG	GGTTTGATGC	AGGAACTTCA	CTCAATAATT	TCAACAATTA	TACCGCTGTG	1440
TATGCCAGCG	ATGAAATCAA	TTCAATAAC	GGCATGCTAA	CGATCACGCC	GGGCTTGAGA	1500
TACACTTTTT	TAAATTACGA	AAAAAAGAC	GCTCCTCCCT	TTAAGGTGGG	TCAAACCCCA	1560
AAAACCACGA	AAGAGCGTTA	TAACCAATGG	AATCCGGCA			1599

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 768 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

ATGAAAAAGA	TTTTTTTAGG	TATGGCATT	GCCTTTAGTG	TGTCCATGGC	AGAAAAAAGC	60
GGCGCGTTTT	TAGGAGGGGG	GTTTCAATAT	TCTAATTTAG	AAAACCAAAA	CACCACCCGC	120
ACCCAAGCG	CTAACAATAA	CACCCCGATA	AACACTTCAA	TGTTTGCGAA	CAATCAAGCG	180
GCTCCAGCCC	AAGAAACGCC	AAGCGTGATC	AACACCAATA	ATTACGGGCA	AATGTATGGG	240
GTAGATGCCA	TGGCAGGGTA	TAAGTGGTTC	TTTGGCAAAA	CCAAACGCTT	TGGCTTTAGG	300
ACTTATGGAT	ACTACAGCTA	TAACCATGCG	AATTTGAGCT	TTGTAGGCAG	TAAGCTTGGA	360
ATCATGGATG	GCGCATCTCA	AGTGAATAAC	TTCACCTTATG	GCGTGGGCTT	TGATGCGCTC	420
TATAACTTCT	ATGAAAGCAA	AGAGGGCTAT	AACACAGCAG	GGTTGTTTCGT	GGGCTTTGGA	480
TTAGGAGGGG	ATTCGTTTAT	CGTTCAAGGA	GAGAGCTACT	TGAAATCTCA	GATGCAAATT	540
TGCAACAACA	CCGCCGGCTG	TTCAGCGAGC	ATGAACACGA	GCTACTTCCA	AATGCCTGTG	600
GAATTTGGTT	TTAGGAGCAA	TTTCTCTAAA	CACAGCGGGA	TTGAAGTGGG	CTTTAAATTG	660
CCTTTATTTA	CCAACCAATT	CTATAAAGAA	AGGGGCGTAG	ATGGATCGGT	AGATGTGTTC	720
TATAAAAGGA	ATTTCTCTAT	CTATTTTAAC	TACATGATCA	ACCTCTAA		768

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1002 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

ATGCTAATCG	CTCGCTTTAA	AAAAGCTTTA	ATTTCTTATT	CTTTAGGGGT	TCTTCTTGTT	60
TCATCGTTAT	TAGGCGTGGC	TAACGCTTCT	AATCAAGAGA	TCCAAGTCAA	GGATTATTTT	120
GGGGAGCAAA	CCATAAAGCT	TCCTGTTTCT	AAAATAATCT	ACTTGGGCAG	CTTTGCAGAA	180
GTGCCTGCCA	TGTTCAATAC	TTGGGATAGG	GTCGTGGGCA	TTTCGGATTA	CGCTTTTAAA	240
TCTGATATTG	TTAAAGCCAC	TCTCAAAGAT	CCTGAACGCA	TTAAACCCAT	GAGCAGTGAT	300
CATGTGGCGG	CGTTGAATGT	GGAATTATTA	AAAAAGCTTA	GCCCTGATCT	TGTGGTAACC	360
TTTGTGGGTA	ACCCTAAAGC	GGTAGAGCAT	GCGAAAAAAT	TTGGGATTTT	ATTCCTTTCT	420
TTCCAAGAAA	AAACCATTGT	AGAGGTCATG	GAAGATATTG	ACGCTCAAGC	TAAGGCCTTA	480
GAAGTTGACG	CTTCTAAAAA	ATTGGCTAAA	ATGCAAGAAA	CTTTGGATTT	TATCAAAGAG	540
CGTTTGAAAA	ATGTCAAAAA	GAAAAAGGGG	GTGGAGCTTT	TCCATAAAGC	CAATAAAATC	600
AGCGGCCATC	AAGCCCTTGA	TTCAGATATT	TTAGAAAAAG	GGGGCATAGA	CAATTTTGGC	660
TTGAAATACG	TCAAGTTTGG	GCGCGCTGAC	ATTAGTGTGG	AAAAAATCGT	TAAAGAAAAC	720

CCTGAGATTA TTTTATTTG GTGGATAAGC CCGCTTAGCC CTGAAGACGT GTTGAACAAC	780
CCTAAATTTT CCACTATCAA AGCCATTAAA AACAAGCAAG TCTATAAGCT CCCCACAATG	840
GATATTGGCG GACCTAGAGC CCCACTCATT AGTCTTTTAA TCGCTTTAAA AGCCCACCCCT	900
GAAGCGTTTA AGGGCGTGGA TATTAATGCG ATAATCAAAG ATTACTATAA AGTGGTCTTT	960
GATTTGAATG ACGCGGAAGT TGAACCCTTT TTGTGGCACT GA	1002

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

ATGAAAAAGC AAATCTTGAC AGGTGTTTTG TTATCAGTTT TGGCAGTGAG TTCTGCATAC	60
GCTCACAAAG ATAAAAAAGA CGCTAAAAAA CCTGAGTTAA GCTCTCAATT AGTGGCTCAC	120
AAAGATAAAA AAGACGCCAA AAAACCTAAA AACTCAGTGG CCTAA	165

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

ATGTATAAAT TAGGAATATT TTTATTAGCC ACCTTACTAT CAGCTAACAC GCAAAAAGTG	60
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AGCGATATTG	CTAAAGACAT	CCAACATAAA	GAAACCCTTT	TGAAAAAAAC	CCATGAAGAA	120
AAAAACCAAC	TGAACAGTCG	TTTGAGTTCT	TTAGGCGAAG	CGATCCGCTC	TAAAGAGCTT	180
CAAAAGGTTG	AGATTGAACG	CCAAATGGTC	GCCTTAAAAA	AGAGTCTTGA	AAAAAATCGT	240
AACGAAAAGT	TGGTGCAAGA	AAAAGTCCTA	ACCAACTACC	GCAAGTCTTT	AGATCATTTG	300
CAAAAACAAC	GATCGTTTTT	ACAAAAGAGA	GTGTTTGATA	CGCTTTTAGA	GGATTTTCTT	360
TTCTCACAA	GCCTTAAAGG	GCAGAATTTA	GCCTCTTCTA	ATGATGTGAT	TTTGCTAAGT	420
GGCGTTTGA						429

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

ATGGATAAAA	ACAACAATAA	TAATCTCCGC	TTGATTTTAG	CGATCGCTCT	GTCTTTCTTG	60
TTTATCGCTC	TTTATAGCTA	TTTTTTCCAA	GAACCAAACA	AAACAACAAC	CGAAACCACA	120
AAGCAAGAAA	CAACCAACAA	CCACACAGCA	ACAAGCCCCA	CCGCGTCCAA	TACCATCACC	180
CAAGATTTTA	GCGTTACCCA	AACCATCCCT	CAAGAGAGTT	TGTTAAGCAC	GATTTCTTTT	240
GAACATGCCA	AAATTGAAAT	TGATTCTTTA	GGGCGCATCA	AACAGGTTTA	TCTCAAAGAT	300
AAAAAGTATC	TAACCCCTAA	AGAAAAGGGC	TTTTTAGAGC	ATGTGAGCCA	TCTTTTTAGC	360
TCCAAAGAAA	ACTCGCAACC	CTCCCTAAAA	GAGCTCCCCC	TTTTAGCAGC	CGATAAACTC	420
AAGCCTTTAG	AAGTGCCTTT	TTTAGACCCC	ACGCTCAATA	ATAAAGCGTT	CAACACCCCT	480
TATAGCGCCT	CAAAAACCAC	CCTTGGGCCT	AACGAACAGC	TCGTTTTAAC	CCAAGATTTA	540
GGCACTCTTA	GCATCATTA	AACCCTGACT	TTTTATGATG	ATTTGCATTA	TTGA	594

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

ATGGCGTGTT	GGCATAAAAG	ATTGGCAGTT	GGTTGTTGTA	TCGTTTTATT	GTCATGCGTA	60
ATGAGTGCTA	ATAATGTTAG	TATCGTTAGA	GACGATCCGC	CCCTTGATCC	AACGCTCCCT	120
GCATGGATTT	ATTCTGTTGC	GTTATTGAAA	GTGTATTTTA	GCGATGGGAC	TTATAAAGAA	180
GGCTATGCGA	CTTTGCTAGA	AAACGGGCGT	TATATCGCTT	CTTCTGAAAC	GCTCTATTCT	240
AATGGCTTGT	ATCCTAAAAT	GATTTTAGCC	AAAATGCAAG	ACAGCAGTGC	TAAAGAGCTG	300
ATTTGCATAG	CCAGCTTGCA	CCTTGAAGCG	ATGGATAGGG	ATCAAGGGCT	TTCGCTCTTA	360
AAAACCGCCG	ATTTTAGAGA	CGATTATTGT	CATAAAAGAG	AAGAGAGCTA	TTATCATGCA	420
AGGATTTATG	CCAAATACGC	TCAAACCTTC	CATTCAAATC	CTTATACCAA	TCAAAAAACA	480
CCCCTTCCG	ATCTCTACTA	CCCGGCGTTA	AATGAGGGGA	ATTCTTTTTC	CATACAGACA	540
ACGGACATTT	CTGTGGCTGA	ACTTTTGAAA	TCTAAAAAGT	TTCTTTCGCT	TGATGCTTCT	600
TTTAAAAAGG	GGAGCGTGTT	GTGGGGAGGG	AGGCCTTATT	TTAGCGAGGT	AGGGGAGTTT	660
ATGGGAATGG	CTAGCAGCAC	TTAGAAAAAC	CAAGAAAGTT	TGGTGATTAT	CCCTAAAGAA	720
AAGATTGCGC	GATTTTAAAG	CGCTCTAAAA	AATCAAAATA	TTTTTCCAAA	CATTCCCTAA	780

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

ATGAAAAATC	AACACAAAAA	TCCCCTAACA	AAAGCTTTAA	TGAAAACTTA	TCCATATAAC	60
CATTTTTTAT	TTTTCTGCTT	TATTCTAGGA	GCGTTTTTAT	TAGGTTTGCT	CAGTCCAGCT	120
TATGCTTTAA	GTATTATCAC	CACTAAAGAA	ATTGACGCTA	ATTTGCTTAA	TGGAGCGATA	180
GAAAGCAGGG	TGGTGTTAGG	CAAGAGGGTG	TTTAAAGTAG	AAGCTCATGG	GTTTTATTTT	240
AGAAACAATG	CGACTAACAG	CATAGATATA	GAAATCACCA	GTCTTTTAAG	AGACAATCAA	300
TCGTTTCCTT	TGACTAGCAG	TGCTAAAACC	AGTTTAAAAA	TACCTCCTAA	CGCCAAGATT	360
AAAAAATCCA	CTATCCTTGT	TTTGAAAGGC	GAGAACGCTG	AAGAAGTGGC	TAAGATTTTA	420
GGCGTTAGCA	AAGAAGAATA	CCAAAAGCTA	GAAAACATCG	CTCAAACCAA	AGCGGCTAAT	480
GACCCTATGT	ATGCTAACAC	GCCTTTTAGT	AATGGTTCTG	ATAGTTCCTT	TTACGATAAC	540
AATCCTAATA	GCCCTAGCAA	TAACGCTATC	AATGGCAAAG	ATGGCGCAAA	TGGGAGTAAC	600
GGCTATGGGG	CAAATGGCAA	TGATGGGGTA	AATGGGATCA	GTGGGAGTAA	TGGTGCAAAAT	660
GGGAGTCATT	CAAATAATAA	TGCAATAGGC	AGTGGTATTG	ATACAGATGG	CGTGTTAGGG	720

GTGGATGGGG	TGAATGGCTC	TAGTTCCTTCA	AGTGGCGGCT	CTGTAGGGGG	TTATGAGAAT	780
AATTTCACTA	ATCATGGCTC	TACTAACAAAT	AACACAGGAG	GGTATGACAA	TTTTAATAAT	840
GGCAGCTCAA	GTGGTGGGAG	TTTAGGGAAT	GGGGGGCTTT	TCCCTATTCC	TTTTGGTAAT	900
GGAGACACAA	ACAATTCCAA	TAATTCCTACT	AACACCACTA	GCCCAACTAA	TGGCAGTAGT	960
TCTAATAACG	CCACTAATCC	TAGTTCGCAA	GAAAACAATT	ACTCCAGCCA	GTATTGTAAA	1020
GTGCCAGAGT	TAAGCCCCAA	CAACACGATG	AAACTAGATG	TTATCGCTAA	AGATGGCTCT	1080
TGTATTTCTA	TGAACGCTTT	AAGAGATGAC	ACTAAATGCG	CTTATAGATA	CGATTTTGAA	1140
GCCGGTAAAG	CCATCAAGCA	AACGCAATAC	TACTATGTAG	ATAGGGAAAA	TAAAACGCAA	1200
AATATCGGTG	GTTGTGTGGA	TTTACAAGGC	GCTCAATACG	CCATGCAACT	TTACAAAGAT	1260
GACAGCAAAT	GCGCCTTACA	AACCACGAGC	GATAAAGGTT	ATGGTATGGG	GAAAACGCAA	1320
ACCTTTCAAA	CTGAAATCGT	GTTTCGTGGG	ATGGACAATT	TAATCCATGT	CGCTGTGCCT	1380
TGCAGCGATT	ATGCAAGGGT	GCAAGACAGG	ATTGTTAGGT	ATGAAAAAAA	TGATAAAACC	1440
CAAACCTTAA	CGCCTATAGT	GGATCAGTAT	TATAATGATC	CTAACAACCC	TAACAAGCAA	1500
GAGATTTTAA	ATCGTGCGGAT	TGCCACCCAA	TTAAGCTCGC	AATATCAAGA	ATTTGCATGC	1560
GGTCAATGGG	AATACAATGA	CGCTAAATTA	GAAGCCAAAA	GACCTACAAT	GCTAAAAAGC	1620
TATAACAAGC	TTAATGGAGA	ATGGGTAGAA	GTTACGCCCT	GTAATTTTGA	AGCAGGGATT	1680
AAAAGCGGTG	CGGTTGTTAG	CCCTTATGTG	ATGGGCGTGC	CTAGTTCTAA	AGTCTTAAGC	1740
GATATTACTA	CAAGCCATTA	TTTTAGGATA	GAAAGGAAAA	ATTATGGTGA	GAGAGAACAA	1800
TGCCAAAAAC	TTTATGGAGT	CAATCGTTGC	CAACCGCAAT	ATTCCATACT	GATCCTAGTA	1860
TCACCGATTG	GAGCGCCACT	TACAAAACCA	CTACCACCCA	AACCACTCAA	CCTTATTTAC	1920
GCCCAGCCCA	AGATAATGAA	AAACACCCCA	CAACCTATAA	TCTTATCACC	ACTCAAACCA	1980
CCATCAACAG	GACTCAAAGC	GTTTTGA				2007

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 987 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

ATGACTTATA	AAGAACGACT	CATACACGAA	AAAATATTAA	ACCAAAACGA	CAAGGGTTTT	60
AAAACAGAAC	TGCGCATTTT	GAGCGTTTTT	ATCGTGGAAT	TTTTGGTGAA	TATTCTAGGG	120
TTTATGTTGG	CTAAAATGCC	TCATTTTTTG	TTTTTAAGGT	GCGTTAAAGC	TTTAGCGTGG	180
CTCATGAAAA	CTTTTGATAG	GCGCCGTTAT	TTTGACGCTA	AGGCCAATTT	GGATTTGTG	240
TTTGGGGATT	CTAAAAGCGA	AGAAGAAAAA	AAAAGGATCA	TTAAAAAGGG	GTATGAAAAT	300
TTTGCTTTCA	TTATTTTAGA	AACCATTAGA	GTGATCTTTA	TCCCTAAAGA	TGAATACGAC	360
GCTCGTTTCA	CGCTCATCAA	TGAAGAAAAC	GTGTGGAAGT	CCTTAAACAA	GGAAGGCCAA	420
GCGATCACTT	TGTGCATGCA	TTTTGGCTAT	TGGGAAGCGG	TAGGCACGAC	TTTGGCGCAA	480
TATTATGAAA	ATTATGGTAG	GGGGTGTTTG	GGGCGTTTGA	CTAAATTCGC	TCCCATCAAT	540
CACATGATCA	TGAGTAGGCG	AGAGGCGTTT	GGGGTGCGTT	TTGTCAATAA	AATAGGGGCG	600
ATGAAAGAAC	TCATTAAAAAT	GTATAATCAA	GGCAATGGCC	TGGTGGGGAT	TTTAGTGGAT	660

CAAAATGTCG	TGCCTAAAGA	CGGGGTGGTG	GTGAAATTTT	TCAATAAAGA	CGCTACGACC	720
ACCACGATCG	CTTCTATTTT	GTCGCGCCGT	TACAATATAG	ACATTCAGCC	GGTATTCATT	780
GATTTTAACG	ATGATTATTC	GCATTACACA	GCGACTTATT	ACCCAAGTAT	CCGCTCTCAA	840
ATCACTGATA	ACGCGCAAAA	CGATATTTTA	GAATGCACGC	AAGCCCAAGC	GAGTTTGTGC	900
GAAGAGGTGA	TTAGAAACCA	CCCGGAAAGT	TATTTTGGT	TCCACAGGCG	TTTAAAAGC	960
ACCCACCCTG	AGATTTATCA	AAGATAG				987

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

ATGTTATATC	TAAGGAAAGA	AAATGGGGTT	AGGACACTAA	TAAGTTTAGG	GATTTTGTTA	60
AGCGTTTTGA	ATGGCGATGA	TCTGAGATTG	TATTCAAAAC	CTTTGGTCTA	TTCGGCTGGA	120
AGTGGGATTA	TTGGGATTGA	TATTGACAAA	CGGACATTCT	ATAAACGAGC	GTTTCGCTTTC	180
ACGATGAAAT	CGTTGTTTGG	TGAAAACCTG	CTTTTGTTTG	TTAAATTGAA	GCATTCTGCG	240
TTGATGAGCA	AACACATGAA	AGGGCCTTTA	GAAAACCGCC	ACCACCATTC	TTTCGCTAAA	300
AATTATGAAA	AAGCGGTTAA	TGGTTGTCAA	AAATATGTCC	ATATCAAATT	GCCTGAAGGC	360
GCTCCTAGCA	ACTTCCAATC	AGGCTCATAC	ATGGCGACTA	TGGTGATGCG	TTTTTAA	417

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 987 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

ATGCGTAAGG	TTTTATACGC	TCTCATGGGC	TTTTTGTTGG	TTTTTAGTGC	TTTAAAAGCC	60
GATGATTTTT	TAGAAGAAGC	GAACGAAACA	GCCCCAGCGA	ATTTAAACCA	CCCCATGCAG	120
GATTTAAACG	CCATTCAAGG	GAGCTTTTTT	GACAAAAACC	GCTCCAAAAT	GTCCAACACT	180
TTGAACATTG	ATTACTTTCA	AGGGCAAAC	TATAAAATCC	GCTTGCGTTA	TGCGATGGCG	240
ACTTTATTGT	TTTTTTCAAA	ACCCATTAGC	GATTTTGTTT	TGGGGGATAA	GGTGGGTTTT	300
GATGCGAAAA	TTTTAGAAAG	CAATGATCGC	ATTTTACTCA	TCAAACCCCT	ACAAATCGGC	360
GTGGATTCTA	ATATCAGCGT	GATTGATAGC	GAGGGTAAGA	TTTTTTCTTT	CTATGTGTTT	420
TCTACCACTT	TCACCAGCTC	CAAACACCCT	AATTTACAGG	TTTTTATAGA	AGATAAAAAC	480
TATTACACTA	ACGCTTTTAT	CAAGCCCCAA	AAAGAAAATC	AAGAAAATAT	GTCTGAAAAT	540
GCCCCATAAG	ATGCCCAAAA	AAATAATAAG	CCCCTAAAAG	AAGAAAAAGA	AGAACTAAA	600
GAAAAAGAAG	AAGAGACTAT	AATTATTGGC	GATAACACCA	ACGCGATGAA	AATTATTAAA	660
AAAGACATCC	AAAAAGGCTA	TAAGGCTTTA	AAAAGCTCTC	AAAGGAAATG	GTATTGTTTA	720
TGGGCTTGTT	CTAAAAAATC	CAAACTCTCC	TTAATGCCTA	AAGAAATCTT	TAACGACAAG	780
CAATTCACCT	ATTTCAAATT	TGACAAAAGA	TTAGCACTCT	CTAAATTCCC	GGTGATTTAT	840
AAGGTCGTTG	ATGGTTATGA	TAATCCGGTG	AATACAAGGA	TTGTGGGCGA	TTACATTATC	900
GCTGAAGACG	TTTCTACTAA	ATGGACTTTA	AGGTTGGGTA	AGGATTATCT	GTGTATCCGT	960
TTTGTCAAAA	GGCGCAAAGG	TGAATAA				987

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1008 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

GTGATGTTTC	ACAAAGCCCT	TATTACCTTT	ATCGTTCTAT	GGTTTTTTTT	GAATGGCTTA	60
GGGGCTTATG	ATTTCAAGCA	TTGTCAGGCT	TTTTTTAAAA	AAGCGAGCCT	TCAAAAAGGG	120
GGCGTGGCTT	TAAAGGAATT	GCCTAAGGGC	GTGTATTTGT	ATTATCTAA	AACCTACCCC	180
AAACACGCTA	AAGTCATCAA	ATCCGATCCT	TTTATAGGGC	TGTATTTGTT	GCAAAGCGCG	240
CCAAGCGAGT	ATGTTTATAC	ATTAAGGGAT	TTAGACAAAG	ACGCCCTTAT	AAGACCCATG	300
GCCAGTATAG	GGGCTAATCA	AGCCACAGAA	GCGCGATTAT	TGGTAGGGCA	AAAAGGCTAT	360
GACCGCTACG	CTCAAAATTC	ACAAAAAACC	CAAAAAAATG	GCGTTATCAG	CAATATTTGT	420
TATCAAAATG	CAGGGCTAGG	GGTAGGGGGG	AACGGCTTTA	TAGAAACGAA	ATTCATCAAG	480
CGCTTTTTTA	ACCAACAAGA	GCCTTATTAT	GGGGATATTG	GGGTGCGTTT	AGAAGAACGT	540
CATAAGCGTT	TGGTGGTAGC	GCAATTTGAT	CCCTTTTTCC	CTAAAAACCC	TTTTTTAAAA	600
AACGATGAAA	TCCTAGCGAT	CAATGATTAC	AAGATCCACT	CGTTAGCGGA	GTTTGAATGG	660
GTGGTGAGCA	ATCTTTCATA	CCAAAGCCTC	GCCAAAGTGA	AAATCAAACG	AAACCATCAA	720

314

ATCAAAGAAG	TAACGCTCAA	AGTCAATAAA	CGCTATGGGG	GGTTTTTGCT	CAAAGACACT	780
TTTTTAGAGC	GCTATGGCAT	CGCTTTAGAC	GAGCGTTTTA	TCATCACTAA	AATAGGCGCT	840
CATTTGCCCA	AAGGCTTGGA	TTTTTTAAAG	CTTGGGGATA	GGATTTTATG	GGTGAATCAT	900
AGAAGCGTTT	CGTTCAACCC	GAAAGCTTTA	AGAGAAGCGT	TAAGCACGCC	TAAAATTGAA	960
TTATTAGTCT	GGCGTCAAGG	CTTTGAATTT	TACATTAAAG	TCCGTTGA		1008

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

ATGCTAGGAA	CGGTTAAAAA	AACCCTTTTT	GGGGTCTTGT	GTTTGGGCGC	GTTGTGTTTG	60
AGAGGGTTAA	TGGCAGAGCC	AGACGCTAAA	GAACCTTGTTA	GTTTAGGTAT	AGAGAGCGTG	120
AAGAAACAAG	ATTTCGCTCA	AGCTAAAGCG	CATTTTGAAA	AAGCGTGTGA	GTTAAAAGAA	180
GGTTTTGGGT	GTGTTTTTTT	AGGGGCGTTT	TATGAAGAAG	GGAAAGGAGT	GGGAAAAGAC	240
TTGAAAAAAG	CCATTCAATT	TTACACTAAA	GGTTGTGAAT	TAAATGATGG	TTATGGGTGT	300
CGCCTACTAG	GAAATTTATA	CTATAACGGA	CAAGGCGTTT	CTAAAGACGC	CAAAAAAGCC	360
TCACAATATT	ACTCTAAATC	TTGTGAATTG	AACCATGCTG	AAGGGTGTAC	GGTCTTAGGA	420
AGCCTACACC	ATTATGGCGT	AGGCACGCCT	AAGGATTTAA	GAAAGGCTCT	TGATTTGTAT	480
GAAAAAGCTT	GCGATTTAAA	AGACAGCCCT	GGGTGTATTA	ATGCAGGATA	CATGTATGGT	540
GTGGCAAAGA	ATTTTAAGGA	GGCTATCGTT	CGTTATTCTA	AAGCATGCGA	ATTAAAAGAT	600
GGTAGGGGGT	GCTATAATTT	AGGGGTTATG	CAATACAACG	CCCAAGGCAC	AGCAAAGGAC	660
GAAAAGCAAG	CGGTAGAAAA	CTTTAAAAAA	GGCTGCAAAT	CAAGCGTTAA	AGAAGCATGC	720
GACGCTCTCA	AGGAATTAAA	AATAGAGCTT	TAG			753

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

ATGCGTTTAT TGATCGCGCT AGTTTTGTTC TTATGGTGGT TAAATTTAGG CGCTAAAGAA	60
GCGGATTTCA TCTCTGATTG GGAATACGGA CTGGCCCTTT ATAAAAACCC TAGGGGTGTT	120
GCGTGCGCAA AATGCCATGG CATTAAAGGC GAACAACAAG AAATCACCTT TTATTATGAA	180
AAAGGCGAAA AAAAAATCCT TTACGCCCTT AAAATCAACC ATTTGGATTT TAAAACCTTT	240
AAAGACGCTT TGAGTTTGGG CAAAGGCATG ATGCCTAAAT ACAACCTGAA TTTAGAAGAA	300
ATCCAAGCGA TTTACCTTTA CATCACCTCT TTAGGGCATA AAGACGAGCG TAAGGATCCT	360
TCCAAGCCTT AA	372

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 543 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

ATGTTAAACA AGTTTAAAAA AATCGTTGGC GTGGGTGTGT TAGTGGGCTG TTTAGGGGTT	60
TTGCAAGCTA AAAACAGCTT ATTTGTCTTA CCTTATGAGC AAAGAGACGC TCTCAATTCT	120
TTAATTTCTG GGATTAGCAG CGCTAGAGAG AACGTGAAAA TCGCTATTTA TAGTTTCACG	180
CACAGAGATA TTGCAAGAGC GATTAAAAGC GTAGCGAGTA GGGGGATTAA GGTGCAAATC	240
ATTTATGATT ATGAAAGCAA TCACAATAAC AAGCAATCCA CTATTGGCTA TTTAGACAAA	300
TACCCTAACA CGAAAGTGTG CTTATTAAAG GGGCTTAAGG CTAAAAACGG GAATTATTAC	360
GGCATCATGC ACCAAAAAGT AGCGATCATT GATGATAAAA TCGTGTTTTT AGGCTCAGCG	420
AATTGGAGCA AAAACGCTTT TGAAAACAAT TATGAAGTGC TTCTAAAAAC CGATGACACA	480
GAGACGATCC TCAAAGCCAA GAGTTATTAT CAAAAGATGC TAGAAGGTTG CGTTGGGTTT	540
TAA	543

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...423
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

ATGAGAAGGA GTTTGGCTTT TTGCCTTTTA GCTTTGCTTG GATTACAGGT TTTAGGTGCT	60
AGAGACTTTT CGCAACTCAA AAACGAAGAA CTTTAAAAAT TAGCAGGAAC TCTGCCTTCT	120
AATGAAGCGA TTGATTATCG CATGGAAGTG TCTAAACGCC TTAAAGCCTT AAGTGCTGAA	180
GACGCTAAGA AATTCGCGC GAATTTTCAGC CGGATCGCTA GGAAGAATCT TTCTAAAATG	240
AGCGAAGAGG ATTTCAAAAA AATGCGTGAA GAAGTGCCTA AAGAATTAGA AGAAAAAACC	300
AAAGGTCTAA GCGCTGAAGA AATCAAGGCA AAAGGACTTA ATGTGAGCGT TTGCAGCGGC	360
GATACGAGAA AAGTTTGGTG TAGGGCTGTT AAGAAAAAAG ACGAACATTG CTCTCCTAAG	420
TGA	423

(2) INFORMATION FOR SEQ ID NO:301:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 459 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...459
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

ATGAAAAAAG CGTTGAAAAT ACTTTCTGTT GGCGCGTTGC TATTTGTGGC TTAAACGCC	60
AAAGATTTCA GCAAAACAAG CGATGAAGAT TTGGCTAAAA TGGCTGGCGT TGTCGCTCCG	120
CAGGATATTG TGGATTACAC AAAAGAGTTG AAAAAGCGCA TGGAAAAGAT GCCTGAAGAC	180
AAGAGAAAGG CGTTCCATAA ACAATTGCAT GAATACGCGA CTAAAAACAC AGACAAAATG	240
ACCGTGGCGG ATTTTGAAGC CCGCCAAAAA GCCATTAAAG AAGCGCTTAA AAAAGGCAAT	300
ATGGAAGACA TGGATGATGA TTTTGGGTTG AGATCATGCA AGCATGGGAA AAAGCACAAA	360
CACGATAAGC ATGGCAAGAA GCATGGCAAA AAACATGACA AAGATCATGA CGATAAAGAC	420
CATGACCACC ATGATGAAGA TCACAGCGAT AAGCACTAA	459

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

```

ATGCTAAAAA AGTTATTGCT CATTTCACCTA TTTTtagggT TTTTAAGAGC AGAGGGCGAA      60
CATTATGAAA TCATCGCTGA ACTTTCcAAG GCTTTTTTTGA AAGCCAAAGA GGTTTTGACT      120
GCGATCAATA AAACCTGTAT TGAAACCGGG CATGATCGCA CTCAAATACG CCTTCAAAAC      180
GATTTTTTTAG AGAATTTGTC TCAAACAGAG CAACAATTTG ATGATTATTT TGAAAAGGAT      240
TTTAAAAGCG TAGGGGTTTT AAAAACCTTG CTTAAAGACA TCCAATCCTT AGAAAAAACT      300
TCCAACAAGC TCGTATGCGT TGCCCCAAAA AACGCTAAAA ATTTTGAAAT ATTAGAGGGA      360
GCGATAACGC AAATCATAGG ATTAGAAGAG CAGATGAATC AATTTATCAA TGGCGCGAAA      420
TAA                                          423

```

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

```

TTGAGTGGGG AACTGAGATT GTCTTGGTGG TTAGTGGCTC GTTGCAAAAC ATTGTTTCGTT      60

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CTTTTTTGCG AAGGATCAGC GTTTCTTCA TTATTGATTT CATCAATTTT ATTTTCGTTA	120
TTGATCAGAT CATTCACCTC TTTGGTGACT TTTTCATCTT CTTCTTCATG CTCAATCTTT	180
TTTATATCCT TATTAGGTTG A	201

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

TTGGTGTTA GTGGCTCGTT GCAAAACATT GTTCGTTCTT TTTTGCGAAG GATCAGCGTT	60
TTCTTCATTA TTGATTTTCA CAATTTTATT TTCGTTATTG ATCAGATCAT TCACTTCTTT	120
GGTGACTTTT TCATCTTCTT CTTTCATGCTC AATCTTTTTT ATATCCTTAT TAGGTTGATT	180
GATTGATTG TTTTGAGTGG TTTTAGTGTT GTTTTGGTGC GATTGGGAYG ATTTTTTAGG	240
CTCATCTTTG CATGCGCTCA ACACGCTTAA	270

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

ATGAAAAAAT CCCTTTGTTT GTCTTTCTTT CTGACCTTCT CTAACCTCT TCAAGCCCTT	60
--	----

GTCATTGAGC	TTTTAGAAGA	GATTAAAACT	TCGCCGCATA	AAGGCACTTT	TAAGGCTAAA	120
GTCCTTGATT	CTAAAGAACC	AAGACAAGTT	TTAGGCGTTT	ATAATATCTC	CCCACACAAA	180
AAACTCACGC	TCACATATCAC	TCACATATCC	ACGGCAATCG	TCTATCAACC	CCTTGATGAA	240
AAACTTTCTT	TAGAAACGAC	CTTAAGCCCT	AACCGCCCTA	CTATCCCCTAG	AAACACCCAA	300
ATCGTTTTTT	CTTCAAAGA	ATTGAAAGAA	CCGCACTCAA	ACCCAATACC	TTCTTAA	357

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 738 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

TTGAAAGCGT	TTCAAACCTT	TGGCGTGTTT	GGGACAAGCG	TGATCACTTG	CATCACCGCT	60
CAAAACACAC	AGGGCGTGCA	TGGGGTGAT	CCATTGAGTG	TAGAGAGCGT	GAAAGCGCAA	120
ATCCTAGCTA	TTAGAGATGA	TTTTTCGATC	AAGGCGTTCA	AAATGGGGGC	GTTATGCAAC	180
GCTCAAATCA	TTGAATGCGT	AGCGAACGCT	TTAGAAACTT	GTGATTTTGG	GTTGTGCGTT	240
TTAGATCCGG	TGATGGTGCG	AAAGAATGGG	GCTTTGCTTT	TAGAAGAGGA	GGCGATTTTA	300
AGCTTAAAAA	AACGCCTTTT	ACCTAAAACC	AATTTACTAA	CCCCTAACCT	CCCTGAAGTC	360
TATGCGCTCA	CAGGCGTTCA	AGCGCGAGAC	GATAAAAGCG	CTTCAAAGC	GATGGGTGTT	420
TTAAGGGATT	TAGGCGTTAA	AAACGCTGTG	ATTAAAGGGG	GGCATAACAG	ACATTTTCAA	480
GGGGAATTTA	GCAACGATTG	GGTGTTTTTA	GAAGACGCTG	AATTTACTTT	AAGCGCCAAG	540
CGATTCAACA	CCAAAAACAC	GCATGGCACG	GGTTGTACTT	TGTCTAGCTT	GATTGTGGGC	600
TTACTCGCTC	AAGGGCTGGA	TTTAAAAAAC	GCTATCACAA	AGGCTAAAGA	GCTTTTAACT	660
ATCATCATTC	AAAACCCCTT	AAACATTGGG	CATGGGCATG	GGCCTTTGAA	TTTGTGGAGC	720
ATCAAAAAGC	ATGTTTGA					738

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

GTGCTAGAAA	AACAAGATAA	AGACCTTTTT	CTTTTGCAAG	TGGGTAACAG	GATTATCCCC	60
ACCAAAAGCG	AACAGGAATT	AAAAATCAAT	CAGCCTTATT	TTGCGACTAT	GCAAAGAAAT	120
CAGCTGGGCG	ACATTGTGCT	TAAAAATTTA	GTGCCTGCCC	CAAAAATCTT	AGACGCATTG	180
GACGATTTGC	CCGTTATTGA	AATGAAGAAA	TTAAAAGAAA	TATTGAGCGC	CAAAGACAAC	240
ACCCCCCTAA	AAGAATACAA	AGAACTTTTG	AGCGAAAAAT	TAATCCATGC	TAAAAGCTCG	300
CAAGAGTTTT	TGAATACAGC	CAACATGCTT	TTAAGCTTGC	AATCGCAGGT	TTTAAGCTTT	360
GTGGTTGAAA	ACGAACGCAA	AAAAGCTTTT	TTACAGATGA	AAGCCAAAAA	ACAAAGCGTT	420
GATTTTTTACG	CTCTGTACCC	TAACCTGGGC	GAAATTGGCG	GCGTTATTTA	TTTAAAAGAA	480
AAAGAGAAAC	AGCTTTTTTTT	AAAAACCACC	CTCCAAAGGA	CCAAAGAGGT	TTTAAAAGAG	540
GCTCAAAACA	CCCTTTTAGG	CTTTTCTTTT	GTGGAAATTG	TGTGCGAAAA	AACCCCATG	600
CTTTTTCCT	TTGAAGATCG	CTTATTGGAC	ACGCTAGGGT	AA		642

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

ATGTCAGATG	AAATCACGCA	AGAAAACGAG	TTAGAAATTA	ACTCCAATAA	TCAAAACCAA	60
GAGCCAAAGG	AAGTAGAAAA	AATGCCATTG	AATAATATTC	AAAAAGCTAA	GAAATTAAAA	120
AACCACGCCA	ATTTAATTGT	TCGACGCACT	GATGAGTTAG	ATAAGGTTAT	CAATAAGCGT	180
GAAAGCTTGC	AAAGAGAGTT	TAAAAGACGC	ATTAAGCACT	TGGATAACAA	GATTGAAACG	240
CTTAGTAACA	ATATTGAAGA	ATTAAAAAGA	AAGTAA			276

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 519 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...519
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

ATGAAAAAAT ATCAAAACAA ACGAAAGCTG GGTAAGCGTA TCAATTGCTT TATTTCAAAT	60
GAATGTAAGG ACATTTTAGA AAATTATTTA AAAGTCAAAA AAATTAGCGT TACTGAGTGT	120
ATAGAAAGCC TTTTATTAGC CCTAGACCCT AGCAAAGAAA CACTAAGAGC AAGGGATTTT	180
TATGAAAGTT TGTTTAAAGT CATCAGTCTT AACCAACATG TCTATAAAGA ACTCATGGCT	240
AATGGTAATA ACATTAACCA AATAGCCAAG AACACCAACA TTGCCATTAA GTATAACAAG	300
CCCTTTTATT TGCAGAATTT AGCATTCTTA GAAGAGATTT TTAAGGTTAT GGATACACTT	360
AATAAAAATG TAGAAGAATG TAAAAAAATC TCTTTGGAAT TATTACTTCA AATTTACAAA	420
GAACAAAAAA GCCAAACAGA ATTTAACGCC ATTTCAAAAA TTCTCAACGC TCTTAATGAA	480
AAACAATCTA CTACTGAGCC AAAAAAGGAC AACGCATGA	519

(2) INFORMATION FOR SEQ ID NO:310:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 963 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...963
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

ATGAACACTA ATTTAAAGAA AGCCTTGTTT TTAAC TACTC TTGGTTATTT GCAAGCTAAT	60
GAGGGCTTTT TAGCCATTAT GCCTGATGAA AATAAACAAG AAGACATTTT TCAAGAACAG	120
AAATTAGAAC ACAAATGGA GCAAAAAATT GCTCCACAAA ATACCCTTAA AAAGCAACAA	180
TCAGCTCCTT TACAAAGTGC TGAGTTGTTA CAAAGTCAAG TTAAAAGAGA AGTTAAAGAG	240
CAAAAAAAGT CTCAAAAACA CCTAGTAGCT ATGCAAACTA AAAATGGCTT TTTCTTAGGC	300
TCAGAAATTG CTATTACAGG CACAAGTTTA AAACAAAGTT TAAGCCTTAT TTCTAATGCT	360
ACAGATGATT TACTCACTTA TAGCAAGACT TCTAAAAACG CTAATTTTAA TATGGGACTA	420
TTAATAGGTT ATCAGCATTA TTTTGGAGCT AGTAAAAGGC ATGGGATTAA AATCTCAAGC	480

CATTTGTATG	GAGGCACACC	TAGTGATGTA	AGCACAGACA	TAAAAATTTA	CAAATCTAAA	540
GTTAGCACCA	ATTACACGCC	TTTAAATTTT	GGCATAGATG	TGAAGTATTT	GTTTGATTTT	600
TTAAATGTCA	TTAAAAAGAA	CCGCCATACA	CTAGGATTAA	GTGTGGGCTT	TGGCTGGCGT	660
ATGCAATATT	ATTTTGCAAA	AATAGACCCC	ATAAAAACCA	GCCATAGTGA	GTTTATCACT	720
AATAAACCTA	AAGATATTTT	TAATCATGGT	TTTTATCCCA	CTATTGGACT	ACATTATTAC	780
TTAAACCATC	ATCAATTGTA	AGTGAATTAT	CGCTTTGGAG	GAGCAATTAA	CTATCACTCA	840
GTTGTGCCTA	GCAAAATTGT	CGTTCAAAAC	GGGAATTTTA	AGGGCGAGGT	CTTGTTTCT	900
AATTTTCTTA	CCAAAGCGAC	TAATTC TAGC	TACATAGCGT	TCAACTACGC	TTATTTATTT	960
TAA						963

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

TTGGCTATTA	AAAGGGAAAA	AATGAAAAAT	AGCGCGCCTT	TAAAGAATAA	AGTTTTTTTGT	60
GGGTTATACG	TTTTAAGTTT	AAGCGCTTCT	GTGCAAGCGT	TTGATTATAA	AAATTGAAGTT	120
TTGGCAGAGT	CCTTTTCTAA	AGTTGGCTTT	AATAAAAAAA	AGATTGACAT	AGCTAGGGGG	180
ATTTATCCTA	CAGAGACTTT	TGTAACCGCT	GTGGGTCAGG	GCAATATTTA	TGCGGATTTT	240
TTATCCAAAA	GCCTTAAAGA	TCAAGGGCAT	GTTTTAGAGG	GAAAAGTCGG	CGGCACAATC	300
GGTGGGATTG	CTTATGACAG	CACGAAATTC	AATCAAGGCG	GATCGGTTAT	TTATAATTAT	360
ATCGGTTATT	GGGATGGCTA	TTTAGGGGGT	AAAAGGGCCT	TGCTTGATGG	CACGAGTATC	420
CATGAGTGCG	CGCTTGGCTC	TGATGGCAAG	GTGATTGATT	CTATAGCGTG	CGGGAACGCT	480
AGAGCCAATA	AAATCCGCCG	TAATTACTTG	ATGAATAACG	CTTTTTTAGA	ATACCGCTAT	540
AAGGATATAT	TTGCGGCTAA	AGGGGGGCGT	TATCAATCCA	ATGCTCCTTA	TATGAGCTCT	600
TATACGCAAG	GCTTTGAAAT	CAGCGCTAAA	ATCAAGGATA	AAAATGAGGG	GAGCCATAAA	660
TTATGGTGGT	TTAGCTCATG	GGGTAGGGCG	TTCGCTTATG	GGGAGTGGAT	TTATGATTTT	720
TACTCTCCAA	GAACCGTGAT	TAAAAACGGG	CGCACTCTAA	ATTATGGTAT	CCATTTAGTG	780
GATTACACTT	ACGAAAGGAA	AGGGGTTAGC	GTCAGCCCCT	TTTTCCAGTT	TTCGCCCCGG	840
ACTTATTATA	GCCCTGGGGT	GGCTGTAGGC	TATGATAGTA	ACCCTAATTT	TAATGGCGTG	900
GGCTTTAGAT	CCGAAACGAA	GGCTTATATT	TTGCTCCCTG	TCCATGCCCC	CCTTAAAAGG	960
GATACTTATC	GTTACGCTGT	GAAAGCTGGC	ACCGCTGGGC	AAAGCCTGCT	CATTAGGCAA	1020
CGATTTGATT	ACAATGAATT	TAACTTTGGG	GGAGCGTTTT	ATAAAGTATG	GAAAAACGCA	1080
AACGCTTACA	TAGGCACGAC	AGGAAACCTT	CTAGGCATTG	ATTTTTGGAC	CAATAGCGTT	1140
TATGATATAG	GGCAAGCCTT	AAGCCATGTG	GTAACCGCTG	ATGCCGCTC	TGGTTGGGTT	1200
TTTGGTGGAG	GCGTGCATAA	AAAATGGCTG	TGGGGGACTT	TGTGGCGTTG	GACTAGCGGC	1260
GCTTTAGCCA	ATGAAGCGAG	CGCGGCTGTT	AATGTGGGCT	ATAAGATCAG	TAAGAGTTTG	1320
ACAGCGAGCG	TGAAATTAGA	ATATTTGGGC	GTGATGACGC	ATTCAGGCTT	TACGGTAGGG	1380
AGTTACAGAC	CCACGCCCGG	CTCTAAAGCA	CTTTATTTCAG	ACAGGAGCCA	TCTAATGACA	1440

ACCCTTAGCG CCAAATTCTA A

1461

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

GTGTGCATTA TTTTGTATGC AGACATAAAA AAAGAGAACC AAGAAAGCGA TGCAGGTTTT	60
GATAACAAGC TTAAGCATAT TCGTGAAAAA TTCAAAGAAA AAGGGACTGA TTTTCCCCAA	120
GAACAAATCT TTTTATTCCC TAACAATCAA GATGATGGCG ATTTAGAAAC CCTATTATTA	180
GAAATTGCTA AACACGATGA ATTTCTTAAA TGCTTTGAAG GATACTTAGA ATGTATTAAA	240
AGTAAAGAAC ATTATAAACC GATTAAAAAC ATAAGAAAAA ATATGCTGTA TGCCTATTTA	300
GAAGCGCTTG GATTAGAGAA TTTGACCAAG ACCAATATAG ATGTTTTTGA TAGTAAAGGT	360
AAAATAAAGA GTAGATATGA AGAAACTAC AAAAAATTAA CAGAAGAAGT TATTGATTTT	420
AGCTCGAATT CTCTCATGCC CCTTAAAAAT TTTCTAGGGC AATTCGCAGA AAATAAACAA	480
AAAACAAATC CTAATAATTT CTAA	504

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

ATGGTATTGA	AAACAAAATT	AAAAATTATA	AGCTCGGTGA	TTTTGAGTAC	TTTATTGTGG	60
GTGGGTGCT	CAAGCGAAAT	GGCGACTTAT	CAAAATGTGA	ATGACGCCAC	TAAAAATACG	120
ACTGCAAGTA	TTAATAGCAC	GGATTTATTG	CTAACCGCTA	ACGCGATGTT	AGATTCCATG	180
TTTAGCGACC	CTAATTTTGA	GCAACTCAAG	GGCAAGCATT	TGATTGAAGT	TTCAGATGTG	240
ATTAACGACA	CCACTCAGCC	CAATTTGGAC	ATGAATCTTT	TGACGACCGA	AATCGCGCGG	300
CAGTTGCGAT	TGCGATCTAA	TGGGAGGTTT	AATATCACAA	GGGCGAGTGG	AGGGAGTGGT	360
ATTGAAGCAG	ACAGCAGAAT	GGTGAAACAG	CGCGAAAAAG	AACGAGAGAG	CGAAGAGTAT	420
AATCAAGACA	CCACTGTAGA	AAAAGGCACT	TTAAAAGCCG	CTGATTTATC	TTTAAGTGGT	480
AAAGTATCCA	GTATCGCAGC	CTCTATTAGT	AGTTCTAGGC	AACGCTTAGA	CTACGACTTC	540
ACCCTAAGCC	TTACCAATAG	GAAAACGGGT	GAAGAGGTAT	GGAGCGATGT	TAAGCCTATT	600
GTGAAAAATG	CTAGCAATAA	GCGTATGTTT	TAA			633

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

ATGAAAGCTT	TTTTAAAGAT	TGCGATGGTT	TTGATTTTTG	TGGGTGTCGC	TCATGCTAAA	60
AATCCTTTAA	CCCTTTCTAA	AGAAGAAGAA	GTTTTACAAA	ATTTGCAAAG	TTTtagCGCG	120
CATTTCAAGC	AAGTGTAA	AAATGAAAAG	CCCTTAGTTT	ATTATGGGGT	TTTAAAGGCT	180
AAAGCCCCTA	ATTGGGCTTT	ATGGGTTTAT	GAAAAACCTT	TAAAAAAAGA	AATTTACATG	240
AACGATAAGG	AAGTGGTGGT	TTATGAGCCT	AATTTATTCC	AAGCGACTAT	CACGCCCTTA	300
AAAGACAAGA	CGGATTTTTT	CACCATTCTC	AAGCAATTGA	AAAAGCAGAC	TGACGGCTCT	360
TTTAAAACGA	CTATCAACAA	GACCACTTAT	CGTTTGTTT	TTAAAGACGG	CAAGCCTTTT	420
TCGTTGGAAT	TTAAAGATGA	CATGAATAAT	CTTGTTACGA	TCACTTTTTC	TCAAGCAGAA	480
ATCAACCCTA	AAATTCCTAA	TGAAATCTTT	GTTTTTAACC	CTAAAGATGA	AAATATTGAT	540
ATTGTACGCC	AGTGA					555

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

ATGAGAATTA	AGGCTTATTT	TTTGCGTTTT	ATCGCACTGG	TTTTTATCGT	TTTGTGGGT	60
TTTAGCGCTT	GTAAAACTC	TCAAAAATCT	CAAGATTCTC	AAAACAATAC	CACCCAACAA	120
GATAGCCCTA	AAACCTACAC	CGCTATGGAT	CTGAATAACC	AAGAATACAC	GATTATGGGC	180
GATTTAGATT	CTCTAAACAT	CAGCCCGGAT	CCTAACACCC	CTACCCTATT	GATTTTAAGC	240
GCTTTAGATA	ATTCTTTAAA	AGATTACGCC	CCCACCTTTA	ACGTCTTAAA	AAAAACTTTT	300
AAAGATCGTT	TGAGGGTGCT	TATTTTACTC	AATCAACCCT	ATTCAAGCGA	TGCAATCAAA	360
GGCTTTATTG	CGCCTTCTCA	AACTGATTTG	ATGATTTTAA	ACCCTAAAGA	TACCGCTCTT	420
TTTGATCATT	TAAACCATGA	CGCTTTAAAC	CATTCTTTTA	ACATGCTCTT	ATATGACAAA	480
CACCAATTGA	TTAAATGTA	TCAAGGGATC	GTGCCAGCAG	AAATGCTCCA	ATTTGATATT	540
TCCAATTTAA	AGGACTGA					558

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1092 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

ATGGTATCAA	CACTCAAACC	GCTAAAAATC	GGTAAACACA	CCATAAAATT	CCCTATTTTT	60
CAAGGGGGCA	TGGGTGTGGG	GATTAGCTGG	GATGAAGTAG	CTGGAAATGT	TGCCAAAGAA	120
GGGGCTTTAG	GAGTGATTTC	AGCCGTAGGG	ACTGGTTATT	ATAAAAACAT	GCGTTTTGTA	180
GAAAGGATTG	TGGCTAAAAA	ACCCTTTGAA	GCCTTGAATT	TTTACTCCAA	AAAAGCGTTG	240
AATGAGATTT	TTGCAAACGC	TAGGAAAATT	TGCGGGAACA	AGCCTTTGGG	GGCGAATATT	300
TTATACGCTA	TCAATGACTA	TGGCCGTGTT	TTAAGGGACT	CTTGTGAGGC	GGGGGCGAAT	360
ATTATCATT	CAGGGGCTGG	TTTGCCCACT	AACATGCCTG	AATTCGCTAA	GGATTTTAGC	420
GATGTGGCGC	TCATCCCTAT	CATTTCCTCA	GCGAAGGCTT	TAAAAATCCT	TTGTAAAAGA	480
TGGAGCGATC	GCTATAAAAG	AATCCCGGAC	GCATTCATTG	TGGAAGGGCC	TTTGAGTGGG	540
GGGCATCAGG	GCTTTAAATA	CGAAGATTGT	TTCAAAGAAG	AATTCCAATT	AGAAAACCTA	600

GTGCCTAAAG	TCGTGGAAGC	TTCTAAAGAA	TGGGGGAATA	TCCCTATCAT	CGCCGCGGGG	660
GGGATTGGG	ATAAGAAAGA	TATAGACACC	ATGTTAAGCC	TTGGAGCGAG	TGGGGTGCAA	720
ATGGCGACTC	GTTTTTTTAGG	CACGAAAGAA	TGCGACGCTA	AAGCGTATGC	CGATCTTTTG	780
CCCACGCTCA	AAAAAGAAGA	TATTTTACTC	ATCAAATCGC	CTGTAGGCTA	TCCGGCTAGG	840
GCTATCAATA	CGGGGGTGAT	CAAACGCATT	GAAGAGGGTA	ACGCGCCTAA	AATCGCATGC	900
GTGAGCAATT	GTGTAGCGCC	TTGTAACAGG	GGTGAAGAAG	CTAAAAAGGT	GGGCTATTGT	960
ATCGCTGATG	GTTTGGGGCG	CAGTTATTTA	GGAAACAGAG	AAGAGGGGCT	TTATTTTACC	1020
GGGGCTAATG	GCTATAGAGT	GGATAAGATT	ATCAGCGTGC	ATGAATTGAT	TAAAGAGCTT	1080
ACAGAGGGTT	AA					1092

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

ATGGTATCAA	CACTCAAACC	GCTAAAAATC	GGTAAACACA	CCATAAAATT	CCCTATTTTT	60
CAAGGGGGCA	TGGGTGTGGG	GATTAGCTGG	GATGAACTAG	CTGGAAATGT	TGCCAAAGAA	120
GGGGCTTTAG	GAGTGATTTT	AGCCGTAGGG	ACTGGTTATT	ATAAAAACAT	GCGTTTGTGA	180
GAAAGGATTG	TGGCTAAAAA	ACCCTTTGAA	GCCTTGAATT	TTTACTCCAA	AAAAGCGTTG	240
AATGAGATTT	TTGCAAACGC	TAGGAAAATT	TGCGGGAACA	AGCCTTTGGG	GGCGAATATT	300
TTATACGCTA	TCAATGACTA	TGGCCGTGTT	TTAAGGGACT	CTTGTGAGGC	GGGGGCGAAT	360
ATTATCATT	CAGGGGCTGG	TTTGCCCACT	AACATGCCTG	AATTCGCTAA	GGATTTTAGC	420
GATGTGGCGC	TCATCCCTAT	CATTTCTCA	GCGAAGGCTT	TAAAAATCCT	TTGTAAAAGA	480
TGGAGCGATC	GCTATAAAAG	AATCCCGGAC	GCATTCATTG	TGGAAGGGCC	TTTGAGTGGG	540
GGGCATCAGG	GCTTTAAATA	CGAAGATTGT	TTCAAAGAAG	AATTCCAATT	AGAAAACTTA	600
GTGCCTAAAG	TCGTGGAAGC	TTCTAAAGAA	TGGGGGAATA	TCCCTATCAT	CGCCGCGGGG	660
GGGATTGGG	ATAAGAAAGA	TATAGACACC	ATGTTAAGCC	TTGGAGCGAG	TGGGGTGCAA	720
ATGGCGACTC	GTTTTTTTAGG	CACGAAAGAA	TGCGACGCTA	AAGCGTATGC	CGATCTTTTG	780
CCCACGCTCA	AAAAAGAAGA	TATTTTACTC	ATCAAATCGC	CTGTAGGCTA	TCCGGCTAGG	840
GCTATCAATA	CGGGGGTGAT	CAAACGCATT	GAAGAGGGTA	ACGCGCCTAA	AATCGCATGC	900
GTGAGCAATT	GTGTAGCGCC	TTGTAACAGG	GGTGAAGAAG	CTAAAAAGGT	GGGCTATTGT	960
ATCGCTGATG	GTTTGGGGCG	CAGTTATTTA	GGAAACAGAG	AAGAGGGGCT	TTATTTTACC	1020
GGGGCTAATG	GCTATAGAGT	GGATAAGATT	ATCAGCGTGC	ATGAATTGAT	TAAAGAGCTT	1080
ACAGAGGGTT	AA					1092

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

TTGTTAGGGA	GGAATGGCGT	TACTTTAAAT	ATCCGCCAGG	TTTTTTGGTG	GGATAATTC	60
AACTGGTCCA	TTGGCTTTTA	TAACACCTTT	GGCAATTCAG	ACGCTTTTTT	AGGCTCTCAC	120
ACCATGCCAA	GGGGGAATAA	CACTTCCTAT	ATCAGTAATG	AAATCTCAGT	AACGACTAGG	180
CATGCCGGAA	TGATCGGCTA	TGATTTTTGG	GATAATACGG	CTTATGATGG	GCTGGCTGAT	240
GCGATCACTA	ACGCGAACAC	TTTCACTTTT	TACACTTCGG	TTGGAGGGAT	CCATAAGCGT	300
TTTGCAATGGC	ATGTTTTTGG	GCGCGTCTCT	CATGCGAATA	AAAATGCGTT	AGGGCAAGTG	360
GGGAGGGCTA	ATGAATATTC	CTTGCAATTC	AATGCGAGCT	ATGCGTTCAC	TGAATCGGTT	420
CTCCTTAAC	TTAGGATCAC	TTATTATGGG	GCTAGGATCA	ATAAAGGGTA	TCAAGCAGGG	480
TATTTTGGAG	CGCCCAAATT	CAATAACCCG	GATGGCGATT	TTAGCGCTAA	TTACCAAGAC	540
AGAAGTTACA	TGATGACCAA	CCTCACGCTG	AAGTTTTGA			579

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1065 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

ATGCAACAAC	AGCTCACCTA	CTTGAATGCG	GGGAATGTGT	TTTTTAATGC	GATGAATAAG	60
GCTTTAGAGA	AGAATGGGAC	TGCTACTGCT	AATAGCACTA	GTAGCACTAG	CGGTGCGACT	120
GGTTCAGATG	GTCAAACCTA	CTCTCAACAA	GCTATTCAAT	ACCTTCAAGG	CCAACAAAAT	180
ATCTTAAATA	ACGCAGCGAA	CTTGCTCAAG	CAAGATGAAT	TGCTCCTAGA	AGCTTTCAAC	240

TCTGCCGTAG	CTGCTAACAT	TGGGAATAAG	GAATTCAATT	CAGCCGCTTT	TACAGGTTTG	300
GTGCAAGGCA	TTATTGATCA	ATCTCAATTG	GTTTATAACG	AGCTCACTAA	AAACACCATT	360
AGCGGGAGCG	CGGTAAATAA	CGCTGGGATA	AACTCCAACC	AAGCTAACGC	TGTGCAAGGG	420
CGTGCTAGTC	AGCTCCCTAA	CGCTCTTTAT	AACGTGCAAG	TAACTTTGGA	TAAAATCAAC	480
GCGCTCAACA	ATCAGGTGAG	AAGCATGCCT	TACTTGCCCC	AATTCAGAGC	CGGGAACAGC	540
CGTGCAACGA	ATATTTTAAA	CGGGTTTAC	ACTAAAGTGG	GCTATAAGCA	ATTCTTCGGG	600
AAGAAAAGGA	ATATCGGTTT	GCGCTATTAT	GGTTTCTTTT	CTTATAACGG	AGCGAGCGTG	660
GGCTTTAGAT	CCACTCAAAA	TAATGTAGGG	TTATACACTT	ATGGGGTGGG	GACTGATGTG	720
TTGTATAACA	TCTTTAGCCG	CTCCTATCAA	AACCGCTCTG	TGGATATGGG	CTTTTTTAGC	780
GGTATCCAAT	TAGCCGGTGA	GACCTTCCAA	TCCACGCTCA	GAGATGACCC	CAATGTGAAA	840
TTGCATGGGA	AAATCAATAA	CACGCACTTC	CAGTTCCTCT	TTGACTTCGG	TATGAGAATG	900
AACTTCGGTA	AGTTGGACGG	GAAATCCAAC	CGCCACAACC	AGCACACGGT	GGAATTTGGC	960
GTAGTAGTGC	CTACGATTTA	TAACACTTAT	TACAAATCAG	CAGGGACTAC	CGTGAAGTAT	1020
TTCCGTCCTT	ATAGCGTTTA	TTGGTCTTAT	GGGTATTCAT	TCTAA		1065

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

ATGGAAGACT	TTTTGTATAA	CACCTTATAT	TTCATAGAGG	ATTATAAGTT	GGTTGTTATT	60
TTTAGTTTCA	TAGGGTTAAT	AGCGTTATTT	TTCCTCTACA	AATTCATAAA	AACTCAAAAA	120
AAGGTTTTTA	AAGATAAAGC	TAACCAGCCT	CAAAAGAAAA	AAAGCTTTAA	AGAAATCATT	180
ATAGATGGGC	TGAAAGAAAG	GGTTAAAACC	TTTGGCTTTT	GGTTGCAAGC	TATACTATTA	240
CTATCCTATT	CTTTTATCAC	ATCAGGGTTA	TTTTTCTTGA	TTCTCTTAGG	TAATTTTTAT	300
GATGATAATA	GATTGCCTGA	GAGCGATGAT	GATCTTTTTG	ATATATGGGT	CTATGCCGATA	360
CAAGATTTTC	CTGCATACTA	TTTAAAGGCA	CTCACTTTTA	GCTCGCTCAA	GATTTATGGG	420
TTCAATATAT	CCTTAGTCGT	ATATAGTTCT	ATTTTATGCT	CTTATATATT	CATTACCTTT	480
TTTGTGTGGT	TCTTAAAATA	CTTAACTCGG	ACTAGGGACA	TAGGAGCGAA	TAAAAAAGTT	540
GATGATCTCT	TTGGTAGCGC	GAGTTGGGAA	ACTGAAGAGA	AAATGATCAA	AGCCAAGCTT	600
ATCACACCCA	ACAATAAAAA	ACGCGCCTTT	GACAAACGAG	AGGTTATTGT	AGGCAGGCGT	660
GGCTTAGGGG	ATTTTATCGC	TTACGCAGGA	CAGGCGTTTA	TTGGCTTGAT	TGCTCCTACT	720
AGGAGCGGTA	AGGGTGTGGG	TTTCATCATG	CCCAATATGA	TCAATTACCC	TCAAAATATC	780
GTTGTGTTTG	ATCCTAAGGC	TGACACTATG	GAAACTTGCG	GGAAAATCAG	AGAAAAACGC	840
TTCAACCAAA	AAGTGTTTCA	CTATGAACCT	TTCTCCTTAA	AAACACACCG	ATTTAATCCT	900
TTGCTTATG	TGGATTTTGG	TAATGATGTG	GTTTTGACTG	AAGACATACT	CTCTCAAATT	960
GACACACGCC	TAAAAGGGCA	TGGCATGGTG	GCTAGTGGAG	GGGATTTTTC	CACTCAAATC	1020
TTTGGATTGG	CTAAGTTGGT	GTTCCCTGAA	AGACCTAATG	AAAAAGATCC	TTTTTTTTAGC	1080
AATCAGGCGC	GAAACCTTTT	TGTCATCAAT	TGCAATATTT	ATAGGGATCT	CATGTGGACT	1140

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AAAAAGGGGC TTGAGTTTGT CAAAAGAAAA AAAATCATCA TGCCTGAAAC CCCCACGATG 1200
TTTTTCATAG GTTCTATGGC AAGCGGTATC AACTTGATTG ATGAAGACAC AAACATGGAA 1260
AAAGTCGTGT CTTTAATGGA ATTTTTTGGG GGTGAAGAAG ATAAGAGTGG CGACAATCTA 1320
AGAGCGCTTA GTCCTGCCAC TAGAAACATG TGAATAAAT TCAAGACAAT GGGTGGCGCT 1380
AAAGAACTT ACAGCTCGGT TCAAGGGGTC TATACATCAG CGTTTGCGCC TTACAATAAC 1440
GCCATGATCA GGAATTTTAC GAGCGCTAAT GATTTTGATT TCAGGCGTTT AAGGATCGAT 1500
GCAGTGAGTA TTGGTGTGAT CGCTAATCCT AAAGAAAGCA CTATTGTTGG ACCGATATTA 1560
GAGCTGTTTT TCAACGTGAT GATTATAGC AATTTGATTC TGCCAATCCA TGATCCACAA 1620
TGCAAAAGAA GCTGCTTGAT CCTCATGGAT GAATTTACGC TCTGTGGCTA TTTAGAGACC 1680
TTTGTTAAAG CGGTAGGGAT CATGGCAGAA TACAACATGC GCCCCGCTTT TGTGTTCAA 1740
AGTAAGGCGC AATTAGAAAA CGACCCCCCA CTTGGTTATG GTAGGAATGG CGCTAAGACT 1800
ATTTTAGACA ACCTTTCTTT GAATATGTAT TATGGGATCA ACAACGATAA CTACTATGAA 1860
CATTTTGAAG AGCTTTCTAA AGTGTTAGGG AAATACACAA GGCAAGATGT GAGCCGGAGC 1920
ATTGATGATA ATACGGGTAA GACCAACACT TCTATCAGCA ACAAGGAGCG GTTTTGTATG 1980
ACCCCTGATG AATTGATGAC TATGGGCGAT GAGCTTATCA TTTTAGAAAA CACGCTCAAA 2040
CCCATCAAGT GCCACAAGGC GCTTTACTAT GATGATCCCT TCTTCACCGA TGAGCTCATT 2100
AAGGTGAGTC CAAGCTTGAG CAAGAAATAC AAATTGGGGA AAGTGCCTAA TCAAGCAACA 2160
TTTTATGATG ACTTGCAAGC CGCTAAAACC AGAGGCGAAT TGAGCTATGA TAAATCTTTA 2220
GTGCCTGTGG GTTCAAGCGA ACTGTGA 2247

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(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

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TTGAGCCATT TATTTCTCGT AAAACGCCCT TACAGTCGCC TTTATTTACA TAATCAGAGC 60
AACCATAAAA TGAGACACCA TTCAATCCTC TTTGTATCAT TTTAG 105

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(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

ATGGAACACC ATAAAGCGCA CACAACCATT CAGGCTTTAC AAGCCAAACG CAAAAGGTTG	60
CTAACCGAAT TAGCCGAGTT AGAAGCAGAA ATAAAGGTGA GCAGCGAACG AAGGAGCAGT	120
TTTAACGTTT CGCTCTCGCC GAGTTTGTTA GCCGAAATAG AAGAGATAGA ATACGAAGAA	180
AAAATGAGCA AAGAGCGAAG AATCCATCAC AATCTTTTGC TTTCGCCCAG TTTCATGGCT	240
AAAGTGATG AATACATGAA AGAGAAAGGT TTTCCTAATC GATCGCTTCT CTTTGAAAAA	300
GCGTTGGAGT TTTATATGCT AAAACACCCA TAA	333

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

GTGATGCGTT TCTTTTCATT CTGTTATTTT TTATTTTATT TTTTAGGGGT TTCTTTGCAT	60
GCCCTTAGCC CCCTAGAAGA ACAAGAATTT TTAATTTTCGT ACCGCTTGAA AATCGTTGAT	120
TCTAGAGTGA TGGGTGAAGA GTATTCTGTT TCTAAACCTA TCGTTAGTCG CATTAAAACA	180
GCCCCCTATG TTTTAGACTA TCATTGCTCT ATCATCACTC GCAACTTGCC CGATTTGAAA	240
AACCCCTTGC TCCAAATAAA GCTAGAACGC TTCCTTTTAG AAATAGCGTT AAAAAAAGAA	300
AAAGAGCGAG TCATTGACTG CCTTTTAAAA AGCCAAGTCG CTATCACGCA TTATGATCAC	360
AGCTATAAAA ACGGCACCAC TACCACAAGC ATTCTTAACC TCAAAGCCTT AAGCGTTAAA	420
GCGAGTTTAG AGGGAGATAT GCTGTCTTTA GATATTTTGA GAAAGGAAGA AGAATGA	477

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

ATGGAGTTAA TTAAGAAATT GGAAAAAGAA AGCGAAGTTT TAAAGAAAGA TTTACAACAA	60
CATTCAAACG AGCTTTTAA AATGTTGATT ATTGATAATG AAGATTGTT TAAAGAGCAA	120
TTTGAGATTA TGTTTAAAGC ATGGGTTGAA ATCGTAAAAA TGATGTTTGA ATTAACCAA	180
AAAACCAAT TTGATGGCGA AATGATTGGC TACACAGAAG AACTTTTAAC CTTTTTAGTT	240
AGAGATTTTT TTAATGGGAT TTTTAAATCC AAAGTAATAC CTAAAATGCC TATTTTTTGC	300
GGTGATGTTA AATGCGAAGA TTTTAATGCC CTAAGAAGTT TAGTTTATCT T	351

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 834 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

TTGAAACGAG CGTTATGGTT AATTTTAGGG CTTTTTTACG CGCTTAATGC AGAGAGCTTT	60
AAAGATGTTT TGAATAAAGG GGATTACACT TTTTTTAATA AAAAGGTGGT TTCGCCTATC	120
AAACGCTATG CGGATAGATC GCGGTTTTAT CTGGGGCTTG GGTATCAATT AGGGAGCATT	180
CAGCACAACCT CTAGCAACTT GAATTTATCC CAACGATTTA ATAAGAGTCA GATTATTTTC	240
AGCGATAGTC TAAGCCCTGT TTTTAAAAAT TCGTATGTGT CTAATGGTCT TGGCGTTCAA	300
GTGGGCTATA AGTGGGTGGG TAAGCATGAA GAGACGAAAT GGTGTTGGCTT CAGGTGGGGG	360
CTGTTTTATG ATTTGAGCGC TTCTCTTTAT GGCTCTCAAG AATCGCAGTC TATCATCATT	420
TCCACTTACG GCACTTATAT GGATTTATTG CTTAACGCTT ATAATGGGGA TAAGTTTTTT	480
GCCGGGTTCA ATCTGGGGAT CGCTTTTGCT GGAGTGTATG ACAGATTGAG CGATGCGTTA	540
TTGTATCAAA CTCTCTTCA AACACTTTT GGCGGGAAAG TGAATTTAA CCGCTTCCAG	600

TTTTTGGTGG	ATTTAGGGGT	TCGTTTAGGG	AATGAACACA	ACCAATTTGG	CTTTGGGATT	660
AAAATCCCTA	CTTATTATTT	TAACCATTAT	TATTCCATGA	ATAACATTAG	CAATAATAGT	720
GAAAATGTCT	TAAAAGTTTT	ACGATTTTTA	GAATACGGGA	TCAACAGCTT	GTTGTATCAA	780
GTTGATTTCA	GGCGCAATTA	CTCGGTTTAT	TTCAACTACA	CTTATAGTTT	TTAA	834

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

ATGCCTGCCT	TGAATAGCTC	CAAAAATATG	G TAGTCAATA	TCAATCAAAC	TTTCACAAAA	60
AACCCTACCA	CAGAATACAC	TTACCCCGAT	GGGAATGGCA	ATTATTATTC	AGGCGGTTC	120
TCAATCCCAA	TCCAGCTAAA	GATTAGTAGC	GTCAATGACG	CTGAAAACCT	TTTGCAACAA	180
GCCGCTACTA	TCATCAATGT	CCTTACCACC	CAAAACCCGC	ATGTGAATGG	TGGCGGTGGG	240
GCATGGGGGT	TTGGCGGTAA	GACCGGGAAT	GTGATGGATA	TTTTTGGCGA	TAGTTTTAAC	300
GCTATTAACG	AAATGATCAA	AAACGCTCAA	GCCGTTTTAG	AAAAAACCCA	ACAGCTTAAC	360
GCTAATGAAA	ACACCCAAAT	CACGCAACCA	GACAATTTCA	ACCCCTACAC	TTCTAAAGAC	420
ACGCAGTTTC	CTCAAGAAAT	GCTCAATAGA	GCTAACGCTC	AAGCAGAGAT	TTTGAGCTTA	480
GCCCAACAAG	TAGCGGACAA	TTTCCACAGC	ATTCAAGGGC	CTATCCAACA	AGATCTAGAA	540
GAATGCACCG	CAGGATCAGC	TGGTGTGATT	AACGACAACA	CTTATGGTTC	AGGTTGCGCG	600
TTTGTGAAAG	AGACTCTCAA	TTCTTAGAG	CAACACACCG	CTTATTATGG	CAACCAGGTC	660
AATCAGGATA	GGGCTTTGTC	TCAAACCAT	TTGAATTTTA	AAGAAGCCCT	TAGCACTTTA	720
GGGAACGACT	CAAAAGCGAT	CAATAGCGGT	ATCTCTAACT	TGCCTAACGC	TAAGTCCCTT	780
CAAAACATGA	CGCATGCCAC	TCAAACCCCT	AATTCCCCAG	AAGGTTTGCT	CACTTATTCT	840
TTGGATACCA	GCAAATACAA	CCAGCTCCAA	ACTGTTGCGC	AAGAATTAGG	CAAAAACCCC	900
TTTAGGCGCA	TCGGCGTGAT	TAACATCAA	AACAATAACG	GGGCGATGAA	CGGCATCGGC	960
GTGCAAGCGG	GCTATAAGCA	ATTCTTTGGC	AAAAAAAGGA	ATTGGGGGTT	AAGGTATTAT	1020
GGTTTCTTTG	ATTATAACCA	TGCTTATATC	AAATCTAATT	TTTTTAACTC	GGCTTCTGAT	1080
GTGTGGACTT	ATGGGGTGGG	TATGGACGCG	CTTTATAACT	TCATCAACGA	TAAAAACACC	1140
AACTTTTTAG	GCAAAAATAA	CAAGCTTTCT	GTGGGGCTTT	TTGGTGGCTT	TGCGTTAGCC	1200
GGGACTTCGT	GGCTTAATTC	CCAACAAGTG	AATTTGACCA	TGATGAATGG	CATTTATAAC	1260
GCTAATGTCA	GCGCTTCTAA	CTTCCAATTT	TTGTTTGATT	TAGGCTTGAG	AATGAACCTC	1320
GCTAGGCCCA	AGAAAAAAGA	CAGCGATCAT	GCCGCTCAGC	ATGGCATGGA	ATTGGGCGTG	1380
AAAATCCCCA	CCATTAACAC	GGATTATTAT	TCTTTCATGG	GGGCTGAACT	CAAATACAGA	1440
AGGCTCTATA	GCGTGTATCT	CAATTATGTG	TTTGCTTACT	AG		1482

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

333

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

GTGCTAAACA	CCACCCAAAA	AAGCCTATTG	GTTTTTCATGG	GGGTTTTTTTT	CCTTATCTTT	60
GGCGTGGATC	AAGCGATTAA	ACACGCTATT	TTAGAGGGGT	TTCACATGA	AAGTTTGGTT	120
ATAGATATTG	TTTGTAGTGT	CAATAAAGGC	GTGGCGTTTT	CCTTACTCAG	TTTTTTAGAG	180
GGGGGTTTGA	AATACTTGCA	AATCCTTTTA	ATTTTAGGGC	TTTTTATCTT	TTTAATGCGC	240
CAAAGGAGC	TTTTTAAAG	CCATGCGATA	GAGTTTGGCA	TGGTGTGTTG	CGCTGGGGTT	300
TCTAATGTTT	TAAATCGGTT	AGTATCATTG	GGGCAATTGT	ATATCTTTA	TGATGTATTG	360
GCTATTAGAA	GGGAAAAAAT	GAAAAATAGC	GCGCCTTTAA	AGAATAAAGT	TTTTTGTGGG	420
TTATACGTTT	TAAGTTTAAG	CGCTTCTGTG	CAAGCGTTTG	ATTATAAAAT	TGAAGTTTTG	480
GCAGAGTCCT	TTTCTAAAGT	TGGCTTTAAT	AAAAAAAAGA	TTGACATAGC	TAGGGGGATT	540
TATCCTACAG	AGACTTTTGT	AACCGCTGTG	GGTCAGGGCA	ATATTTATGC	GGATTTTTTA	600
TCCAAAAGCC	TTAAAGATCA	AGGGCATGTT	TTAGAGGGAA	AAGTCGGCGG	CACAATCGGT	660
GGGATTGCTT	ATGACAGCAC	GAAATTCAAT	CAAGGCGGAT	CGGTTATATA	TAATTATATC	720
GGTTATTGGG	ATGGCTATTT	AGGGGGTACA	AAGGCCTGCT	TGATGGCACA	AGTATCCATG	780
ACTGCGCGCT	TGGCTCTGAT	GGCAAGGTGA				810

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

```

ATGTTAGTTA CAAAAC TTGC CCCC GATTTT AAAGCGCCTG CCGTTTTAGG AAACAATGAG      60
GTTGATGAAC ACTTTGAGCT TTCTAAAAAT TTAGGCAAAA ATGGTGTGAT CCTTTTCTTT      120
TGGCCAAAAG ATTTTACTTT TGTATGCCCT ACAGAAATCA TTGCGTTTGA CAAAAGAGTG      180
AAAGACTTCC ACGAAAAAGG CTTTAATGTG ATTGGCGTGT CTATTGACAG CGAACAAGTG      240
CATTTTCGAT GGAAAAACAC CCCTGTGGAA AAAGGCGGTA TCGGTCAAGT GTCTTTCCCT      300
ATGGTGGCTG ATATCACTAA GAGCATTCTT AGAGACTATG ATGTGCTGTT TGAAGAAGCG      360
ATCGCTTTGA GAGGTGCTTT TTTGATTGAT AAAAACATGA AAGTAAGACA CGCAGTGATC      420
AATGACTTGC CATTAGGTAG GAATGCAGAT GAAATGCTTC GCATGGTAGA CGCTCTCTTA      480
CACTTTGAAG AACATGGTGA AGTATGCCCA GCAGGTTGGA GAAAAGGCGA TAAAGGCATG      540
AAAGCAACTC ACCAAGGCGT TGCAGAGTAT CTTAAAGAAA ATTCCATTAA GCTTTAA      597

```

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

```

ATGTTAAAAC TCGCCAGTAA AACGATTTGT TTGTCCCTAA TCAGCTCATT CACGGCTGTA      60
GAAGCCTTTC AAAAACACCA AAAAGACGGC TTTTTCATAG AAGCCGGCTT TGAAACCGGG      120
CTATTACAAG GCACACAAAC CCAAGAACAA ACCATAGCCA CCACTCAAGA AAAACCCAAA      180
CCCAAACCCA AACCAAAACC CATTACCCCT CAAAGCACCT ATGGGAAATA CTACATCTCC      240
CAAAGCACCA TTTTAAAGAA TGCGACTGAG TTGTTTGCAG AGGATAATAT CACCAACTTA      300
ACCTTTTACT CTCAAAACCC TGTGTATGTA ACCGCTTATA ACCAAGAAAG CGCTGAAGAA      360
GCTGGCTATG GTAATAACAG CTTGATTATG ATACAAAAC TCTTGCCTTA TAACTTGAAC      420
AACATTGAGC TGAGTTACAC GGACGATCAA GGCAATGTGG TCAGTTTGGG CGTGATAGAG      480
ACTATCCCTA AACAATCTCA AATCATTCTG CCCGCAAGCT TGTTTAACGA CCCACAGCTT      540
AACGCCGATG GTCCTCAACAA CTCCAAACCA ACACCACACG ATTTTCTGAT GCCAGCACGC      600
AGAATCTGTT TAACAAGCTC AGCAAGGTTA CAACCAATCT TCAAATGA      648

```

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

ATGTTATCTT CTAATGATTT GTTTATGGTC GTTTTAGGGG CGATTTTATT GGTGTTGGTG	60
TGCTTGGTGG GGTATTTGTA TCTTAAAGAA AAAGAGTTTT ACCATAAAAT GAGGCGTTTA	120
GAAAAAACTT TAGATGAATC CTATCAAGAA AATTATCTCT ATTCTAAGCG TTTGAGAGAA	180
TTAGAGGGGC GTTTGGAAGG CCTTCTTTA GAAAAAAGCG CTAAAGAGGA CAGCTCATTA	240
AAAACGACTC TTTCGCACCT TTATAACCAG TTGCAAGAAA TCCAAAAATC CATGGATAAA	300
GAGCGCGATT ACTTAGAAGA AAAAATCATT ACTTTAGAAA ACAAATTTAA AGACATGGGG	360
CATTATGCCG CTAGCGATGA AGTCAACGAA AAACAGGTTT TGAAAATGTA TCAAGAAGGC	420
TATAGCGTGG ATTCTATTTC TAAAGAATTT AAAGTGAGTA AGGGCGAGGT GGAATTTATA	480
TTGAACATGG CAGGGTTAAA ATGGTAG	507

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1017 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

GTGGGTTTTG AATATTCCAT CAGTCATGCC GTTGAACACA ATAACCCTTT TTTGGATCAA	60
GAACGCATCC AAGCGATTTT TAACGCTCGA GGCGAAGTCT GTGGACTCGA TCGAGTCAAA	120
AATGAAATCA CAGACATGCC CAACACCTTT AACTACATCA ACAACGCTTT AAAAAACAAT	180
GCTAAATTAA CCCCTACTGA AAAGCAAGCC GAAACCTACT ACCTGCAATC TACCCTTCAA	240
AACATTGAAA AAATAGTCAT GCTTAGCGGG GGCGTTGCGT CTAACCCTAA ATTAGCCCAA	300
GCGTTAGAAA AAATGCAAGA ACCCATTACT AACCCTTTAG AATTGGTAGA AAACTTAAAA	360
AATTTAGAA TACAATTCAG CCAATCTCAA AACAGCATGC TTTCTTCTTT GTCTTCTCAG	420
ATCGCTCAA TTTCAAATTC TTTGAACGCG CTTGATCCCA GCTCTTATTC TAAAAACGTT	480
TCAAGCATGT ATGGGGTAGG TTTGAGCGTA GGGTATAAGC ATTTCTTTAC CAAGAAAAAA	540
AATCAAGGGT TTCGTTATTA CTTATTCTAT GACTATGGTT AACTAATTT TGGTTTTGTG	600
GGTAATGGCT TTGATGGTTT AGGCAAAATG AATAACCACC TCTATGGGCT TGGCATAGAT	660

336

TATCTTTTCA	ATTTTCATTGA	TAATGCGCAA	AAACATTCTGA	GCGTGGGGTT	TTATGTAGGC	720
TTTGCTTTAG	CGGGGAGTTC	GTGGGTAGGG	AGTGGTTTAT	GCATGTGGGT	GAGTCAAATG	780
GATTTTCATCA	ACAACATTTT	GACGGATTAT	CGGGCTAAAA	TGCACACGAG	TTTTTTTCCAA	840
ATCCCTTTGA	ATTTTGGGGT	TCGTGTGAAT	GTGGATAGGC	ACAATGGTTT	TGAAATGGGC	900
TTAAAGATCC	CTTTAGCGGT	CAATTCCTTT	TATGAAACGC	ATGGCAAGGG	GTAAACGCT	960
TCCCTCTTTT	TCAAACGCCT	TGTCATGTTT	AACGTGAGTT	ATGTTTATAG	TTTTTAG	1017

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

ATGATGTTTG	AATTAACCAA	AAAAACCAA	TTTGATGGCG	AAATGATTGG	CTACACAGAA	60
GAACCTTTTAA	CCTTTTTAGT	TAGAGATTTT	TTTAATGGGA	TTTTTAAATC	CAAAGTAATA	120
CCTAAAATGC	CTATTTTTTG	CGGTGATGTT	AAATGCGAAG	ATTTTAATGC	CCTAAGAAGT	180
TTAGTTTATC	TTTCTGTGCT	TGAGTTGGAA	GAAACGATAA	ATCCTAATAA	AATCCCATTT	240
TAA						243

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

GTGCAATTAC TCAAAGACAA TAAAGAAGTG GTTGTTTTAG ATACAGATAG CCAAAAGTCT	60
ATGGAAACTT TTGCTACAAT TCGTGCTGAA AAAGAACGCC CCACTTTTAG CTTATTTAAT	120
CGTAGTAGTG GCTTTAGCGA TACTTTAAAG CAAATGGTAT CTAAGTATGA AAATATCCTT	180
ATTGATACTA AGGGGGAATA CAGCAAAGAA ACCCAAAAAG CTATGCTTTT AAGTAATATT	240
GTGCTAGTGC CAACAAC TCC TAGCCAATTA GACACTGAAG TCTTAGCTAA TATGCTAGAA	300
AGAATTGAGC AACTCCAAGA GCTTAATGAA AATCTAAGAG CCTTAATTGT CATCAATAGA	360
ATGCCTACTA TTCCTACCCT TAAAGAAAGA CAAGCCTTAA TAGAGTTTAT TAAAGAAAAT	420
AACCCTAGCG ATAGGATTAC ACTTTTAGAA AGCTCTTTGA GTGAGCGCAT TGTTTATAAG	480
CGCAGTGTA GCGAAGGCTT AGGGGTCATA GAATACAGCG ATAAAAAGGC TATCAATGAG	540
TGGGTTAATT TTTATAACGA ATTAAAAAGC CATTTAGAAA AAGAGAAAAT ACATACGTTT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

ATGCGGTCGG ATGTTGAAGT TTTATCGCCT TTGCATAAAA TAGATGAAAA ATACCTTTTC	60
CATTTAAAGA TTGCGGGGGA ATTGGCGAGC ATGGGTAAGA TTTTAAGTGT ATATTTAGCC	120
CACAAGCACA GCGCGTATTT CATTTTAAAC GCTTTGAGTT ACGGCTTTAG CCACCAGGAT	180
AGGGCGATCA TTTGCTTATT GGGCGCAATT TAG	213

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

ATGAGTGC GA	TGATGCCAAG	CCTTTTGACC	TTGCAGTGGC	TGAGTTTAT	CCTTTCTTTA	60
GCCGAAAATT	TGTGCCTGAC	AGACAGCCAT	CATTTAAAAT	ACACGCTAGA	AAAAACAAG	120
CTTGTGATCC	ATTCTAATGA	TGCGCTTTAC	TTGGCTAAAG	AAATGCTCCC	CAAAC TCATT	180
AAGCCCATTC	CTTTGACGAT	AGAGTTTGCT	TGA			213

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1437 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

TTGAAGAAAA	TCGCCCTTAT	TTTAGATGGC	ATTGTAGCAA	AAAATTTTTT	AGACTTGGTG	60
CTAAGGCATT	ATTCTAATCA	TAATTTTTAT	ATAGTGGTTG	TCAAAGATGA	GAGCCTTATC	120
CCTAAAAATT	ACCCGAGCAC	TTTCGCTTTT	CATTGTTTTG	ATGCGACTTC	CAGTTTTAGG	180
CTTTTGCAGG	TGTTAAATGA	TGAGGTGAGC	GATGCGTTTT	TAATCATACA	AGATTTTAAA	240
GAGCAGCGCA	TCATCCATAA	AATCATTCAA	ACCCATTTC A	AACGCATGCG	TGTGGTTTTG	300
AGCGTGAAAA	GAGATAGCGA	AAAACTTTA	GAAAACAATG	AAGAAAATAA	AGATGAAAAG	360
CTCATTTTGA	TTGATGAATT	TGAAGTTTTA	GCCAATAAAT	TCATTTCTCG	TTTGCCTAAT	420
ATCCCTAGCA	CCCCTAGAGA	GTTTGGGTTA	GGCAAGGGCG	AGATCATGGA	GATTGATGTG	480
CCTTTTGGGA	GCATTTTTGC	TTATAGGCAT	ATTGGCTCTA	TCAGGCAAAA	AGAATACAGG	540
ATTGTAGGGC	TTTATCGCAA	CGATGTTTTG	TTGCTCTCCA	CTAAATCTTT	AGTCATCCAA	600
CCACGAGACA	TTCTTTTAGT	GGCAGGCAAT	CCGGAAATTT	TAAACGCGGT	GTACCATCAA	660
GTCAAAAGCA	ATGTGGGGCA	GTTCCCAGCC	CCCTTTGGTA	AGAGCATTTA	TTTATACATT	720
GATATGCGAT	TGCAGAGCCG	AAAAGCGATG	ATGCGCGATG	TGTATCAAGC	CTTGTTTTTG	780
CACAAGCGTT	TAAAGAGCTA	CAAGCTCTAC	ATTCAAGTTT	TACACCCAC	TAGCCCTAAG	840
TTTTATCATA	AATTTTTTATC	GCTAGAAACC	GAAAGCATTG	AAGTGAATTT	TGATTTTTAT	900
GGGAAGAGTT	TTATCCAAAA	ACTCCATGAA	GACCACCAAA	AAAAAATGGG	TTTGATTGTG	960
GTAGGCAGAG	AGCTTTTTTTT	CTTGAAAAAA	CACCGAAGAG	CCTTGACAA	AACAGCCACA	1020
CCGGTTTATA	AAACCAACAC	CTCTGGCCTG	TCTAAAACCA	CTCAAAGCAT	TGTGGTTTTG	1080
AATGAAAGTT	TAAGCATTAA	TGAAGACATG	TCTTCAGTGA	TTTTTGATGT	GTCTATGCAA	1140
ATGGATTTGG	GCTTGTGTGCT	TTATGATTTT	GACCCTAACA	AGCACTATAA	AAACGAGATT	1200
GTCAATCATT	ACGAAAATTT	AGCCAACACC	TTTAACCGCA	AGATTGAGAT	TTTTCAAACC	1260

GATATTAAAA ACCCTATCAT GSTATCTCAAT TCTTTAAGAA ATCCCATTTT GCATTTTCATG	1320
CCTTTTGAAG AGTGCATCAC GCAAACGCGC TATTTGTGGT TTTTATCCAC TAAAGTGGA	1380
AAATTAGCGT TTTTGAACGA TGATCACCT CAAATTTTTC TCCCTGTAGC GGAGTGA	1437

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

ATGAAAAAAG TCTATTTTAA AACTTTTGGG TGTAGGACGA ATCTTTTGA CACGCAAGTG	60
ATGGGCGAAA ATTTAAAGGA TTTTAGCGCG ACTTTAGAAG AACAGAAGC CGATATTATT	120
ATTATCAATT CTTGCACCGT AACCAATGGG ACCGATAGCG CGGTAAGGAG TTACGCTAGA	180
AAAATGGCAC GATTGGATAA AGAAGTGCTA TTTACTGGTT GCGGGGTGAA AACCCTAAGGC	240
AAAGAGCTTT TTGAAAAAGG GCTTTTAAAG GCGGTTTTTG GGCATGACAA TAAAGAAAAG	300
ATTAACGCGC TTTTACAAGA AAAAAAGCGT TTTTTCATAG ATGACAATTT AGAAAACAAA	360
CATTTAGACA CCACGATGGT GAGCGAGTTT GTGGGAAAAA CCAGGGCGTT TATCAAGATC	420
CAAGAGGGCT GTGATTTTGA TTGCAATTAT TGCATTATCC CAAGCGTGAG AGGGAGGGCT	480
AGGAGTTTTG AAGAGAGGAA AATTTTAGAG CAAGTGGGCC TTTTATGCTC TAAAGGGGTT	540
CAAGAAGTGG TTTTAACCGG CACTAACGTG GGGAGCTATG GGAAAGATAG AGGAAGCAAT	600
ATCGCGCGAT TGATTAAAAA ATTAAGCCAG ATTACTGGAT TGAAACGCAT TAGGATTGGG	660
AGTTTAGAGC CTAATCAAAT CAACGATGAA TTTTLAGAGC TTTTAGAAGA GGATTTTTTA	720
GAAAAACATT TGCATATCGC TTTACAGCAC AGCCATGATT TCATGCTAGA GAGAATGAAT	780
CGAAGAAACC GCACTAAAAG CGATAGGGAA TTATTAGAGA TAATCGCTTC TAAGAATTTT	840
GCTATCGGCA CGGATTTTAT TGTGGGGCAT CCGGGCGAGA GTGAAAGCGT TTTTGAAAAG	900
GCGTTTAAAA ATTTAGAAAG CTTGCCTTTA ACGCATATCC ACCCTTTTAT TTACAGCAAG	960
CGAAAAGACA CCCCCTCTAG TTTGATGCGT GATAGCGTGA GTTTGGAAGA TTCTAAAAAG	1020
CGTTTGAATG CGATTAAAGA TTTGATTTTT CATAAAAAATA AGGCGTTCAG GCAATTGCAA	1080
CTCAAACTCA ACACGCCCT AAAAGCCCTA GTGGAAGCGC AAAAAGACGG CGAATTTAAA	1140
GCCTTAGATC AATTTTTTCAA CCCCATTAAA ATCAAAAGCG ATAAGCCTTT AAGGGCTAGT	1200
TTTTTAGAAA TCAAAGAGTA TGAAATTAAG GAGAGGGAAA ATCATGCCGT TTTCTAA	1257

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...528
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

TTGAAAATCG	CTTACAGGCT	TTTAGGTTTG	ATGAGCTTTA	TCGCGCTTGT	CTTAGCGATC	60
GTTTTAATCA	GTATCCTGCC	CTTACAAAAA	ACCGAACACC	ATTTTCGTGGA	TTTTTTAAAC	120
CAGGACAAGC	ATTACGCCAT	TATCCAAAGA	GCGGATAAAA	GCATTTCCAG	TAATGAAGCG	180
TTGGCTCGTT	CGCTCATTGG	GGCGTATGTG	TTAAACCGAG	AGAGCATTAA	TCGCATTGAC	240
GATAAATCCC	GCTATGAACT	GGTGCCTTG	CAAAGCAGCT	CTAAAGTGTG	GCAACGCTTT	300
GAAGATTTGA	TTAAAGCCCA	AAACAGCATC	TATGTGCAAA	GCCATTTAGA	AAGAGAAGTC	360
CATATCGTCA	ATATTGCGAT	CTATCAGCAA	GACAATAACC	CCATTGCGAG	CGTGTCCATT	420
GCGGCTAAAC	TTTTGAATGA	AAACAAGCTC	GTGTATGAAA	AGCGTTATAA	AATCGTATTG	480
AGCTATTTGT	TTGACACCCC	GGATTTTGAT	TACGCTTCCA	TGCCCTAA		528

(2) INFORMATION FOR SEQ ID NO:339:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 561 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...561
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

TTGTTGCTTG	TTTCTCGCTT	TTTAAACGCC	ATTGATCCTT	TTAATTTAGG	GGTGTGTTG	60
AGCCGTTTCC	AAATTAAAAA	TGGTTGTATT	TATGGGGTGT	GTTCTTACAA	GGTTTCAAAA	120
TTTACCCCTG	GATATGAAGA	AAGCAAAGCG	CGAGTTTTTA	ACGCTCTCAA	TATTTTAAGC	180
AAGCATCAAA	TTTGCCAATC	CAATCAAGAA	AGCGTTACAA	AAGTCAAAGG	AACTTTTGTT	240
TTCATTTTAG	AAAATGACCT	GCATTTAGAC	GAAACTCTT	TTTATAAGAA	ACTTTTAAAT	300
CTGATTATAG	ACAATGACTT	TTTTAACCGC	TCTCATTTAG	TAAGTCCGAG	CAATGGCACC	360
AACTCCCACC	CTGAATTGCA	CCGCTCTATC	ACGCCCAGAG	AAGCCGCTAG	GATACAAAGT	420
TTTAGCGATG	ATTATATCTT	TTATGGCAAT	AAAACGAGCG	TTTGCAAGCA	AATCGGTAAC	480
GCCGTGCCTC	CTCTTCTAGC	CCTAGCCTTA	GGCAAAGCGA	TCTTAAAAAG	CGCAAGAAAT	540

341

GATACAAATC CATCACGCTA A

561

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

ATGGGGTTAA AGAATAAAAT CAAGGGTTTT GTTAAAGAGA GAATGCCTTT TGTAATGAGA	60
TGCGTTCGTG GTTTAAAAGG GGCCAAAGAC ACCCATGAAA ACGCCCATGA TAGGGACGCT	120
TATTGTGGAA TCAATCGTGA AATTAAGGAA ATGCTAGAGG CTAAAAAACT TCATTTTCTT	180
CAAGAAAAAG CTTTATTCAA CCACGACCAT CAAGAAAGCG TGTTTTTAGC TATCGCCTCT	240
TTAAATAATG AAAGTTTCAT TGAATACAAC AAGAGTATTT ATAAAAATAG TTCTCTTAAT	300
TATAATTATG GGGGGCATTT AGAAGATAGG GTCATCCATC CCACTTTAAC TTTACCCAAT	360
CCCACGCATT CGGGTTATTT TGACTATGAT AAAAAAAGTC AAAACCCTAA AAGCCCTCTA	420
AACCCATGGG CTTTATTAG AGTCAAAAC GAAATCGTTA CTTTAGAAGA GAGTTTGTTT	480
TCTATGCTTC CTGCCGTTCA AAGGGGGGT CATTGGTTTT AA	522

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

342

TTGTGGCACC	AACTCTATCA	TTACTGTAAT	TATACGCTTT	CTTTTATCCC	TAAAAATGAG	60
TGGGTAGTAA	AAATTGATTG	CGATCATATC	TATGACGCTA	AAAAGCTTTA	TAAAAGTTTT	120
TATATTCCTA	AGAATATTAA	AGAGGTTGTG	ATGTATTCGC	GCATTAATTT	TGTGGTGCGA	180
GATTTTGAAG	TGTTTGTTTCG	TAACGATGGG	GATTTTGGGT	TTTGTAGACGC	ATGGGGGGAT	240
CATTGGTTAT	TGTATAACGA	TTGCGAGCCT	TTTGAAATTT	GGCGCTACAA	TGATGAAAGT	300
TATGAAGTCC	TAAAGCTTAA	AGATAAACAC	CATATTAAAG	ATAAGGAAAT	GGTGCAATGG	360
CACTTCCCTT	TGGCTAAAAA	GAGGCGAAAC	GCTATTGTTT	ATGACGATTT	GATCCCTTTA	420
GAAGAATTCA	AAAAACGCCA	TGCCGATTTG	ATAGGCACAA	GGATTGAAGA	AAGCATGCTA	480
GATGAAAAGA	GGATTTTAGA	GGTATATCAA	AAATTCGCT	TGCCTTAA		528

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

ATGCAAAAAC	CACAAAATAA	ACCCAGCTCA	TCGCAACAAT	CTCCTCAAAA	CTTTTCTTAC	60
CCAGAGTCCA	AACTAGGCTC	TAAAAACTCT	AAAAACAGCC	TTTACAGCC	TTTAGTAACT	120
CCTAGCAAAG	TAAGCCCCAC	TAACGAAGTT	AAAACGCCAA	CAAACGACGC	TAATCCCCCT	180
TAAAGCATT	CTTCACAAGA	TCAAGAAAAC	AACCTCTTTG	TAGCGCCACC	CACTGAAAAA	240
ACGCTCCCTA	ACAACACCTC	TAGTGCTGAT	GCGAGTGAAA	ACAATGAAAG	CAACGAAAAT	300
AGGGATAATG	TGGAAAAACA	AGCGATTAGA	GATCCTAATA	TCAAAGAATT	CGCATGCGGG	360
AAGTGGGTTT	ATGATGATGA	AAATTTACAA	GCCTATCGCC	CAAGCATTTT	AAAACGCGTT	420
GATAAAGACA	AAGAGATTAC	AACAGACATT	ACCCCTTGCG	ATTACAGCAC	CGCTGAAAAT	480
AAAAGCGGTA	AAATCATTAC	CCCCTATACT	AAAATCTCTG	TTCATAAAAC	AGAGCCTTTA	540
GAAGACCCTC	AAACTTTTGA	AGCTAAAAAT	AATTCGCCA	TTCTCCAAGC	CAGAAGCTCT	600
ACAGAAAAGT	GTAAAAGGGC	TAGAGCGAGA	AAAGACGGCA	CGACCAGGCA	ATGCTATCTG	660
ATAGAAGAGC	CTTTAAAACA	AGCGTGGGAG	AGCGAGTATG	AAATCACCAC	GCAATTAGTG	720
AAAGCCATAT	ATGAACGCCC	CAAACAAGAC	GATCAAGTAG	AGCCGACTTT	TTATGAAACC	780
AGCGAATTGG	CTTATTCTTC	CACACGAAAA	AGCGAAATAA	CGCGTAATGA	ATTGAATTTG	840
AATGAAAAAT	TCATGGAATT	TGTGGAAGTG	TATGAGGGGC	ATTATTTAAA	CGATATAATC	900
AAAGAGAGCA	GCGAATACAA	AGAATGGGTT	AAAAACCATG	TGCGCTTTAA	AGAAGGGGTG	960
TGCATGGCCT	TAGAAATAGA	AGAGCAACCA	CGAGCCAAAA	GCACGCCTTT	GAGTATTGAA	1020
AACTCTCGTG	TTGTGTGTGT	CAAAAAGGGG	AATTATTTAT	TCAATGAAGT	TTAA	1074

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs

343

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

ATACAATACC CCAAGTCATC TTTTTCCTCA AAAAGGGGTA GGAATGGCAA CCATTCAACC	60
ATTCAACCAT TCAACCATTC AACCATTCAT CCATTCAACC ATTCAATCAT TCAATCATTC	120
AATCATTCAA TCATTCAATC ATTCAATCAT TCAATCATTC AATCATTCAA TCATTCAACC	180
ATTCAAGCAA CGCTACCTTA TTTTATAAC TATTTATCTT TTTACAAAAA CCTATTATAA	240
AATCCCCTAT TTTTATTAT TCCCCCTTTT ATTAACCCTT TTATTAACCC TTTTATTAAC	300
CCTTTTATTA ACCCTTTTAT TAACCCTTTT ATTAACCCTT TTATTAACCC TTTTATTAAC	360
CCTTTTATTA ACCCTTTTAT TAACCCTTTT ATTAACCCTT TTATTAACCC TTTTATTAAC	420
CCTTTCATAT AA	432

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 729 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

TTGAAAGTCA ATTTCTTGC CACTTGTCTA GGAGCAGCTA TTTATAGCAA CGCATCGCTT	60
AACGCTATCA AATTACTCCG CAAGGAAAAT TTGGAAGTGG TTTTAAAAA AGACCAGACA	120
TGTTGTGGCC AGCCAAGCTA CAACTCAGGA TACTATGAAG AGACTAAAAA AGTCGTTTTA	180
TACAATATCA AACTTTATTC CAATAACGAC TACCCTATTA TTTTGCCTAG CGGTTCATGC	240
ACAGGGATGA TGCGGCATGA TTATTGGGAA TTGTTTGAAG GGCATGCGGA ATTTAACATG	300
GTAAAGATT TTTGCTCTAG GGTGTATGAA TTGAGCGAGT TTTTGGATAA AAAATTGCAA	360

GTCAAATACG AAGATAAGGG CGAACCTCTC AAAATCACAT GGCATTCTAA TTGCCATGCC	420
TTAAGGGTGG CTAAAGTGAT TGA CTGCGGCG AAAAATCTCA TCAGACAGCT TAAAAATGTG	480
GAAGTCATTG AATTGGAAAA AGAAGAAGAA TGCTGCGGGT TTGGGGGGAC TTTTTCAGTT	540
AAAGAGCCTG AAATTTTCAGC GGTATGGTC AAAGAAAAGA TTAAAGACAT AGAGAGCCGT	600
CATGTGGATG TGATCGTTTC AGCGGATGCT GGGTGCTTGA TGAATATCAG CACCGCTATG	660
CAAAAAATGG GCTCTTTGAC AAAACCCATG CATTTTTATG ACTTTTTTAGC CTCAAGGCTT	720
GGACTTTAA	729

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

ATGATTTTTG GGGATTTTAA ATATCAAAAA AGCGTTAAAA AACTCACAGC CACTAACCTT	60
AACGAGCTTA AAAACGCCCT GGATTTTATC TCTCAAAATA GGGGAAGGG GTATTTTGTG	120
GGGTATCTTT TGTATGAAGC GCGCTTAGCG TTTTITAGATG AAAATTTTCA AAGCCAAACC	180
CCTTTTTTGT ATTTTGAACA ATTTTITAGAA AGAAAAAAT ACCCTTTAGA GCCTTTAAAA	240
GAGCATGCGT TTTACCCTAA AATCCACAGC TCTTTAGATC AAAAAACTTA TTTCAAGCAG	300
TTTAAGGCCG TTAAAGAGCA TCTCAAAAAC GGCATACCT ATCAAGTGAA TTTGACAATG	360
GATTTATTGT TAAACACTAA AGCCAAACCA AAGCGCGTTT TTAAGGAAGT GATACACAAC	420
CAAAACACGC CTTTAAAGGC TTTTATAGAA AATGAGTTTG GGAGCGTTT AAGCTTTTCG	480
CCGGAATTGT TTTTGAATT AGAGTTTTTA GACACAGCGA TTAAGATTAT CACAAAACCC	540
ATGAAAGGCA CGATCGCTCG CTCAACAAC CCCTTGATAG ATGAAAAAAA CCGATTGTTT	600
TTGCAAAATG ATGACAAAAA TAGAAGCGAA AATGTGATGA TCGTGGAATT ATTGCGTAAC	660
GATTTGAGCC GCTTGGCCTT AAAAAATAGC GTGAAAGTCA ATCAATTGTT TGAAATCATC	720
AGTTTGCCGA GCGTGATCA AATGATAAGC GAGATTGAAG CTCAATTGCC CCTAAAAACA	780
AGCTTGTTTG AGATTTTTAA GCGTTGTTT CCTTGCGGCT CTGTGACCGG ATGCCCTAAA	840
ATCAAAACCA TGCAATCAT TGAAAGTTTA GAAAAACGCC CTAGGGGGGT GTATTGTGGG	900
GCGATAGGCA TGGTTGGAGG AAAAAAGCC CTTTTTAGCG TGCCTATCCG CACTTTAGAA	960
AAAAGAGCGC ATGAAGATTT TTTGCATTTA GGGGTAGGGA GTGGGGTAAC TTATAAAAGT	1020
AAAGCTTCAA AGGAATATGA AGAGAGCTTT TTTAAATCCT TTTTGTGAT GCCCAAAATA	1080
GAATTTGAGA TCGTGAAAC GATGAGAGTT ATCAAAAGGG ATCAAAAATT AGAGATTAAAC	1140
AATAAAACG CCCATAAAGA ACGCTTAATG CATAGCGCCC AATATTTTAA CTTTAAATAC	1200
AGATGA	1206

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 base pairs

345

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...795
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

ATGAAAATCA GTGTTAGTAA AAACGATTTA GAAAACACTT TCGCTACTT GCAAGCTTTT	60
TTGGATAAAA AGGACGCTTC CTCTATCGCT TCACACATCC ATTTAGAAGT CATTAAGAA	120
AAGCTCTTTT TAAAAGCCAG CGATTCAGAT ATTGGACTAA AAAGCTATAT TTCTACGCAA	180
TCTACCGATA AAGAGGGCGT AGGCACGATC AACGGGAAGA AGTTTTTAGA TATTATCTCA	240
TGTTTGAAAG ACTCTAATAT TGTTTTAGAG ACTAAAGATG ACAGCTTGGT GATCAAACAA	300
AATAAAGCT CTTTCAAAC CCCCATGTTT GACGCTGATG AGTTCCTGA ATTCCCTGTT	360
ATTGATCCAA AAGTGAGTTT AGAAATCAAT GCCCCCTTTT TGGTGGATGC GTTAAAAAG	420
ATCGCTCCTG TGATTGAGCA AACTAGCCAT AAAAGGGAAT TAGCCGGTGT TTTAATGCAA	480
TTCAATCAAA AACACCAAAC CCTTTCAGTG GTAGGCACGG ATACCAAGCG GCTCTCTTAC	540
ACGCAGTTAG AAAAAATCTC TATCCATTCC ACCGAAGAAG ACATCTCTTG CATTTTGCCT	600
AAAAGGGCTT TATTGGAAAT CCTTAAACTT TTTTATGAAA ATTTAGTTT TAAAAGCGAC	660
GGCATGTTAG CGGTGGTTGA AAACGAAACG CACGCTTTTT TCACCAAGCT CATTGATGGG	720
AATTACCCTG ATTATCAAAA AATCCTCCCT AAAGAATACA CTTCTTCTTT CACTTTAGGC	780
AAGGAAGAAT TTAA	795

(2) INFORMATION FOR SEQ ID NO:347:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 939 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...939
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

TTGAATAATT	TAGAGCCTTT	GGGCGCGGAA	GTGTTTGTGG	GGTTAGACGG	CATTGATGCG	60
ATGATAGAGG	AGTGCGTTTC	CAATTTAGTC	ATTAACGCCA	TTGTGGGCGT	AGCCGGATTG	120
AAAGCGAGCT	TTAAAAGCTT	ACAAAGGAAC	AAAAAACTAG	CCCTAGCGAA	TAAAGAAAGT	180
TTAGTGAGCG	CGGGGCATTT	ATTAGACATT	TCACAAATCA	CGCCCGTTGA	TAGCGAGCAT	240
TTTGGTTTGT	GGGCGTTGTT	GCAAAACAAG	ACTTTAAAGC	CTAAATCTTT	AATCATTAGC	300
GCGAGTGGGG	GGGCTTTTAG	GGACACGCCC	TTAGATCTTA	TCGCTATTCA	AAATGCGCAA	360
AACGCGCTCA	AGCACCTTAA	TTGGAGCATG	GGGGATAAAA	TCACCATTGA	TTCAGCGAGC	420
ATGGTCAATA	AACTTTTTGA	AATTTTAGAA	ACCTATTGGC	TTTTTGGTGC	GTCTTTAAAG	480
ATTGACGCGC	TGATTGAAAG	AAGTTCTATC	GTGCATGCTT	TGGTGGAGTT	TGAAGACAAC	540
TCTGTCATTG	CGCATTTAGC	GAGTGC GGAC	ATGCAATTAC	CCATAAGCTA	TGCCATTAAC	600
CCTAAATTAG	CTTCTTTGAG	TGCTTCCATT	AAACCCCTAG	ATTTATACGC	TTTAAGCGCG	660
ATTAAATTTCG	AACCCATTAG	CGTGGAGCGC	TACACTTTGT	GGCGTTATAA	AGATTTGTTG	720
TTGGAAAACC	CAAAGCTTGG	CGTGGTGCTG	AATGCGAGCA	ATGAAGTGGC	GATGAAGAAG	780
TTCTTGAATC	AAGAAATCGC	TTTTGGTGGC	TTTATCCAAA	TCATCTCTCA	AGCTTTAGAA	840
TTGTATGCTA	AAAAATCTTT	CAAGCTCTCT	AGTTTAGATG	AAGTGCTAGC	GTTAGATAAG	900
GAAGTTAGGG	AGCGTTTTTG	AAGGTAGCG	AGAGTGTAG			939

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 873 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

ATGTTAGAAA	ATGTCAAAAA	ATCCCTTTTT	AGGGTTTTGT	GCTTGGGCGC	GTTGTGTTTA	60
GGGGGGCTAA	TGGCAGAGCA	AGACCCTAAA	GAGCTTGTCG	GTTTGGGGGC	AAAGAGCTAC	120
AAAGAGCAGG	ATTTCACTCA	GGCTAAGAAA	TATTTTGAAA	AAGCTTGCGA	TTTGAAAGAA	180
AATAGCGGGT	GTTTTAATTT	AGGGGTGCTT	TATTATCAAG	GGCATGGGGT	GGAAAAGAAT	240
TTGAAAAAAG	CCGCTTCATT	TTACTCTAAA	GCTTGCGATT	TAAATTACAG	CAATGGGTGT	300
CATTTGCTAG	GGAATTTATA	TTATAGCGGG	CAAGGCGTGT	CCCAAAACAC	CAACAAAGCC	360
TTGCAATACT	ACTCTAAAGC	GTGCGATTTG	AAATACGCTG	AAGGGTGTGC	GAGCTTAGGG	420
GGGATCTATC	ATGATGGCAA	AGTGGTTACT	AGGGATTTTA	AAAAAGCGGT	GGAATATTTT	480
ACTAAAGCTT	GCGATTTGAA	CGATGGCGAT	GGTTGCACGA	TATTAGGGAG	CTTGTATGAT	540
GCAGGCAGAG	GCACGCCTAA	AGATTTGAAA	AAAGCGCTCG	CTTCGTATGA	TAAAGCTTGC	600
GACTTAAAG	ACAGCCCAGG	GTGCTTTAAC	GCAGGGAACA	TGTATCATCA	TGGCGAAGGT	660
GCGGCGAAGA	ATTTTAAAGA	GGCCCTCGCT	CGTTATTCTA	AGGCATGCGA	GTTGGAAAAT	720
GGCGGAGGGT	GTTTCAATTT	AGGGGCTATG	CAATACAATG	GCGAAGGCGC	AACAAGGAAT	780
GAAAAGCAAG	CCATAGAAAA	CTTTAAAAAA	GGCTGTAAAT	TAGGCGCTAA	AGGGGCATGC	840
GATATTCTCA	AGCAGCTCAA	AATCAAAGTT	TAG			873

(2) INFORMATION FOR SEQ ID NO:349:

347

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 714 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...714
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

ATGAAGTCAA ATAAAAAGTC CAATCATTTA AGAGCGATTT ATAGGGCTTT AGTGATCGCT	60
ATAGGCTTAG CCGTTATCAT TGTTTTCAAT TATTTTAAACC GCAAAAACAA TAACGCCCGC	120
TCCAGCCGTA GGGCTTGTTT GTGTTTTTTT TCTCTCACCG GGGTTAATTT AGAAAAATA	180
GGTTCCTTTG ACACGGGCGC TAAACTCATT GTCTTAAACC ACCAAAGCTT ACTAGACATT	240
ATTTATTTAG AAGCCTACCA CCCTAGTAAT ATTTGCTGGA TCGCTAAAAA AGAGCTGGGC	300
GAAATCCCTT TTTATGGGCA TGCTCTAACG GATACCGGAA TGATCTTAAT TGACAGAGAG	360
GATAAAAAGG GGATAGTGAG CCTTTTGAAA GCATGTAAAG AAAAGCTAGA TCAAAACCGC	420
CCTTTAGTGA TTTTTCCTGA AGGCACTAGA GGCAAAGGAG GAGAAAAATT CCTCCCCTTT	480
AAGCAAGGGG CTAAAATCAT CGCTGAAAAA TTCCAGCTCA AAATCCAGCC CATGGTGTTA	540
ATCAATTCCA TTAAAATCTT TAATTCCAAG CCCCTAGAAG CTTATAAAGC GCGCACCCGT	600
TTGGTCATGC TAGAAAGCTA TACGCCTGAT TTTAGCTCGC CCACCTGGTA TGAAGAATTA	660
CAAGAACGCA TGCAAAAAGA ATATTTAAAA CACTACCACG AACTAAACGC ATGA	714

(2) INFORMATION FOR SEQ ID NO:350:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2046 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2046
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

ATGGGTTTTG	AAAAAAGCAT	TTTAGACAAT	TTGAACGGAG	CGCAAAAAAT	TGCCGCATGC	60
CACATTCAAG	GGCCTTTATT	GATTTTAGCG	GGAGCTGGGA	GCGGTAAGAC	TAAGACTTTA	120
ACGAGCCGTT	TAGCGTATTT	GATTGGCGCT	TGTGGCGTGC	CTAGCGAAAA	CACTTTAACG	180
CTCACTTTCA	CCAATAAAGC	GAGTAAAGAA	ATGCAAGAAA	GGGCTTTGAA	ATTGTTGAAA	240
AACCAAGCCC	TTATCCCCC	CTTGCTTTGC	ACTTTCATC	GTTTTGGTTT	GCTGTTTTTA	300
AGGCAACACA	TGAATCTTTT	AAAAAGGGCG	TGCGATTTTT	CGGTGCTAGA	TAGCGATGAA	360
GTGAAAACGC	TCTGCAACA	GCTCAAATT	TCAAATTTCA	GGGCGAGCAT	TTCTCAAATC	420
AAAAACGGCA	TGATGGATT	GAGCGTGCAA	GATAGCGAAT	GTTACAAAGC	GTATGAGCTT	480
TATCAAAACG	CGCTCAAAAA	AGACAATTTA	GTGGATTTTG	ACGATTTGCT	TTGTTTGAGC	540
CTTAAGATTT	TACAAGATAA	TGAAAACTC	GCCAAAGAGA	CCAGCGAACG	CTACCATTAC	600
ATTATGGTAG	ATGAGTATCA	AGACACGAAC	GCCCTGCAAC	TGGAATTTTT	AAAACAATTG	660
AGTTTCACGC	ACCATAATTT	GTGCGTGGTG	GGCGATGACG	ATCAGAGCAT	TTATGGGTTT	720
AGGGGGGCTG	ATATTTCTAA	CATTTTAAAT	TTTTCCAAGC	ATTTTAAAGG	GGCTAAAATA	780
GTGAAATTAG	AGACCAACTA	CCGCTCTAGC	GCTGAAATCT	TAGCGTGCGC	TAATCCCCTG	840
ATCAGCCATA	ACCAACACCG	CCACATTAAA	ACGCTTCAAA	GTTTCAAAGG	TTCGCACAAA	900
AGCGTGATTT	GTAAAGAATA	CCCCACGCAA	AAAGAAGAGA	GCCTGGATGT	GGCTTATCAG	960
ATCAAAGCCC	TTTTTAAAGAA	GGGCGAGAAT	TTAGAAAATA	TCGCTATTTT	GTATCGTTTA	1020
AATGGGCTTA	GGCGCAGCAT	TGAAGAGAGC	TTGAACGCTT	TGAATATCCC	TTATAGGCTC	1080
ATTGGTGCGG	TGAGTTTCTA	TGAAAGAGCC	GAGGTTAAAG	ACGCTTTGGC	ACTCATGCAT	1140
GTGGTGCGGA	AAAAAGACGA	TCGCTTTTTT	ATTAAACGCG	TTTTTAAACAA	CCCCCAAGA	1200
GGCCTTGCGA	AGATCACTCA	AGAATGGATT	TTTTCTCTTT	TAGATGAAGA	GGGTTTGAAT	1260
TTAGAAGAAG	CGCTAAAAAT	TGGGGCGTTT	AAAGACAAAC	TCAACCCATA	AAACGAATAC	1320
GCTTTAAAGA	AATTCACCGC	TATGATAGGG	CGTTTGAGGG	AGGCTTTTGA	AATTCAGTA	1380
GAGAAGTTTT	GCGAGCGGTT	TTTAGAAGAG	ACTAACCTTT	TAAAAAGCTA	TGAAAAAGAA	1440
GACAATTACG	AAGAAAGAGA	GGGCTTTGTT	AAAGAGCTTT	TAAGTTTAGT	GAAAGAGCAT	1500
TTTAAACTA	ACCCACGCA	TTCTTTACTG	GATTTTTTGA	ATGAAAGCGC	ACTGGATGTC	1560
CATAATACAG	AAAACGCGCA	AAAAGTGAGT	TGCATGAGCG	TGCATATGAG	TAAGGGCTTA	1620
GAGTTTAAGC	ATGTGTTTGT	GATCGGGTTA	GAAGAGGGGT	TTTTCCCGCA	TAGGGGGTTC	1680
AATCAAGAAA	GCGATTTGGA	AGAAGAAAGG	CGCTTGCGTT	ACGTGGCGAT	CACTAGGGCT	1740
AAAGAAGAAT	TACAACCTTC	TTATGTCAAA	GAGCGTTCGT	ATTTTGGGAG	GAAAATTTCT	1800
TGCTCGCCCT	CTGTGTTTTT	AGAAGAAGCC	CAGTTGCTCC	AACAAGACAA	GCCTCCTAAA	1860
CAAAATCACC	AAAAAGATAC	GCCCATTAAA	GTGGGGGATT	TGATCAAACA	TAAGATTTTT	1920
GGCACCGGGA	GGGTTTTAGG	CGTAGAAAAA	GGCTTGAGCG	GTTTGTGCTT	GAAAATCAAT	1980
TGCGGAGGGA	ATGTCTATGA	TAAAATTTCA	GAAAAATTTG	TAGAAAAAGT	GGATAACGAG	2040
TTTTGA						2046

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

ATGAAACTT	CTAACACAAA	AACCCCTAAA	CCCGTTTTAA	TCGCCGGGCC	ATGCGTCATT	60
GAGAGTTTAG	AAAATCTAAG	AAGTATCGCT	ATTAAATTAC	AACCCCTAGC	CAACAACGAG	120
CGGTTGGATT	TTTATTTTAA	AGCGAGTTTT	GATAAGGCTA	ACCGCACGAG	TTTGGAGAGT	180
TACAGAGGAC	CTGGTTTAGA	AAAAGGCTTA	GAAATGTTAC	AAACTATCAA	AGATGAATTT	240
GGTTATAAAA	TTTTAACCGA	TGTGCATGAG	AGCTATCAAG	CAAGCGTGGC	AGCCAAGGTA	300
GCGGATATTT	TACAAATCCC	GGCGTTTTTG	TGCCGCCAAA	CGGATCTGAT	TGTAGAAGTG	360
AGCCAAACTA	ACGCCATTGT	CAATATCAAA	AAAGGGCAAT	TCATGAACCC	AAAAGACATG	420
CAATATTCGG	TTCTAAAAGC	CCTTAAAACA	AGGGATAGTA	GCATTCAAAG	CCCCACTTAT	480
GAAACAGCGT	TAAAAAATGG	CGTGTGGCTG	TGTGAAAGGG	GGAGCAGCTT	TGGGTATGGG	540
AATTTAGTGG	TGGATATGCG	CTCTTTAAAA	ATCATGCGAG	AATTTGCCCC	TGTGATTTTT	600
GACGCTACCC	ATAGCGTGCA	AATGCCAGGG	GGAGCGAACG	GGAAAAGTTC	AGGAGACAGC	660
TCTTTTCCCC	CTATTTTACC	CAGAGCGGCG	GCGGCGGTGG	GGATTGATGG	GCTGTTCGCT	720
GAAACGCATA	TTGATCCTAA	AAACGCCCTA	AGCGATGGAG	CAAACATGCT	AAAACCTGAC	780
GAGCTAGAAC	ACTTAGTAAC	CGACATGTTA	AAAATCCAAA	ATTTATTTTA	A	831

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

ATGATGAAAT	TTTTTCTTTT	AAAGAAATTC	AGCGAATTTT	TAAACACTCA	AACGCATTTT	60
AACCTCAAAC	GCTTGAACGC	GTCTAGTTTT	TTATTAGAGA	CTTTTCTTAA	AGAAAAACAC	120
GCCTTTGTTG	TGGATTGAG	CGCGCCTTAT	ATTGGTTTGT	CCAAAAAACC	CCCAGAGAGC	180
GTTTTAAAAA	ACACTTTAGC	GTTAGATTTT	TGTTTGAATA	AATTCACCAA	AAACGCCAAA	240
ATTTTACAAG	CAAACGTCAT	TGATAACGAT	CGGATTTTAG	AAATCAAGGG	CGCTAAAGAT	300
TTAGCTTATA	AGAGTGAAAC	TTTTATTTTG	CGTTTAGAAA	TGATCCCTAA	AAAAGCCAAT	360
CTCATGATTT	TAGATCAAGA	AAAATGCGTG	ATAGAGGCTT	TTCGTTTAA	TGACAGGGTG	420
GCTAAAAACG	ATATTTTAGG	GGCATTGCCT	CCTAATATTT	ACGAGCATCA	AGAAGAGGAT	480
TTGGATTTTA	AGGGATTGTT	GGACATTTTA	GAAAAAGATT	TTTTATCCTA	TCAGCACAAA	540
GAATTGGAAC	ACAAAAAAA	TCAAATCATC	AAGCGATTAA	ACGCCCCAAA	AGAACGCTTG	600
AAAGAAAAAT	TAGAAAAACT	AGAAGATCCT	AAAACTTTAC	AGCTGGAAGC	GAAAGAATTG	660
CAAACCTCAAG	CCTCATTTGT	GCTCACTTAC	CAGCATTTAA	TCAACAGGCG	TGAAAATCGC	720
GTGATTTTAA	AGGATTTTGA	AGATAAAGAA	TGCATGATTG	AAATTGATAA	GAGCATGCCC	780
TTAAACGCTT	TTATCAATAA	AAAATTCACT	CTCAGCAAGA	AAAAGAAACA	AAAATCGCAA	840
TTCTTGATTT	TAGAAGAAGA	GAATCTGAAA	GAAAAAATCG	CTTTTAAGGA	AAATCAAATC	900
AACTATGTTA	GAGACGCTGC	AGAAGAAAGC	GTTTTAGAAA	TGTTTATGCC	GGTAAAAAAC	960

TCTAAAATCA AACGCCCCGAT GAACGGGTAT GAAGTGCTGT ATTATAAGGA TTTTAAAATC	1020
GGTTTAGGGA AAAACCAAAA AGAGAATATC AAGCTTTTAC AAGACGCAAG AGCGAATGAT	1080
TTGTGGATGC ATGTGAGAGA TATTCCTGGA TCGCATTGGA TCGTTTTTTG CCAAAAAGAT	1140
ACGCCTAAAG ATGAGGTCAT TATGGAATTA GCCAAAATGT TGATTAAAAT GCAAAAAGAT	1200
GCGTTTAATG GTTACGAGAT TGACTACACG CAACGAAAAT TTGTCAAAAT CATCAAAGGA	1260
GCTCATGTCA TTTACTCAA ATACCGAACT ATTAGTCTAA AGGACACTTA A	1311

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

ATGTTTAAAA AAATCATTTT TTTGTGCGTT TTTTGTATAG GGGGATTGT CATTCACCC	60
CTTGAAGCCA TGCCTATTTT GCGCAATAAA ACCCCCAAAA AAAATTACCA AGAAGCCCAT	120
GAAAAGCTCT ATAGAAGCAT CATTAAACGC CAAAAGCTCA CGCGTAAAAA AAGCGGGTGG	180
TATTTTTTAG GGGGGTTGG CGCTGTAGAA GCCATTAAGG ACTATCAAGG CAAGGAAATG	240
AAAGATTGGA TCGCCACGCT CAATTTAAAA ACCGGCGTGC AAAGTTTTTT TAAAAATAC	300
ATCGGGATTA GGGGGTTTT TGCATGGGAT CTTGGGTCAG GAAAAGTGAA TTATCAAAGC	360
TATAAAGATC CTACCAACTC TTTTTTTACC ATGCTTGCGG TGGGTTTGA TGTGATCATG	420
GAATTCCTC TAGGGAGTTA TAAGCATTAT TTAGGGGCGT TTGGGGGAGC TAGGGGGGCT	480
TTAGTTGTTT ATACAGACAA GCAAATTTT AAGTTTTTTA AACATTCTGT GGTTCAGGG	540
GGATTAGCGA TTAGTGAGG GGTCATGCTC ACGCTTTTTT TAAGGCACCG CATTGAATTA	600
GGGTTTAAGA TCTTGCCAC CGCCAGATTG CTTTCTAGCT CTAGTCGCTT TGAAACTTCG	660
CCCCTATTTT ATGCGGCATA CAGCTATAAA TTTTAA	696

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1983 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

ATGCTAAAAA	AGATTTTTTA	TGGTTTTATC	GTTTTATTTT	TGATTATCGT	AGGGTTGTTG	60
GCCGTTCTTG	TCGCTCAAGT	TTGGGTAAC	ACGGATAAGG	ATATTGCTAA	AATTAAAGAT	120
TATCGCCCCA	GTGTCGCTTC	ACAGATTTTA	GACAGAAAAG	GGCGTTTGAT	CGCTAATATT	180
TATGATAAGG	AATTTTCGTTT	TTATGCGCGT	TTTGAAGAAA	TCCCCCACG	ATTTGTTGAA	240
AGCCTTCTAG	CGGTAGAAGA	CACCTCTTTT	TTTGAGCATG	GGGGGATCAA	TTTAGACGCT	300
GTCATGCGCG	CTATGATTAA	AAACGCTAAA	AGTGGTCGTT	ACACTGAAGG	GGGTAGCACT	360
CTAACCCAAC	AACCTCGTTAA	AAACATGGTG	CTCACACGGG	AAAAAACCTT	AACCAGAAAA	420
CTCAAAGAAG	CTATCATCTC	CATACGCATT	GAAAAAGTCT	TAAGCAAAGA	AGAAATTTTA	480
GAGCGTTATT	TGAACCAAAC	TTTTTTTGGG	CATGGGTATT	ATGGCGTGAA	AACCGCAAGT	540
TTAGGGTATT	TTAAAAAACC	CCTTGACAAA	CTCACGCTTA	AAGAAATCAC	CATGTTAGTC	600
GCCTTACCTA	GGGCTCCAAG	TTTTTATGAC	CCTACCAAAA	ATTTAGAATT	TTCCTCTCT	660
AGGGCTAATG	ATATTTTAAG	GCGGTTGTAT	TCTTTAGGCT	GGATTTCTTC	TAACGAGCTC	720
AAATCCGCTC	TCAATGAAGT	GCCAATCGTC	TATAACCAAA	CTTCCACGCA	AAATATCGCT	780
CCCTATGTCG	TGGATGAAGT	GTTGAAGCAA	TTGGATCAAT	TAGACGGGTT	AAAAACTCAA	840
GGCTATACCA	TAAAACTCAC	GATAGATTTG	GATTACCAAC	GCTTAGCGTT	GGAGTCTTTG	900
CGTTTTGGGC	ATCAAAAAAT	CTTAGAAAAA	ATCGCTAAAG	AGAAGCCAAA	AACTAACGCT	960
TCTAATGATA	AAGATGAAGA	CAACTTAAAC	GCCAGCATGA	TAGTTACAGA	AACGAGCACC	1020
GGTAAGATTT	TAGCCTTAGT	GGGGGGGATT	GATTATAAAA	AAAGCGCTTT	CAATCGCGCC	1080
ACGCAAGCCA	AACGGCAGTT	TGGGAGCGCG	ATCAAGCCTT	TTGTGTATCA	AATCGCTTTT	1140
GATAATGGCT	ATTCCACCAC	TTCCAAAATC	CCTGATACCG	CGCGAAATTT	TGAAAATGGC	1200
AATTATAGTA	AAAACAGCGT	GCAAAACCAC	GCATGGCACC	CTAGCAATTA	TACTCGCAAA	1260
TTTTTAGGGC	TTGTAACCTT	GCAAGAAGCC	TTGAGCCATT	CGTTAAATCT	GGCTACGATT	1320
AATTTAAGCG	ATCAGCTTGG	CTTTGAAAAA	ATTTATCAAT	CTTTAAGCGA	CATGGGGTTT	1380
AAAAACCTCC	CTAAAGATTT	GTCTATTGTG	TTAGGGAGCT	TTGCTATCTC	ACCGATTGAT	1440
GCGGCTGAAA	AGTATTCTCT	ATTTTCTAAT	TACGGCACCA	TGCTCAAACC	CATGCTCATT	1500
GAAAGCATCA	CCAACCAACA	AAACGAAGTC	AAAACTTTCA	CGCCCATTTGA	AACCAAAAAG	1560
ATCACTTCCA	AAGAACAAGC	TTTTTTAACC	CTTTCAGCGC	TGATGGATGC	GGTAGAAAAC	1620
GGCACAGGGA	GTTTGGCTCG	CATTAAAGGT	TTAGAAATTG	CCGGTAAAAC	CGGGACTTCT	1680
AACAACAATA	TTGACGCTTG	GTTCAATTGGC	TTTACCCCCA	CCTTACAAAG	CGTGATCTGG	1740
TTTGGGAGAG	ACGATAACAC	GCCTATTGGC	AAAGGAGCGA	CAGGAGGCGT	TGTGAGCGCG	1800
CCTGTGTATT	CGTATTTTCAT	GCGCAATATC	TTAGCGATTG	AACCTTCTTT	AAAAAGAAAG	1860
TTTGATGTCC	CCAAAGGCTT	GCGTAAAGAA	ATCGTGGATA	AAATCCCCCTA	CTACTCAAGC	1920
CCTAATTCCA	TCACCCCCAC	CCCCAAAAAA	ACAGACGATA	GCGAAGAACG	CTTGTTGTTT	1980
TAA						1983

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 972 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

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ATGAAATATT TATGGCTTTT TTTAATATAC GCTATAGGGC TTTTTCGAAC AGATAAAACG      60
CTAGATATTA TTAAAACCAT TCAAAAACCTT CCTAAGATTG AAGTGCGCTA CTCCATAGAT      120
AACGATGCCA ATTACGCTTT AAAATTGCAT GAAGTCTTAG CGAACGATTT AAAGACTAGC      180
CAGCATTTTG ATGTTTCTCA AAACAAAGAG CAAGGTGCTA TCAATTACGC AGAACTCAAG      240
GATAAAAAAG TCCATCTTGT AGCGCTTGTG AGCGTGGCGG TAGAAAACGG CAATAAAATT      300
TCACGATTAA AACTTTATGA TGTGGATACA GGAACGCTCA AAAAGACTTT TGA CTACCCC      360
ATTGTAAGTT TAGATCTATA CCCTTTTGCA GCGCACAACA TGGCCATTGT GGTGAATGAT      420
TATTTAAAAG CCCCTTCTAT CGCTTGGATG AAGCGCCTGA TTGTTTTTTC TAAATACATT      480
GGACCAGGAA TCACAAACAT CGCACTAGCG GATTATACGA TGC GTTATCA AAAAGAAATC      540
ATCAAAAACA ACCGACTCAA TATTTTCCCC AAATGGGCGA ACGCTGAGCA AACGGAGTTT      600
TATTACACGC AGTATGGCGA AAAAACGCCC ATGATTTTAA AATACAACAT TCAAAAAGCC      660
ACTCATGAGA ATATCGCTAG CTCTCAAGGA ATGGCTGTGG TCTCTAGCGT GAGTTCTGAT      720
GGCTCTAAAA TTTTAATGTC TTTAGCCCCT GATGGCCAAC CGGATGTTTA TTTGTATGAC      780
ACGCATAAAA AAATAAAAC CAAAATAACG CGCTATCCGG GGATAGATGT TTCAGGCGTG      840
TTTTTAGAAG ATGACAAGTC TATGGCTTTT GTTTCAGATA GATCCGGTTA TCCTAACATC      900
TATATGAAGA AATTGGGGTT AAAAGAGAGC GCGGAGCAAC TCCTTTATGA AGGAAGAAGC      960
AATGAATCCA TT

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(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3867 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...3867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

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ATGGAAATAC AACAAACACA CCGCAAAATC AATCGCCCTT TAGTTTCTCT CGTTTTAGCA      60
GGAGCGTTGA TTAGCGCCAT ACCGCAAGAG AGTCATGCCG CCTTTTTCAC GACCGTGATC      120
ATTCCAGCCA TTGTTGGGGG TATCGCCACA GGCCTGCTG TAGGAACGGT CTCAGGGCTT      180
CTTAGTTGGG GACTCAAACA AGCCGAAGAA GCGAATAAAA CCCCAGATAA ACCCGATAAA      240
GTTTGGCGCA TTCAAGCAGG AAAAGGCTTT AATGAATTTT CTAACAAGGA ATACGACTTA      300
TACAAATCCC TTTTATCCAG TAAGATTGAT GGAGGTTGGG ACTGGGGGAA CGCCGCTAGG      360

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CATTATTGGG	TCAAAGGCGG	GCAATGGAAC	AAGCTTGAAG	TGGATATGAA	AGACGCTGTA	420
GGGACTTATA	AAC TATCAGG	GCTTAGAAAC	TTTACTGGTG	GGGATTTAGA	CGTGAATATG	480
CAAAAAGCCA	CTTTGCGTTT	GGGCCAATTC	AATGGCAATT	CTTTCACAAG	CTATAAGGAT	540
AGCGCTGATC	GCACCACGAG	AGTGAATTTT	AACGCTAAAA	ATATTTCAAT	TGATAATTTT	600
GTAGAAATCA	ATAATCGTGT	GGGTTCTGGA	GCCGGGAGAA	AAGCCAGCTC	TACGGTTTTG	660
ACTTTGCAAG	CTTCAGAAGG	GATCACTAGC	AGTAAAAATG	CGGAAATTTT	TCTTTATGAT	720
GGCGCCACGC	TCAATTTGGC	TTCAAACAGC	GTTAAATTAA	ATGGTAATGT	GTGGATGGGC	780
CGTTTGCAAT	ACGTGGGAGC	GTATTTAGCC	CCTTCATACA	GCACGATCAA	CACTTCAAAA	840
GTTCAAGGGG	AAGTGGATTT	TAACCATCTC	ACTGTGGGGG	ATCAAAACGC	CGCTCAAGCG	900
GGCATTATCG	CTAGCAATAA	GACTCATATT	GGCACACTGG	ATTTGTGGCA	AAGCGCCGGG	960
TTAAATATCA	TTGCCCTTCC	AGAAGGTGGC	TACAAGGATA	AACCTAATAG	TACCACTTCT	1020
CAAAGTGCGA	CTAAAAACGA	CAAGAAAGAG	ATCAGTCAAA	ATAACAATAG	CAACACAGAG	1080
GTCATTAACC	CACCCAATAA	CACGCAAAAA	ACAGAAACTG	AACCCACGCA	AGTCATTGAT	1140
GGGCCTTTTG	CTGGCGGCAA	AGACACGGTT	GTCAATATTT	TCCACTTAAA	CACTAAAGCC	1200
GATGGCACGA	TTAAAGTGGG	AGGGTTTAAA	GCTTCTCTTA	CCACGAATGC	GGCTCATTTG	1260
AATATCGGCA	AAGGCGGTGT	CAATCTGTCC	AATCAAGCGA	GCGGGCGCAC	CCTTTTAGTG	1320
GAAAATCTAA	CCGGGAATAT	CACCGTTGAT	GGGCCTTTAA	GAGTGAATAA	TCAAGTGGGT	1380
GGCTATGCTT	TGGCAGGATC	AAGCGCGAAT	TTTGAGTTTA	AGGCTGGTGT	GGATACTAAA	1440
AACGGCACAG	CCACTTTCAA	TAACGATATT	AGTTTGGGAA	GATTTGTGAA	TTTAAAGGTG	1500
GATGCTCATA	CAGCTAATTT	TAAAGGTATT	GATACGGGTA	ATGGTGGTTT	CAACACCTTA	1560
GATTTTAGTG	GTGTTACAGA	CAAAGTCAAT	ATCAACAAGC	TCATCACAGC	TTCCACTAAT	1620
GTGGCCGTTA	AAAACCTTAA	CATTAATGAA	TTGATTGTTA	AAACCAATGG	GATAAGTGTG	1680
GGGGAATACA	CTCATTTTAG	CGAAGATATA	GGCAGTCAAT	CGCGTATCAA	TACCGTGCCT	1740
TTGGAAACTG	GCACTAGGTC	AATCTTTTCT	GGGGGTGTCA	AATTTAAAAG	CGGTGAAAAA	1800
CTAGTTATCA	ATGATTTTTA	CTATAGCCCT	TGGAATTATT	TTGACGCTAG	GAATGTTAAA	1860
AATGTTGAAA	TCACCAGAAA	ATTCGCTTCT	TCAACCCAG	AAAACCCTTG	GGGCACATCA	1920
AAGCTCATGT	TTAATAATCT	AACCTTGGGT	CAAAATGCGG	TCATGGACTA	TAGTCAATTT	1980
TCAAATTTAA	CCATTACAGG	GGATTTTATC	AACAATCAAG	GCACTATCAA	CTATCTGGTC	2040
CGAGGCGGGA	AAGTGGCAAC	CTTAAATGTA	GGCAATGCAG	CAGCTATGAT	GTTTAATAAT	2100
GATATAGACA	GCGCGACCGG	ATTTTACAAA	CCGCTCATCA	AGATTAACAG	CGCTCAAGAT	2160
CTCATTAATA	ATACAGAGCA	TGTTTTATTG	AAAGCGAAAA	TCATTGGTTA	TGGTAATGTT	2220
TCTACAGGTA	CCAATGGCAT	TAGTAATGTT	AATCTAGAAG	AGCAATTCAA	AGAGCGCCTA	2280
GCCCTTTATA	ACAATAATAA	CCGCATGGAT	ACTTGTGTGG	TGCGAAATAC	TGATGACATT	2340
AAAGCATGCG	GTATGGCTAT	CGGCAATCAA	AGCATGGTGA	ACAACCCTGA	CAATTACAAG	2400
TATCTTATCG	GTAAGGCATG	GAGAAATATA	GGCATCAGTA	AAACGGCTAA	CGGCTCTAAA	2460
ATTTCCGGTG	ATTATTTAGG	CAATCTACG	CCTACTGAGA	ATGGTGGCAA	TACCACCAAC	2520
TTACCCACAA	ACACCACTAA	TAATGCGCAT	TCTGCTAACT	ACGCTCTCGT	GAAGAACGCT	2580
CCTTTCGCTC	ACAGCGCCAC	TCCTAATTTA	GTCGCTATCA	ATCAGCATGA	TTTTGGCACT	2640
ATTGAGAGCG	TGTTTGAATT	GGCTAACCGC	TCTAAAGATA	TTGACACGCT	CTATACTCAT	2700
TCAGGCGCGC	AAGGCAGGGA	TCTCTTGCAA	ACTTTATTGA	TTGATAGCCA	TGATGCGGGT	2760
TATGCCAGAC	AAATGATTGA	TAACACAAGC	ACCGGTGAAA	TCACCAAGCA	ATTGAATGCG	2820
GCCACTGACG	CTTTAAACAA	CGTAGCCAGT	TTAGAGCATA	AACAAAGCGG	CTTACAAACC	2880
TTGAGCTTGA	GTAATGCGAT	GATTTTAAAT	TCTCGTTTAG	TCAATCTCTC	TAGGAAGCAC	2940
ACCAACCATA	TTAACTCGTT	CGCTCAACGC	TTACAAGCTT	TAAAAGGCCA	AGAATTCGCT	3000
TCTTTAGAGA	GCGCGGCAGA	AGTGTGTGAT	CAATTTGCCC	CTAAATATGA	AAAACCTACC	3060
AATGPTTGGG	CTAACGCTAT	TGGGGGAGCG	AGCTTGAATA	GCGGCTCTAA	CGCTTCATTG	3120
TATGGCACAA	GCGCCGGCGT	AGACGCTTTC	CTTAACGGGA	ATGTGGAAGC	CATTGTGGGC	3180
GGTTTGGGAA	GCTATGGTTA	TAGCTCCTTT	AGCAATCAAG	CGAACTCTCT	TAACTCTGGG	3240
GCCAATAACG	CTAATTTTGG	CGTGTATAGC	CGTTTTTTTG	CCAACCAGCA	TGAATTTGAC	3300
TTTGAAGCTC	AAGGGGCGCT	AGGGAGCGAT	CAATCAAGCT	TGAATTTCAA	AAGCACTCTA	3360
TTACAAGATT	TGAATCAAAG	CTATAATTAC	TTAGCCTATA	GCGCCACAGC	AAGAGCGAGT	3420
TATGGTTATG	ACTTCGCGTT	TTTTAGGAAC	GCTTTAGTGT	TAAAACCAAG	CGTGGGCGTG	3480
AGCTATAACC	ATTTAGGTTT	AACCAACTTT	AAAAGCAATA	GCCAATCACA	AGTGGCTTTA	3540
AAAAATGGCG	CGAGCAGTCA	GCATTTATTC	AACGCTAACG	CTAACGTGGA	AGCGCGTTAT	3600
TATTATGGGG	ACACTTCATA	CTTTTATTTG	CATGCGGGAG	TTTTTACAAGA	GTTTCGCTCAC	3660
TTTGGATCGA	ATGATGTGGC	GTCTTTAAAC	ACCTTTAAAA	TCAATGCCGC	TCGCGAGTCT	3720
TTAAGCACCT	ATGCAAGAGC	GATGATGGGT	GGGGAATTGC	AATTGGCTAA	AGAAGTGTTT	3780

TTGAATTTGG GCGTGGTTTA TTTGCACAAT TTGATTTCCA ACGCAAGCCA TTTCGCTTCC 3340
 AATTTAGGAA TGAGGTATAG TTTCTAA 3867

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

ATGAAAGATA	GTTTTCTTTT	CACTTCCGAA	TCAGTAACCG	AAGGGCATCC	TGATAAAATG	60
GCCGATCAGA	TCAGCGATGC	GGTTTTAGAT	TACATTATTG	AGCGGGATAA	AAAAGCCAAA	120
GTCGCATGCG	AGACTTTAGT	TTCTAATGGT	TTTTGCATGA	TCACTGGCGA	GTTAAAAACT	180
TCTGTTTATG	CCCCGATGCA	AGAGATCGCA	AGAGAAGTGG	TTAAAAAAAT	TGGCTATACA	240
GACGCTCTTT	ATGGCTTTGA	TTACAGAAGC	GCGGCGGTTT	TAAATGGCAT	TGGCGAGCAA	300
AGCCCTGATA	TTAATCAAGG	CGTGGATAGA	GAAGATGGCG	AGATTGGGGC	GGGGGATCAA	360
GGGCTTATGT	TTGGTTATGC	ATGCAAAGAG	ACTGAAACGC	TCATGCCTTT	ACCCATCCAT	420
TTAGCGCACC	AGCTCGCTTT	CGCTCTAGCT	CAAAAAAGAA	AAGACAACAC	CTTGCCTTTT	480
TTAAGGCCTG	ATGGCAAGTC	TCAAGTGAGC	GTGCGTTATG	AAAACAACAA	GCCTGTAAGC	540
GTTGATACGA	TTGTCAATTC	CACCCAACAT	TCCCCAGAAG	TTTCACAAAA	GCATTTAAAA	600
GAAGCGGTGA	TTGAAGAGAT	CGTGTATAAG	GTTTTACCCA	AAGAATATTT	GCATGACAAT	660
ATCAAGTTTT	TTATAAACCC	TACAGGAAAA	TTCGTCATCG	GTGGGCCCTCA	AGGCGATGCG	720
GGTTTGACAG	GTAAGAAAAT	CATCGTGGAT	ACTTATGGAG	GGTTTTGCCC	GCATGGAGGG	780
GGAGCGTTTA	GCGGGAAAGA	CCCTAGCAAG	GTGGATAGGA	GCGCGGCTTA	TGCGGCCCGC	840
TATGTGGCTA	AAAATTTGGT	AGCGAGCGGG	GTTTGCGATA	AAGCGACCGT	GCAGCTTGCT	900
TATGCGATTG	GGGTGATAGA	GCCTGTGTCT	ATTTATGTGA	ACACGCATAA	CACGAGCAAG	960
CATTCAAGCG	CGGAGTTGGA	AAAATGCGTG	AAATCGGTTT	TCAAACACAC	GCCAAAAGGC	1020
ATCATTGAAA	GCTTGGATTT	GTTAAGACCC	ATTTATTTCG	TCACTTCAGC	TTATGGGCAT	1080
TTTGGGCGCG	AGTTAGAAGA	ATTCACCTGG	GAAAAGACTA	ACAAGGTGA	AGAGATTAAA	1140
GCGTTCTTTA	AGCGTTAA					1158

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

ATGAAATTTT TAAACGGATT AGCAGGGAAT TTA CTGATTG TGGTTATCTT ATTGTGTGTG	60
GTCGTTTTTT TCGCGCTCAA AGCGATCCAT ATCCAAAAG AGCAAGCCAC CAATTATTAC	120
CGCTATAAGG ATATTAACGC TTTAGAGGCA AAAACACCC AAAACCACGC TAATTATGAA	180
TTAGTCAATC AAGGGAGTAA AAAATGA	207

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1509 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

TTGAAATCT TTTTAGTTAT TCTAAGCGTC TTTTTTTT TA ATGGGTGTTT TGGGCTAGTC	60
TATAAGACTC CCATTTCAA CCCCCCTATC TCTTATGACC CCTACACTAC CACCATTGGG	120
AGCTTGATG CTAAAAATTT AAAAGAAAAC CCTAAACATA GTGCGGCCAT TCTTTTAGAA	180
GACGGCTTTG ATGCCTTGTT GCACAGAGTG GGTCTTATTA GAATGAGCCA AAAAAGCATT	240
GACATGCAA CTTATATCTA TAAAAACGAC CTTTCTTCTC AAGTGATCGC TAAAGAACTT	300
TTAAACGCGG CCAATCGTGG GGTAAAAGTG CGCATCCTTT TAGATGACAA CGGGTTAGAT	360
TCAGATTTTT CAGACATCAT GCTTTTAAAT TTCCACAAAA ACATTGAAGT GAAAATCTTT	420
AACCCCTACT ATATCCGCAA TAAAGGCTTG CGTTATTTTG AAATGCTTGC GGATTATGAA	480
CGCATTAATA AACGCATGCA CAACAAGCTT TTCATCGTGG ATAATTTTCGC TGTCATTATA	540
GGGGGGCGCA ACATTGGGGA CAATTATTTT GATAACGATT TAGACACGAA TTTTTTAGAT	600
TTAGACGCTT TGTTTTTTGG GGGGGTTGCT TCAAAGGCCA AAGAAAGCTT TGAAAATTAT	660
TGGCGATTCC ACCGCTCTAT CCCTGTTTCA TTATTAAGAA CCCATAAAAG ACTCAAAAAC	720
AACGTTAAAG AAATCGCTAA GCTCCATGAA AAAATCCCTA TCAGCGCTGA AGACGCAAAC	780
GAATTTGAAA AAAAAGTCAA TGATTTTATA GAACGCTTCC AAAAATACCA ATACCCCAT	840
TATTATGGGA ATGCCATTTT TCTAGCCGAT TTGCCCCGCA AAATTGACAC GCCCTTGTAT	900
TCGCCCATCA AAATCGCTTT TGAAAAAGCC CTTAAAAACG CTAAAGACTC CGTTTTTTATC	960

356

GCTTCATCGT	ATTTTATTCC	AGGTAAAAAG	ATAATGAAAA	TCTTTAAAAA	TCAAATTTCT	1020
AAGGGGATTG	AATTGAATAT	TCTTACCAAT	TCCCTTTTCAT	CTACGGACGC	TATCGTGGTC	1080
TATGGGGCGT	GGGAAAGGTA	TCGCAATAAA	TTAGTGCGAA	TGGGCGCGAA	TGTCTATGAA	1140
ATACGAAACG	ATTTTTTCAA	CCGCCAGATT	AAAGGGCGCT	TTAGCACCAA	ACATTCCTTA	1200
CACGGCAAGA	CAATTGTTTT	TGACGATGCC	CTAACGCTTC	TAGGGAGTTT	TAATATTGAT	1260
CCGCGCTCTG	CATATATTAA	CACTGAAAGT	GCGGTCTTGT	TTGACAACCC	GTCTTTTGCC	1320
AAAAGGGTGC	GTTTGTGCT	TAAAGATCAT	GCCCAACAAT	CATGGCATT	AGTCTTGTAT	1380
CGGCATAGAG	TGATTTGGGA	AGCTACAGAA	GAAGGCATCT	TAATCCATGA	AAAAAACTCG	1440
CCTGATACCT	CTTTCTTTTT	GCGTTTGATT	AAAGAATGGT	CTAAAGTCCT	TCCTGAAAGA	1500
GAACTTTAA						1509

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

ATGCGTTTTA	GTTACATTGA	GCCAAGAGCG	AAATACTTAA	TCAGCAAGCT	TTCTAAAATT	60
TGGGTTTTTT	ACATTTTTTT	ATCTTTTGTG	CTAATAGGGG	GGTTAGTGTG	GTTTATGCAC	120
AACGCCATTA	AACGCGCTCA	AGACAACGCG	TCTAGTTTGA	CGATCCAAGA	AAGGCTTTAC	180
CGCCATGAAA	TCAGCCGCTT	GCAGGTAAAG	ACTGATGAAA	CTTTAAAAC	CATTAAAGAA	240
GCCAAAAGC	GTTTGAATTA	TAACGATGAT	ATACGAGATG	TTTTGCAAGG	GCTTTTGAAT	300
ATTGTGCCGG	ATCTTATCAC	CATTAATAGC	ATTGAAATAG	ACCAACAAAG	CGTGGTGGTT	360
AGCGGTAAAA	CCCCCTCTAA	AGAAGCCTTT	TACTTTTTGT	TTCAAAACAA	ACTAAACCCC	420
ATGTTTGATT	ATTCTAGGGC	GGAATTTTTC	CCTTTAAGCG	ACGGGTGGTT	TAATTTTGTC	480
TCCACCAACT	TTTCTAATTC	CTTACTGATA	AAAACCCGG	AGTCTATTAA	ATGA	534

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

```
ATGCGTAAGA TCTTGTTAAT GGGCTTGATT TTACAAGCGC TCTTTGGCGA AGAAGCCGCG      60
CAAGAATTGT TGCAATGCTC TGCGATTTT GAATCTAAAA AAGCCGAATT GAAAGAGGAT      120
TTGCGCCAAT TGAGTGAAAA AGAGCAGTCT TTGAGGATCT TGCAAACCGA AAACGCCCCG      180
CTTTTAGATG AAAAAAGCGA TCTGTTAAAC AAGAAAGAAA AAGAAATAGA CGAAAAACTG      240
AAAAATTTAG CCGCTAAAGA AGAAGCCTTT AAAACCTTAC AAACAGAAGA AAAAAACGC      300
CTTAAAAATT TGATAGAAGA AAATGAAGGC ATTTTAAGAG AAATCAAGCA GGCTAAAGAC      360
AGCAAGATTG GCGAGACTTA TTCTAAAATG AAAGATTCTA AATCGGCTCT GATTTTAGAA      420
AATTTACCCA CTCAAACGC TTTAGAAATT TTAATGGCGC TAAAGCCTCA AGAATTAGGC      480
AAAATTCTAG CCAAATGGA TCCTAAAAAA GCGGCGGCTT TGACAGAGTT GTGGCAAAAA      540
CCCCCAAAG AAAATAAGA AAATAAGAA AGCCAAAAAA CCACAGATCC CACGCCCCC      600
ACACCACCA CGCCTCTAA AGAGCCAACC CTAAAGATC CTAATGTAAA AGAGCCAACA      660
GGGGTATGA
```

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1296 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

```
ATGAATATTC AAACAAAGAA AAGATTTTTA GCAAATTTAT TGCTTTT TAG CCTGTTTCT      60
TGCTTAAAGG CTGAAACCCT TTCAGAAGAC CATCAAATCC TGTTGAGTTC AGACGCTTTC      120
CATAGAGGGG ATTTTGCCAC CGCTCAAAAA GGCTATATGA ATCTCTATAA GCAAACCAAT      180
AAAGTGGTGT ATGCTAAAGA GGCGGCCATT TCAGCGGCCGA GTTTAGGGGA CATTAAACC      240
GCTATGCATT TAGCCATGCT TTATCAAAAA ATCACCATA ATCGTAACGA TGTTTCTATC      300
AATAAGATTT TAGTGATGG CTATGCACAA ATGGGGCAGA TTGATAAGGC GATTGAACTA      360
TTACACAAGA TTCGTAAGGA AGAAAAACC ATAGCCACAG ACAATGTGTT AGGGACTTTG      420
TATTTGACTC AAAAGCGTTT GGATAAGGCT TTCCCGTTGT TGAATAAGTT TTATAACCAA      480
GTGCATGATG AAGACAGCCT AGAAAACTC ATTACGATCT ATTTT TACA AAACCGCAAA      540
AAAGAGGGTT TGGATCTGTT GCAATCTCAT ATAGACAGGT ATGTTTGCTC AGAGCAATTG      600
TGCCAAAAAG CGCTCAACAC CTTACGCAA TTTAACGAGC TTGATTGGC TAAAACGACT      660
```

TTCGCTCGTT	TGTATGAAAA	AAACCCTATT	GTTCAAAACG	CCCAATTTTA	CATAGGGGTA	720
TTAATCTTGT	TAAAAGAGTT	TGATAAGGCC	CAGCAAATCG	CAGAATTATT	CCCCTTTGAC	780
AGGCGTTTGT	TGCTAGACTT	ATACACCGCG	CAAAAAAAT	TTGATCAAGC	TTCCAAACAG	840
GCTTCTTTAA	TCTATCAAGA	AAGAAAAGAC	CCTAAATTCT	TAGGCTTAGA	GGCGATTAT	900
CATTATGAAA	GCTTGAGCGC	GAATAAGAAA	AAGCTCACCA	AAGAAGAGAT	GTTGCCCATC	960
ATTCAAAAAT	TAGAGCAAGC	CACCAAAGAG	CGCCAAGCAT	GGCTTGCTAA	AACTAAAGAT	1020
AAAGAAGACG	CGCAAGACGC	TTCTTTTAT	AATTTTTTAG	GGTATTCCTT	AATAGATTAT	1080
GACATGGATG	TTAAAAGGGG	CATGGATCTT	GTGAGGAAAG	CCTTAGCGTT	AGATTCTAAC	1140
TCAGTGCTTT	ATTTGGATTC	TTAGCATGG	GGTTATTACA	AATTAGGGAA	TTGTTTGGAG	1200
GCTAAAAAAA	TCTTTTCTAG	CATCGCTAAA	GAGCTTATCC	AAAACGAACC	CGAATTGAAA	1260
GAACACAATA	AAATCATTC	AGAATGCAAG	AAATAG			1296

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

ATGCTTTATG	CATCAAAAGC	GCGTTTATTT	TTACAAATCA	AAGGAAAGTT	TATGTTAAGA	60
ATTTTAATCC	CCTTACTCAT	TATTGTGTGG	GTTTTATGGC	GTTTGTTTT	GAGGCAAAAA	120
CCCCACAAAG	ATGACCACAG	AGACAACCAC	TCTTACACGC	AACAAACCCC	CAAAGAATTA	180
GAAGATCACA	TGATTGTATG	CTCTAAATGC	CAAACCTATG	TCTCTAGTAA	AGACGCCATT	240
TATAGTGGGG	CGGTAGCCTA	TTGCAGTGAA	ACTTGTTTGA	AGGATAAGGG	GTAA	294

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

```

ATGAAAAATA GCGCGCCTTT AAAGAATAAA GTTTTTTGTG GGTATACGT TTTAAGTTTA      60
AGCGCTTCTG TGCAAGCGTT TGATTATAAA ATTGAAGTTT TGGCAGAGTC CTTTCTAAA      120
GTTGGCTTTA ATAAAAAAA GATTGACATA GCTAGGGGGA TTTATCCTAC AGAGACTTTT      180
GTAACCGCTG TGGGTCAGGG CAATATTTAT GCGGATTTTT TATCCAAAAG CCTTAAAGAT      240
CAAGGGCATG TTTTAGAGGG AAAAGTCGGC GGCACAATCG GTGGGATTGC TTATGACAGC      300
ACGAAATTCA ATCAAGGCGG ATCGGTTATT TATAATTATA TCGGTTATTG GGATGGCTAT      360
TTAGGGGGTA AAAGGGCCTT GCTTGATGGC ACGAGTATCC ATGAGTGCGC GCTTGGCTCT      420
GATGGCAAGG TGATTGATTC TATAGCGTGC GGAACGCTA GAGCCAATAA AATCCGCCGT      480
AATTACTTGA TGAATAACGC TTTTTTAGAA TACCGCTATA AGGATATATT TCGCGCTAAA      540
GGGGGGCGTT ATCAATCCAA TGCTCCTTAT ATGAGCTCTT ATACGCAAGG CTTTGAAATC      600
AGCGCTAAAA TCAAGGATAA AAATGAGGGG AGCCATAAAT TATGGTGGTT TAGCTCATGG      660
GGTAGGGCGT TCGCTTATGG GGAGTGGATT TATGATTTTT ACTCTCCAAG AACCGTGATT      720
AAAAACGGGC GCACTCTAAA TTATGGTATC CATTTAGTGG ATTACACTTA CGAAAGGAAA      780
GGGGTTAGCG TCAGCCCTTT TTTCCAGTTT TCGCCCGGGA CTTATTATAG CCCTGGGGTG      840
GCTGTAGGCT ATGATAGTAA CCCTAATTTT AATGGCGTGG GCTTTAGATC CGAAACGAAG      900
GCTTATATTT TGCTCCCTGT CCATGCCCCC CTTAAAAGGG ATACTTATCG TTACGCTGTG      960
AAAGCTGGCA CCGCTGGGCA AAGCCTGCTC ATTAGGCAAC GATTTGATTA CAATGAATTT     1020
AACTTTGGGG GAGCGTTTAA TAAAGTATGG AAAAACGCAA ACGCTTACAT AGGCACGACA     1080
GGAAACCCTC TAGGCATTGA TTTTGGACC AATAGCGTTT ATGATATAGG GCAAGCCTTA     1140
AGCCATGTGG TAACCGCTGA TGCCGTCTCT GGTGTTGGTT TTGGTGGAGG CGTGCATAAA     1200
AAATGGCTGT GGGGGACTTT GTGGCGTTGG ACTAGCGGCG CTTTAGCCAA TGAAGCGAGC     1260
GCGGCTGTTA ATGTGGGCTA TAAGATCAGT AAGAGTTTGA CAGCGAGCGT GAAATTAGAA     1320
TATTTGGGCG TGATGACGCA TTCAGGCTTT ACGGTAGGGA GTTACAGACC CACGCCCGGC     1380
TCTAAAGCAC TTTATTCAGA CAGGAGCCAT CTAATGACAA CCCTTAGCGC CAAATTCTAA     1440

```

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii)-MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

```

ATGAAAAATA GCGCGCCTTT AAAGAATAAA GTTTTTTGTG GGTATACGT TTTAAGTTTA      60
AGCGCTTCTG TGCAAGCGTT TGATTATAAA ATTGAAGTTT TGGCAGAGTC CTTTCTAAA      120

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360

GTTGGCTTTA	ATAAAAAAAA	GATTGACATA	GCTAGGGGGA	TTTATCCTAC	AGAGACTTTT	180
GTAACCGCTG	TGGGTCAGGG	CAATATTTAT	GCGGATTTTT	TATCCAAAAG	CCTTAAAGAT	240
CAAGGGCATG	TTTTAGAGGG	AAAAGTCGGC	GGCACAATCG	GTGGGATTGC	TTATGACAGC	300
ACGAAATTCA	ATCAAGGCGG	ATCGGTTATT	TATAATTATA	TCGGTTATTG	GGATGGCTAT	360
TTAGGGGGTA	AAAGGGCCTT	GCTTGATGGC	ACGAGTATCC	ATGAGTGCGC	GCTTGGCTCT	420
GATGGCAAGG	TGATTGATTC	TATAGCGTGC	GGGAACGCTA	GAGCCAATAA	AATCCGCCGT	480
AATTACTTGA	TGAATAACGC	TTTTTTAGAA	TACCGCTATA	AGGATATATT	TGCGGCTAAA	540
GGGGGGCGTT	ATCAATCCAA	TGCTCCTTAT	ATGAGCTCTT	ATACGCAAGG	CTTTGAAATC	600
AGCGCTAAAA	TCAAGGATAA	AAATGAGGGG	AGCCATAAAT	TATGGTGGTT	TAGCTCATGG	660
GGTAGGGCGT	TCGCTTATGG	GGAGTGGATT	TATGATTTTT	ACTCTCCAAG	AACCGTGATT	720
AAAAACGGGC	GCACTCTAAA	TTATGGTATC	CATTTAGTGG	ATTACACTTA	CGAAAGGAAA	780
GGGGTTAGCG	TCAGCCCCCT	TTTCCAGTTT	TCGCCCCGGA	CTTATTATAG	CCCTGGGGTG	840
GCTGTAGGCT	ATGATAGTAA	CCCTAATTTT	AATGGCGTGG	GCTTTAGATC	CGAAACGAAG	900
GCTTATATTT	TGCTCCCTGT	CCATGCCCCC	CTTAAAAGGG	ATACTTATCG	TTACGCTGTG	960
AAAGCTGGCA	CCGCTGGGCA	AAGCCTGCTC	ATTAGGCAAC	GATTTGATTA	CAATGAATTT	1020
AACTTTGGGG	GAGCGTTTTA	TAAAGTATGG	AAAAACGCAA	ACGCTTACAT	AGGCACGACA	1080
GGAAACCCTC	TAGGCATTGA	TTTTTGGACC	AATAGCGTTT	ATGATATAGG	GCAAGCCCTTA	1140
AGCCATGTGG	TAACCGCTGA	TGCCGTCTCT	GGTTGGGTTT	TTGGTGGAGG	CGTGCATAAA	1200
AAATGGCTGT	GGGGGACTTT	GTGGCGTTGG	ACTAGCGGCG	CTTTAGCCAA	TGAAGCGAGC	1260
GCGGCTGTTA	ATGTGGGCTA	TAAGATCAGT	AAGAGTTTGA	CAGCGAGCGT	GAAATTAGAA	1320
TATTTGGGCG	TGATGACGCA	TTCAGGCTTT	ACGGTAGGGA	GTTACAGACC	CACGCCCCGC	1380
TCTAAAGCAC	TTTATTCAGA	CAGGAGCCAT	CTAATGACAA	CCCTTAGCGC	CAAATTCTAA	1440

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

ATGGGCTTGA	AAAATCTCTC	AACACTTCTG	GTGTTTTTAT	TCTTTTGTTT	GGGGTGTGTG	60
AGCAATTTTA	ATGAAGACAC	TTACACGCTA	GACTTAGTTT	TAGAAAAAAA	GATCCAAGCC	120
AGTAGGAAAG	GCGAAATCAC	CCAAGATAAT	GTGCCTATCA	TCACGGCTAT	CGCTACGCAT	180
TTAAACGATG	TGGATAGCGG	CACTTACTAC	GATCATGAGT	ATTTTTTAGT	GGAGATTTTC	240
ACGCAAAATA	ACGACTGGAT	AGATGATGGC	TATATTTCTT	ATGAACTTTT	TGGCACAAAA	300
CCTACAGGAT	CAGAACCCTT	ATGGGTGCGA	GAGATTACAA	GAGATGAATT	TGATGGCATT	360
TTAGAAACCA	CGAACCAGTG	GAGCCGAGCC	TTTTTGATCG	CTTTTGACAA	ATTGGATTAT	420
TTAGCGGTGC	AAGAAGCCAA	ACTAGAGCTT	GATGCCTATA	GTTTAGGCAA	AATTGTTTTT	480
AATTCGCTT	ACCAAGTCCC	CTTACCTCAA	TTTTAA			516

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

GTGAATAAAA AGCACCGCTT GGCTTTTTTA GGGCTAATTG TTGGGGTTCT ATTCTTCTTT	60
AGCGCGTGCC AACACCGCCT GCACATGGGG TATTATTCAG AAGTTACAGG GGATTATTG	120
TTCAATTATA ATTCCACTAT CGTGGTGGCT TATGACAGAA GCGATGCGAT GACTTCTTAT	180
TATATCAATG TGATTGTTTA TGAATTGCAA AAATTAGGCT TTTATAATGT CTTACGCAA	240
GCGAATTCCC GCTAG	255

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

ATGCAATATA AGAAAAATAA GAAAAGATAT TATCATTTAG CGTTAGGGAT CCTTTTTTGT	60
AATGGTCTGT CTTTGAAAGC TTTAGAAATT GCCGTCAAAC CCTTTGGCTA TCTGGGGCTA	120
TTGTATAATC AAGGGACGCA AAAAAACCCT CACAGCTATG TGGGGGCTTT AGCGCGTCTT	180
GGGGTGGATT TTTCTTATAG CAATGGGTGG TCGTTTGGTA TTGGGGCTAT TGGGGCTTGG	240
AATATTTATA ACAAACAGCG TTTGGCTAAC CTTTACATCA GTCTAGGGAA TTTTTTGGT	300
AACCCTAACA ACGTTAAGCC TTATTTGAGC GCCGGCGATG TTTCTGATGC GTATCTTCAA	360

362

TACGCTAACC	AGCGTTTTAA	AATCGCTTTA	GGGCGTTTTA	ATACCGATTT	TGTGGATTTT	420
GATTGGATAG	GGGGCAATAT	TCAAGGGGTC	TCTGTGGCTT	TCAAGCAAAA	TTCCATGCGT	480
TATTTTGGGA	TTTTTATGGA	TAGCATGCTT	TATAATGGGC	ATCAAATCAA	TAAAGAGCAA	540
GGGAATCGGA	TCGCCACTTC	CCTAAACGCT	CTAGCGTCTT	ATGATCCTGT	GTCTAAACGC	600
TTGTATGTAG	GGGGGGAAGT	GTTTGTTTTG	GGCGCAGAAT	ACAAAAATAA	AAATTTGATA	660
TTCGTTCTTT	TTATTTTAAC	GGACACCCGC	TTGCCTTTGC	CCACCCAAAA	TGTTTTAGTG	720
CAAGTGGGGG	GTAAGTTGGA	GTATCGACGC	TTCTTT			756

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

ATGGTGCAAA	AAATTGGCAT	TTAGGGGCG	ATGAGAGAAG	AAATAACCCC	TATACTAGAA	60
TTGTTTGGCG	TGGATTTTGA	AGAGATCCCT	TTAGGGGGGA	ATGTTTTCCA	TAAAGGCGTT	120
TATCATAATA	AGGAAATCAT	TGTCGCTTAT	AGCAAGATTG	GCAAGGTGCA	TTCCACTTTA	180
ACCACAACAA	GCATGATTTT	AGCGTTTGGC	GTTTCTAGAG	TGCTTTTTAG	CGGGGTGGCT	240
GGAAGCTTAG	TTAAAGATTT	AAAAATCAAT	GATTTGTTAG	TGGCTACTCA	ATTAGTCCAG	300
CACGATGTGG	ATTTGAGCGC	GTTTGATCAC	CCTTTAGGGT	TTATCCCCGA	AAGCGCGATT	360
TTTATTGAAA	CGAGTGGAAG	TTTAAACGCT	TTAGCTAAAA	AGATCGCTAA	TGAGCAACAT	420
ATCGCGCTCA	AAGAAGGCGT	CATCGCATCA	GGCGATCAGT	TTGTGCATAG	CAAAGAAAGG	480
AAAGAATTTT	TAGTTAGCGA	GTTTAAAGCG	AGCGCGGTGG	AAATGGAGGG	GGCGAGCGTG	540
GCGTTTGTGT	GCCAAAAATT	TGGCGTGCCA	TGCTGCGTGC	TAAGGAGCAT	TAGCGATAAC	600
GCCGATGAAA	AAGCCGGTAT	GAGTTTGTAT	GAATTTTGTAG	AAAAAAGCGC	TCACACTTCA	660
GCGAAATTCT	TAAAAAGCAT	GGTGGATGAG	CTTTAG			696

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

ATGAGAGCTA	CGGCGATAAA	AATCTTTTCA	TTCTCATCAG	CGCTCGCCCT	ATTGCTTCAG	60
GGTTGCTTGA	GCATTAATTT	AAAACAAATG	CTGCCAGAAA	TCAGAACTTA	TGATTTAAAT	120
GCGAGTTCTT	TTGAAATGAC	GCAATGCCCT	AAACCTTTGA	CTGAAGTGAG	GCTCATTAGC	180
ATTTTGAGCG	CGGATTTATT	CAACACTAAA	GAGATCGTGT	TTAAAGCGCA	AGACGGGCAG	240
ATCACGCATG	GGAAGCACCA	AAAATGGATA	GACTTGCCTC	GCAACATGTT	AAAAACCATG	300
TTCATGCAAG	AAGCGCAAAA	AGCATGCTTA	GGCGTGCTT	TGCCCCCTTA	TGGCGCGGGC	360
GCGCCCACTT	ATGCGGTTCG	TTTTACGATT	TTATCGTTTT	CTCTTTTAGA	AAAAGAAAT	420
TCTACTTACA	GGGCGGAATT	CGCGCTAGGC	TATGATATTA	GCGTGAAAGG	CGATTCGCAT	480
TCTGGAGTGA	TCATTAAGCA	TGAAAATATT	TCTAGCTTGG	AAAATAAAAC	GACCAAAACG	540
AGTAAAAATG	GCAGTCAAGA	TTTCCAAGAA	AGCGCGATAC	AATCCCTCCA	ACATGTCAGC	600
ACGCAAGCGA	TGCAAGAAGC	GATTTCTTTG	ATTAAAAAAG	CGGTTGAAGC	GCAAAGCGTA	660
AGCCCGTTAA	AAAAATAA					678

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 816 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

TTGGAAAGGC	ATGTGAATTA	CACTTTAATC	GGCGGGCTCT	TCTTTTATG	CTTAGTGTGC	60
ATGGTAGGCT	TTATTTTATG	GCTAGGCCAT	TTGGGATTAG	ATGATGGGAA	GTATTATGAA	120
TATGTGGTCT	ATACGGACAA	AGACTTGGGA	GGCATTGCGA	CCAACTCGCC	CATTAATTAC	180
AAAGGGATTC	AAGTGGGTAA	TGTCATCAAA	GTGGGTTTTG	CAAAGGATAA	AGTGGGGGTG	240
GTCCGTTTGG	ATTTGATGAT	CAAATCCAGC	GTTAAGATCC	GTAAAGATTC	CAAAGTGGCG	300
GTTTCTTCTA	GAGGGTTTAT	GGGGTTAAAA	TTTTTAGCCT	TAGAGCAAAG	CCACAATGAA	360
GAATTTTATG	GTAGCGGCGA	TAAAGGGGAG	CGGATTTTAA	TCTTTAAAGA	AGGGCTTATG	420
GATCGCTTGA	GCGGTGATGC	TAATCAAGTG	GTGCAAGAAG	TGATGAAAGC	GATCAGGAAT	480
GTGAATAGGA	TTTTAGACGA	TGAAAACGTG	GAGAAATTCA	AGCACATTCT	CGCTTCAGTG	540
GATGATCTCA	TCGCTAACTT	GGATTCAAGA	AAGACTCAAT	TTGATTCCTT	GATCAACAAC	600
GCTAACAACC	TTGTTTCTAA	TGTCAATAAT	GTGGCTTTGG	ATGTGGATAA	ACGCGTCAAA	660

364

CAGGGGCAAT	ACGACTTTAA	GGCGATGTT	CTCCTTTAA	TCATGCAAGC	GCAGTTGAGC	720
TTAAGAAACA	TTGATAATTT	TGTGGAAAAA	GGCTCTGCTT	TGATAGATAA	ATTTGACGCT	780
AACCCCTATA	AAACGATTTT	TGGAGAAAGG	AAATAA			816

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

ATGAAAAAAA	CTATTCTATT	GAGCGCTCTT	TTAGCTTTTT	CTTGCGCTCA	TGCTTTAAGC	60
GATATGGATT	TGATTAAAAA	AGCGAAGGAA	AGCCAATTAG	AACCCATGCC	TATGGGCAAA	120
GCGCTCAAAG	AATACCAGAT	CAAAAAAACC	AGAGATGTGG	GCATTGGCGC	TAAAAACAGC	180
GAAATCATGA	CCTCCGCTCA	AGTGGAATTA	GGCAAAATGC	TCTATTTTGA	CCCTAGGATT	240
TCCACTTCCT	ATCTTGTGTC	TTGCAACACA	TGCCATAATT	TGGGCTTAGG	CGGGGTGGAT	300
CTAATCCCAA	GCGCTATAGG	CTCTCAATGG	AAGAAAAACC	CCCACCTTTT	AAGTTCCCCA	360
ACGGTGTATA	ACTCTGTGTT	TAACGATGTG	CAGTTTTGGG	ATGGTAGGGT	TACGCATTTA	420
AACGAACAAG	CGCAAGGGCC	AATCCAATCT	TCTTTTGAAA	TGGGGGCTGA	TCCTAAAGTC	480
GTGGTAGAAA	AAATCAATTC	CATACCAGGC	TATGTCAAGC	TCTTTAGAAA	AGCTTATGGC	540
TCTAAAGTCA	AAATTGATTT	TAAATTGATC	GCTGATAGTA	TCGCTATGTT	TGAAGCCACG	600
CTCATTACCC	CAAGCCGTTA	CGATGATTTT	TTAAGGGGCA	ATCCTAAAGC	GCTCAGTAAA	660
GCCGAAAAAG	AAGGGCTGGA	TTTATTTCATT	TCTAAAGGCT	GTGTGGCGTG	TCATAATGGC	720
ATCAATCTTG	GGGGGACGAT	GCAGCCTTTT	GGGGTGGTCA	AACCTTATAA	ATTCGCTAAT	780
GTGGGCGATT	TCAAGGGCGA	TAAAAACGGG	CTTGTGAAAG	TGCCTACTTT	AAGGAATATC	840
ACCGAAACGA	TGCCTTATTT	CCATAACGGG	CAATTCTGGG	ATGTTAAGGA	TGCGATTAAA	900
GAAATGGGCT	CTATCCAGTT	AGGCATTGAA	ATCAGCGATG	CAGAAGCGAA	AAAGATTGAA	960
ACCTTCTTTG	AAGCCTTAAA	GGGTAAAAAA	CCTAAAATAA	TCTATCCAGA	ACTCCCTGTG	1020
ATGACAGACA	AAACCCCTAA	ACCCTCTTTT	TGA			1053

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

ATGATGGATT TAGAAAGTTT GAGAGGTTTT GCGTATGCGT TTTTACCAT TCTTTTACG	60
CTCTTTTGT ATGCTTATAT TTTTAGCATG TATAGAAAGC AAAAAAGGG CATCGTGGAT	120
TATGAGCGAT ACGGTATTT AGCGTTAAAT GATGCTTTAG AAGACGAGTT GATTGAACCA	180
CGCCATAAAG AAGTTCATGA TAAAGGCATA AAGGAAAGTT GA	222

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 828 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

TTGCTAGATG TCAAAGCCAA TTCCCCCGCC TATCAAGCGG TGCTTTTAGC ATTGAACGCT	60
GCAGTGGGCT TGTGGCAAGT TACAAGCTAT GCCTTTACCG CTTGTGGTCC TGGTAGCAAT	120
GAGAACGCGA ATGGAGGTAT CCAAACCTTT AATAATGTGC CAGGACAAA CACGACGACC	180
ATCACTTGTA ATTCTGATTA TGAGCCAGGA CATGGCGGGC CAATATCCAC TGAAAATTAT	240
GCGATCATCA ACAAGGCTTA TCAAATCATT CAAAAGGCTT TGACAGCCAA TGGAGAAGGG	300
ATCCCAGTTT TAAGCAACAC CACTACAAA CTTGATTTC CTATCAATGG AGACAAAAGA	360
ACGGGTGGCG AACCATAA AAAATTAGTA TACCCATGGA GTCATGGGAA ACCTATTTCA	420
ACCTCGTGGA ATGCAACCAT AACAGTACCA ACAACAGAAA ATATCAATAC AACCATAGC	480
GCTCAAGAGC TTTTAAAACA AGCGAGCATC ATTATCACTA CCCTGAATAG TGCATGCCCA	540
AACTTCCAAA ATGGTGGTAG CGGTATTGG GCAGGGATAA GTGGCAATGG GACAATGTGT	600
GGGATGTTTA AGAATGAAAT CAGCGCTATC CAAGGCATGA TCGCTAACGC GCAAGAAGCT	660
GTCGCGCAAG CCAAATCGT TAGTGAAAAC ACGCAAAATC AAAACAGCCT AGACGCTGAA	720
AACCATTCAA CCCCTACACA GACGCTAGTT TTGCTGAAAAG CATGCTCAA AACCGAAGC	780
CCAAGCGGAG ATTTTAAACC AAGCCGAACA AGTGGTGAAA AACTTTGA	828

(2) INFORMATION FOR SEQ ID NO:375:

366

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

ATGCTGACGA TTGAAACCAG TAAAAAATTT GATAAGGATC TTAAAATTCT TGTAAAAAAT	60
GGGTTTGATT TAAAGCTTTT GTATAAAGTG GTTGGAATT TAGCCACAGA GCAACCCCTA	120
GAACCCAAAT ACAAAGACCA CCCACTCAAA GCGCTTTAA AAGACTTTAG GGAATGCCAC	180
CTAAACCGG ATTTATTGCT TGTCTATCAA ATTAAAAAC AAGAAAACAC TCTTTTTTTA	240
GTAAGGCTAG GCAGTCATAG CGAGCTGTTT TGA	273

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

ATGCTAGAAA TTGAATTAAA AAAGAAATTC ACTAAGGATT TAAAAAGCA TATTTTAAAT	60
CAAAAAATTG AGTTAGAAGT TTTTGACTTA GTGGTTGAAA ATTTAAGAAA TCAAATCCCA	120
TTGGACAAA GATTTAAAGA CCATGCTTTA AGTGGAACAT ACAAAGGCTG TAGAGAGCGC	180
CACATTAAGC CTGATGTTTT GCTTGTGTAT AGAGTGAAAG GCAATGTTTT AACTTTGGTT	240
AGGCTTGGCA GTCATAGCGA GCTGTTTTGT AAACCGCCA CACCACTCAT AACGCTTAAA	300
TGA	303

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

TTGGTGGTTA GTGGCTCGTT GCAAAACATT GTTCGTTCTT TTTTGCGAAG GATCAGCGTT	60
TTCTTCATTA TTGATTTTCAAT CAATTTTATT TTCGTTATTG ATCAGATCAT TCACTTCTTT	120
GGTGACTTTT TCATCTTCTT CTTCATGCTC AATCTTTTTT ATATCCTTAT TAGGTTGATT	180
GATTTGATTG TTTTGAGTGG TTTTAGTGTT GTTTGGTGC GATTGGGACG ATTTTTTAGG	240
CTCATCTTTG CAGGCGCTCA ACACGCTTAA	270

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

ATGAAAAAAT CCCTTTGTTT GTCTTCTTT CTGACCTTCT CTAACCCTCT TCAAGCCCTT	60
GTCATTGAGC TTTTAGAAGA GATTAAACT TCGCCGCATA AAGGCACTTT TAAGGCTAAA	120
GTCCTTGATT CTAAAGAACC AAGACAAGTT TTAGGCGTTT ATAATATCTC CCCACACAAA	180
AAACTCACGC TCACTATCAC TCACATATCC ACGGCAATCG TCTATCAACC CCTTGATGAA	240
AAACTTCTT TAGAAACGAC CTTAAGCCCT AACCGCCCTA CTATCCCTAG AAACACCCAA	300

ATCGTTTTTT	CTTCAAAAGA	ATTGAAAGAA	CCGCACTCAA	ACCCAATACC	TTCTTTAAAC	360
GCGCCCATGC	AAAAACCACA	AAATAAACCC	AGCTCATCGC	AACAATCTCC	TCAAAACTTT	420
TCTTACCCAG	AGTCCAAACT	AGGCTCTAAA	AACTCTAAAA	ACAGCCTTTT	ACAGCCTTTA	480
GTAACTCCTA	GCAAAGTAAG	CCCCACTAAC	GAAGTTAAAA	CGCCAACAAA	CGACGCTAAT	540
CCCCCTTTAA	AGCATTCTTC	ACAAGATCAA	GAAAACAACC	TCTTTGTAGC	GCCACCCACT	600
GAAAAAACGC	TCCCTAACAA	CACCTCTAGT	GCTGATGCGA	GTGAAAACAA	TGAAAGCAAC	660
GAAAATAGGG	ATAATGTGGA	AAAACAAGCG	ATTAGAGATC	CTAATATCAA	AGAATTCGCA	720
TGCGGGAAGT	GGGTTTATGA	TGATGAAAT	TTACAAGCCT	ATCGCCCAAG	CATTTTAAAA	780
CGCGTTGATA	AAGACAAAGA	GATTACAACA	GACATTACCC	CTTGCGATTA	CAGCACCGCT	840
GAAAATAAAA	GCGGTAAAAT	CATTACCCCC	TATACTAAAA	TCTCTGTTCA	TAAAACAGAG	900
CCTTTAGAAG	ACCCTCAAAC	TTTTGAAGCT	AAAAATAATT	TCGCCATTCT	CCAAGCCAGA	960
AGCTCTACAG	AAAAGTGTA	AAGGGCTAGA	GCGAGAAAAG	ACGGCACGAC	CAGGCAATGC	1020
TATCTGATAG	AAGAGCCTTT	AAAACAAGCG	TGGGAGAGCG	AGTATGAAAT	CACCACGCAA	1080
TTAGTGAAAG	CCATATATGA	ACGCCCCAAA	CAAGACGATC	AAGTAGAGCC	GACTTTTTTAT	1140
GAAACCAGCG	AATTGGCTTA	TTCTTCCACA	CGAAAAAGCG	AAATAACGCG	TAATGAATTG	1200
AATTTGAATG	AAAAATTCAT	GGAATTTGTG	GAAGTGATG	AGGGGCATTA	TTTAAACGAT	1260
ATAATCAAAG	AGAGCAGCGA	ATACAAAGAA	TGGGTAAAA	ACCATGTGCG	CTTTAAAGAA	1320
GGGGTGTGCA	TGGCCTTAGA	AATAGAAGAG	CAACCACGAG	CCAAAAGCAC	GCCTTTGAGT	1380
ATTGAAAAC	CTCGTGTGT	GTGTGTCAA	AAGGGGAATT	ATTTATTCAA	TGAAGTTTAA	1440

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

ATGAAAAAAT	CCCTTTGTTT	GTCTTTCTTT	CTGACCTTCT	CTAACCCCTCT	TCAAGCCCTT	60
GTCATTGAGC	TTT TAGAAGA	GATTAAAACT	TCGCCGCATA	AAGGCACTTT	TAAGGCTAAA	120
GTCCTTGATT	CTAAAGAACC	AAGACAAGTT	TTAGGCGTTT	ATAATATCTC	CCCACACAAA	180
AAACTCACGC	TCACTATCAC	TCACATATCC	ACGGCAATCG	TCTATCAACC	CCTTGATGAA	240
AAACTTTCTT	TAGAAACGAC	CTTAAGCCCT	AACCGCCCTA	CTATCCCTAG	AAACACCCAA	300
ATCGTTTTTT	CTTCAAAAGA	ATTGAAAGAA	CCGCACTCAA	ACCCAATACC	TTCTTTAAAC	360
GCGCCCATGC	AAAAACCACA	AAATAAACCC	AGCTCATCGC	AACAATCTCC	TCAAAACTTT	420
TCTTACCCAG	AGTCCAAACT	AGGCTCTAAA	AACTCTAAAA	ACAGCCTTTT	ACAGCCTTTA	480
GTAACTCCTA	GCAAAGTAAG	CCCCACTAAC	GAAGTTAAAA	CGCCAACAAA	CGACGCTAAT	540
CCCCCTTTAA	AGCATTCTTC	ACAAGATCAA	GAAAACAACC	TCTTTGTAGC	GCCACCCACT	600
GAAAAAACGC	TCCCTAACAA	CACCTCTAGT	GCTGATGCGA	GTGAAAACAA	TGAAAGCAAC	660
GAAAATAGGG	ATAATGTGGA	AAAACAAGCG	ATTAGAGATC	CTAATATCAA	AGAATTCGCA	720
TGCGGGAAGT	GGGTTTATGA	TGATGAAAT	TTACAAGCCT	ATCGCCCAAG	CATTTTAAAA	780
CGCGTTGATA	AAGACAAAGA	GATTACAACA	GACATTACCC	CTTGCGATTA	CAGCACCGCT	840

GAAAATAAAA	GCGGTAAAAT	CATTACCCCC	TATACTAAAA	TCTCTGTTCA	TAAAACAGAG	900
CCTTTAGAAG	ACCCTCAAAC	TTTGAAGCT	AAAAATAATT	TCGCCATTCT	CCAAGCCAGA	960
AGCTCTACAG	AAAAGTGTA	AAGGGCTAGA	GCGAGAAAAG	ACGGCACGAC	CAGGCAATGC	1020
TATCTGATAG	AAGAGCCTTT	AAAACAAGCG	TGGGAGAGCG	AGTATGAAAT	CACCACGCAA	1080
TTAGTGAAAG	CCATATATGA	ACGCCCCAAA	CAAGACGATC	AAGTAGAGCC	GACTTTTTAT	1140
GAAACCAGCG	AATTGGCTTA	TTCTTCCACA	CGAAAAAGCG	AAATAACGCG	TAATGAATTG	1200
AATTTGAATG	AAAAATTCAT	GGAATTTGTG	GAAGTGTATG	AGGGGCATTA	TTTAAACGAT	1260
ATAATCAAAG	AGAGCAGCGA	ATACAAAGAA	TGGGTAAAA	ACCATGTGCG	CTTTAAAGAA	1320
GGGGTGTGCA	TGGCCTTAGA	AATAGAAGAG	CAACCACGAG	CCAAAAGCAC	GCCTTTGAGT	1380
ATTGAAAAC	CTCGTGTGT	GTGTGTCAA	AAGGGGAATT	ATTTATTCAA	TGAAGTTTAA	1440

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

ATGAGAAAAA	CGATTTTCAGC	GTTGTTTTTA	TCAGCGTGTA	TAGGGTTATC	GTCTGTTTCAT	60
GCGAGTAACG	CTTTGATTTT	ACAAACAGAT	TTTAGCCTAA	AAGATGGGGC	CGTCTCGGCG	120
ATGAAAGGCG	TCGCTTTCAG	CGTTGATTCT	AATCTTAAAA	TCTTTGATTT	AACGCACGAA	180
ATCCCCCGT	ATAACATTTG	GGAAGGCGCT	TACCGCTTGT	ATCAGACCGC	TAGTTATTGG	240
CCAAAAGGCT	CGGTATTTGT	GAGCGTAGTG	GATCCGGGCG	TAGGCACTAA	TCGTAAATCG	300
GTGGTATTGA	AAACTAAAAA	CGGCCAGTAT	TTCGTCTCTC	CAGATAACGG	CACGCTGACT	360
TTGGTAGCGC	AAACTTTGGG	GATTGATAGC	GTGCGTGAAA	TTGATGAAAA	AGCCAACCGC	420
TTGAAAGGTT	CTGAAAAATC	CTATACTTTC	CATGGCCGTG	ATGTGTATGC	TTACTACTGGG	480
GCGCGCTTGG	CTTCTGGGGC	GATCACATTC	GAGCAGGTCG	GGCCAGAGCT	TCCTATAAAA	540
GTTGTTGAAA	TTCCTTACCA	AAAAGCGAAA	GCCACAAAAG	GGGGAGTGAA	AGGCAATATC	600
CCGATTTTGG	ATATTCAATA	TGGCAATGTT	TGGAGCAATA	TCAGCGATAA	ACTGCTCAAT	660
CAAGCAGGGA	TCAAACGAAA	CGATACAGTG	TGTGTAAC	TTTTTAAAAA	TTCCAAGAAA	720
CAATACGAAG	GGAAAAATGCC	GTATGTCGCG	AGCTTTGGCG	ATGTGCCAGA	AGGCCAGCCG	780
TTGGTCTATT	TAAACAGCTT	GTTGAATGTT	TCCGTGGCGT	TGAATATGGA	TAATTTTCGCG	840
CAAAAACATC	AAATTAAATC	TGGTGCTGAC	TGGAATATTG	ATATAAAGAA	GTGCGCTAAA	900
TAA						903

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

TTGACTAAAA	AATTCATGTC	TTGGATGGTG	GTTATCGGGG	CTTTAATTG	CGTGCTTTTA	60
GGGGTGTTTA	TCTTCTTCAC	TAGCATGTCG	GTTAAAAAAT	CTTTAACCGC	TTATCTTAAC	120
GCTTATTTAG	AGCAACGCCC	AAATATCGAG	GGCATGGGGA	TTATAGGAGT	TCCTTTTAAA	180
TGCGAAAGGT	TTTTTAAAAT	CGCATGCGTT	TCTAAAGAAC	TTCGTTTTTT	AGATCCTCAA	240
AACTCTCCTA	TTATGGATTT	TAAAAATTA	AAGATCAAGC	TCCATTCTTT	AGATAAAAGC	300
TCTCTTACCC	TTTCTATCCA	TTCTCAAATC	CAATCCCCTA	TTTTAGAACA	ATCCATTGAG	360
CAAAAAATCA	GCCAAATCCC	CTTAAAAAAC	TTGAATGCCT	TATTGGAAAA	ATTCAAACCC	420
ACGCGCTTGA	ATTGCTCTTT	AACATTCAAC	GCTTTAGATG	AAAAAACCTA	A	471

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 858 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

ATGCAAGATT	TTATTAAGAT	TTTATTTC	AAAGAGTT	GTCTCT	CTACTTTAGA	AGGGTTAGTG	60
GGTAAGGCTC	CAAGCGTAGG	ATTAGAAAA	GAAGTTTCTA	ACAATGAAGA	AGCGAGTTTA		120
ATCAGCACTC	CTTATGCAAG	GGTTAAGATT	AGCGCGATTG	AAAAAAATGA	AAGTCCTATT		180
GAATTACTGG	CTCCGGTAGA	TTAGTTACC	GCTTTGAGCG	ATTTGATGCT	AGGAGGTGAG		240
GGGGCGAGCA	AGGAAGAAAT	GGATAATGAC	GATTTAGACG	CTTTTAAAGA	AATGGCTTCT		300
AATATTTTTG	GTGCGATCGC	TACAAGCTTG	AAGTCTCAAG	AATTGCTCCC	TAAACTCAAT		360
TTCACCACCA	CGAACGCTGA	AATCGCTAAA	GAGCTTCCTA	AAAAAGAAGA	TTACGCTAAG		420
CGGATGGTGT	TTTCTTTTAA	AATGGAAGCC	ATCAAAGAAA	GCCAAATCGT	TTTATTGATC		480

ACTTCAGCGT	TTGAGGGCCA	ATTTGAAAAA	ACGCATAAAG	AAGAAAAAGA	AGAAACGACA	540
AAAAGCGCTA	CTGAAGAGAG	TAAACCCAC	GACGCGTCTT	TAGAAAATAT	AGAAATCCGC	600
AATATCAGCA	TGCTTTTAGA	CGTGAAATTG	AACGTTAAGG	TGCGTATCGG	TCAAAAAAAG	660
ATGATTTTAA	AAGATGTGGT	CTCTATGGAT	ATAGGGAGCG	TGGTGGAGTT	GGATCAATTG	720
GTGAATGACC	CTTTAGAAAT	CCTCGTAGAT	GACAAGGTGA	TCGCTAAGGG	CGAAGTGGTG	780
ATCGTGGATG	GGAATTTTGG	CATTCAAATC	ACGGATATTG	GCACTAAAAA	GGAACGATTA	840
GAGCAACTGA	AAAATTAA					858

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

ATGACGACTA	AAAGAGTGAA	TACTGCCACA	AACAAGATAA	TGACATTAAA	CACTTCTCTG	60
GATACATGTT	TTCTTTTCTT	CATCAGTATT	CTTTTTTACC	TAAGTATACC	AATTTATCCT	120
AACAAAGTGG	TGGTTGTCCC	GCAAGGTTCC	CTCAAAAAAG	TGTTTTTTTC	TTTGAAAGAG	180
CAAGGCGTGG	ATATTAACGC	TTTAGATTTG	CTTTTGTTGC	GCCTAATGGG	CATGCCTAAA	240
AAAGGCTATA	TTGACATGGG	CGATGGGGCT	TTAAGGAAGG	GGGATTTTTT	AGTCCGTTTG	300
ATCAAAGCGA	AAACGGCGCA	AAAAAGCGTT	ACTTTAATCC	CTGGAGAAAC	CCGCTATTTT	360
TTCACGCAAA	TTTTGAGCGA	GACTTACCAA	CTAGAAACAA	GCGATCTCAA	TGAAGCTTAT	420
GAAAGCATCG	CTCCACGATT	AAACGGCGCT	GTGATAGAAG	ATGGGGTGAT	ATGGCCAGAC	480
ACTTATCATT	TACCTTTAGG	GGAGGACGCT	TTTAAAATCA	TGCAAACTTT	GATTGGTCAA	540
TCCATGAAAA	AACACGAAGC	CTTAAGCAAA	CAATGGCTTG	GATACTACCA	TAAAGAAGAG	600
TGGTTTGAAA	AAATCATTCT	CGCTTCCATT	GTGCAAAAAG	AAGCCGCTAA	TGTTGAAGAA	660
ATGCCCTGA	TTGCGAGCGT	GATTTTAAAC	CGCTTGAAAA	AAGGCATGCC	TTTACAAATG	720
GATGGGGCTT	TGAATTATCA	GGAATTTTCA	CACGCTAAAG	TAACCAAAGA	GCGCATTAAA	780
ACCGATAACA	CCCCCTACAA	TACCTATAAA	TTTAAGGGCT	TGCCTAAAAA	TCCTGTAGGG	840
AGCGTGAGCT	TAGAAGCGGT	TAGAGCCGTG	GTTTTCCCTA	AAAAAACGGA	TTTCTGTAT	900
TTTGTGAAAA	TGCCGGATAA	AAAACATGCT	TTCAGCGCAA	CTTATAAGGA	GCATTTAAAA	960
AACATTAATA	TTTCTAATAA	TCATTTTTAA				990

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

372

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...441
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

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ATGAGATTGT TGTTCTTGTT ACTGAGCGCT ACTTTGATGT TACTGGCTGA AGAAAAAATA      60
CCTTTAAGCG ATGACGCCCC CATTAAATTG GTTCATTGGC AAAATGCGCT AAAAGAAGTC      120
CAACCCGATT CAAACGCTCC GGCAACGCCA CCTATAAAGG CCGTGCAAAC CACGCTCACT      180
TTTGAAACGC CTTTTAATAA AACGCCTAAA ATCATGGAGG TTGAAGGGCA AAAAGTCATC      240
GTGTTAAAAA ACGCTCAATT GGATTCTAAA AAAACGATGG ATTTTAAAGA AGCCTCTTTG      300
AATGCCTTAG AAATGTTTTT CTACCAAAAT GACATCTACC TCTTGTCTAA AAAAGCTAAA      360
GCGGGATTAG AAATCCAAGC TTCAAGCAGC AAGGATAAAA AGCAACTCGC TTTCTTTTTT      420
TACCCAAAGG TTTTCATTTA G                                     441

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(2) INFORMATION FOR SEQ ID NO:385:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1983 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1983
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

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ATGCTAAAAA AGATTTTTTA TGGTTTTATC GTTTTATTTT TGATTATCGT AGGGTTGTTG      60
GCCGTTCTTG TCGCTCAAGT TTGGGTAAGT ACGGATAAGG ATATTGCTAA AATTAAAGAT      120
TATCGCCCCA GTGTCGCTTC ACAGATTTTA GACAGAAAAG GGCGTTTGAT CGCTAATATT      180
TATGATAAGG AATTTGTTTT TTATGCGCGT TTTGAAGAAA TCCCCCACG ATTTGTTGAA      240
AGCCTTCTAG CCGTAGAAGA CACCCTCTTT TTTGAGCATG GGGGGATCAA TTTAGACGCT      300
GTCATGCGCG CTATGATTAA AAACGCTAAA AGTGGTCGTT AACTGAAGG GGGTAGCACT      360
CTAACCCAAC AACTCGTTAA AAACATGGTG CTCACACGGG AAAAAACCTT AACCAGAAAA      420
CTCAAAGAAG CTATCATCTC CATACGCATT GAAAAAGTCT TAAGCAAAGA AGAAATTTTA      480
GAGCGTTATT TGAACCAAAC TTTTTTGGG CATGGGTATT ATGGCGTGAA AACCACAAGT      540
TTAGGGTATT TTAATAAAC CTTTGACAAA CTCACGCTTA AAGAAATCAC CATGTTAGTC      600

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GCCTTACCTA	GGGCTCCAAG	TTTTTATGAC	CCTACCAAAA	ATTTAGAATT	TTCACCTCTCT	660
AGGGCTAATG	ATATTTTAAG	GCGGTTGTAT	TCTTTAGGCT	GGATTTCTTC	TAACGAGCTC	720
AAATCCGCTC	TCAATGAAGT	GCCAATCGTC	TATAACCAAA	CTTCCACGCA	AAATATCGCT	780
CCCTATGTCG	TGGATGAAGT	GTTGAAGCAA	TTGGATCAAT	TAGACGGGTT	AAAAACTCAA	840
GGCTATACCA	TAAAACTCAC	GATAGATTTG	GATTACCAAC	GCTTAGCGTT	GGAGTCTTTG	900
CGTTTTGGGC	ATCAAAAAAT	CTTAGAAAAA	ATCGCTAAAG	AGAAGCCAAA	AACTAACGCT	960
TCTAATGATA	AAGATGAAGA	CAACTTAAAC	GCCAGCATGA	TAGTTACAGA	AACGAGCACC	1020
GGTAAGATTT	TAGCCTTAGT	GGGGGGGATT	GATTATAAAA	AAAGCGCTTT	CAATCGCGCC	1080
ACGCAAGCCA	AACGGCAGTT	TGGGAGCGCG	ATCAAGCCTT	TTGTGTATCA	AATCGCTTTT	1140
GATAATGGCT	ATTCCACCAC	TTCCAAAATC	CCTGATACCG	CGCGAAATTT	TGAAAATGGC	1200
AATTATAGTA	AAAACAGCGT	GCAAAACCAC	GCATGGCACC	CTAGCAATTA	TACTCGCAAA	1260
TTTTTAGGGC	TTGTAACCTT	GCAAGAAGCC	TTGAGCCATT	CGTTAAATCT	GGCTACGATT	1320
AATTTAAGCG	ATCAGCTTGG	CTTTGAAAAA	ATTTATCAAT	CTTTAAGCGA	CATGGGGTTT	1380
AAAAACCTCC	CTAAAGATTT	GTCTATTGTG	TTAGGGAGCT	TTGCTATCTC	ACCGATTGAT	1440
GCGGCTGAAA	AGTATTCTCT	ATTTTCTAAT	TACGGCACCA	TGCTCAAACC	CATGCTCATT	1500
GAAAGCATCA	CCAACCAACA	AAACGAAGTC	AAAACTTTCA	CGCCCATTTGA	AACCAAAAAG	1560
ATCACTTCCA	AAGAACAAGC	TTTTTTAACC	CTTTCAGCGC	TGATGGATGC	GGTAGAAAAC	1620
GGCACAGGGA	GTTTGGCTCG	CATTAAAGGT	TTAGAAATTG	CCGGTAAAAC	CGGGACTTCT	1680
AACAACAATA	TTGACGCTTG	G TTCATTGGC	TTTACCCCCA	CCTTACAAAG	CGTGATCTGG	1740
TTTGGGAGAG	ACGATAACAC	GCCTATTGGC	AAAGGAGCGA	CAGGAGGCGT	TGTGAGCGCG	1800
CCTGTGTATT	CGTATTTTAT	GCGCAATATC	TTAGCGATTG	AACCTTCTTT	AAAAAGAAAG	1860
TTTGATGTCC	CCAAAGGCTT	GCGTAAAGAA	ATCGTGGATA	AAATCCCCTA	CTACTCAAGC	1920
CCTAATTCCA	TCACCCCCAC	CCCCAAAAAA	ACAGACGATA	GCGAAGAACG	CTTGTTGTTC	1980
TAA						1983

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

ATGGCTAAAA	TGAACGCTCC	AGATGGGGTT	GCCGTTTGGG	TGAATGAAGA	CAGGTGTAAG	60
GGTTGTGATA	TTTGC GTGTC	GGTATGCCCC	GCTGGAGTTC	TTGGCATGGG	GATTGAAAAA	120
GAAAGGGTGC	TTGGAAAAGT	GGCCAAAAGTA	GCCTATCCAG	AGAGCTGTAT	TGGTTGCGTG	180
CAATGCGAGT	TGCACTGCCC	GGATTTTGCG	ATTTACGTGG	CTGACAGGAA	GGATTTCAAA	240
TTGCTAAAG	TTTCTAAAGA	AGCCCAAGAA	AGAAGCGAAA	AGGTTAAGGC	CAATAAATAC	300
ATGCTCTTAG	AAGAGACTAT	TTTAGAAGGG	AGAGGCAAAT	AA		342

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1020

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

ATGATTTTCA	TTGACGCATG	TTT TAGAAAG	GAAACGCCTT	ACACACCCAT	TTGGATGATG	60
AGGCAAGCGG	GGCGTTACCT	TAGCGAATAC	CAAGAGAGCC	GTAAAAAAGC	GGGGAGCTTC	120
TTGGAATTGT	GTAAAAATAG	CGATTTAGCC	ACAGAAGTTA	CCCTACAGCC	GGTAGAGATT	180
TTAGGCGTGG	ATGCGGCTAT	TTTGTTTAGC	GATATTTTAG	TAGTGCCTTT	GGAAATGGGC	240
TTGAATTTGG	AGTTTATCCC	CAAAAAGGGG	CCGCATTTTT	TAGAGACGAT	TACGGATTTA	300
AAAAGCGTGG	AAAGCCTAAA	AGTAGGGGTT	TATAACAAC	TAAACTATGT	CTATGATACG	360
ATTTCTCAAA	CGCGCCAAA	GCTTTCTAAA	GAGAAAGCGC	TAATCGGTTT	TTGCGGATCG	420
CCTTGGAATT	TAGCGACTTA	CATGATAGAA	GGCGAGGGGA	GCAAATCGTA	TGCCAAAAGC	480
AAGAAAATGC	TTTATAGCGA	GCCTGAAGTT	TTAAAAGCGC	TTTTAGAAAA	GTAAAGCCTT	540
GAATTGATAG	AGTATTTGAG	CCTTCAAATC	CAAGCAGGGG	TCAATGCAGT	GATGATCTTT	600
GACTCATGGG	CTAGCGCTTT	AGAAAAAGAA	GCGTATTTGG	AATTCAGTTG	GGATTATTTG	660
AAAAAATCT	CTAAAGAGCT	TAAAAACGC	TATGCGCACA	TCCCAGTTAT	CCTTTTCCCT	720
AAAGGGATTG	GCGCTTATTT	GGATAGCATA	GATGGGGAAT	TTGATGTGTT	TGGCGTGGAT	780
TGGGGCACGC	CTTTAACTGC	GGCAAAAAG	ATTTTAGGCG	GTAAGTATGT	TTTGCAAGGG	840
AATTTAGAGC	CCACCCGCCT	TTATGATAAA	AACGCTTTAG	AAGAAGGGGT	TGAAAAGATT	900
CTAAAAGTCA	TGGGCAATCA	AGGGCATATT	TTTAATTTAG	GGCATGGGAT	GTTGCCGGAT	960
TTGCCCAGAG	AAAACGCCAA	GTATTTAGTG	CAATTAGTGC	ATGCTAAAAC	CAGGCGATAG	1020

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

GTGTTAGAAA AATCTTTTTT AAAAAGCAAG CAATTGGTTT TATGCGGGTT GGGTGTTTTA	60
ATGTTGCAGG CTTGCACTTG CCCAAACACT TCACAAAGAA ATTCTTTTTT ACAAGATGTG	120
CCTTATTGGA TGTGCAAAA TCGCAGCCAG TATCTCACGC AAGGGGTGGA TAGCTCGCAC	180
ATTGTAGATG GTAAGGCAAC TGAAGAGATA GAGAAAATCG CTACCAAAAG AGCGACAATA	240
AGAGTGGCGC AAAATATCGT GCATAAACTT AAAGAAGCTT ATCTTTCTAA ATCCAACCGC	300
ATCAAGCAAA AGATCACTAA TGAAATGTTT ATCCAAATGA CAAAGCCCAT TTTTGACAGC	360
TTGATGAATG TGGATCGTTT AGGGATTTAT ATCAATCCTA ACAATGAAGA AGTGTTTGCG	420
TTGGTGC CGCGTTCCTT TGATAAGGAC GCTTTGAGCG AAGGGTTGCA TAAAATGTCT	480
TTAGACGATC AAGCGGTGAG TATCCTTGTT TCTAAAGTGG AAGAAATCTT TAAAGATTCT	540
ATCAATTACG GAGACGTTAA AGTCCCTATA GCCATGTAG	579

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

ATGCTTAGAA ATCAATTTCTG TATCGTGTTT GTCTCTTGTA TTGTCGCTAG CAGTTTGCAA	60
GCTCAAGAAA ATACCCACAC TTTGGGTAAAG GTAACCACTA AGGGTGAAAG GACTTTTGAA	120
TACAACAATA AAATGTATAT TGACAGGAAA GAGCTCCAAC AACGCCAAAG CAACCAAATC	180
CGTGATATTT TTAGGACTAG GCGGGATGTG AATGTGGCCA GTGGGGGCTT AATGGCGCAA	240
AAAATCTATG TTAGGGGGAT TGAGAGCCGT CTCTTAAGGG TAACGATAGA TGGCGTCGCT	300
CAAAATGGTA ACATTTTCCA CCATGACGCT	330

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GTGATGAAAA	AAATCGTTGT	GAGTTTATGC	GTGGCGTTAG	GTTTTTTAAG	CGCGGATCCA	60
GCGCAGGCCA	ATAAAGCGAT	CAGTGATGCG	GATTTGATTG	AAGAGATAAG	GGACTTGAAA	120
AAAATCATCA	GCGCACAAAA	CACGGAGATT	AACCAATTAA	GAAAAGTGCA	AGAAGTCTTA	180
TCTGGGCAAT	TAGGGGACAT	GCGTAAGGAT	ATATTAAGCA	CTAGAGATTA	CTGTATCAGC	240
TTAAGGCCTT	ATATTTATAA	TTGGCGCTAG				270

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

TTGAATAAAT	TTGGTTGGCG	TGCGTGTTTT	CTAACCCTTT	TTTTTAGCGG	GTATTCTAAA	60
AAAGCTCCTG	GAACGATAGG	GAGTTTAGTG	GCGTTGTAC	TGGGCTTACC	TATTTTAATT	120
TTTTCGGCTA	ACACTTTGTT	TTAGGGGCG	ATTTTGTG	GGCTTATCGC	TATTACTCAA	180
ATAGATAAGG	AAGAAGAAGA	ACTAAGAGG	CATGACAGCT	CTTACATTGT	GATAGACGAA	240
TTAGTGGGCA	TGTGGCTTGC	GATGGCGATT	AGCGGATTAT	CGTTAGTGGG	TGTGATCTTG	300
AGTTTTATCT	TTTTTAGGAT	CTATGATATT	ACTAAACCCT	CACTCATTGG	CAAAATAGAC	360
AAAGAAGTTA	AAGGGGGCTT	AGGGGTTGTG	GCTGATGACG	CTTTAGCCGG	GGTTTTAGCC	420
GGATTGAGCA	CGTTATTAGC	CATCAATATT	TTAGGATTTT	TTAACATTAA	GTTTTAG	477

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 402 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...402
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

ATGGAGTTAA TTAAGAAATT GGAAAAAGAA AGCGAAGTTT TAAAGAAAGA TTTACAACAA	60
CATTCAAACG AGCTTTTTTAA AATGTTGATT ATTGATAATG AAGATTTGTT TAAAGAGCAA	120
TTTGAGATTA TGTTTAAAGC ATGGGTTGAA ATCGTAAAAA TGATGTTTGA ATTAACCAAA	180
AAAACCAAAT TTGATGGCGA AATGATTGGC TACACAGAAG AACTTTTAAC CTTTTTAGTT	240
AGAGATTTTT TTAATGGGAT TTTTAAATCC AAAGTAATAC CTAAAATGCC TATTTTTTGC	300
GGTGATGTTA AATGCGAAGA TTTTAAATGCC CTAAGAAGTT TAGTTTATCT TTCTGTGCTT	360
GAGTTGGAAG AAACGATAAA TCCTAATAAA ATCCCATTTT AA	402

(2) INFORMATION FOR SEQ ID NO:393:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 402 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

ATGGAGTTAA TTAAGAAATT GGAAAAAGAA AGCGAAGTTT TAAAGAAAGA TTTACAACAA	60
CATTCAAACG AGCTTTTTTAA AATGTTGATT ATTGATAATG AAGATTTGTT TAAAGAGCAA	120
TTTGAGATTA TGTTTAAAGC ATGGGTTGAA ATCGTAAAAA TGATGTTTGA ATTAACCAAA	180
AAAACCAAAT TTGATGGCGA AATGATTGGC TACACAGAAG AACTTTTAAC CTTTTTAGTT	240
AGAGATTTTT TTAATGGGAT TTTTAAATCC AAAGTAATAC CTAAAATGCC TATTTTTTGC	300
GGTGATGTTA AATGCGAAGA TTTTAAATGCC CTAAGAAGTT TAGTTTATCT TTCTGTGCTT	360
GAGTTGGAAG AAACGATAAA TCCTAATAAA ATCCCATTTT AA	402

(2) INFORMATION FOR SEQ ID NO:394:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...378
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

ATGAAAAAGT TAGCCGCTTT ATTTTATAGTA AGCGCGTTGG GGGTTATGAG TTTGAACGCA	60
TGGGAGCAAA CCCTAAAAGC TAATGATTTG GAAGTGAAAA TCAAATCCGT GGGCAACCCC	120
ATTAAAGGCG ATAACACTTT TGTGCTTAGC CCCACTTTAA AAGGTAAGGC TTTAGAAAAA	180
GCTATCGTTA GGGTGCAGTT TATGATGCCT GAAATGCCCC GCATGCCAGC GATGAAAGAA	240
ATGGCGCAAG TGAGTGAAAA AAACGGCCTT TATGAAGCTA AAACCAATCT TTCCATGAAC	300
GGGACATGGC AGGTTAGGGT GGATATTAAA TCCAAAGAAG GCCAAGTTTA TCGCACTAAA	360
ACAAGCCTGG ATTTATGA	378

(2) INFORMATION FOR SEQ ID NO:395:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1026 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1026
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

ATGAAACGGC TTTTATTGTT AGCCTTGGCC CTCTTTTTTA GCCTCTCATG CACTAACGCT	60
CAAGAAATTA AAGAACTCA AGAGACTAAA AAAACTAAAG AAACTAAAAG CCAAACCCGT	120
TTTAACATTT CCACCACTAA GGTCATAGAA AAAGAATTTT CTCAAAGCCG GCGCTATTAC	180
GCGCTTTTAG AGCCTAATGA AGCGCTGATT TTTTCTCAAA CCCTGCGTTT TGATGGCTAT	240
GTGGAAAAGC TTTATGCGAA TAAAACCTAT ACCCCCATTA AAAAGGGCGA TAGGCTATTG	300

AGCGTGTATT	CCCCTGAATT	AGCGGGCGTT	CAAAGCGAGC	TGTTATCGTC	ATTGAAATTC	360
AACCAGCAAG	TGGGAGCGAT	TAAAGAAAAA	TTAAACTAC	TAGGGCTAGA	AAACTTTAGC	420
ATTGAAAAAA	TCATCAGCAG	CCATAAAGTC	CAAAATGAAA	TCACTATTTA	CTCTCGTTTC	480
AACGGCGTTA	TTTTTAAAAA	AAGCCCGGAT	CTCAATGAGG	GGAGTTTCAT	TAAAAAAGGG	540
CAAGAGCTTT	TCAAAATCAT	AGATTTAAGC	CGATTGTGGG	CGCTTGTTAA	AGTCAATCAA	600
GAGGATTTAG	AATTTTTTAAA	AAACACGCAT	CAAGCGATTT	TGTTCTAGTA	GGGGGTAA	660
GGCAAGCAAG	CAATCACGCT	TGAAAACATC	AACCCCATCA	TAAATGCGCA	AGATAAAATG	720
CTAGAAGCGC	GCTTCAATGT	GCCTAATCTT	AAATTGCTTT	ATTACCCTAA	CATGTTTCGCT	780
CAAGTAGAAA	TCTTTCACAA	ACCCCAAAAA	ATGAAGATCT	TGCCTAAAGA	AGCGGTTTTG	840
ATTAAGGGGG	GGAAAGCTAT	CGTGTTTAAA	AAAGATGATT	TTGGCTTAAG	CCCGTTAGAA	900
ATTAAAGCCG	TCCGCTTGAG	CGATGGGAGT	TATGAAATTT	TAGAGGGTTT	AAAAGCGGGC	960
GAAGAAGTCG	CTAATAACGC	TTTATTCGTG	CTAGACGCTG	ACGCTCAAAA	CAATGGGGAT	1020
TATTGA						1026

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

ATGGGCGTAG	CGGTTGTTTT	ATTTTAAACG	CTAATTTTAT	TGTTTTTAGT	TTTAAGGGAT	60
TTTGGTTTAG	CTAGCCCCAA	ACAAAAGATT	TTAGCTTTTT	TAATCGTAGG	GATTATAGGA	120
GCGAGCATCA	GCGTTTATAC	TTATAAACAA	AACCAACAAA	ACCAACAAGA	AATCGCTTTG	180
CAAAGAGCGT	TTTTAAGGGG	GGAAACCTTG	TTGTGTAAAG	GCATCAAAGT	CAATAACCAA	240
ACCTTTAATT	TAGTGAGCGG	GACTTTGAGC	TTTTTAGGCA	AAAAACAAAC	CCCTATGAAA	300
GATGTTCTTG	TGGATTGGA	TTCTTGTCAG	ACGCTTCAAA	AAGATCCCTT	AATCCAACCT	360
TAA						363

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

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ATGCGTTTTT TTATTTTATT TTTTATGGGT ATGCTTGGCG TTGGTTTTTC TCAAACCGAG      60
TTGGATTAA AGGATTTAGA AAAAAAGCCC GCCGGGATCG TTAGGGATTA TTATTTATGG      120
CGTTATATTA GCGATAAAAA AACGAGTTTA GAAAACGCTA AAAAAAGCCTA TGAATTGACT      180
CAAAATAAAA ACAGCGCCCT ACAAAAAGCC ATGCAAGAAA AAGGCGTAGA AAATTCAGAT      240
AAAAGCCCTG ATGCCAAAAT GCCTGAAGAT ATTTATTGCA AGCAAATTAC CTTAGAAAGC      300
ATGTTAGAAA CAACAGACGC TTTCCAAGCG AGTTGTATCG CTATCGCTTT AAAATCAAAA      360
ATCAGAGATT TTGATAAAAT CCCCATTCOA ACCTTTAAAC CTTTACAAGA AAAAATCAAA      420
GAGGCTTACC CCATTCTTTA TGAAGAATTA GAAATCTTGC AAAGTAAGAA CGTGAGCGCT      480
TCTTTGTTTA AGGCTAACGC GCAAGTGTTT AGCGCGCTCT TTAATCATTT GAGTTATGAA      540
AAAAAGCTCC AAATTTTTGA AAAGCATATC CCGATTAAAG AGTTAAACCG CCTTTTAGAT      600
GAAGATTACC CGGCGTTTAA CCGCTTGATC TATCAAGTCA TCTTAGATCC TAAATTGGAT      660
CATTTTAAAG ACGCTCTCGC TAAAAGTAAC GCCACCCAAA GCAACGCGCA AACCTTTTTT      720
ATTCTAGGAA TCAATGAAAT CTTGCACAAA AAAACTTCTA AAGCGCTCAA GTATTTTGAA      780
CGCTCAGAAG CGGTTGTCAA GGACGATGAT TTTTCAAAAG ACAGAGCGAT TTTTGGCAG      840
TATTTAGCCT CTAAAAGAA AAAAAGTTT GAGCACCTT CACAAAGCCC AGCCCTAAAC      900
CTCTATAGTC TTTATGCGAG CCGCAAACCT CAAAACCACG CCCAGTTATC GCATCATTTT      960
TCATATCCAA AATTAAAGCC AAGAGAACCC TCCTTTTAA      999

```

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 474 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

```

GTGCATCTAG CCCACTACCT CAAAAGGAAT TTTTCTTTTT TCCCTAGCGT GGATATTGTG      60
GATGGGGGGA CTATGGCTCA GCAACTCATT CCTTAAATCA CTTCGTATGA AAAGGTTTTG      120
ATTTTAGATT GCGTGAGCGC TAAAGGCGTT GAAATGGGCT CAGTTTATGC CTTTGATTTT      180
AAGGACGCTC CTAAAGAAAT CACATGGGCT GGGAGTGCGC ATGAAGTGA AATGCTGCAC      240
ACTTTAAGGC TCACGGAGTT TTTAGGGGAT TTGCCTAAAA CTTTATCGT GGGGCTTGTC      300

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CCTTTTGTGA TAGGGAGCGA GACCACTTTC AAGCTTTCAA GCGAAATGTT AAACGCTTTA	360
GAAACAGCCC TAAAAGCCAT AGAAACCCAA CTCAACGCAT GGGGAGTTAA AATGCAACGC	420
ACCGATCATA TTGCCCTAGA TTGTATCGCT GAACTCTCTT ATAAGGGTTT TTGA	474

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

ATGAAAAAAG TCCTCTTACT AACTCTCTCT CTCTCTCTCT CGTTTTGGCT CCACGCTGAA	60
AGGAACGGAT TTTATTTAGG TTTAAATTTT GCAGAAGGAA GCTATATTCA AGGACAAGGT	120
AGCATCGGCG AAAAAGCTTC AGCAGAAAAC GCCTTAAATC AAGCGATCAA TAACGCAAAA	180
AATTCATTAT TCCCTAACAC AAAAGCCATA AGAGATGTGC AAAACGCCTT AAATGCAGTG	240
AAAGATTCAA ACAAATCGC TAACCGATTC GCAGGAAATG GTGGATCGGG CGGTATTTTC	300
AATGAACTCA GCTTGGGGTA TAAATATTTT TTGGGTAAAA AAAGGATTAT AGGGTTTAGG	360
CACTCTCTTT TTTTCGGTTA CCAACTTGGT GCGTTTGGTT CTGTTCTGG CAGCGGTTTA	420
ATAGCTTTTT TACCCTATGG TTTCAATACG GATTTGCTCA TTAATTGGAC TAACGATAAG	480
CGAGCGTCTC AAGAATACGT TGAAAGAAGG GTAAAAAGGC TCTCTATATT TTACAAAGAT	540
ATGACCGGCA GAACGCTAGA CGCTGATACA TTAAAAAGAG CATCAAGGCA CATAATCAGA	600
AAATCTTCAG GGCTTGTGAT TGGCATGGAA CTAGGGGCTA GCACTTGGTT TGCAAGTAAC	660
AATCTCACCC CTTTAAATCA AGTCAAGAGT CGCACGATTT TTCAGTTACA AGGGAAATTT	720
GGCGTTCGTT TTAGTAGTGA TGAATACGAT ATTGATCGCT ATGGCGATGA AAATATCTT	780
GGGGTTCTA GTGTTGAATT AGGGGTAAA GTGCCAGCGT TTAAAGTCAA TTATTATAGC	840
GATGATTACG GGGATAAATT GGATTATAAA AGAGTGGTGA GCGTTTATCT TAACTATACG	900
TATAACTTTA AAAACAAACA TTAA	924

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1737 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

ATGTCAAAAA	AAATCGTAGT	CGATCCTATC	ACTAGGATTG	AGGGGCATTT	AAGGATTGAG	60
GTGATCGTAG	ATGATGATAA	TGTGATCACC	GATGCGTTTT	CTTCTTCTAC	GCTTTTTTAGG	120
GGGCTAGAAA	CGATCATTAA	GGGCAGAGAC	CCACGAGATG	CAGGCTTTAT	CGCTCAAAGG	180
ATTTGTGGGG	TATGCACCTA	TTCGCATTAT	AAAGCCGGTG	TTACTGCGGT	AGAAAACGCT	240
TTAGGAATCA	CTCCCCCATT	AAACGCGCAA	TTGGTGCGAT	CTTTGATGAA	CATGGCGTTG	300
CTTTTTCACG	ATCATGTGGT	GCATTTCTAT	ACTTTGCATG	GGCTTGATTG	GTGCGATATT	360
TTGAGCACTT	TAAAAGCTGA	TCCCATTCAA	GCAGCAAAAC	TTTCTTTCAA	ATACAGCCCT	420
TATCCCATTA	ATACCGGTGC	GGGCGAATTA	AAAGCGGTTT	AAAAACGCTT	GAATGATTTT	480
GCTAAAAGCG	GATCTTTTAGG	GCCTTTTAGC	AATGGCTATT	ATGGGCATAA	AACCTATCGT	540
TTAAACCCAG	AACAAAATTT	AATCGTCTTA	AGCCACTACC	TCAAGCTTTT	AGAAATCCAA	600
AGGGAAGCGG	CGAAAATGAC	CGCTATTTTT	GGGGCCAAAC	AACCTCACCC	ACAAAGCCTA	660
ACGGTGGGGG	GTGTTACGAG	TGTCATGGAT	ATATTGGATC	CAACAAGGTT	GGCTGAATGG	720
AAGAGCAAGT	TTGAAGTGGT	GGCTAATTTT	ATCAACCATG	CTTACTACCC	TGATTTGGTG	780
ATGGCAGGCG	AAATGTTTCG	TAACGAACCA	TCTGTTATTA	AAGGCTGTGG	TTTAAGGAAT	840
TTTATCGCTT	ATGAAGAAGT	GTTGCTTGGG	AAGGATAAAT	ACCTTTTGAG	TAGTGGGGTG	900
GTGCTTGATG	GGGATATTTT	TAAATTACAC	CCCATTGATG	AAAGTTTGAT	TAAAGAAGAG	960
GTTACGCATT	CTTGGTATCA	ATATGAAGAC	ACTAAAGAAG	TGCAACTCCA	CCCTTATGAC	1020
GGGCAAACTA	ACCCGCATTA	TACCGGTTTA	AAAGACGGCG	AGAGCGTGGG	GATTGAAAAT	1080
AAAATAATCC	CTGCTAAAGT	GCTTGACACT	AAGGATAAAT	ATTCTTGGAT	AAAATCGCCC	1140
AGATACGATA	GTAAGCCCAT	GGAAGTAGGG	CCTTTAAGTT	CCGTAGTGGT	AGGTTTAGCG	1200
GCGAAAAACC	CTTATGTTAC	TGAAGTGGCT	ACTAAATTTT	TAAAAGACAC	GAAACTGCCT	1260
TTAGAGGCGT	TGTTTTCAAC	GCTTGGGCGC	ACAGCTGCAA	GGTGTATTGA	AGCTAAGACT	1320
ATCGCTGATA	ATGGTCTTTT	GGCGTTTGAC	GCGTTAGTGG	AAAATCTAAA	GAGCGATCAA	1380
AGCACTTGTT	CTCCTTATCA	TATTGATAAA	AATCAAGAAT	ATAAAGGGCG	CTACATTGGT	1440
CAAGTGCCAA	GGGGCATGTT	AAGCCATTGG	GTGCGTATTA	AAAACGGCGT	GGTGGAAAAT	1500
TATCAAGCGG	TAGTGCCTTC	CACTTGGAAT	GCAGGGCCTA	GAGATTCTAA	AAATCAAAGG	1560
GGGGCTTATG	AAATGAGCTT	GATTGGCACT	AAAATCGCTG	ATTTAACCCA	GCCTTTAGAA	1620
ATCATTAGGA	CTATCCATTE	TTTTGATCCA	TGCATCGCAT	GCTCAGTGCA	TGTGATGGAT	1680
TTTAAAGGGC	AGTCTTTGAA	CGAGTTCAAA	GTAGAGCCTA	ATTTGCTTAA	ATTCTAA	1737

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

383

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

ATGAATAGTT CTAACCTCAA AAATTGGCTA TTCCCCACTA TTTGCTTTTT TTTATTTTGT	60
TATATTTTAA TTTTTTTGAT ATTTTTTATG TTAAAAAACT TGCAATCGCA ATCTTTTGGC	120
TCTGTGGCAG AAACCGGAAA AAAACCCATC ACCACCACCA AGAAATTTGG TAAGGAATTG	180
CAAAAACAGA TTTCAAAAAT CCATTAA	207

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

GTGGTCTTGC CTAAAGAAAC CTTATCTTCT ATCGCTAAAC GCTATCAAGT CAGCATTTCC	60
AGTATCCAAT TAGCCAATAA CCTCAAAGAT TCTAATATCT TTATCCACCA GCGCTTAATC	120
ATCCCCACTA ACAAAAAATT ACTCGCTACA AGGGAATTTT AA	162

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...1059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

TTGTATTTCC	TTAATGGTGG	TTATAATCGG	CTTCATAAAT	CATACGAAAG	GATTGTCATG	60
CTAATCGCTC	GCTTTAAAAA	AGCTTTAATT	TCCTATTCTT	TAGGGGTTCT	TCTTGTTTCA	120
TCGTTATTAG	GCGTGGCTAA	CGCTTCTAAT	CAAGAGATCC	AAGTCAAGGA	TTATTTTGGG	180
GAGCAAACCA	TAAAGCTTCC	TGTTTCTAAA	ATAATCTACT	TGGGCAGCTT	TGCAGAAGTG	240
CCTGCCATGT	TCAATACTTG	GGATAGGGTC	GTGGGCATTT	CGGATTACGC	TTTTAAATCT	300
GATATTGTTA	AAGCCACTCT	CAAAGATCCT	GAACGCATTA	AACCCATGAG	CAGTGATCAT	360
GTGGCGGCGT	TGAATGTGGA	ATTATTAAAA	AAGCTTAGCC	CTGATCTTGT	GGTAACCTTT	420
GTGGGTAACC	CTAAAGCGGT	AGAGCATGCG	AAAAAATTTG	GGATTTCATT	CCTTTCTTTC	480
CAAGAAAAAA	CCATTGTAGA	GGTCATGGAA	GATATTGACG	CTCAAGCTAA	GGCCTTAGAA	540
GTTGACGCTT	CTAAAAAATT	GGCTAAAATG	CAAGAACTT	TGGATTTTAT	CAAAGAGCGT	600
TTGAAAAATG	TCAAAAAGAA	AAAGGGGGTG	GAGCTTTTCC	ATAAAGCCAA	TAAATCAGC	660
GGCCATCAAG	CCCTTGATTG	AGATATTTTA	GAAAAAGGGG	GCATAGACAA	TTTTGGCTTG	720
AAATACGTCA	AGTTTGGGCG	CGCTGACATT	AGTGTGGA	AAATCGTTAA	AGAAAACCTT	780
GAGATTATTT	TTATTTGGTG	GATAAGCCCG	CTTAGCCCTG	AAGACGTGTT	GAACAACCTT	840
AAATTTTCCA	CTATCAAAGC	CATTAAAAAC	AAGCAAGTCT	ATAAGCTCCC	CACAATGGAT	900
ATTGGCGGAC	CTAGAGCCCC	ACTCATTAGT	CTTTTATCG	CTTTAAAAGC	CCACCCTGAA	960
GCGTTTAAGG	GCGTGGATAT	TAATGCGATA	ATCAAAGATT	ACTATAAAGT	GGTCTTTGAT	1020
TTGAATGACG	CGGAAGTTGA	ACCCTTTTTG	TGGCACTGA			1059

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

ATGAAGTGCT	CAAGCTTTAC	CTCTAATAGC	GTCTTAAACT	TTTTTGTA	TTTGTCTTTC	60
ATCACGATAG	GGCTAGTGTT	TTTCTTTTTG	CGTTCCCAAC	CAACTAGCGT	AGTTTCTAAA	120
GAAAATATCC	CTAAAAATTGA	ATTAGAAAAT	TTTAAAGCGT	TTCAAATCAA	CGATAAAATC	180
CTTGATCTGT	CCATAGAGGG	CAAAAAAGCC	CTACAATACG	ATGATCATGA	AATCTTTTTT	240
GATTCTAAAA	TCAAGCGCTA	TGATGAAGAC	ACCATTGAAA	GCGTTGAGTC	CCCTGAAGCC	300
AAACGGCAGC	AGGATTGTGA	TTTCTTCCCT	AACGGGGTAA	CTTATAAAAAG	AAGCGATGAT	360
TCCAGTTTTT	GGAGTGAAAC	AGGGATTTAT	AACCATAAGG	AGCAAAATTT	TAAAGGCAAG	420
GGCCGTTTCA	TTCTCACTTC	AAAGGACAGC	AAGGTTGAAG	GGCTTGACAT	TTCTTATTCG	480
CATGCATTAG	CTATTATTGA	AGCTCAAAGC	ATTCAAGCCA	ATTTGTTTTT	AGATGAAATC	540
AAACAAAGCC	AGAAAGAAAA	GAAAAAATTC	CCCCTTTTCA	AAGGAGGGTT	TTAA	594

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

ATGCGTTGGT GGTGTTTTTT GGTGTGTTGT TTGAGCGTTT TAAGCGTGAT GGACGCTAAA	60
AAATTAGAGA ATAAAGGCTT GAAAAAGAA AGAGAGCTTT TAGAAATTAC CGGCAACCAA	120
TTTGTAGCGA ACGACAAAAC CAAAACCGCC GTTATTCAAG GCAATGTGCA GATCAAAAAA	180
GGTAAAGACC GGTGTTTTCG GGATAAAGTG AGCGTGTTTT TAAACGATAA ACGAAAGCCA	240
GAACGCTATG AAGCCACAGG GAACACGCAT TTTAACATCT TTACAGAAGA TAATCGTGAA	300
ATCAGCGGGA GCACTGACAA GCTCATTTAT AACGCGCTGA ATGGGGAATA CAAATTATTG	360
CAAAATGCGG TGGTTAGAGA AGTGGGAAAA TCTAATGTCA TCACCGGCGA TGAAATCATT	420
TTAAACAAAA CCAAGGGTTA TGCTGATGTG TTGGGGAGCG CGAAGCGGCC CGCTAAATTT	480
GTGTTTGATA TGGAAGACAT TAATGAAGAA AATCGTAAGG CTAAATTGAA GAAAAAAGGC	540
GCTAAGGAAA AACCATGA	558

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

TTGATCCAAC	AAAATTTTAA	AACACTTAAG	GAGTTGTATA	TGTTAGTTAC	AAAACCTGCC	60
CCCGATTTTA	AAGCGCCTGC	CGTTTATAGGA	AACAATGAGG	TTGATGAACA	CTTTGAGCTT	120
TCTAAAAATT	TAGGCAAAAA	TGGTGTGATC	CTTTTCTTTT	GGCCAAAAGA	TTTACTTTT	180
GTATGCCCTA	CAGAAATCAT	TGCGTTTGAC	AAAAGAGTGA	AAGACTTCCA	CGAAAAAGGC	240
TTTAATGTGA	TTGGCGTGTC	TATTGACAGC	GAACAAGTGC	ATTTTCGCATG	GAAAAACACC	300
CCTGTGGAAA	AAGGCGGTAT	CGGTCAAGTG	TCTTCCCTA	TGGTGGCTGA	TATCACTAAG	360
AGCATTCTTA	GAGACTATGA	TGTGCTGTTT	GAAGAAGCGA	TCGCTTTGAG	AGGTGCTTTT	420
TTGATTGATA	AAAACATGAA	AGTAAGACAC	GCAGTGATCA	ATGACTTGCC	ATTAGGTAGG	480
AATGCAGATG	AAATGCTTCG	CATGGTAGAC	GCTCTCTTAC	ACTTTGAAGA	ACATGGTGAA	540
GTATGCCCAG	CAGGTTGGAG	AAAAGGCGAT	AAAGGCATGA	AAGCAACTCA	CCAAGGCGTT	600
GCAGAGTATC	TTAAAGAAAA	TTCCATTAAG	CTTTAA			636

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

GTGCCGTTGT	GGATTATGGT	AGTAGGGGCA	GCTGGGATCG	CTTTAGGCTT	GAGCTTGTAT	60
GGGCCAAAGC	TCATTAATAAC	GGTGGGGTCT	GAAATCACAG	AATTAGACAA	AATGCAAGCT	120
TTTTGCATCG	CGCTTTCAGC	GGTCATCACC	GTGCTTTTAG	CCTCTCAATT	AGGCTTACCG	180
GTAAGCTCTA	CGCATATTGT	GGTGGGCGCG	GTGTTTGGGG	TGGGCTTTTT	AAGGGAGCGT	240
TTGAGGGAGC	AATCCAGAAG	GCGTTTTGCT	AGAATCAGAG	ACAACATTGT	AGCGGCGCAC	300
TTTGGGGAAG	ATTTAGAAGA	AATTGAAGGC	TTTTTAGAGC	GCTTTGATAA	AGCCAATTTG	360
AAAGAAAAAT	CGCTCATGCT	AGAGAGCTTG	AAAAAAGCA	AGAACACCGC	TATCGCTTTG	420
GAATTGAAAA	AGAAAGAAAA	AAAGTCGCTT	AAAAAAGTGT	ATAAAGAAGA	AGTGATCAAA	480
CGCTCCATTT	TGAAAAAGAT	TGTTACCGCT	TGGTTGGTAA	CCGTGCCGGT	TTCTGCGCTT	540
TTAGGGGCGC	TTCTTTTTGT	AGCTCTTGGT	TTTATAGAAA	AGTATTCTA	G	591

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

ATGTCAAATA	GCATGTTGGA	TAAAAATAAA	GCGATTCTTA	CAGGGGGTGG	GGCTTTATTG	60
TTAGGGCTAA	TCGTGCTTTT	TTATTTGGCT	TATCGCCCTA	AGGCTGAAGT	GTTGCAAGGG	120
TTTTTAGAGG	CTAGGGAATA	CAGCGTGAGC	TCTAAAGTCC	CTGGCCGCAT	TGAAAAGGTG	180
TTTGTTAAAA	AAGGCGATCG	CATTAAAAAG	GGCGATTTAG	TTTTTAGCAT	TTCTAGCCCT	240
GAATTAGAAG	CCAAGCTCGC	TCAAGCTGAA	GCCGGGCATA	AAGCCGCTAA	AGCCGTTAGC	300
GATGAAGTGA	AAAGAGGCTC	AAGAGATGAA	ACGATCAATT	CTGCGAGGGA	CGTTTGGCAA	360
GCGGCAAAAT	CCCAAGCGAA	TTTGGCTAAA	GAGACTTATA	AGCGCGTTCA	AGATTTGTAT	420
GACAATGGCG	TGGCGAGTTT	GCAAAAGCGC	GATGAAGCCT	ATGCGGCTAT	GAAAGCACCA	480
AATACAACGA	GAGCGCGGCT	TACCAAAAGT	ATAAAATGGC	TTTAG		525

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

ATGGAATTTT	TGAGCGGGTA	TTTTTTATGG	GTAAAGCTT	TCCATGTGAT	AGCGGTCATT	60
TCGTGGATGG	CAGCGTTATT	TTATTGCCA	CGCCTTTTTG	TCTATCATGC	AGAGAACGCG	120
CATAAAAAAG	AGTTTGTAGG	CGTGTTCAA	ATCCAAGAGA	AAAAGCTCTA	TTCTTTTATC	180
GCTTCGCCGG	CGATGGGTTT	CACGCTTATT	ACAGGGATTT	TGATGTTGTT	GATCGCCCCCT	240
GAAATGTTTA	AAAGCGGGGG	TTGGTTGCAT	GCTAAATTGG	CTTTAGTGGT	ATTGCTTTTA	300
ATCTATCATT	TTTATTGCAA	AAAATGCATG	CGCGAGCTGG	AAAAAGACCC	TACAGGGGAA	360
AACGCAAGGT	TTTATCGTGT	GTTTAATGAA	ATACCCACGA	TTTAAATGAT	CCTTATTGTG	420
ATCTTAGTGG	TTGTCAAGCC	TTTTTAA				447

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

ATGAAACCAA TTTTTTTGTT AATCTTTTGT TTGTTAGCGA GCCTTATTGC TAGAGAAAAG	60
GACGCTTCTT CAAACCTTTT TGATTGTATC GATAAGGGGA TTAACAGAGA ACAAGAATTG	120
AAAGAGCAGG AGCAAAAAAC GCGCTTGAAA CTGGCTCAAA GCCCTTTAGT GGCCTTAGAA	180
ATTGTCCCCC AAGAAACGCC CTATTTAGAA TGGCAAGGGG CTAGGGAGTC GTATTATTTG	240
AAAGTGAGCG CTGTAGTGGA GAGCGTGGTT ATTTTAAAGA TTGACATCAA TCAGGGGCGT	300
TCTTGCTCGC TCTACCCAC GCCTAAAAGC GTTCTTTAG TGAGGAATCA AAGCGTAGCC	360
TATGAAATTT TATGCGAAAA CCAGCCGCTA TGGATAGAAG TTAGCACCAA TTTAGGCAAA	420
CGCACCTTTC AGTTTAA	438

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

ATGGCTAAGA AAAACAAACC CACCGAATGC CCCGCCGGCG AAAAATGGGC GGTTCCTTAT	60
GCGGACTTTT TGTCGTTGTT GCTCGCGCTT TTTATCGCTC TTTATGCCAT TTCAGCGGTC	120
AATAAATCCA AAGTGGAAGC CTTAAAAACC GAATTTATTA AGATTTTTAA TTACGCCCCA	180
AAGCCAGAGG CGATGCAGCC GGTGTAGTGT ATCCCCCTG ATTACAGGGAA AGAAGAAGAG	240
CAAATGGCGA GCGAAAGCTC CAAGCCGGCT TCGCAAATA CCGAAACAAA AGCCACTATC	300

GCTCGCAAGG	GCGAAGGCAG	TGTTTTAGAG	CAAATTGATC	AAGGCTCTGT	TTTAAAGCTC	360
CCCTCTAGTT	TGCTGTTTGA	AAACGCCACT	TCAGACGCTA	TCAATCAAGA	CATGATGCTT	420
TATATTGAAC	GGATCGCTAA	AATCATTCOA	AAACTCCCTA	AAAGGGTGCA	TATTAATGTG	480
AGAGGTTTTA	CGGATAACAC	GCCTTTAAAT	AAAACCCGTT	TTAAAAGCCA	CTATGAATTA	540
GCCGCCAATC	GCGCTTATAG	GGTGATGAAA	GTCCTTATAC	AATACGGCGT	GGATCCTAAC	600
CAATTGTCTT	TTTCTTCTTA	CGGCTCTACC	AACCCTATTG	CGCCCAATGA	TTCCCTAGAA	660
AACAGAATGA	AAAACAATCG	TGTGGAAATC	TTTTTTTCAA	CCGATGCGAA	CGATTTGAGC	720
AAGATCCATT	CTATTTTAGA	TGAAGAATTC	AATCCCCATA	AACAGCAAGA	ATGA	774

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

ATGAGAAAGG	TTATCATAAT	GAATGGTTAT	TTGAGGGTAA	AAACCCCGTA	TTTTTTAGCG	60
TCGGTCGTTT	TGACTTTTTG	GACTTTTAAT	TCTTTTATGA	GCGCGAAAGA	TAAGCACCAT	120
TTTTTAAAAA	AAGTTACAAC	CACCGAGCAA	AAATTCAGTT	CTAGTGCCCC	AATTTTCATGG	180
CAAAGCGAAG	AGGTGCGTAA	TTCCACAAGC	TCTCGCACGG	TGATTTCCAA	CAAAGAACTC	240
AAAAAAACGG	GGAATTTGAA	TATTGAAAAC	GCCTTGCAAA	ATGTGCCAGG	GATTCAAATC	300
AGAGACGCTA	CAGGCACGGG	CGTGCTGCCT	AAAATTTCCG	TGCGCGGTTT	TGGTGGGGGC	360
GGTAACGGGC	ATAGCAACAC	CAACATGATT	TTAGTCAATG	GTATCCCCAT	TTATGGCGCG	420
CCGTATTCCA	ATATTGAACT	GGCGATTTTC	CCTGTAACTT	TCCAGTCAGT	GGATAGGATT	480
GATGTGATTÀ	AGGGGGGAAC	GAGCGTCCAA	TACGGCCCTA	ACACTTTTGG	AGGCGTGGTG	540
AATGTCATCA	CTAAAGAAAT	CCCCAAAGAG	TGGGAAAATC	AAGCGGCTGA	AAGGATCACT	600
TTTTGGGGGC	GCTCCTCTAA	TGGGAATTTT	GTCGATCCCA	AAGAAAAAGG	CAAGCCCTTA	660
GCCCAAACTT	TAGGAAACCA	AATGCTGTTT	AACACTTATG	GGCGAACGGC	TGGGATGTTG	720
GGTAAATATA	TAGGCATTAG	CGCTCAAGGC	AATTGGATTA	ATGGGCAAGG	TTTCAGGCAA	780
AATAGCCCTA	CAAAGGTGCA	AAACTACTTG	TTGGATGCGA	TTTATAAGAT	CAATGCGACC	840
AATACTTTTA	AAGCTTATTA	CCAGTATTAT	CAATACAACT	CTTACCATCC	AGGCACTTTG	900
AGCGCGCAAG	ATTACGCCTA	TAACCGCTTC	ATCAATGAGC	GCCCTGACAA	TCAAGATGGA	960
GGGCGAGCCA	AGCGCTTTGG	GATCGTGTAT	CAAAACTACT	TTGGCGATCC	GGATAGGAAA	1020
GTGGGGGGCG	ATTTTAAATT	CACTTATTTT	ACGCATGACA	TGAGTAGGGA	TTTTGGGTTT	1080
TCCAACCAAT	ACCAAAGCGT	GTATATGAGC	GGTCAAAATA	AGATTTTACC	CTTTAAAGGC	1140
AAGGGAGAAA	TCAGCGCAAA	AAACCCTAAT	TGCGGTCTGT	ATTCTTATAG	CGACACGAAT	1200
AGCCCTTGCT	GGCAATTTTT	TGACAATATC	CGCCGATCCG	TGGTGAATGC	CTTTGAGCCA	1260
AAACTCAATC	TTATCGTCAA	TACTGGTAAA	GTCAAACAAA	CTTTTAACAT	GGGAATGCGC	1320
TTTTTAACTG	AAGATTTATA	CCGCCGATCC	ACCACCAGGA	AAAACCCTAG	CATGCCTAAT	1380
AATGGGAGTG	GTTTGTATGC	AGGAACCTCA	CTCAATAATT	TCAACAATTA	TACCGCTGTG	1440
TATGCCAGCG	ATGAAATCAA	TTTCAATAAC	GGCATGCTAA	CGATCACGCC	GGGCTTGAGA	1500

TACACTTTTT	TAAATTACGA	AAAAAAGAC	GCTCCTCCCT	TTAAGGTGGG	TCAAACCCCA	1560
AAAACCACGA	AAGAGCGTTA	TAACCAATGG	AATCCGGCAG	TCAATGTCGG	CTATAAACCC	1620
ATTAAAGAAT	TATTGTTTTA	TTTCAATTAC	CAAAGAAGCT	ACATTCCGCC	CCAATTCAGC	1680
AATATCGGTA	ATTTTGTAGG	CACAAGCACG	GATTATTTTC	AAATCTTTAA	TGTCATGGAA	1740
GGCGGCTCAA	GATATTATTT	TAACCATCAA	GTGAGTTTTA	ACGCGAACTA	TTTTGTGATT	1800
TTTGCGAATC	ATTATTTTAC	CGGGCGCTAT	GGGGACAACA	GAGAGCCGGT	CAATGCGAGA	1860
TCGCAAGGCG	TGGAGCTGGA	ACTCTACTAC	ACGCCTATTA	GGGGGCTTAA	TTTCCATGCG	1920
GCTTACACTT	TTATAGACGC	TAATATCACA	AGCCACACGA	TGGTTACTAA	CCCTGCTAAT	1980
CCTAAAGGGC	CTAAAAAAGA	TATTTTGGC	AAAAAGCTCC	CTTTTGTGAG	CCCGCACCAA	2040
TTCATTTTAG	ACGCGAGTTA	CACCTACGCT	AAAACCACGA	TTGGGTAAAG	CTCTTCTTTT	2100
TATAGCCGCG	CTTATAGCGA	TGTGTTAAAC	ACCGTGCCTT	TTACAGAATA	CGCGCCACG	2160
ATTAAAAATG	GGGCTATCGT	TACCAAAACA	GCGGGCATGA	CGCCGTAATA	TTGGGTGTGG	2220
AATTTGCAAA	TTTCTACCAC	TTGTGGGAA	CGCAAAATC	AAAGCGTGAA	TGCGAGCTTG	2280
CAAATCAATA	ACATTTTTAA	CATGAAATAT	TGGTTTAGCG	GGATAGGCAC	TAGCCCTAAC	2340
GGGAAAGAAG	CTGCGCCTCC	CAGGAGCATC	ACAGCGTATG	TGAGTTATAA	TTTTTAA	2397

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

ATGAGAAAGG	TTATCATAAT	GAATGGTTAT	TTGAGGGTAA	AAACCCCGTA	TTTTTTAGCG	60
TCGGTCTGTT	TGACTTTTTG	GACTTTTAAAT	TCTTTTATGA	GCGCGAAAGA	TAAGCACCAT	120
TTTTTAAAAA	AAGTTACAAC	CACCGAGCAA	AAATTCAGTT	CTAGTGCCCC	AATTTTCATGG	180
CAAAGCGAAG	AGGTGCGTAA	TTCCACAAGC	TCTCGCACGG	TGATTTCCAA	CAAAGAACTC	240
AAAAAAACGG	GGAATTTGAA	TATTGAAAAC	GCCTTGCAAA	ATGTGCCAGG	GATTCAAATC	300
AGAGACGCTA	CAGGCACGGG	CGTGCTGCCT	AAAATTTCCG	TGCGCGGTTT	TGGTGGGGGC	360
GGTAACGGGC	ATAGCAACAC	CAACATGATT	TTAGTCAATG	GTATCCCCAT	TTATGGCGCG	420
CCGTATTCCA	ATATTGAACT	GGCGATTTTC	CCTGTAACTT	TCCAGTCAGT	GGATAGGATT	480
GATGTGATTA	AGGGGGGAAC	GAGCGTCCAA	TACGGCCCTA	ACACTTTTGG	AGGCGTGGTG	540
AATGTCATCA	CTAAAGAAAT	CCCCAAAGAG	TGGGAAAATC	AAGCGGCTGA	AAGGATCACT	600
TTTTGGGGGC	GCTCCTCTAA	TGGGAATTTT	GTCGATCCCA	AAGAAAAAGG	CAAGCCCTTA	660
GCCCAAACCT	TAGGAAACCA	AATGCTGTTT	AACACTTATG	GCGGAACGGC	TGGGATGTTG	720
GGTAAATATA	TAGGCATTAG	CGCTCAAGGC	AATTGGATTA	ATGGGCAAGG	TTTCAGGCAA	780
AATAGCCCTA	CAAAGGTGCA	AACTACTTG	TTGGATGCGA	TTTATAAGAT	CAATGCGACC	840
AATACTTTTA	AAGCTTATTA	CCAGTATTAT	CAATACAAC	CTTACCATCC	AGGCACTTTG	900
AGCGCGCAAG	ATTACGCCTA	TAACCGCTTC	ATCAATGAGC	GCCCTGACAA	TCAAGATGGA	960
GGGCGAGCCA	AGCGCTTTGG	GATCGTGTAT	CAAACTACT	TTGGCGATCC	GGATAGGAAA	1020
GTGGGGGGCG	ATTTTAAATT	CACCTATTTC	ACGCATGACA	TGAGTAGGGA	TTTTGGGTTT	1080

TCCAACCAAT	ACCAAAGCGT	GTATATGAGC	GGTCAAAATA	AGATTTTACC	CTTTAAAGGC	1140
AAGGGAGAAA	TCAGCGCAAA	AAACCCTAAT	TGCGGTCTGT	ATTCTTATAG	CGACACGAAT	1200
AGCCCTTGCT	GGCAATTTT	TGACAATATC	CGCCGATCCG	TGGTGAATGC	CTTTGAGCCA	1260
AAACTCAATC	TTATCGTCAA	TACTGGTAAA	GTCAAACAAA	CTTTTAACAT	GGGAATGCGC	1320
TTTTTAACTG	AAGATTTATA	CCGCCGATCC	ACCACCAGGA	AAAACCCTAG	CATGCCTAAT	1380
AATGGGAGTG	GGTTTGATGC	AGGAACTTCA	CTCAATAATT	TCAACAATTA	TACCGCTGTG	1440
TATGCCAGCG	ATGAAATCAA	TTTCAATAAC	GGCATGCTAA	CGATCACGCC	GGGCTTGAGA	1500
TACACTTTTT	TAAATTACGA	AAAAAAAGAC	GCTCCTCCCT	TTAAGGTGGG	TCAAACCCCA	1560
AAAACCACGA	AAGAGCGTTA	TAACCAATGG	AATCCGGCAG	TCAATGTCGG	CTATAAACCC	1620
ATTAAAGAAT	TATTGTTTTA	TTTCAATTAC	CAAAGAAGCT	ACATTCCGCC	CCAATTCAGC	1680
AATATCGGTA	ATTTTGTAGG	CACAAGCACG	GATTATTTTC	AAATCTTTAA	TGTCATGGAA	1740
GGCGGCTCAA	GATATTATTT	TAACCATCAA	GTGAGTTTTA	ACGCGAACTA	TTTTGTGATT	1800
TTTGCGAATC	ATTATTTTAC	CGGGCGCTAT	GGGGACAACA	GAGAGCCGGT	CAATGCGAGA	1860
TCGCAAGGCG	TGGAGCTGGA	ACTCTACTAC	ACGCCTATTA	GGGGGCTTAA	TTTCCATGCG	1920
GCTTACACTT	TTATAGACGC	TAATATCACA	AGCCACACGA	TGGTTACTAA	CCCTGCTAAT	1980
CCTAAAGGGC	CTAAAAAAGA	TATTTTGGC	AAAAAGCTCC	CTTTTGTCAG	CCCGCACCAA	2040
TTCAATTTAG	ACGCGAGTTA	CACTTACGCT	AAAACCACGA	TTGGGTAAAG	CTCTTCTTTT	2100
TATAGCCGCG	CTTATAGCGA	TGTGTTAAAC	ACCGTGCCTT	TTACAGAATA	CGCGCCCACG	2160
ATTAAAAATG	GGGCTATCGT	TACCAAAACA	GCGGGCATGA	CGCCGTACTA	TTGGGTGTGG	2220
AATTTGCAAA	TTTCTACCAC	TTTGTGGGAA	CGCAAAAATC	AAAGCGTGAA	TGCGAGCTTG	2280
CAAATCAATA	ACATTTTTAA	CATGAAATAT	TGGTTTAGCG	GGATAGGCAC	TAGCCCTAAC	2340
GGGAAAGAAG	CTGCGCCTCC	CAGGAGCATC	ACAGCGTATG	TGAGTTATAA	TTTTTAA	2397

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

ATGAAAACAA	ACGGGCTTTT	TAAAATGTGG	GGGCTATTTT	TAGTTTAAAT	CGCTTTAGTC	60
TTTAACGCAT	GCTCTGATAG	CCATAAAGAA	AAGAAGGACG	CTTTAGAAGT	CATTAAACAA	120
AGGGGGGTTT	TAAAGGTGGG	GGTTTTTAGC	GATAAGCCTC	CTTTTGCTC	TGTGGATTCT	180
AAAGGGAAC	ATCAAGGCTA	TGATGTAGTC	ATCGCTAAAC	GCATGGCCCT	TGATTTATTG	240
GGCGATGAAA	ATAAGATTGA	GTTTATCCCT	GTAGAAGCCT	CAGCTAGGGT	GGAATTTTTA	300
AAAGCCAATA	AAGTGGATAT	TATCATGGCT	AATTTACGC	GCACTAAAGA	AAGAGAAAAA	360
GTCGTGGATT	TCGCTAATCC	GTATATGAAA	GTCGCTTTGG	GGGTGATTTT	TAAAGATGGG	420
GTCATTAAAA	ATATAGAAGA	GCTGAAAGAT	AAAGAGTTGA	TCGTGAATAA	AGGCACGACA	480
GCGGATTTTT	ATTTCACTAA	AAATTACCCC	AATATCAAAC	TTTTGAAATT	TGAACAAAAC	540
ACAGAGACTT	TTTLAGCCCT	TTTAAACAAT	AAGGCCATCG	CATTAGCCCA	TGATAACACT	600
TTGTTGCTCG	CTTGGGTGAA	ACAACACCCT	GAATTTAAAT	TAGGCATTAC	AAGCCTTGGC	660

GATAAGGATG	TGATCGCTCC	AGCGATTAAA	AAAGGCAACC	CTAAGCTTTT	AGAGTGGTTG	720
AATAACGAGA	TTGATTCCCT	CATTTCTAGC	GACTTTTTAA	AAGAAGCTTA	TCAAGAGACT	780
TTAGAGCCTA	TTTATGGCGA	TGGAATCAAA	CCGGAAGAAA	TTATTTTGA	ATGA	834

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

TTGGATAATT	TCATCTCACA	ATACGCGCAA	CGCTTGATCG	TAACCAATTT	GAGTCAAGCG	60
ATTCGCATTT	ATGGCTATGA	AGTGGGTGGG	ACTTTTAGAT	ACAAGGGCGT	GAGTTTGAAT	120
GTGGGGATCT	CGCGCACTTG	GCCCACCACT	AGGGGGTATT	TAATGGCGGA	CAGCTATGAG	180
CTTGCCGCAA	GCACCGGTAA	TGTTTTTATC	ATTAAATTGG	ATTACACCAT	TCCAAAAACA	240
GGGATCAATC	TTGCATGGCT	TAGCCGCTTT	GTTACCGGTT	TGGATTATTG	CGGGTTTGAT	300
ATTTACTTGC	CTGATTATGG	GACAGCTGAA	AAACCCAAA	CCCCTACCGA	TTTAGCCAAA	360
TGCGGATCCC	AATTGGGGTT	AGTGCAATG	CACAAACCGG	GCTATGGCGT	GAGTAATTTT	420
TATATCAATT	GGAGCCCTAA	AACCAAAAGC	CACTGGAAGG	GTTTGCTGCT	TTCAGCCGTG	480
TTTAATAATG	TTTTCAACAA	ATTCTATGTG	GATCAAACAA	GCCCCTATGT	CATGAGCCCG	540
GATATGCCAG	GCACTGACGC	TATTAAAAGA	GCGATCGCAG	AGCCTGGGTT	TAATGCGCGT	600
TTTGAAGTGG	CTTACAAATG	G TAG				624

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

ATGAAAAAAG	CGGGTTTTCT	TTTTTTGGCG	GCGATGGCTA	TCATTGTTGT	GAGTTTAAAC	60
GCCAAAGATC	CGAATGTGTT	GCGTAAGATT	GTTTTTGAGA	AATGTTTGCC	TAATTATGAG	120
AAAAATCAAA	ATCCTTCACC	ATGCATAGAA	GTCAAACCCG	ACGCCGGCTA	TGTGGTTTTA	180
AAAGATATTA	ACGGTCCGTT	GCAATATTTG	TTGATGCCAA	CGACTCACAT	TAGTGGCATT	240
GAAAACCCTT	TGTTGCTTGA	TCCTTCTACG	CCTAACTTTT	TTTACTTGTC	ATGGCAAGCG	300
CGCGATTTTA	TGAGTAAAAA	ATACGGAAAA	CCCATTCCCTG	ATTATGCGAT	CTCTTTGACG	360
ATCAATTCTA	AAAAAGGGCG	ATCGCAAAAC	CATTTTCACA	TCCATATTTT	TTGCATTAGC	420
CTTGATGTGC	GCAAACAGCT	GGATAATAAT	CTAAAAAATA	TCAACAGCCG	TTGGTCGCCA	480
TTATCAGGTG	GCTTGAACGG	GCATAAATAT	TTGGCGCGTC	GGGTAACAGA	GAGCGAATTA	540
GCGCAAAAAA	GCCCGTTTTGT	CATGCTTGCT	AAAGAAGTGC	CTAACGCGCA	CAAACGCATG	600
GGAGACTATG	GCTTGGCGGT	GGTGCAACAG	AGCGATAACT	CCTTTGTCTT	GTTAGCGACA	660
CAATTTAACC	CATTGACTTT	AAATCGCGCT	TCAGCCGAAG	AGATTCAAGA	TCATGAATGC	720
GCGATTTTGC	GTAA					735

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 687 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

ATGGTATTTG	ACAGAACAAAC	AAGCGTAAGA	GAAAAAAAG	CGGCTAAGGC	GCTTGGGATT	60
GTGGGGATCG	TCTTTTTTAT	TTTGTGTTGC	ATCGTGATAA	GCGGGGTGGC	TTCTCAAAAA	120
GAGTGGGTGC	AACAATTGGA	TTTATTTTTT	ATAGACTTGA	TCCGCAACCC	TGCCCCCAT	180
CAAGGGAGCA	CGTGGCTTTC	TTTCGTGTTT	TTTAGCACTT	GGTTTGCGCA	AAGCAAGCTC	240
ACCACTCCTA	TAGCCTTACT	CATTGGCTTG	TGGTTTGGGT	TTCAAAAACG	CATCGCTTTG	300
GGGGTGTGGT	TTTTCTTTAG	CATCTTATTA	GGTGAATTCA	CCTTAAAATC	CCTTAAGCTT	360
TTAGTGGCGC	GCCCACGGCC	TGTAACCAAT	GGCGAATTGG	TTTTTGCGCA	TGGCTTTAGT	420
TTCCCTAGCG	GGCATGCTTT	AGCTTCAGCG	CTTTTTTACG	GCTCTTTGGC	GTTGTTGTTA	480
TGCTATTCTA	ACGCAAACAA	TCGCATTAAA	ACTATTGGTG	CTATTATTTT	ACTTTTTTGG	540
ATTTTTTTTAA	TGGCGTATGA	TAGGGTTTAT	TTAGGGGTGC	ATTACCCTAG	CGATGTTTTA	600
GGAGGGTTTT	TATTAGGGAT	TGCTTGCTCG	TGCTGCTCTT	TAGCGCTTTA	TTTGGGGTTT	660
TTGAAACGCC	CTTATAAAGC	CGCTTAA				687

(2) INFORMATION FOR SEQ ID NO:418:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...474
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

ATGAAAAAAT TTGGTTTAGG GGTGTATTTG CTTCTTTTAG GTATTTTGGG CGGCTCTTTG	60
ATCATTCTAG GAGCGATAGT CGCGCCCAT TTTTCAAAG CTTCAAGCAT TTTACCTGAA	120
TTGAATCTGA CTCCCTTTGA GAGTGGGAAA CTCATGGCGC AAATCTTTGT GCGTTTCAAT	180
TATGTTTTAG GCGCGATCGG TTTTGTGGTG TTA CTTTATG AAATCATTTC GTTTATCTAC	240
TATAAAAGAT CGTTAGTGTA TTTGATCCTT GGCGTGCGGA TAGGGGCGTT GTGTTTGCTC	300
TTTGTTTTTT ATTACACGCC TTATATTTTA AACGCTCAA AGGTGGGTGA AGTTGCGCTT	360
CAAAGTGCTG AATTTGCCCG CTCGCACGCT CAAAGCGAAT GGCTGTTTAA GGAATTGTTT	420
GTGCTGGTGT GTGCTTTGTT TTTTGGCGT TTGTTTGGGA AAAATGCGCT TTAG	474

(2) INFORMATION FOR SEQ ID NO:419:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...333
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

TTGATCAATT TATTGCCCCA CCATTACCAT AAATTCCCCC CCAATATCAA CCCCTCTCTC	60
ATCTCTCTAA AAGATCGCTT TTTACCCCAT GAAAAGCACA GCCAAAAGGT CAAAAAGAA	120
TGCGTCAACT TGTTTGAAGT TTTATCGCCT TTGCATAAAA TAGATGAAAA ATACCTTTTC	180
CATTTAAAGA TTGCGGGGGA ATTGGCGAGC ATGGGTAAGA TTTTAAGTGT ATATTTAGCC	240

CACAAGCACA GCGCGTATTT CATTTTAAAC GCTTTGAGTT ACGGCTTTAG CCACCAGGAT 300
AGGGCGATCA TTTGCTTATT GGGCGCAATT TAG 333

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

ATGAAATCTT TTTTAAACT TTTTGCACAG CCTTTGTTGG TGGTTTTAGC GTTCATGTTG	60
TTGTATGCTT TAGCGCATGC TGTGCTTGGT TTTTACGTGA AAAAAGACAG CGCTCCAATG	120
AGTCCAAATG TAGAAAAAAG CGAGACAGAG CGCCAAAACA GCACGTTTTC GCCTAAAGAA	180
GAAGCCAACG CAACCACAAC CGCCACAGAA CAAAACCCCA CCAAAGACAC AGTGCCACCT	240
TTAGACACAG CCACACAAAA ACAAGAGATT AAACAAGAGA TTAAACAAGA GATTAAACAA	300
GAGATTAAAC AAGAGATTAA ACAAGAGATT AAACAAGAGA TTAAACAAGA AACTAAACAA	360
GAGCAAGAAA AAGAAAATAA GCCTAAACAA AACAGTGTCT CGCCCGTTCA AAACGATCAA	420
AAAACCCCCA CAACCCCTT AATGGGAAAA AAACCTCTAG AGTATAAAGT CGCAGTCAGT	480
GGCGTGAACG TGCGCGCTTT TCCTAGCACA AAAGGCAAAA TCATTGGCTC GCTTATAAAA	540
AATAAAGCG TGAAGGTTTT AGAAATCCAA AACGATTGGG CTGAAATTGA ATTTCTCAC	600
GAAACAAAGG GATATGTGTT TTTAAACTT TTAATAAAGG CTGAATGA	648

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

ATGTGGCCTG	TGGCTCTCAA	GCAGCCTAAT	AGGGTGTCCC	ATCATTTTTA	TATCATGGCC	60
ATGCTTTTTA	TTTTATTTGA	TGTAGAAATC	GTTTTCATGT	TCCCTTGGGC	GATTGATTTT	120
AAAAAGTTAG	GCTTGTGG	GCTCGTTGAA	ATGCTAGGCT	TTGTCTTCTT	TTTGGCAATC	180
GGTTTTATTT	ACGCTTTAAA	GCGAAACGCT	TTGAGCTGGC	AAAAATTAGA	GGTGAAATAA	240

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

ATGTGTGGGA	TGTTTAAGAA	TGAAATCAGC	GCTATCCAAG	GCATGATCGC	TAACGCGCAA	60
GAAGCTGTCG	CGCAAGCCAA	AATCGTTAGT	GAAAACACGC	AAAATCAAAA	CAGCCTAGAC	120
GCTGGAAAAC	CATTCAACCC	CTACACAGAC	GCTAGTTTTG	CTGAAAGCAT	GCTCAAAAAC	180
GCGCAAGCCC	AAGCGGAGAT	TTTAAACCAA	GCCGAACAAG	TGGTGAAAAA	CTTTGAAAAA	240
ATCCCTACAG	CCTTTGTAAA	TGACTCTTTA	GGGGTGTGTT	ATGAAGTGCA	AGGAGGTGAG	300
CGTCGTGGCA	CCAATCCGGG	TCAGACGACT	TCTAACACTT	GGGGGGCAGG	CTGTGCGTAT	360
GTAGGACAAA	CGATAACAAA	TCTTAAAAAC	AGCATCGCCC	ATTTTGGCAC	TCAAGAGCAG	420
CAGATACAGC	AAGCCGAAAA	CATCGCTGAC	ACTCTGGTGA	ATTTCAAATC	TAGATACAGC	480
GAATTGGGCA	ACACTTATAA	CAGCATCACC	ACTGCGCTCT	CTAATATCCC	TAACGCGCAA	540
AGCTTGCAAA	ATGCGGTGAG	TAAAAAGAAT	AACCCCTATA	GCCCGCAAGG	CATAGACACC	600
AATTACTACC	TCAATCAAAA	CTCTTACAAC	CAAATCCAAA	CCATCAACCA	AGAACTCGGG	660
CGTAACCCCT	TTAGGAAAGT	GGGGATTGTT	AGTTCTCAAA	CCAATAATGG	CGCGATGAAT	720
GGGATCGGTA	TTCAGGTGGG	TTACAAACAA	TTCTTTGGCC	AAAAAAGAAA	ATGGGGCGCT	780
AGGTATTACG	GCTTTTTTGA	TTACAACCAT	GCGTTCATTA	AATCCAGCTT	CTTCAACTCG	840
GCTTCTGACG	TGTGGACTTA	TGGCTTTGGA	GCGGACGCTC	TTTATAATTT	CATCAACGAT	900
AAAGCCACCA	ATTTCTTAGG	CAAAAACAAC	AAGCTTTCTG	TGGGGCTTTT	TGGGGGTATT	960
GCATTAGCCG	GGACTTCATG	GCTTAATTCT	GAGTATGTGA	ATTTAGCCAC	CATGAATAAC	1020
GTCTATAACG	CTAAAATGAA	CGTGGCGAAT	TTCCAATTCT	TATTCAACAT	GGGAGTGAGG	1080
ATGAATTTAG	CCAGGCCTAA	GAAAAAAGAC	AGCGATCATG	CGGCTCAGCA	TGGGATTGAG	1140
TTAGGGCTTA	AAATCCCCAC	CATCAACACG	AACTACTACT	CCTTTATGGG	GGCTGAACTC	1200
AAATACCGAA	GGCTCTATAG	CGTGTATTTG	AATTACGTGT	TCGCTTACTA	A	1251

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

397

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

ATGGCAACCA TTCAACCATT CAACCATTCA ACCATTCAAC CATTCAACCA TTCAACCATT	60
CAACCATTCA ATCATTCAAT CATTCAATCA TTCAATCATT CAACCATTCA AGCAACGCTA	120
CCTTATTTTT ATAACATTTT ATCTTTTTAC AAAAACCTAT TTAAAAATCC CCTATTTTTT	180
ATTATTCCCC CTTTTATTAA CCCTTTTATT AACCCTTTTA TTAACCCTTT TATTAACCCT	240
TTTATTAACC CTTTTATTAA CCCTTTTATT AACCCTTTTA TTAACCCTTT TATTAACCCT	300
TTTATTAACC CTTTTATTAA CCCTTTTATT AACCCTTTCA TATAA	345

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

TTGGTTTCAG AATACTGGTT AAAATTCTTC ACGCGCTCTT TTTCTAAATC AACCATGCTC	60
TTTAAACCCC TCTTGCGGTC TTTTTTCACA TTCCCTGTGG AGCTTTCAGA AAACATAACA	120
TTGGGATCAA CTGTAGTGTT AATAGTAGCA GAAGCCGTTT CTGCTCTCAA CAAAAAAGTC	180
GTAGCCGCTA AAAAAAATAA AATTCGCTTC ACACCAAACCT CCTATATCCA TAACCGCAAC	240
AAAAACAGAC GCTATTCTTC ATTAAGCCCT CTTTAAAT CTTCTTCTAT TTATAAAAC	300
CCACCTAGAA TTCAAGCTAT TTTGATTATC TTAAATACA GACTTTCAA GGGTATTTAT	360
CATTTGGGTA TGATACTATA A	381

(2) INFORMATION FOR SEQ ID NO:425:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 861 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...861
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

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ATGAAGAAAT CTGTTATAGT AGGTGCTATC TCTCTAGCAA TGACAAGCTT ATTGTCAGCA      60
GAGACCCCTA AGCAAGAAAA GGCTATTAAG ACTAGCCCTA CCAAAAAAGG TGAAAGAAAT      120
GCTGCTTTTA TAGGGATTGA TTACCAGTTG GGTATGCTCA GCACTACCGC TCAAAATTGT      180
TCCCATGGGA ATTGCAATGG TAATCAAAGT GGGGCTTACG GCTCTAATAC GCCTAACATG      240
CCTACAGCGT CAAACCCAAC AGGAGGCCTT ACTCATGGCG CTCTAGGGAC TCGTGGGTAT      300
AAAGGCTTAA GCAACCAACA ATACGCTATC AATGGTTTTG GGTGTGTTGT AGGGTATAAG      360
CATTTTTTTA AGAAAGCCCC ACAATTTGGA ATGCGTTATT ACGGATTCTT TGATTTTGCA      420
AGCTCTTATT ATAAGTACTA CACTTATAAT GATTATGGCA TGAGAGACGC TCGCAAGGGT      480
TCTCAAAGTT TCATGTTTGG CTATGGGGCT GGCACAGATG TGTTGTTTAA CCCAGCTATT      540
TTCAATCGTG AGAACTTGCA TTTGGGGTTT TTCTTGGGCG TTGCGATTGG TGGCACCTCT      600
TGGGGTCCAA CAAACTATTA TTTTAAGGAC TTAGCTGAAG AGTATAGAGG GAGTTTCCAC      660
CCATCAAATT TCCAGGTCTT AGTTAATGGC GGGATCCGCT TAGGCACTAA ACACCAAGGT      720
TTTGAAATTG GCTTGAAAAT CCAAACCATT CGCAATAATT ACTATACCGC TAGCGCGGAT      780
AATGTGCCTG AAGGGACTAC TTATAGATTC ACTTTCACC GCCCTTACGC CTTTTATTGG      840
CGTTACATTG TAAGCTTTTA A                                     861

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(2) INFORMATION FOR SEQ ID NO:426:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 858 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

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GTGAAGCGAA TTTTATTTTT TTTAGCGGCT ACGACTTTTT TGTTGAGAGC AGAAACGGCT      60
TCTGCTACTA TTAACACTAC AGTTGATCCC AATGTTATGT TTTCTGAAAG CTCCACAGGG      120
AATGTGAAAA AAGACCGCAA GAGGGTTTTA AAGAGCATGG TTGATTTAGA AAAAGAGCGC      180
GTGAAGAATT TTAACCAGTA TTCTGAAACC AAGATGAGTA AGGGCGATTT ATCCGCTTTT      240
GGAGCTTTCT TTAAGGGGAG TTTGGAAGAT TCGGTGGAGC AAAAGATTTG TTAATATGAG      300
CATAGGAATG GCAAGGTTTC TTTTGTGGTG AATGACAGAG AAAAGTTTTA TAAGCATGTG      360
CTTAAAGACT TAGGGACAGA GCTTTCACCT CCCTTGTTCA ACTGGCTTTA CAAAGGCTCA      420
GATTTTGGGG CTTTGCATGA GCAGTTTGGG GACATGTATG ATGGGTATAT CAAATACTTG      480
ATCAGCATGG TTAGGGTGAG CCAAAAAGAA AAGGCTAGAA AAGTGGATGC AATCGTTCTT      540
AAAAAATGG AAGAACAAGC TGAGAAAGAC ACTAAGGCAG CATTCCAAAA GAGGAGCAGT      600
GGGGAGCTTG AAAGCCATAC TGATAGCCCT GAATTTATAA GCTCTTCTAA GACACAGAAT      660
TCTTCTAACC CAGATCTAGA CCCTATGACT AACGCTAACA CGCTCAAAGA AACAGCTTCA      720
AAAGAGCCAG AGACTTCTTC AAAAAAGGAA AAAAAGCCCA AGAAAAACG ACGCCTTTCA      780
AAGAAAGAAA AGCAACAACA GGCCTTACAA CAAGAGTTTG AAAAGCAAAT TAGCGACTCT      840
AGTAAGTCTG AAAAATAG                                     858

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(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

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ATGCCAAAAG AAAACACCAC CCACGAAGAC GCTTTAGCGA AATGCTTTGC GCCTGCAATT      60
TTTAAAGCCA TCATGCTGAA TAAATTGATA TTGGCGGTTG TGGCTGCTCC CATTATAAAG      120
ATGCTTAAAT TGAGTAAAGA GATTTGGTGG AAAAAAATGG GCAAAAAACA TGCGATAGAT      180
TTTAAATGA GGATAAAGAT ATTGGCTTCT TTAGCCCCTA GCTTTTGA                228

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(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

400

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...405
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

ATGTGCCAAA	TCCAATGCTT	GCTTATTTTG	CTTCTATCA	ATATAGTTAG	CGCGATTATC	60
GTTTATTTT	TCCAAGCATT	TCAAGGGGTT	TTGAATTTTG	AAGGGGGGTT	TTAGGGTTT	120
TTTATCGTGG	CGTTGTCTTC	GTATTACGGC	GTTAAAAAGC	GTTTGGATTT	GAGGAAACAA	180
GATTCAAAAG	AAAAAGAAGA	AAAGCAAAA	TTCCAAAAT	TCGCCCTAGG	TTTGAAATG	240
TCTTTCAATG	TGTGGCGTTT	AGGGGGGTAT	GGGGTTTTAT	TAGGTATTTT	AGGAGTGCTT	300
TTATTCTTGC	ATCTTTTAA	CGGATTGCCG	TTTCTTATCG	GCGTGTTTGT	GAGCTCGCTC	360
TCTAGCGCGT	TATTACGATT	CTTAAACAAT	AATGGTAAGT	TTTGA		405

(2) INFORMATION FOR SEQ ID NO:429:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...279
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

ATGGCGTGTG	AATTTTTGAA	AAAGCCAAAG	TATTACAAGT	TTATAGAGGG	GGCGAATTAT	60
TTGAGCTTAG	GGCTTTCTAT	GGTGGTGGCG	ATCCTTATGG	GCGTGGCTAT	AGGCTATGGG	120
CTTAAAAAAC	TCACTCACAT	TTCGTGGCTT	TTTGGGCTTG	GGGTATTATTG	GGGCGTGTTA	180
GCGAGCTTTC	TCAATGTCTA	TAAGGCTTAT	AAAAACATGC	AAAAAGACTA	TGAAGAACTA	240
GCCAAAGACC	CTAAATACAC	GCAAAATAAA	ACAAAATAA			279

(2) INFORMATION FOR SEQ ID NO:430:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs

401

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

ATGGAAGACT TTTTGTATAA CACCTTATAT TTCATAGAGG ATTATAAGTT GGTGTTATT	60
TTAGTTTCA TAGGGTTAAT AGCGTTATTT TCCTCTACA AATTCATAAA AACTCAAAAA	120
AAGGTTTTTA AAGATAAAGC TAACCAGCCT CAAAAGAAAA AAAGCTTTAA AGAAATCATT	180
ATAGATGGGC TGAAAGAAAG GGTAAAACC TTTGGCTTTA GGTGCAAGC TATACTATTA	240

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

ATGGCCATTG ATTTAGCAGA AGTTACAGGA GCTAAAGCCG CGCAAGAAAG GAAAAAGAA	60
CAGCCCACCA TCGCTAACGG GTTGGATAAA AACGCTTTCA TGAAACTCTT TTAGAGCAA	120
TTGAAAAATC AAGACCCAC CGCTCCTATG GAAACGGATA AAATCATCAC CCAACCGCG	180
CAACTCACGC AAGTGGAAT GCAAGAAGAA AACAAAAAGA CCATGCAAGA AGTCGCCAGT	240
GCGATGAAAT CCAATAAAGA AACTAACGAA TCTTTAAAAG ACTTTCAAGG CGCTTTAAAA	300
GACACCATGG AAAACCTGAA CAAAGGCATG GACGATAGCT TAAAGGCTAA CAACGCTTTA	360
AGGGAAGTAA GCGCCCTTAA TTCTGTGAGC ATGATAGGCA AAATCGCTGA AACCGATGTG	420
AGTGGGGCGA ATTTTGACGG CAACAACAAG CTTTCTTTT CGCTCTTTT TGATGAAAAA	480
ATTGACGCTT CTAAGGAGT GCCAGCGATT CAAATCTTAA ACGAAAACAA TGAATTGGTC	540
AAAACGATTC CTTTAAAGA TTATAACGGG CAAAAGGGT ATATCAATTT TGAATGGGAC	600

GGCACAAACG	AAAAGGGCGA	AAAAGTCCCT	AAAGGCAATT	ACAAAATCAA	GGCTGAATAC	660
AATTTAGACT	CTCAAAGCAA	GCAGTATTTG	CAAACGCGCA	TTGGTAGGGG	CGAAGTGGAA	720
AGCGTGATTT	TTGATAAAGG	CAAACCCATG	TTAAGAATGG	GCGAAATGAT	TTTACCCATA	780
GACAGCGCGA	TAGAGTTTTA	CAAACCGGAT	CAAAAACCGC	TTGATCAAAA	ACTCTCGGAT	840
CAAAAACCTC	AAAAACTCTC	TGAACAAAAA	GCCCTTGAAC	AGAAAATCTC	TGAACAAAAA	900
CCGCAAGAAC	CCCTTGATCA	AAAACCTCTG	GATCAAAAAC	CACAGAAACC	GCTTGAACAG	960
AAAATCTCTG	AACAGAAACC	GCTAGATCAA	AAACTCTCGG	ATCAAAAACC	ACAGAAACCG	1020
CTTGAACAGA	AAATCTCTGA	ACAGAAACCG	CTAGATCAAA	AACCCCAAAC	CCCCCCTAAA	1080
GAGACAGCAT	GA					1092

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

TTGAAACATT	TAGCCCCACT	CATTCATATC	CCTTTTAAAG	CCTTATGGCT	AGGCACAGCC	60
TTAAGCATGT	TCTTAAGTTT	GAATTTGAAC	GCTGAAGAAA	ACCCTACTAA	AACAGAGCCT	120
AAGCCCGCTA	AAGGGGTAA	AAACAAGCCC	AAATCGCCTG	TTACTAATGT	CATGATGACC	180
AATTGCGATA	ACCTTAAAGA	CTTTAACGCT	AAGCAAAAAG	AAGTTTTAAA	AGCCGCTTAT	240
CAATTCGGAT	CTAAAGAAAA	TTTAGGCTAT	GAAATGGCGG	GCATTGCGTG	GAAAGAATCA	300
TGCGCAGGGA	CTTATAAAAT	CAATTTTTCG	AATCCGAGTG	CGGGCATTTA	CCATGCGTAT	360
ATCCCTAGCG	TTTTAAAAAG	CTATGGGCAT	AATAATAGCC	CCTTTTTCG	TAACGTGATG	420
GGGGAATTGC	TCATTAAAGA	CGATGCGTTT	GCTTCTGAAG	TGGCCCTAAA	AGAATTGCTA	480
TATTGGAAAA	CGCGCTACCA	TGACAACCTA	AAAGACATGA	TCAAGTCTTA	CAATAAGGGC	540
AGTCGTGGG	AAAAAACGA	GAAAGCTAAC	GCTGATGCTG	AAAAATATTA	TGAAGAGATA	600
CAAGATAGAA	TCAGGCGTTT	GAAAGAATCT	AAAATCTTTG	AATCGCAGT	CTAG	654

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

ATGCAATTTT	AAAAAACCTT	ACTTTCTTTA	TCTTTATTAT	TTTTATCTTA	TTGTATCGCT	60
GAAGAAAATG	GGGCGTATGC	GAGCGTGGGT	TTTGAATATT	CCATCAGTCA	TGCCGTTGAA	120
CACAATAACC	CTTTTTTTGAA	TCAAGAACGC	ATCCAAACGA	TTTCTAACGC	TCAAAACAAA	180
ATCTATAAAC	TCAATCAAGT	CAAAAATGAA	ATCACAAACA	TGCCCAACAC	CTTTAACTAC	240
ATCAACAACG	CTTTAAAAAA	CAATGCTAAA	TTAACCCTTA	CTGAAAAGCA	AGCCGAAACC	300
TACTACCTGC	AATCTACCCT	TCAAAACATT	GAAAAAATAG	TCATGCTTAG	CGGGGGCGTT	360
GCGTCTAACC	CTAAATTAGC	CCAAGCGTTA	GAAAAAATGC	AAGAACCCAT	TACTAACCTT	420
TTAGAATTGG	TAGAAAACCT	AAAAAATTTA	GAATTACAAT	TCAGCCAATC	TCAAAACAGC	480
ATGCTTTCTT	CTTTGTCTTC	TCAGATCGCT	CAAATTTCAA	ATTCTTTGAA	CGCGCTTGAT	540
CCCAGCTCTT	ATTCTAAAAA	CGTTTCAAGC	ATGTATGGGG	TAGGTTTGAG	CGTAGGGTAT	600
AAGCATTTCT	TTACCAAGAA	AAAAAATCAA	GGGTTTCGTT	ATTACTTATT	CTATGACTAT	660
GGTTACACTA	ATTTTGGTTT	TGTGGGTAAT	GGCTTTGATG	GTTTAGGCAA	AATGAATAAC	720
CACCTCTATG	GGCTTGGCAT	AGATTATCTT	TTCAATTTCA	TTGATAATGC	GCAAAAACAT	780
TCGAGCGTGG	GGTTTTATGT	AGGCTTTGCT	TTAGCGGGGA	GTTTCGTGGT	AGGGAGTGGT	840
TTAGGCATGT	GGGTGAGTCA	AATGGATTTC	ATCAACAAC	ATTTGACGGA	TTATCGGGCT	900
AAAATGCACA	CGAGTTTTTT	CCAAATCCCT	TTGAATTTTG	GGGTTCGTGT	GAATGTGGAT	960
AGGCACAATG	GCTTTGAAAT	GGGCTTAAAG	ATCCCTTTAG	CGGTCAATTC	CTTTTATGAA	1020
ACGCATGGCA	AAGGGTTAAA	CGCTTCCCTC	TTTTTCAAAC	GCCTTGTCAT	GTTTAACGTG	1080
AGTTATGTTT	ATAGTTTTTA	G				1101

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1101 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

ATGCAATTTT	AAAAAACCTT	ACTTTCTTTA	TCTTTATTAT	TTTTATCTTA	TTGTATCGCT	60
GAAGAAAATG	GGGCGTATGC	GAGCGTGGGT	TTTGAATATT	CCATCAGTCA	TGCCGTTGAA	120
CACAATAACC	CTTTTTTTGAA	TCAAGAACGC	ATCCAAACGA	TTTCTAACGC	TCAAAACAAA	180

ATCTATAAAC	TCAATCAAGT	CAAAAATGAA	ATCACAAACA	TGCCCAACAC	CTTTAACTAC	240
ATCAACAACG	CTTTAAAAAA	CAATGCTAAA	TTAACCCCTA	CTGAAAAGCA	AGCCGAAACC	300
TACTACCTGC	AATCTACCCT	TCAAAACATT	GAAAAAATAG	TCATGCTTAG	CGGGGGCGTT	360
GCGTCTAACC	CTAAATTAGC	CCAAGCGTTA	GAAAAAATGC	AAGAACCCAT	TACTAACCCT	420
TTAGAATTGG	TAGAAAACCT	AAAAAATTTA	GAATTACAAT	TCAGCCAATC	TCAAAACAGC	480
ATGCTTTCTT	CTTTGTCTTC	TCAGATCGCT	CAAATTTCAA	ATTCTTTGAA	CGCGCTTGAT	540
CCCAGCTCTT	ATTCTAAAAA	CGTTTCAAGC	ATGTATGGGG	TAGGTTTGAG	CGTAGGGTAT	600
AAGCATTTCT	TTACCAAGAA	AAAAAATCAA	GGGTTTCGTT	ATTACTTATT	CTATGACTAT	660
GGTTACACTA	ATTTTGGTPT	TGTGGGTAAT	GGCTTTGATG	GTTTAGGCAA	AATGAATAAC	720
CACCTCTATG	GGCTTGGCAT	AGATTATCTT	TTCAATTTCA	TTGATAATGC	GCAAAAACAT	780
TCGAGCGTGG	GGTTTTATGT	AGGCTTTGCT	TTAGCGGGGA	GTTTCGTGGT	AGGGAGTGGT	840
TTAGGCATGT	GGGTGAGTCA	AATGGATTTC	ATCAACAAC	ATTTGACGGA	TTATCGGGCT	900
AAAATGCACA	CGAGTTTTTT	CCAAATCCCT	TTGAATTTTG	GGGTTTCGTG	GAATGTGGAT	960
AGGCACAATG	GCTTTGAAAT	GGGCTTAAAG	ATCCCTTTAG	CGGTCAATTC	CTTTTATGAA	1020
ACGCATGGCA	AAGGGTTAAA	CGCTTCCCTC	TTTTTCAAAC	GCCTTGTCAT	GTTTAACGTG	1080
AGTTATGTTT	ATAGTTTTTA	G				1101

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

TTGAATACAA	TGAATAGCGT	GTTAGAATGT	AAAGAATTAG	CGCTCTATGG	AGGGAGTTTT	60
GATCCTTTGC	ACAAGGCTCA	TTTAGCCATT	ATTGAGCAAA	CTTTAGAATT	ATTGCCATTC	120
G TTCAGCTGA	TTGTCTTGCC	CGCTTATCAA	AACCCTTTCA	AAAAGCCATG	TTTTTTGGAC	180
GCAAAAACCC	GTTTTAAGGA	ATTAGAAAGA	GCTTTAAAGG	GAATGCCTAG	GGTGCTGTTG	240
AGCGATTTTG	AAATCAAGCA	AGAAAGGGCT	GTGCCTACGA	TAGAAAGCGT	TCTTCATTTT	300
CAAAAACCTCT	ACCGCCCTAA	AACGCTTTAT	TTAGTCATAG	GAGCGGATTG	TTTGAGGCAT	360
CTTTCTTCTT	GGACTAACGC	TAAAGAGCTT	TTAAAAAGGG	TGGAATTAGT	GGTTTTTGAA	420
AGGATTGGCT	ATGAAGAAAT	TCAATTTAAG	GGGCGTTATC	ACCCTTTAAA	AGGCATTGAC	480
GCGCCGATTT	CTTCTAGCGC	GATTAGGGCT	AGTTTAGGGG	TTTAA		525

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1131
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

ATGAGATTTT	TTTGCTTCTT	TTTATTTTTT	CTAACCTTTT	CAAACGCGCA	GATAATGATG	60
ACTTTTGATT	CCCAAATAA	CGCCAACTT	TCGCGCTCCA	ACGAACAGCT	TTCTGACATG	120
CTTTACAAAC	TCAATGAAAG	TTTAAGAATC	TATCAAAACG	TGCTTTCTAA	CAACCAGGAT	180
CAACTTAAAG	AAATCAAAAA	GGCTAACAGC	ACCCTAACTA	GCCAAAGGCG	TTTTTTTAAC	240
GCTAGCCAGA	TCCGCCTTAT	GGACACTGAT	GCACTATTGA	AACAAAGCGC	TTTGGAATTA	300
GAAAAATTAC	AAGCTTTAGA	AAAACACTTA	AAAGAGAGCA	TGGAGCATGA	ACGCTTAATC	360
AAAGAATCCC	AAGCGCTTTT	TTTGCAAGAG	CATTGCCCTT	ATTTGAGCGG	CGTTAAGAAT	420
TTAGAAGAGG	CATCAAACGC	TTTAGAAGTC	CAAGAAAAAA	ATAACGCCCT	TTTCTTACTC	480
AAAGAGCCTA	AACTCTTTCA	TTTGCTCTCA	CGATTGGATT	TGATGAGCGC	TTTAAACGCC	540
TTATGCGATC	AGGTTTTAGA	AAATGAAATA	CAGGATCAAC	AATCCCATAA	CAAAACCCTA	600
GAATACAACG	CCCTTATGAA	CCATGATTTT	CAAGCCTATA	AAGCCATGCG	TTTGAAAAAA	660
ATTAAAAACA	AGCTTCAAAG	CCAAATCCAA	GCTAAAGAAG	ACGCCCTAAA	AACCTTTTTA	720
CCCCTAGAAA	AACGCCTAGA	AACTTTAAAA	TCGCGCTTTT	TATGCGACAA	AGAAAAATCTC	780
AAATCATGCG	CTAACCAATT	ACAGCAACGC	TACCAAAACG	CCCTAATAGA	GCGAGATAAG	840
GAATTAAAAA	ACGCTAAAAA	CAACAAAGAA	AAGCATGCTC	TAATCTTAGC	CAATTACGAA	900
CACACTTTAA	AAACCTTGAA	TATAGAATTT	TTAAGCGAAT	TGAGTGAGCA	AATGGCGTTT	960
TTGAATGAGA	CCATGGCGTT	AAACGCCCAA	GTTTTAGCCC	TTTLAGCCCA	ACAACAGACT	1020
AAAAAGCCCT	TCAATGTGAG	CGATGGTTTG	AGCGGTGGGA	AAGCCCTTAT	TAAAAATATC	1080
CGCTTAGATC	CGCATGGATT	CCCTAGCTTT	AAAAATTTTA	AGCAAGAGTG	A	1131

(2) INFORMATION FOR SEQ ID NO:437:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 690 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

GTGAAAGGCG	AGAAAAACGC	TTGGTATCTG	GGGATTAGCT	ATCAAGTCGG	TCAGGCTTCA	60
CAAAGCGTTA	AAAACCCCC	CAAAGCAGT	GAATTTAACT	ATCCTAAGTT	CCCTGTGGGT	120
AAAACCGACT	ATCTGGCCGT	TATGCAAGGC	TTAGGGCTTA	CTGTGGGTTA	TAAGCAGTTT	180
TCGGGGGAGA	AAAGATGGTT	TGGTGCGCGC	TATTACGGCT	TTATGGATTA	TGGGCATGCC	240
GTGTTTGGAG	CGAACGCTTT	GACATCAGAT	AATGGTGGGG	TGTGCAAAC	CAATGAGCCA	300
TGCGCGACCA	AAGTAGGGAC	TATGGGCAAT	CTGTCTGACA	TGTTCACTTA	TGGTGTGGGT	360
ATTGACACTT	TATACAATGT	CATTAATAAG	GAAGACGCGA	GTTTTGGTTT	CTTTTTTGGG	420
GCTCAAATCG	CGGGTAACTC	TTGGGGTAAT	ACGACAGGGG	CCTTTTTTGA	AACTAAAAGC	480
CCTTATAAGC	ACACCTCCTA	TAGCCTTGAT	CCGGCGATTT	TCCAGTTCCT	TTTTAATTTA	540
GGGATTCGCA	CCCATATTGG	TCAGCATCAA	GAATTTGACT	TTGGCGTGAA	GATTCCTACT	600
ATCAATGTTT	ATTATTTTAA	CCATGGGAAC	TTGAGCTTCA	CTTACCGCCG	TCAATACAGC	660
CTTTATGTAG	GGTATCGTTA	CAATTTCTGA				690

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

TTGAAAAACC	ACTCCTTTAA	AAAAACGATC	GCTCTTTCCT	TGCTGGCGAG	CATGTCTTTG	60
TGTAACGCTG	AAGAAGATGG	GGCGTTTTTT	GTCATTGATT	ACCAAACGAG	TTTGGCCAGA	120
CAGGAATTGA	AAAATCCAGG	CTTCACTCAA	GCGCAAGAAT	TAAAGCAACT	CATTAGAGAT	180
GGGGCTGTGA	GGTTGCAAAC	TTCTGCCATT	CCCTTATCCT	ACTACTTGGA	TATTTTAGGG	240
AATAAAACAA	AAACTCTTTT	GAGTGAAAGC	CTAAAAAACA	ATCCGCAACA	ACCAAACGGG	300
CAACCCAACC	AAGCTTTAGT	CAATTTAGAG	CAATCTCTAG	GGATTTTAGG	AAAACACTA	360
GATCTATCCC	AACAATACGC	TTCAGAAGGT	GTCATTAAGC	CTTTGGTGGT	GGATGTAGGG	420
AAAGAACAAA	TCGGTATCAC	GGATAGCATG	CTCTTGGTGG	CTCAAAACAT	CGTTTTAGCT	480
TTAGGGCAAG	TGGATTTGAG	CAAAATCCAA	CAAAACAATG	GTAACCAACA	GCTATACGAA	540
AACATCATGA	AAGTCATGCT	TTAGGCACA	GGCGGGACTA	ATGGAGCGTA	TAATGGCGTG	600
AGTGTGGGCG	ATATCGCCAC	AGGCATGCAA	AATTTTCCTT	CGCAAACGGG	CTTGATTGGG	660
GCTAATTCTA	CGGTGAGCGA	GCTCAACGCT	TTGATTAAGA	GCGGGATTTT	TTTAGATCGT	720
GAACTTTTGG	GGTTAGGGAG	TTTATTTGAA	AAAAATATCT	GCAGCGGTGC	ATCGTCTTGT	780
TTTAGTGGGA	ATCAGCTTAT	CTATAAGAAA	GGGCTAGACA	GAACCATAAA	CATCATTAAT	840
GCGGTATTAG	GTCAGTTTGA	ATCTTCGGCT	AGTTCTCTTT	ATAAGATTTT	TTATATCCCT	900
AACCTCTTTT	CGCTCAAAGA	TTACCAGTCA	GCGAGCATGA	ACGGCTTTGG	GGCTAAAATG	960
GGTTATAAAC	AATTTTTCAC	CCATAAGAAA	AATATCGGCT	TAAGGTATTA	TGGGTTTTTG	1020
GATTATGGCT	ATGCGAATTT	TGGCGATACG	AATTTAAAG	TGGGAGCGAA	TCTTGTTACT	1080
TATGGGGTAG	GAACGGATTT	TTTATACAAT	GTGTATGAAC	GCTCTAGAAG	GAGAGAAAGG	1140

ACTACAATCG	GTCTTTTCTT	TGGCGCTCAA	ATTGCAGGGC	AAACTTGGAG	CACTAATGTA	1200
ACGAACTTAT	TGAGCGGGCA	AAGGCCTGAT	GTCAAGTCCA	GTTTCGTTCCA	ATTCTTATTT	1260
GATTTGGGCG	TGCGCACCAA	CTTTGCAAAA	ACCAATTTCA	ATAAGCACAG	ATTAGACCAA	1320
GGGATAGAAT	TTGGGGTGAA	AATCCCTGTT	ATCGCTCATA	AATATTTTGC	AACCCAAGGC	1380
TCAAGCGCGA	GCTATATGAG	GAATTTTAGC	TTCTATGTGG	GCTATTCAGT	CGGTTTTTAA	1440

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

ATGGCGTCTC	TTGCCTTTGT	TCAAGCTTTT	TTGGAGTCTT	TTAAGGGATT	TTTAAGCCAA	60
GCGACCTTAA	TTAGCGTTTT	AATAGCGAGC	GTTTAAATCC	TTTTTTGCGC	GATTTTGCTC	120
CTTTTGGCTC	TGCTTTTAAG	AAACCGCTGG	GCTAGTTATA	TAACAACAGC	AGCTTTTTTG	180
GGCGCGTTTT	TAAGCATGCC	TTTTGTTTTG	AACGTTTAC	TCACTCAAGC	GATTTACCCC	240
ATAGAAACGC	GCATCTTGCA	CGCTAATCCC	TTAAGTTATA	GCAACGCCTT	TTCTTTGCAA	300
GTGGGAGTCA	AAAACATTTT	CAAATTCAGT	CTAAACAAAT	GCGTTTTACG	CCTAGAAGTC	360
CTTAAAAACC	CTCACAATTT	TGTGGAAGAG	CGAGCTTTTA	AATGGTTTGT	CAAAAAAAGC	420
TATGAAAAAA	CCTTTAAAGA	AAAGATTTTG	CCTGAAGAAT	CCAAGGTCTT	TTCATTCTTT	480
ATTGACGACT	ACCCTTATTC	AAAAACGGCC	CCTTATCAAG	TTTCTTTGTT	TTGTTTGTAG	540

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

TTGGGGGAGT	TGCTGCAAGC	TAGCGCACCT	TATGCGATCG	CTCCTGTGGA	GTTGATCGTT	60
GTTTTTTATA	AAAACGAATA	CAAACGAAAA	AAACAAACTT	CTACGATGAG	TAGAGAGGAA	120
TTTTTACTCT	ACACGAACGG	GCTTTGGAAT	TTTAGCGGTG	AATCCAAAAA	GCGCCTAAAG	180
CACCCAGCCC	CATTCCCAAG	GGAATTACCC	AGGCGTTGCA	TCCAATTGTT	TTCTTTTTTG	240
GAAGACACGA	TTTTTGATCC	CTTTAGCGGC	TCTGGCACGA	CTATTTTAGA	GGCCAACGCT	300
TTAGGGCGTT	TTAGCGTGGG	TTTAGAGATT	GAAAAAGAAT	ATTGCGAGTT	GTCTAAAAAG	360
CGTATTTTAG	AGAGTTTGTC	GTTAGTGTGA				390

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

GTGCTTAAGG	GGTTAAAAAA	AGCGTTTAAG	GAGAGGTTTT	GCTCTCAAGT	GTATATCTCT	60
TTTAATGTGG	ATCACAATCT	TTTATCCGCT	CAAGTTTTTA	GGGTTAAAAA	CCACCGCATC	120
AAAGAGAAAT	TTTTTAAAC	TTTGTGAGCT	AAAGTGGAAG	CTAAAAATGG	TGAAGTCCCC	180
ATTCAAGCCT	TAAAAATCGC	CAGAACTTAT	AGCCAAAAAT	ACCCCTACAC	CTATTTTAGC	240
GCGATGAGTA	AAGCTAAAGA	GGTTTATGCT	GAAAAGCAGG	CGTTTGAACA	AATCAAACAA	300
GAAAATCAAG	ATTATCAGGC	TTGTGAAGTC	AATCAAAAGT	ATTGCGTTTA	TGTGGAATCT	360
AAGGATTTTC	TAAAGGATTT	CAAGCGTTTT	AAAATCCAGG	ATGTGGATTT	TTTGTTTTCG	420
CCCTTTAGCC	TTATTTATGA	TTTGTGCGCT	GATAATTTAG	AAAACAAGCC	GTTGTGTGAT	480
CTGCTTTTAG	AGCGTTCAAG	GTTTTATTTT	TTGATTGCGG	ATAAAAAAGA	GATTTTTTTA	540
GCCAAATCCG	TGTTTTTAGA	AGAGCAACCT	GAAGAGTTTA	TAGAGAGCAA	AGAAGAAGAT	600
TCTATGGGAA	TGGATAATGA	AGCTGTGGAT	TTGTTTTTGA	GTGAAATCCA	AGAAGATATT	660
GACAGCCTTG	AAGAAGCGAT	AGGCCTAGAC	AGCAGCAAGG	ATAATAGCGA	AAAAATAACA	720
GAGGACGCTT	ATAGTTTGAT	TGAAGGCATG	ACGAATATCC	CCTTGATTGC	AGATGTTTTG	780
CAAGAGGGAT	TGCGTGCGCT	CTATCATTCCT	AGAGAGATAG	ACTTTGTAGA	AAAAGTGGTT	840
GTTTTTAGACA	GCTGTCAAAT	CCACCACAAG	GCGTTAATGC	ATTGCAAGA	AACTTTGATG	900
ATAGAAGTGG	ATAGGCTCGA	TTTTTCTTTA	GTGGAGCGGT	TGAATGTTTT	AGCGCGCATG	960
GAGAATGAAA	AGCATGCGTT	TTAG				984

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

409

- (A) LENGTH: 1296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

ATGAATATTC	AAACAAAGAA	AAGATTTT	TGCAATTTAT	TGCTTTT	CTGTTTCT	60
TGCCTTAAGG	CTGAAACCCT	TTCAGAAAGAC	CATCAAATCC	TGTTGAGTTC	AGACGCTTTC	120
CATAGAGGGG	ATTTTGCCAC	CGCTCAAAAA	GGCTATATGA	ATCTCTATAA	GCAAACCAAT	180
AAAGTGGTGT	ATGCTAAAGA	GGCGGCCATT	TCAGCGGCGA	GTTTAGGGGA	CATTAAAAACC	240
GCTATGCATT	TAGCCATGCT	TTATCAAAAA	ATCACCAATA	ATCGTAACGA	TGTTTCTATC	300
AATAAGATTT	TAGTGGATGG	CTATGCACAA	ATGGGGCAGA	TTGATAAGGC	GATTGAACTA	360
TTACACAAGA	TTCGTAAGGA	AGAAAAAACC	ATAGCCACAG	ACAATGTGTT	AGGGACTTTG	420
TATTTGACTC	AAAAGCGTTT	GGATAAGGCT	TTCCCGTTGT	TGAATAAGTT	TTATAACCAA	480
GTGCATGATG	AAGACAGCCT	AGAAAAACTC	ATTACGATCT	ATTTTTTACA	AAACCGCAAA	540
AAAGAGGGTT	TGGATCTGTT	GCAATCTCAT	ATAGACAGGT	ATGGTTGCTC	AGAGCAATTG	600
TGCCAAAAAG	CGCTCAACAC	CTTCACGCAA	TTTAACGAGC	TTGATTGGC	TAAAACGACT	660
TTCGCTCGTT	TGTATGAAAA	AAACCCATAT	GTTCAAAACG	CCCAATTTTA	CATAGGGGTA	720
TTAATCTTGT	TAAAAGAGTT	TGATAAGGCC	CAGCAAATCG	CAGAATTATT	CCCCTTTGAC	780
AGGCGTTTGT	TGCTAGACTT	ATACACCGCG	CAAAAAAAT	TTGATCAAGC	TTCCAAACAG	840
GCTTCTTTAA	TCTATCAAGA	AAGAAAAGAC	CCTAAATTCT	TAGGCTTAGA	GGCGATTAT	900
CATTATGAAA	GCTTGAGCGC	GAATAAGAAA	AAGCTCACCA	AAGAAGAGAT	GTTGCCCATC	960
ATTCAAAAAT	TAGAGCAAGC	CACCAAAGAG	CGCCAAGCAT	GGCTTGCTAA	AACTAAAGAT	1020
AAAGAAGACG	CGCAAGACGC	TTTCTTTTAT	AATTTTTTAG	GGTATTCCTT	AATAGATTAT	1080
GACATGGATG	TTAAAAGGGG	CATGGATCTT	GTGAGGAAAG	CCTTAGCGTT	AGATTCTAAC	1140
TCAGTGCTTT	ATTTGGATT	TTAGCATGG	GGTTATTACA	AATTAGGGAA	TTGTTTGGAG	1200
GCTAAAAAAA	TCTTTTCTAG	CATCGCTAAA	GAGCTTATCC	AAAACGAACC	CGAATTGAAA	1260
GAACACAATA	AAATCATTCA	AGAATGCAAG	AAATAG			1296

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

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TTGATTCAAA AGAACAAGAG CTTATCAATC TTTTAAATCT CAAATTCGGT CGTTTTTCTT      60
GGGAAAATTA TCTTGCATAA AGTTTTTATC ATGGAAGCTT TGGAGTGTTC GAAAAGAATA      120
GAAAAGAAA GCATCCAAAC AATCTATATA GACCCCCCTT ATAACACCAA GAGTTCTAAC      180
TTTGAATATG AAGACGCTCA TGCTGACTAT GAAAAATGGA TTGAAGAACA TTTGATTTTA      240
GCAAAAGCTG TGTTAAAACA AAGTGGTGTG ATTTTATTTT CTATGGACGA TAATAAAATG      300
GCTGAAGTTA AAATCATTGC CAATGAAATT TTTGGAACGC GCAATTTTTT AGGCACTTTT      360
ATCACCAAAC AAGCCACAAG ATCTAACGCT AAACACATCA ATATTACTCA TGAATATGTT      420
TTAAGCTACG CTAAAAATAA AGCGTTCGCT CCTGGTTTTA AAATCTTACG AACGCTTTTG      480
CCCATTTATG CTAAAGCATT AAAAGATTTA ATGCGAACGA TTAAGAATGT TTTTAAACAA      540
AAAGGACAAG CTCAAGCCCA ACTTATTTTA AAAGAACAAA TCAAAGAGTT ATCCCAAAAA      600
GAACATTTTA ATTTTTTAAA AAATTATAAT TTAGTGGATG AAAAAGGTGA GATCTATTTC      660
GCTAAAGATT TATCCACGCC TTCAAACCCG CGCAGTGTAG CGATACAAGA AATCAATCTT      720
TTTTTAGAAC CCTTAAAAAG CAGAGGGTGG AGCAGCGATG AAAAGCTTAA GGAGTTATAT      780
TATCAAAATA GACTTATTTT TAAGAATAAT CGCCCTTATG AAAAATATTA CCTAAAAGAA      840
TCGCAAGATA ATTGTTTGAG CGTGTTAGAT TTTTATAGCC GACAAGGCAC AAAAGATTTA      900
GAAAATTAG GCTTAAAGGG GCTTTTTTAA ACGCCAAAAC CTGTAGCATT GATTAAATAT      960
TTATTATTAT GCTCCACCCC TAAAGATTCT ATTATTTTAG ATTTTTTTGC AGGCAGCGGG      1020
ACAACAGCGC AAGCGGTTAT AGAAGTTAAT AAGGATTATT ATTTGAATTG GTCTTTTAT      1080
TTGTGCCAAA AAGAAGAAAA AATTAAAAAT AACCCGCAAG CTGTTAGCAT TTTAAAAAAC      1140
AAGGGGTATA AAAACACGAT TTCAGACATC ATGCTGTTGC GTTTAGAAAA GATCATCAAA      1200
AGAAGTGAAT ACGAAATTTT AAAAACAAAA TCTATTTTAT TTAA                      1245

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(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

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TTGGAGATTG ATAAACAGA ATGCTCTACT CTTTGTAGCA GCATTCAAAA ACAACAGCTT      60
GTGATACCCG TTGTGGGGAA TTTTAGCGCA GGCAAAAGCA CGCTATTAAA CCGCTTTTTA      120
GGCAGTAGCG TTTTGCCTAC CGGTATCACG CCAGAGACTT CTTTAGCCAC TGAATTGCAC      180

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TATAGCGCTA ATGAACGCAT AGAGGCTTTT TCAAGCAATG ACGAAAAAAC AGAGAGTTTT	240
GAAGTGAATG AGCAAAGTTT TGAGGCGATT AAAGAGAATG CGGCGAAGTA TTCCTACCTT	300
AAGGTTTATT TGAATAATGA AGCCTTAAAA GATAGTGCGC CTTTAGTGTT TGTGGATATG	360
CCCGGGTTTG ATAGCCCCAT TTCAAGCCAC ACCCATGCCA TTTTGAATA TTTGGAAAGG	420
GGCGTGCATT TTGTCATTCT CACAAGCGTA GAAGAGGGTA ACCTCACTAA ACGCATGGTT	480
AGGGAGTTAA AAACCTTTTA G	501

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

ATGAAACTCC CGGTCGTTGA GAGCTTTTTT TCCTTACAGG GTGAAGGAAA AAGGATAGGC	60
AAGCCCAGTC TTTTTTTGCG CTTAGGGGGG TGTAACCTTT CATGCAAGGG CTTTAATTGT	120
AAAACCTTAT TCAATGATGA AATCCTAACA GGTGCGATA GTTTGTATGC GGTGCATCCT	180
AAATTCAAAA CATCTTGGA TTATTACAAT GAGCCTAAGC CTTGATTGA ACGATTAGTT	240
AATTTAGCCC CTAATTATAA GGATTTTGAT TTCATTCTTA CAGGCGGGGA GCCAAGCTTG	300
TATTTTAATA ACCCTATTTT ATTGAGCGTT TTAGAGCATT TTTACCATAA AAAAATCCCT	360
TTATTTGTAG AGAGTAATGG CTCTATTTT TTTGAATTTA GCCCTATTTT AAAAGAATTG	420
CATTTCACCC TAAGCGTCAA ACTCTCTTTT TCTTTGGAGC AAGAAAGCAA GCGGATCAAC	480
CTTAAAGCCT TACAAAATAT CTTAAATAAC GCTAAAAGCG TGCATTTTAA ATTCGTATTG	540
GAGAGTCAAA ACGCCGCTCA TTCTATCGCA GAAATTCAAA GCCTTTTGAA ACAGCTCTCC	600
TTAAAAAATA ATGAAATCTT TTTAATGCCC CTAGGCACAA CTAACAACGA GCTAGACAAA	660
AATCTAAAAA CCCTAGCCCC CCTAGCCATA GAGCATGGTT TTAGGCTGAG CGATAGGCTT	720
CATATCCGCT TGTGGGACAA TAAGAAAGGG TTTTAA	756

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

ATGAATTTAA	ACTTTATGCC	CCTATTGCAT	GCTTATAACC	ATGTAAGCAT	TGATTTTTCAT	60
TTCAATTCTA	GCGCTAGGGA	TTTTTGCGTG	CATGAAGTGC	CTTGTATGA	ATTTAGCAAC	120
ACGGGCGAAC	ATGCCGTTAT	TCAAGTGAGA	AAAAGCGGTT	TAAGCACTTT	AGAAATGCTT	180
CAAATTTTTT	CTCAAATTTT	AGGGGTAAAA	ATCGCTGAAT	TGGGTATGC	GGGCTTGAAA	240
GATAAAAACG	CGCTGACGAC	TCAATTCATC	TCACCTCCCTA	AAAAATACGC	CCCTTTATTA	300
GAAAAAATA	CGAGCAACTT	TCAAGAAAGA	AACCTTAAAA	TCCTGTCTTT	GAATTACCAT	360
CACAATAAAA	TCAAATTAGG	GCATTTAAAG	GGGAATCGCT	TTTTTATGCG	TTTCAAAAAA	420
ATGACCCCCC	TAAACGCTCA	AAAAACGGAG	CAAGTTTTAG	AACAAATCGC	GCAGTTTGGC	480
ATGCCTAATT	ATTTTGGCTC	GCAACGCTTC	GGGAAGTTCA	ATGACAACCA	TAAAGAGGGG	540
TTAAAAATCT	TGCAAAATGA	AACGAAATTC	GCCACCAAAA	AATTAAACGC	TTTTTTAATT	600
TCAAGCTATC	AAAGTTATTT	GTTTAATTCG	CTTTTAAGCA	AGCGATTAGA	AATCAGTAAA	660
ATCATTAGCG	CTTTTAGCGT	CAAAGAAAGT	TTAGAATTTT	TTAAACAAAA	AAATTTAAGC	720
GTCCATTCAA	ACGCCCTAAA	AGCCCTTAAA	AACCAAGCCC	ACCCCTTTAA	AATCTTAGAA	780
GGCGATGTGA	TGCGCCATTA	CCCTTATGGG	AAGTTTTTTG	ACGCTTTGGA	ATTAGAAAAA	840
GAGAGCGAAA	GGTTTTTGAA	CAAAGAAGCT	GTGCCTACGG	GGTTACTGGA	CGGTAAAAAA	900
GCTCTTTATG	CAAAAAATTT	GAGTTTAGAA	ATTGAAAAAG	GATTCCAGCA	TAACCTTTTA	960
AGTGGCCATG	CTAAAACGCT	AGGATCCAGG	CGGTTTTTTT	GGGTGTTTGT	GGAAAATATA	1020
ACTTCTCAAT	ACATCAAAGA	AAAAGCGCAA	TTTGAATTGG	AATTTTACTT	GCCTAAAGGG	1080
AGTTATGCGA	GCGCGCTGCT	CAAAGAAATC	AAGCATGAGA	AAGGAGAAAA	TAATGACGAA	1140
TTTTGA						1146

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2094 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

TTGCAAAACT	TTGTTTTTAA	TAAAAAATGG	CTCATCTATT	CTAGCCTACT	CCCCTTATTT	60
TTTCTTAACC	CTTTAATGGC	AGAAGACGAT	GGGTTTTTTA	TGGGGGTGAG	TTATCAAACT	120
TCTTTGGCCG	TTCAAAGGGT	GGATAACTCA	GGGCTTAACG	CCAGTCAAGA	CGCATCCACT	180

TATATCCGCC	AAAACGCTAT	CGCTCTAGAA	TCTGCGGCGG	TGCCTTTAGC	CTATTATTTA	240
GAAGCGATGG	GCCAACAAAC	GAGAGTCTTA	ATGCAAATGC	TCTGCCCTGA	TCCTTCTAAA	300
AGATGTTTGC	TCTATGCAGG	GGGCTATCAA	AACGGACAAA	ATAATAACGG	CGATACAGGC	360
AACAACCCCC	CAAGAGGCAA	TGTCAATGCC	ACCTTTGATA	TGCAATCTCT	AGTCAATAAT	420
TTAAACAAGC	TCACCCAAC	CATCGGCGAG	ACTTTAATCC	GTAACCCTGA	AAATCTTCCT	480
AACTCCAAAG	TCTTTAACGT	CAAATTTGGC	AATCAAAGCA	CTGTTATTGC	ATTGCCTGAG	540
GGTCTAGCCA	ATACCATGGA	CGCTTTAAAC	AATGACATCA	CCAACGCTTT	AACCACGCTC	600
TGGTATAACC	AAACCTTAAC	GAATAAATCT	TTTAGCACCC	CTAGTAACAC	TTCTGTGAAT	660
TTTAGCCCCC	AAGTCTTGCA	ACACCTTTTA	CAAGACGGCT	TAGCCACAGC	AAATAATAAT	720
CAAACCATT	GCAGCACTCA	AAACCAATGC	ACCGCCACTA	ATGAAGCTAA	ATCTATCGCT	780
CAAAACGCCC	AAAACATCTT	CCAGGCTTTA	ATGCAAGCAG	GGATTTTAGG	GGGCTTAGCC	840
AATGAAAAGC	AATTTGGCTT	CACTTACAAC	AAAGCCCCCA	ATGGCAGCGA	TTCCCAACAA	900
GGCTATCAAA	GCTTTAGCGG	CCCGGGTTAT	TACACCAAAA	ACGACAACAC	CACGCAAGCG	960
CCCTTAAAG	CATTACCCGC	TGGAGCGACA	ATTGGATCAG	GCAATGGCCA	ATACACCTAC	1020
CACCCAGCT	CGGCAGTCTA	TTATTTAGCC	GATAGCATCA	TCGCTAATGG	CATCACCGCT	1080
TCTATGATTT	TTTCAGGCAT	GCAAAATTTT	GCCAATAAAG	CCGCTAAACT	GATAGGCACT	1140
TCAAGCTATA	ACCAGATGCA	AGATGTGATC	AATTACGGGG	AAAGCTTGCT	TAGTAACACC	1200
GTAGCGTATG	GGGATTTTAT	CACCAATTGG	GTCGCCCCCT	ATTTGGATTT	AAACAATAAA	1260
GGTTTGAATT	TCTTGCCTAA	TTATGGGGGG	CAATTGAATG	GCGCTAATAA	TCAAACCCCA	1320
CAATTAACCC	CACAACAAGC	CCAACAAGAA	CAAAAAGTGA	TCATGAACCA	ATTAGAGCAA	1380
GCCACAAACG	CCCCACCCC	CGCGCAAATA	AACAGGATTT	TAGCCAACCC	CTATTCCCCC	1440
ACGGCAAAAA	CTTTAATGGC	TTATGGGCTC	TATCGCTCTA	AAGCAGTGAT	TGGCGGAGTG	1500
ATTGATGAAA	TGCAAACTAA	AGTGAATCAA	GTCTATCAAA	TGGGCTTTGC	TAGGAATTTT	1560
TTGGAGCATA	ACTCTAATTC	TAATAACATG	AACGGCTTTG	GCGTGAAAAT	GGGCTATAAG	1620
CAATTTTTTCG	GCAAAAAGCG	CATGTTTGGG	CTTAGGTATT	ATGGTTTTTA	TGATTTTGGT	1680
TACGCTCAAT	TTGGCACAGA	ATCTTCTTTA	GTGAAAGCCA	CCCTCTCTAG	CTATGGAGCG	1740
GGCACAGACT	TTCTTTATAA	TGTTTTTACC	CGAAAAAGAG	GGACTGAAGC	GATAGATATA	1800
GGTTTTTTTTG	CCGGTATCCA	ACTTGCAGGG	CAAACCTGGA	AAACGAATTT	TTTAGATCAA	1860
GTGGATGGCA	ACCATCTTAA	ACCTAAGGAC	ACTTCTTTCC	AATTCCTTTT	TGATTTGGGC	1920
ATAAGGACCA	ATTTTTCCTA	AATCGCTCAT	CAAAAAGAT	CTCGTTTTTC	TCAAGGGATA	1980
GAATTTGGCC	TTAAATATACC	GGTGCTTTAT	CACACCTACT	ACCAATCAGA	AGGCGTTACA	2040
GCGAAGTATA	GAAGAGCCTT	TAGTTTTTAT	GTGGGCTACA	ACATAGGCTT	TTGA	2094

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2094 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

TTGCAAAACT TTGTTTTTAA TAAAAAATGG CTCATCTATT CTAGCCTACT CCCCTTATTT 60

TTTCTTAACC	CTTTAATGGC	AGAAGACGAT	GGGTTTTTTTA	TGGGGGTGAG	TTATCAAACCT	120
TCTTTGGCCG	TTCAAAGGGT	GGATAACTCA	GGGCTTAACG	CCAGTCAAGA	CGCATCCACT	180
TATATCCGCC	AAAACGCTAT	CGCTCTAGAA	TCTGCGGCGG	TGCCTTTAGC	CTATTATTTA	240
GAAGCGATGG	GCCAACAAAC	GAGAGTCTTA	ATGCAAATGC	TCTGCCCTGA	TCCTTCTAAA	300
AGATGTTTTG	TCTATGCAGG	GGGCTATCAA	AACGGACAAA	ATAATAACGG	CGATACAGGC	360
AACAACCCCC	CAAGAGGCAA	TGTCAATGCC	ACCTTTGATA	TGCAATCTCT	AGTCAATAAT	420
TTAAACAAGC	TCACCCAAC	CATCGGCGAG	ACTTTAATCC	GTAACCCTGA	AAATCTTCCT	480
AACTCCAAAG	TCTTTAACGT	CAAATTTGGC	AATCAAAGCA	CTGTTATTGC	ATTGCCGTGAG	540
GGTCTAGCCA	ATACCATGGA	CGCTTTAAAC	AATGACATCA	CCAACGCTTT	AACCACGCTC	600
TGGTATAACC	AAACCTTAAC	GAATAAATCT	TTTAGCACCC	CTAGTAACAC	TTCTGTGAAT	660
TTTAGCCCCC	AAGTCTTGCA	ACACCTTTTA	CAAGACGGCT	TAGCCACAGC	AAATAATAAT	720
CAAACCATTT	GCAGCACTCA	AAACCAATGC	ACCGCCACTA	ATGAAGCTAA	ATCTATCGCT	780
CAAAACGCCC	AAAACATCTT	CCAGGCTTTA	ATGCAAGCAG	GGATTTTAGG	GGGCTTAGCC	840
AATGAAAAGC	AATTTGGCTT	CACTTACAAC	AAAGCCCCCA	ATGGCAGCGA	TTCCCAACAA	900
GGCTATCAAA	GCTTTAGCGG	CCCGGGTTAT	TACACCAAAA	ACGACAACAC	CACGCAAGCG	960
CCCTTAAAAG	CATTACCCGC	TGGAGCGACA	ATTGGATCAG	GCAATGGCCA	ATACACCTAC	1020
CACCCCAGCT	CGGCAGTCTA	TTATTTAGCC	GATAGCATCA	TCGCTAATGG	CATCACCGCT	1080
TCTATGATTT	TTTCAGGCAT	GCAAAATTTT	GCCAATAAAG	CCGCTAAACT	GATAGGCACT	1140
TCAAGCTATA	ACCAGATGCA	AGATGTGATC	AATTACGGGG	AAAGCTTGCT	TAGTAACACC	1200
GTAGCGTATG	GGGATTTTCAT	CACCAATTGG	GTCGCCCCCT	ATTTGGATTT	AAACAATAAA	1260
GGTTTGAATT	TCTTGCCATA	TTATGGGGGG	CAATTGAATG	GCGCTAATAA	TCAAACCCCA	1320
CAATTAACCC	CACAACAAGC	CCAACAAGAA	CAAAAAGTGA	TCATGAACCA	ATTAGAGCAA	1380
GCCACAAACG	CCCCCACCCC	CGCGCAAATA	AACAGGATTT	TAGCCAACCC	CTATTCCCCC	1440
ACGGCAAAAA	CTTTAATGGC	TTATGGGCTC	TATCGCTCTA	AAGCAGTGAT	TGGCGGAGTG	1500
ATTGATGAAA	TGCAAACATA	AGTGAATCAA	GTCTATCAAA	TGGGCTTTGC	TAGGAATTTT	1560
TTGGAGCATA	ACTCTAATTC	TAATAACATG	AACGGCTTTG	GCGTGAAAT	GGGCTATAAG	1620
CAATTTTTCG	GCAAAAAGCG	CATGTTTGGG	CTTAGGTATT	ATGGTTTTTA	TGATTTTGGT	1680
TACGCTCAAT	TTGGCACAGA	ATCTTCTTTA	GTGAAAGCCA	CCCTCTCTAG	CTATGGAGCG	1740
GGCACAGACT	TTCTTTATAA	TGTTTTTACC	CGAAAAAGAG	GGACTGAAGC	GATAGATATA	1800
GGTTTTTTTTG	CCGGTATCCA	ACTTGCAGGG	CAAACCTGGA	AAACGAATTT	TTTAGATCAA	1860
GTGGATGGCA	ACCATCTTAA	ACCTAAGGAC	ACTTCTTTCC	AATTCCTTTT	TGATTTGGGC	1920
ATAAGGACCA	ATTTTTCCAA	AATCGCTCAT	CAAAAAGAT	CTCGTTTTTC	TCAAGGGATA	1980
GAATTTGGCC	TTAAAATACC	GGTGCTTTAT	CACACCTACT	ACCAATCAGA	AGGCGTTACA	2040
GCGAAGTATA	GAAGAGCCTT	TAGTTTTTAT	GTGGGCTACA	ACATAGGCTT	TTGA	2094

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

ATGATAAAAA	AAGCTAAAAA	ATTATATACCA	CTCTTTTTTAA	TTGGCTCCCT	CTTAGCTGAA	60
GACAATGGCT	GGTATATGTC	TGTAGGCTAT	CAAATCGGTG	GCACGCAGCA	ATTCATCAAT	120
AACAAACAAC	TTTTAGAAAA	TCAAAATATC	ATCAATAGCA	TCACCCAAAG	CGCGATCAAT	180
ATTGCAGGGC	CTACTACCGG	CCTAATCACT	TTAAGCTCTC	AAAGCGTTAT	TGACGCTTTA	240
GGCTATGGCG	TGAGTAACAC	CGTGGGTAAC	CAATTAGAAG	GCATTTCTAA	TATCCTGAAT	300
CAAATTGGCA	AAAGAAAAGA	CTTTTATTCT	AGCCGTCAAA	TCTCTAGCAT	TTCCCAGCAA	360
ATCATAGGGC	TTAAAGGAAG	CTCTGATCCC	TTAAAAGCCC	ATTCTTCACA	AATCACAGCC	420
AAACTCCTTT	CCAACACCCA	AAGCGCGTTT	GATCAGGGCA	TCGCTCTAAG	CTCTAATATC	480
ATTAGTGCAG	TCAATAGCCT	AAACCCTAGC	AACAACCTCC	AAGAAGTCAA	AGCCCAGCTC	540
CAAAACACCG	CGCAATCCAT	GACAGAATTG	TTGCAACAAA	TTGAACACAG	CATCACTAAA	600
ACCACTAGCA	CCACTTACGC	ACAATCCCTA	CTCTCCAATC	TGACCGATGC	GGTGAATGCA	660
TCTAGCAATA	ATACCACTTA	TGTGAGCGCT	CTTGTTAACG	CTTTAAACAC	TTTAGGGGTG	720
GGGGTTTTTC	CCACCACAAC	CTCAACGCAT	GTGGTGCTAA	ACCCACCGGG	ACAAGTCGTA	780
TTCTATCCAA	CTAATTCCCT	TTTAGGCTCT	ACTTCTTCAA	ACAGCAATAA	CCAACAACAA	840
TACAACAACA	CCCTTTTAAT	GAACACCTTA	CAAGGGGAAT	TAAGCACTAA	CAATCAAAAT	900
AACCCCAATG	GTTGCGCCAA	TCAAATCCAG	TGTTTAGAGC	AATTCATCCA	AAATTTAACC	960
CCTTTAGCCG	CAACCCCCAC	TTCAACTAAC	CAGGCCAACC	AGCAAGTCCA	AGCCATCGCT	1020
CAAAAAC TTC	AAAGCGTTGC	TATCAACGCT	TTAGACAACA	ATGCGATCAA	CAACACCACC	1080
TATAATTTAA	ACAACCTGCA	CAACGCTTTG	AATTTCCAAG	CCTATCAAAG	CACGATAGAA	1140
CAATACAATA	ACGCTTTAAA	GCAAATTTG	TGGATTAGTT	TTAGCGAGCC	TAAAAACTTG	1200
CTCAAAAACA	CTTCCAATAA	CTACCAAATC	GGCACGGTTA	CCAACGATCA	AGGGCAAAAT	1260
ATCAGCGCCT	ATGATTGCAC	AAGCGCTACC	GGAAGCCTTT	CTAGCGATGC	TTCTAGTGGG	1320
ATTTTCATGCT	CAGCCACAAG	CTCCACAAAT	AACACAAATA	GTTTTGACAA	TTCTTTAGTC	1380
GCTACCTCCA	AAGTCCAAAC	CATCAACGGC	AAAGAGCAGA	TCGGCGTGAA	TTCTTTTAAT	1440
CTTGCTCTCT	AAGTGTGGAG	CGTTTATAAC	TCTTTAAAAA	CTTCAGAAGA	AAATTGCAA	1500
AAAAACGCCA	AAATATTATG	CAACAATGGA	TCGCAATCTG	GGACAAGCCC	ATGCAATAGC	1560
TCTTCAGGGG	GTTTGAGCAT	CAGCGGGAAC	GCCCAATTGC	AAAATATTTT	AAGCCCTACT	1620
AATGGGACTA	CCACTAATAC	TCAAGCTAAA	AGCAACGCTT	CCAAACTAAA	AGCGATGGTA	1680
ATGGTGAATA	ATGAAGAAGA	AGCCAAAACG	ACCAATTTCA	ATCAAAGCAG	TGGGCCAACC	1740
ACACAATCTT	CTAACAGCAC	GGTGATGGGA	GCTTTAAACA	CCGTATTGCA	AAATGTCAGC	1800
AATTTCCAAC	AAAGCATTC	AAGCGCTTTT	CAAAACCAAG	AAAATAATAT	CCAAGCTTGG	1860
GCGAACGCAC	TTTATAACAC	TAGTAACCTT	AATGGGAATC	AATCGCAAAA	TTTAACCACT	1920
AACAATAACC	AAGATTTACG	CATCCAATTA	AGGGCGAATT	TTTACCAGCT	CATCAATACC	1980
ATTAACCAGC	AAGTGCCTAC	AGACATGAAC	GCTTTAATTA	ATCAAAGCCA	ACAAACCCAG	2040
CAACAAGCG	GATCAGCAAG	CACCACGAAC	AACGCATGCG	CGAGCGGAAT	GGGGAGTAGT	2100
GGCAACTGGT	GCTACCAGCA	GTGGTCCGAT	TCTAAGGCTT	ATTACAGCGG	GTTGCAAAGC	2160
GCTTTAGGGT	ATCAAACACA	AGCGACAAC	CAAAATGGGA	GCAGTGGTGG	GAGCAATATC	2220
ACCTACAATG	TCCAACAAAT	CACGCTCACT	AGCGGTGGTT	TGCTCAATCA	AATTATCACA	2280
AACCTTAAGA	GCGTTAATGG	GGGCAGTAAT	GGGGGAAGCA	GTGGGAATGG	CACTAGTCAA	2340
ATCAACACAG	CCTACCAAAT	GCTCACAGAC	GCTAGCGATG	GGAAATTAGG	GACTTATAAT	2400
AGTAGCAATA	GTAGCAATAG	TAGCAATAGT	GGCAATAATA	ACGGCTATAC	GCCATGCAAT	2460
AGCACCAACG	GGAGCAATGG	GACGAGTGGG	AGCAATTGTT	ATGAACCCAA	CAAAACAACA	2520
AACGCCACCA	CCGCAACCAC	CACGACCGAC	AGCAATTTAC	AAAAAGTCTA	TAATGACGCC	2580
CAAAAAATAG	CCAATATTAT	CGCCAGCTCT	GGGAACAATA	AAGGCGTTGA	AAACGGCTTA	2640
AAACAATTCT	TTGAAGCGTT	AAAAAGTAAT	AGCAGCAGTC	TTAGTAATTT	ATGTGGTAAT	2700
GGTAGTAGCG	GTAGTAGCTC	TACTTGCTCC	GGTGGGCTTA	TCAACCTTTT	AGGGGCAATC	2760
CCCACAAACG	GAGTGAGCGA	TACGAATAAT	TTAATTAATC	TGCTCACTGA	ATTCATTAAA	2820
ACCGCCGGGT	TTATCCAAAA	TAATGATAGT	AATGTATCTA	CTAGTCTTAC	AAGCGCTTTT	2880
CAAGCCATTA	CGAGCGCTAT	TTCTCAAGGG	TTTCAAGCCT	TGCAAAACGA	TATTAGCCCT	2940
AATGCGATTT	TGACCTTGCT	CCAAGAAATC	ACTTCTAACA	CCACCACCAT	TCAGTCATTC	3000
TCGCAAAACCT	TACGGCAGCT	TTTAGGGGAT	AAAACCTTCT	TTATGGTGCA	ACAAAAGCTC	3060
ATTGATGCGA	TGATTAAACG	CAGAAATCAG	GTTCAAAACG	CGCAAAATCA	AGCCAATAAC	3120
TACGGCTCTC	AACCCGTTTT	AAGCCAGTAT	GCGGCCGGTA	AAAGCACCCA	ACACGGCATG	3180
AGCAATGGCT	TAGGGGTTGG	CATAGGCTAT	AAATACTTCT	TTGGTAAGGC	TAGGAAATTA	3240
GGCCTTAGGC	ATTATTTTTT	CTTTGATTAC	GGCTTTAGTG	AAATAGGCCT	AGCCAATCAA	3300
AGCGTGAAAG	CGAATATCTT	TGCTTATGGG	GTAGGCACGG	ATTTTTTATG	GAATCTATTC	3360

AGGAGGACTT	ACAACACTAA	AGCGTTGAAT	TTTGGGCTAT	TTGCCGGGGT	CCAACTGGGC	3420
GGTGCAACTT	GGCTTAGTTC	CTTAAGGCAA	CAAATCATTG	ACAACTGGGG	GAACGCTAAT	3480
GACATCCATT	CAACGAATTT	TCAAGTGGCG	CTGAATTTTG	GGGTGCGCAC	CAATTTTCGCG	3540
GAGTTTAAGC	GTTTTGCTAA	GAAATTCCAC	AATCAAGGGG	TCATCAGCCA	AAAGAGCGTG	3600
GAATTTGGGA	TCAAGGTGCC	TCTCATCAAT	CAAGCGTATT	TGAATAGTGC	TGGGGCTGAT	3660
GTGAGCTACA	GGAGGCTTTA	TACTTTCTAT	ATCAATTACA	TCATGGGGTT	TTAA	3714

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

ATGGAAAAAT	TACCTAAAAA	ACGAGTTTCT	AAAACCAAAT	CACAAAAACT	TATCCATAGC	60
CTAACCACCC	AAAAAACAG	AGCCTTTCTC	CAAAAAACCA	GCGCCAATGA	AATGCTTTTA	120
GAGTTAGAAA	AAGGGGCGTT	TAAAAAAAT	GAAGCCTATT	TTATTTCTGA	TGAAGAAGAT	180
AAAAATTACG	TTTTAGTGCC	GGACAATGTG	ATCTCTCTTT	TGGCAGAAAA	CGCCAGAAAG	240
GCTTTTGAAG	CCAGGCTTAG	GGCGGAATTA	GAAAGGGATA	TTATCACCCA	AGCGCCGATT	300
GATTTTGAAG	ACGTGCGCGA	AGTTTCTTTG	CAATTGTTAG	AAAATTTACG	CCAAAAAGAC	360
GGGAATTTGC	CCAATATCAA	CACCTTAAAT	TTTGTCAAAC	AAATCAAAAA	AGAACCCTCT	420
AATTTATTCT	TTAATTTTGA	CAACATGTTC	AAACAACCCC	CTTTTAATGA	GAATAATTTT	480
GAAAATTTTG	ACAATAGCGA	TGAGGAAAAT	TTTTAA			516

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

ATGAAAAAAAA	TTTAAATCAC	TTAATCACT	TTATTATTAG	GAGTTTTTAT	GGGGTTACAA	60
GCGAGTGCTT	TGACACACCA	AGAAATCAAT	CAAGCTAAAG	TCCCTGTGAT	TTATGAAGAA	120
AACCATTTGT	TACCCATGGG	GTTTATCCAT	TTAGCCTTTA	GAGGGGGTGG	GAGCTTGAGC	180
GATAAAAACC	AGTTGGGTTT	GGCGAAATTG	TTGCGCAAG	TTTTAAACGA	AGGCACTAAA	240
GAGCTTGGCG	CGGTGGGGTT	TGCGCAACTT	TTAGAGCAAA	AAGCGATCAG	TTTGAATGTG	300
GATACCAGCG	CAGAAGATTT	GCAAATCACT	TTAGAATTTT	TAAAAGAATA	CGAAGATGAA	360
GCCATAATGC	GCTTAAAAGA	GCTTTTAAAA	TCCCTTAATT	TCACGCAAAA	CGCTTTAGAA	420
AAAGTCAAAA	CCAGAATGTT	AGCCCAACTT	TTACAAAAAG	AAAGCGACTT	TGATTATTTG	480
GCTAAACTGA	CTTTAAAACA	AGAGCTTTTT	GCTAACACCC	CTTTAGCTAA	TGCGGCCTTA	540
GGCACTAAAG	AGAGTCTTCA	AAAAATCAAG	CTAGACGATT	TGAAACAGCA	ATTTGCTAAG	600
GTTTTTGAAC	TCAATAAACT	CGTGGTGGTG	CTTGGGGGCG	ATTTGAAAGT	CAATCAAACG	660
CTCAATCGTT	TAAATAACGC	CCTCAATTTT	TTGCCGCAAG	GTAAAGCCTA	TGAAGAGCCT	720
TATTTTGAAG	CGAGCGATAA	AAAAAGTGAA	AAAGTCTCT	ATAAAGACAC	TGAGCAGGCT	780
TTCGTGTATT	TTGGCGTGCC	CTTTAAAATC	AAGGATCTAA	AACAGGATTT	AGCGAAATCT	840
AAAGTCATGA	TGTTTGTGCT	TGGGGGGGGG	TTTGGCTCTC	GTTTGATGGA	AAAAATCAGG	900
GTTCAAGAGG	GCTTGGCTTA	TAGCGTGTAT	ATCCGCTCCA	ACTTTTCTAA	AGTGGCGCAT	960
TTTGCAGAGC	GGTATTTGCA	AACCAAGCTC	AGCACTCAAG	CTAAAAGCGT	TGCCTTAGTT	1020
AAAAAATAA	TTAAAGAATT	TATAGAAAAA	GGCATGACGC	AACAAGAATT	AGACGACGCT	1080
AAAAAGTTTT	TACTAGGCTC	TGAGCCTTTA	AGGAATGAAA	CGATCTCAAG	CCGCTTGAAC	1140
ACCACTTACA	ATTATTTTTA	TTTGGGTTTG	CCTTTAGATT	TCAACCAAAC	GCTACTCAAT	1200
CAAATCCAAA	AAATGAGTTT	GAAAGAGATC	AATGATTTCA	TTAAAGAGCA	TACCGAAATC	1260
AACGACTTGA	CCTTTGCTAT	TGTGAGCAAT	AAAAAGAAGG	ACAAATAA		1308

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1845 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

TTGGCTTCTC	CAAAAGAAAC	CCCAAAGAG	GCTCAAAAAA	ATGAAGCTCA	AAACGAAACC	60
TCTCAATCCA	ATCAAACGCC	TAAAGAAATG	AAAGTCAAGT	CCATTCTTA	TGTCGGGCTT	120
TCTTACATGT	CTGACATGCT	CGCTAATGAA	ATTGCAAAGA	TTGCGGTGGG	CGATATGGTG	180
GATTCTAAAA	AAATAGACAC	CGCTGTTTTA	GCTTTGTTCA	ACCAAGGGTA	TTTTAAAGAC	240
GTTTATGCCA	CTTTTGAAAA	CGGCATTTTA	GAGTTTCATT	TTGATGAAAA	AGCCAGGATT	300

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GCCGGGGTAG AAATCAAGGG TTATGGGACT GAAAAGGAAA AAGACGGCTT AAAATCCCAA 360
ATGGGGATCA AAAAGGGCGA CACCTTTGAT GAGCAAAAAT TAGAGCATGC TAAAACGGCT 420
TTAAAAACGG CTTTAGAGGG GCAGGGCTAT TATGGGAGCG TGGTGGAGGT GCGCACAGAA 480
AAGGTCAGTG AGGGAGCGTT ATTGATCGTG TTTGATGTGA ATAGGGGGGA CAGTATTTAT 540
ATCAAACAAT CCATTTATGA GGAAGCGAT AAATTAAAAC GCCGTGTGAT TGAATCTTTG 600
AGCGCGAACA AGCAGCGCGA TTTCATGGGC TGGATGTGGG GCTTGAATGA CGGGAAATTG 660
CGCTTAGATC AATTAGAATA CGATTCTTTG CGTATCCAAG ATGTGTATAT GCGTAGGGGT 720
TACTTAGACG CTCATATTTT TTCGCCTTTT TTGAAAACGG ATTTTCCAC CCATGACGCT 780
AAGCTCCATT ATAAGGTCAA AGAGGGGATC CAATACAGGA TTTCAGATAT TTTAATAGAG 840
ATTGACAACC CGGTAGTCCC CTAAAAACC TTAGAAAAAG CGCTTAAAGT TAAAAGGAAA 900
GATGTCTTTA ATATTGAGCA TTTAAGAGCG GATGCGCAA TTTTAAAAAC CGAAATCGCC 960
GATAAGGGCT ATGCGTTTGC GGTGGTGAAG CCAGACTTGG ATAAAGACGA AAAAAACGGG 1020
CTTGTGAAAG TCATTTATCG TATTGAAGTG GCGGATATGG TGCATATCAA TGATGTCATC 1080
ATTTAGAGGA ACCAGCGCAC GAGCGATAGG ATCATTAGGA GGAATTGTT ACTAGGGCCT 1140
AAAGATAAAT ACAACTGAC CAACTGAGA AATTCCGAAA ATTCTTTGAG GCGTTTAGGG 1200
TTTTTCTCTA AAGTCAAGAT TGAAGAAAAA AGGGTCAATA GCTCATTGAT GGATTTGTTA 1260
GTGAGCGTAG AAGAGGGGCG CACCGGGCAG TTGCAATTCG GGTGGGGCTA TGGCTCTTAT 1320
GGAGGGCTCA TGCTTAATGG GAGCGTGAGC GAAAGGAATC TTTTGGGCAC AGGGCAAAGC 1380
ATGAGCTTGT ATGCTAACAT TGCCACAGGG GGGGGTAGAT CTTATCCGGG CATGCCAAAA 1440
GGGGCGGGGC GTATGTTTGC CGGGAATTTG AGCTTGACTA ATCCAAGGAT TTTTGACAGC 1500
TGGTATAGCT CTACGATCAA TCTTTATGCG GATTACAGGA TAAGCTACCA ATACATCCAA 1560
CAAGGCGGGG GCTTTGGGGT GAATGTCGGG CGCATGCTGG GTAATAGAAC CCATGTGAGC 1620
TTAGGGTATA ACTTGAATGT TACCAAACTC CTTGGTTTCA GCAGCCCCTT ATACAACCGC 1680
TACTATTCCT CTGTTAATGA AGTGGCCTCT CCAAGGCAAT GTTCCACACC CGCATCGGTG 1740
ATTATCAACC GCTTATCAGG CGGTAGAACT CCATTGGTTC CTGAAAGCTG TTCTAGTCCT 1800
GGAGCGATCA CCATCTTCAC CAGAAATAAA AGGTATTTGG GATAG 1845

```

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

```

TTGTGTGAGG GCCCTAACGT GATGAGCGGT TGGAAACCCC ACATCAAGCA TGGCGTTTAT 60
AGAAACTGGA ATAAGTGGCG CAACAATTAC ACAGCGGTCT ATTTGAGCGA TCGCATTGAA 120
GCTTGGGACG GCGCCTTTTT CATCGTGCCT GGTTCGCGCT ACGCTTTTGT GCAATACAAC 180
AACGAAAATG CGTCTAACTG GATGCAAAATC CCTGAGAAGG ATTTAAGAAA AATCAAGCAC 240
ATGAACAATT GGATGCCCTC AACCAACATT GGCTTTATCC CTGTGCAAGG CGATCACAAT 300
GTGCTTACCT ACTTCAACTA CCAACGCTCT TCGTCCCGC CTCAATTAGA CGTTTTGAGC 360
TATGGAGGAG CGGAGTATTT TACCCAACAC TTTGACACGG TGAAGCAGG AGCGCGCTAC 420

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ACCTATAAAG	ATAAATTCAG	CTTCAATGCG	GACTACTTTA	GGATTGGGC	GCGCGATTTT	480
GCCACCGGGC	AGTATTCAGT	CTATACGAGC	GGGCCCATGA	AAGGTAATGT	GCGCCCCATT	540
AATGGCTATT	CTCAAGGCGT	GGAGCTGGAA	TTGTATTACA	GGCCCATTAG	AGGGTTGCAA	600
TTCCATGCCG	CTTTCAACTA	CATTGACACT	CGTGTAAC TA	GCCATGGCCC	TTTAACCGAC	660
TTGAACGGGG	ATGTGCTAAA	AGGGACTAGC	TATAACAAGC	ATTTCCCTTT	TGTAAGCCCT	720
TTCCAATTCA	TTTTTGACGC	TCGCTACAAT	TGGCGTAAAA	CCACCATTGG	TATTTCTAGC	780
TATTTTTTATA	GCCGTGCTTA	TAGCGGGATT	AGCAACAGCG	CAGCAGGAGG	CTATTATGGG	840
ATGCAATACT	ATAGTGGGGG	GAACAACAT	GAAAGCGTTC	TTAATAGCGG	TTATCAATGC	900
GAAGCTTGGT	GTATGACCCA	ACATGAAGGG	CTCTTGCCCT	GGTATTGGGT	GTGGAATATC	960
CAAGTGAGCC	AAATTTTCTG	GGAAAACGGA	AGACACAGAG	TTACAGGAAG	CTTACAAATC	1020
AATAACATCT	TCAACATGAA	GTATTATTTT	ACAGGGATTG	GCTCTAGCCC	TGCAGGCTTG	1080
CAACCTGCGC	CTGGAAGATC	GGTTACAGCG	TATTTGAACT	ACACTTTCTA	A	1131

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1866 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

TTGCATGCTG	AAGACAACGG	CTTTTTTGTG	AGCGCGGGCT	ATCAAATCGG	CGAAGCGGTG	60
CAAATGGTCA	AAAACACCGG	CGAATTGAAA	AAC TTGAACG	ACAAATACGA	GCAGTTAAGC	120
CAATCTTTAG	CCCAACTGGC	TTCGTTAAAA	AAAAGCATTC	AAACGGCGAA	CAACATTCAG	180
GCTGTCAACA	ATGCTTTAAG	CGATTTAAAA	AGCTTTGCGA	GTAACAACCA	CACAAACAAA	240
GAAACATCGC	CCATCTACAA	CACCGCGCAA	GCTGTTATCA	CTTCAGTATT	GGCTTTTTTG	300
AGTCTTTATG	CAGGGAACGC	TCTCAGTTTT	CATGTGACCG	GTTTGAATGA	TGGATCTAAT	360
TCTCCTTTAG	GAAGAATCCA	TAGAGATGGG	AACTGCACAG	GATTACAACA	ATGTTTTTATG	420
AGCAAAGAAA	CTTATGATAA	AATGAAGACA	CTTGCCGAAA	ACCTCCAAAA	AGCTCAAGGC	480
AATCTCTGTG	CCTTATCAGA	ATGCTCTAGC	AATCAATCAA	ATGGAGGCAA	AACTTCCATG	540
ACTACAGCTC	TTCAAACCGC	GCAACAGCTC	ATGGACTTAA	TCGAACAGAC	CAAGGTTTCT	600
ATGGTGTGGA	AAAATATCGT	CATCGCAGGT	GTTACAAACA	AACCCAATGG	TGCTGGCGCT	660
ATCACATCCA	CTGGTCATGT	AACCGACTAT	GCGGTGTTTA	ACAACATCAA	GGCGATGCTA	720
CCTATCTTGC	AACAAGCGCT	TACGCTTTCT	CAAAGTAACC	ACACCCTATC	CACTCAGTTG	780
CAAGCTCGAG	CTATGGGATC	TCAAACAAAT	CGTGAATTCT	CTAAAGACAT	CTACGCTTTA	840
GCTCAAACCC	AAAAGCAAAT	CCTTTCTAAC	GCTTCAAGTA	TCTTCAATCT	CTTTAATTCC	900
ATTCTTAAAG	ACCAACTTAA	GTATTTGGAG	AACGCTTACT	TGAAAGTGCC	ACATTTGGGT	960
AAAACCCCTA	CTAACCCCTA	CAGACAGAA	GTGAATTTGA	ATAAAGAAAT	TAATGCGGTT	1020
CAAGACAATG	TAGCTAATTA	TGGTAATCGT	TTGGATTCTG	CTTTAAGCGT	GGCTAAAGAT	1080
GTTTATAACC	TAAAATCCAA	TCAAACAGAG	ATCGTAACCA	CTTATAACGA	TGCTAAGAAT	1140
TTGAGCGAAG	AGATTTCTAA	ACTTCCCTAT	AACCAAGTCA	ATGTAACAAA	CATCGTTATG	1200
TCGCCTAAAG	ATTCTACAGC	GGGCCAATAC	CAAATCAACC	CAGAGCAGCA	ATCCAATCTT	1260

AACCAAGCTT	TAGCGGCGAT	GAGCAATAAC	CCCTTTAAAA	AAGTGGGCAT	GATCAGCTCT	1320
CAAAACAATA	ACGGCGCTTT	GAACGGGCTT	GGCGTGCAAG	TGGGTTATAA	ACAATTCTTT	1380
GGCGAAAGCA	AAAGATGGGG	GTAAAGGTAT	TATGGTTTCT	TTGATTACAA	CCACGGCTAT	1440
ATCAAATCCA	GCTTTTTTAA	TTCTTCTTCT	GATATATGGA	CTTATGGCGG	TGGGAGCGAT	1500
TTGTTAGTGA	ATTTTATCAA	CGATAGCATC	ACAAGAAAGA	ACAACAAGCT	TTCTGTGGGT	1560
CTTTTTGGTG	GTATCCAAC	AGCAGGGACT	ACATGGCTTA	ATTCTCAATA	CATGAATTTA	1620
ACAGCGTTCA	ATAACCCCTA	CAGCGCGAAA	GTCAATGCTT	CCAATTTC	ATTTTTGTTC	1680
AATCTCGGCT	TGAGGACGAA	TCTCGCTACA	GCTAAGAAAA	AAGACAGCGA	ACGTTCCGCG	1740
CAACATGGCG	TTGAACTGGG	CATTAAAATC	CCTACCATTA	ACACCAATTA	TTATTCTTTT	1800
CTAGGCACTA	AGCTAGAATA	CCGAAGGCTT	TATAGCGTGT	ATCTCAATTA	TGTGTTTGCT	1860
TATTAA						1866

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

ATGATGCGAG	AGATCCTTAC	TAACCGCTTT	TTCCCAAGCC	TTTTTAAAAA	AAGGCTTGAT	60
TTTTCTAACA	GAGTGGTTTT	AGGGCTGGGA	TCTAATCTTA	AAAACCCCTT	AAAAATATTA	120
AAAAGTTGTT	TTTTATATTT	TAAAAATCAT	AGTAAAATCG	GGAAAATTTT	TTCTTCACCC	180
ATTTATATCA	ATCCGCCTTT	TGGTTACACT	AATCAACCTA	ACTTTTATAA	CGCTACGATT	240
ATCCTTAAAA	CATCTTTAGG	TTTGCGCCAT	TTTTTTGCTC	TAGTGTTTTA	TATAGAAAGG	300
CGTTTTGGGC	GTGCAAGGAA	GCGCGATTTT	AAAGATGCTC	CAAGAACTTT	AGATATTGAT	360
ATTATCGCTT	TCAATCAAGT	CATTTTGAGG	CAGAATGATT	TGACTTTACC	TCACCCTAAA	420
TGGAGTGAAA	GAGACTCGGT	GTTAGTGCCT	TAACTTTTAC	AACAAATCCT	TTTTAAAAGA	480
GAAGAGTGGT	GA					492

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

ATGCAAGATT TTATTAAGAT TTTTATTCAA GAGGTTGTCT CTACTTTAGA AGGGTTAGTG	60
GGTAAGGCTC CAAGCGTAGG ATTAGAAAAA GAAGTTTCTA ACAATGAAGA AGCGAGTTTA	120
ATCAGCACTC CTTATGCAAG GGTAAAGATT AGCGCGATTG AAAAAAATGA AAGTCCTATT	180
GAATTACTGG CTCCGGTAGA TTTAGTTACC GCTTTGAGCG ATTTGATGCT AGGAGGTGAG	240
GGGGCGAGCA AGGAAGAAAT GGATAATGAC GATTTAGACG CTTTAAAGA AATGGCTTCT	300
AATATTTTTG GTGCGATCGC TACAAGCTTG AAGTCTCAAG AATTGCTCCC TAAACTCAAT	360
TTCACCACCA CGAACGCTGA AATCGCTAAA GAGCTTCCTA AAAAAAGAAG TTACGCTAAG	420
GCGATGGTGT TTTCTTTTAA AATGGAAGCC ATCAAAGAAA GCCAAATCGT TTTATTGATC	480
ACTTCAGCGT TTGAGGGCCA ATTTGAAAAA ACGCATAAAG AAGAAAAAGA AGAAACGACA	540
AAAAGCGCTA CTGAAGAGAC TAAAACCCAC GACGCGTCTT TAGAAAATAT AGAAATCCGC	600
AATATCAGCA TGCTTTTAGA CGTGAAATTG AACGTTAAGG TCGGTATCGG TCAAAAAAAG	660
ATGATTTTAA AAGATGTGGT CTCTATGGAT ATAGGGAGCG TGGTGGAGTT GGATCAATTG	720
GTGAATGACC CTTTAGAAAT CCTCGTAGAT GACAAGGTGA TCGCTAAGGG CGAAGTGGTG	780
ATCGTGGATG GGAATTTTGG CATTCAAATC ACGGATATTG GCACTAAAAA GGAACGATTA	840
GAGCAACTGA AAAATTAA	858

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

ATGAAAATTT TAGTGATTCA AGGGCCTAAT TTAAACATGT TAGGACACAG AGACCCAAGA	60
CTTTATGGCA TGGTAACCTT AGACCAAATC CATGAAATCA TGCAAACCTT CGTGAAGCAA	120
GGCAATTTAG ATGTGGAATT AGAGTTTTTT CAAACCAATT TTGAGGGCGA AATCATTGAT	180
AAAATCCAAG AGAGCGTGGG CAGCGATTAT GAGGGGATTA TCATTAACCC TGGAGCGTTT	240
TCGCACACTT CTATTGCGAT TGCGGATGCG ATCATGCTAG CGGGCAAACC TGTCATTGAA	300
GTGCATCTCA CTAACATTCA AGCCAGAGAA GAATTCAGGA AAAATTCTTA CACCGGAGCG	360
GCTTGTGGAG GCGTGATCAT GGGATTTGGC CCGCTTGGCT ACAACATGGC TTTAATGGCG	420

ATGGTCAATA TTTTAGCCGA AATGAAAGCG TTCCAAGAAG CCCAAAAAAA CAACCCTAAT 480
 AACCCCAATA ACCCGATCAA CAATCAAAAA TAA 513

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

ATGAGAGGAT TAGAAAGAGA ATCGCATTTT	ACGCTCAATG AAAACGCGAT GTTTTTTGAG	60
TGCGCTTATA GTTGCATAA CGCTTTGTTT	TTGCAATTAG ACGATCGCTC GTTCCTTATC	120
ACTGATTCTC GTTACACCCA AGAAGCTAAA	GAAAGCCTTC AGCCTAAAAA GGGCGTTTTA	180
GTGGAAGTGA TAGAGTCTAG CGATTTAGTC	CAAAGCGCGA TTGATTTAAT TACAAAGAGT	240
TCGGTTAAAA AGCTCTTTTT TGACCCCAAT	CAAGTGAATT TGCAAACCTA CAAGCGTTTG	300
GATTCAGCGG TTGGGAATAA GGTTGTTTTA	GAGGGCGTGC CCAGTTACCA CCGCCAAAAA	360
CGCATCATTA AAAACGAGCA TGAGATCCAA	CTCCTCAAAA AATCTCAAGC GTTGAATGTT	420
GAAGCTTTTG AAAATTTTGC CGAGTATGTG	AAAAAGATTT TTGATGAAAA AGAGTCATTG	480
AGCGAGCGGT ATTTGCAGCA TAAGGTAA	GACTTTTTGA CTAAAGAGGG GGTTTATGAT	540
CTGAGTTTGT AGCCTATTTT AGCCTTGAAT	GCGAACGCGA GCAAACCCCA TGCCTTGCCT	600
AGTGCGAAGG ATTTTTTAAA AGCGGATCAT	AGCATTCTTT TGGATATGGG GATCAAATAC	660
GAACGCTATT GCTCTGATAG GACTCGCACG	GCTTTTTTTG ACCCTAAAGA CTTTGTGTTT	720
AAAAGGGAGC AGAGTTTCAA GGATAAAGAG	CGTCAAAAGA TTTATGACAT TGTGAAAGAA	780
GCGCAAGAAA AGGCTATTTT AGGCATTAGA	GCGGGCATGA CCGGTAAAGA AGCGGACAGC	840
TTGGCTAGGG GAGTGATTAG CGATTATGGT	TATGGGCAGT ATTTCACTCA CAGCACCGGG	900
CATGGCATTG ACTTAGACAT TCATGAGCTT	CCCTATATTT CATCGCGCAG TGAAACCATT	960
TTAGAAGAGG GCATGGTGTT TTCTGTAGAG	CCTGGGATTT ATATCCCTGG GTTTTTTGGG	1020
GTGCGCATTG AGGATTTAGT GGTGATTAAA	AATTCTAGGG CCGAGCTTTT ATGA	1074

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

ATGAAAGATA	GTTTTCTTTT	CACTTCCGAA	TCAGTAACCG	AAGGGCATCC	TGATAAAATG	60
GCCGATCAGA	TCAGCGATGC	GGTTTTAGAT	TACATTATTG	AGCGGGATAA	AAAAGCCAAA	120
GTCGCATGCG	AGACTTTAGT	TTCTAATGGT	TTTTGCGATG	TCCTGGCGGA	GTAAAAAACT	180
TCTGTTTATG	CCCCGATGCA	AGAGATCGCA	AGAGAAGTGG	TTAAAAAAAT	TGGCTATACA	240
GACGCTCTTT	ATGGCTTTGA	TTACAGAAGC	GCGGCGGTTT	TAAATGGCAT	TGGCGAGCAA	300
AGCCCTGATA	TTAATCAAGG	CGTGGATAGA	GAAGATGGCG	AGATTGGGGC	GGGGGATCAA	360
GGGCTTATGT	TTGGTTATGC	ATGCAAAGAG	ACTGAAACGC	TCATGCCTTT	ACCCATCCAT	420
TTAGCGCACC	AGCTCGCTTT	CGCTCTAGCT	CAAAAAAGAA	AAGACAACAC	CTTGCCTTTT	480
TTAAGGCCTG	ATGGCAAGTC	TCAAGTGAGC	GTGCGTTATG	AAAACAACAA	GCCTGTAAGC	540
GTTGATACGA	TTGTCATTTT	CACCCAACAT	TCCCCAGAAG	TTTCACAAAA	GCATTTAAAA	600
GAAGCGGTGA	TTGAAGAGAT	CGTGTATAAG	GTTTTACCCA	AAGAATATTT	GCATGACAAT	660
ATCAAGTTTT	TTATAAACCC	TACAGGAAAA	TTCGTCATCG	GTGGGCCTCA	AGGCGATGCG	720
GGTTTGACAG	GTAAGAAAA	CATCGTGGAT	ACTTATGGAG	GGTTTGGCCC	GCATGGAGGG	780
GGAGCGTTTA	GCGGGAAAGA	CCCTAGCAAG	GTGGATAGGA	GCGCGGCTTA	TGCGGCCCGC	840
TATGTGGCTA	AAAATTTGGT	AGCGAGCGGG	GTTTGGGATA	AAGCGACCGT	GCAGCTTGCT	900
TATGCGATTG	GGGTGATAGA	GCCTGTGTCT	ATTTATGTGA	ACACGCATAA	CACGAGCAAG	960
CATTCAAGCG	CGGAGTTGGA	AAAATGCGTG	AAATCGGTTT	TCAAATCAC	GCCAAAAGGC	1020
ATCATTGAAA	GCTTGGATTT	GTTAAGACCC	ATTTATTCGC	TCCTTCAGC	TTATGGGCAT	1080
TTTGGGCGCG	AGTTAGAAGA	ATTCACTTGG	GAAAAGACTA	ACAAGGTTGA	AGAGATTAAA	1140
GCGTTCTTTA	AGCGTTAA					1158

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 657 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

GTGTTAGATA	GTTTTGAGAT	TTTAAAGGCT	TTAAAGAGCT	TGGATTTATT	GAAAAACGCC	60
CCTGCTTGCT	GGTGGCCTAA	CGCTTTGAAA	TTTGAAGCTC	TACTAGGAGC	GGTTTAAACG	120

CAAAATACTA	AATTTGAAGC	CGTTTTGAAA	TCTTTAGAAA	ATCTAAAAAA	CGCTTTCATT	180
TTAGAAAATG	ATGATGAGAT	CAATCTTAAA	AAAATCGCTT	ATATAGAGTT	TTCAAAGCTT	240
GCAGAGTGTG	TCCGCCCTAG	CGGGTTTTAT	AACCAAAAAG	CCAAACGACT	GATTGATTTG	300
AGCAAGAATA	TTTTAAAAGA	CTTTCAAAGT	TTTGAAAATT	TTAAACAAGA	AGTAACCAAA	360
GAGTGGCTTT	TAGACCAAAA	GGGCATTGGC	AAAGAAAGCG	CGGATGCGAT	TTTATGCTAT	420
GTGTGCGCCA	AAGAAGTGAT	GGTGGTGGAT	AAATACAGCT	ATCTTTTTTT	AAAAAAATTA	480
GGCATAGAGA	TAGAAGATTA	TGATGAATTG	CAGCATTTTT	TTGAAAAGG	CGTTCAAGAG	540
AATTTAAATT	CCGCCTTAGC	GCTTTATGAA	AACACCATTT	CTTTAGCGCA	ACTTTATGCG	600
AGATTCCATG	GAAAGATCGT	GGAATTTTCC	AAACAAAAAT	TGGAATTGAA	GCTTTGA	657

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

ATGAAACAAC	TATTTTTGAT	TATTGGAGCC	CCAGGGAGTG	GTAAAACCAC	TGACGCAGAG	60
CTTATCGCTA	AGAATAACAG	CGAAACAATC	GCTCATTTTT	CTACTGGGGA	TTTACTCAGG	120
GCTGAGAGCG	CTAAAAAGAC	TGAGCGAGGC	TTATTGATTG	AGAAATTCAC	TTCTCAAGGC	180
GAATTAGTGC	CTTTAGAAAT	TGTGGTAGAA	ACGATCCTTT	CAGCGATTAA	AAGCTCTAGT	240
AAAGGGATCA	TTTAAATTGA	TGGCTATCCC	AGGAGCGTGG	AGCAAATGCA	AGCTTTGGAT	300
AAGGAATTGA	ACGCTCCAAA	TGAAGTGATT	TTAAAAAGCG	TGATTGAAGT	AGAAGTGAGC	360
GAAAACACCG	CTAAAGAAAG	GGTTTTAGGG	CAGTTTTAG			399

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

ATGCATTATT CTTATGAAGC CTTTTTAAAA GACAGCCTGG AGTTAGCTAA ACAAGTGGAG	60
CGCCTTTGCG GTATCCCAGA AGCCCTTG TGCGTGATGC GAGGGGGCAT GACTTTAGTG	120
CATTTTTTGA GTTTGCACTG GAATTTAAGG GAAGTTTATG GCATCAATGC GATTTCTTAT	180
GACACCACCA AGCGACAAAA CGCCCTAAAA ATTGAAAATA CCCCCACGAT CAAAGATCAT	240
TTAAAAACCA TTTTAGTGGT AGATGAAATC GTAGATAGCG GTAATTCTTT GGAAGCGGTA	300
CTTAAAGTGT TGCAAGACAA ACACCCTGAT AAAAAGTTTT ATAGCGCGAG TTTGTTCCAA	360
AAAACAAGCG CGAAATACAA AGCCGATGCG TTTTAAAAG ACGCTCCTGA ATGGATTGAT	420
TTCTTTTGGG AAGTGGATTT GAAAAACTTG AAAAGCCACT GA	462

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

TTGTCTGAAC CCATAGATAG ATTCACACGC ATAAGGTGGT TGTTTAAAAA CGATTTTGAA	60
AAAATCCGCC AACAAAGGGT TTTAATCTGT GGCGTGGGGG GCGTTGGAGG CTTTGCACTA	120
GATTCCTTGT ATCGTGTGGG GATAGGGCAA ATCACTATCA TTGATAAAGA CATGTTTGAT	180
GTTACCAATC AAAACCGCCA GATTGGATCA GAAAGGATAG GAGAATCTAA AGTGTTGGTG	240
TTGCAAGATC TCTATAAAGG CATCCAAGCT TFAAATTGTC GCATAGATGA AGCGTTTTTA	300
AATTCATTTA ATTTTAGAGA TTATGATTAC ATTTTAGATT GCATGGACGA TTTGCCTATT	360
AAAACAAGCC TAGCGATAAA ATGTCAAAAT TTCGCTTACG GGAAGTTTAT CAGCTCTATG	420
GGGAGCGCGA AGCGTTTGAA TCCTAAACAC ATCCAAGTGG GGAGCGTGTG GGAAAGCTAT	480
GGCGATAAAT TCGGGCGTAA ATTTAGGGAT TTTTAAAAA AACGCCGTTT TAAGGGGGAT	540
TTTAAGGTGG TTTTAGCCC TGAAGTCCCG CATTCATAG AGCTTGGAAG CTTTAATGCC	600
GTTACGGCGA GTTTTGTTTT GCAAATAGCG AGTGAAGTCG TGCAAGATAT TATCAAAAAT	660
GAAAGGCAAT GGAATGAAAG ATTACGAAGA CGAATTGGAA GATTTTGA	708

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1320 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

ATGCAAGTTA	AAGAAAACAA	ACAACTCTGC	TTGATCTCAT	TAGGTTGTTC	TAAAAATTTA	60
GTGGATTGAG	AGGTGATGTT	AGGCAAGCTT	TATAATTACA	CGCTCACTAA	TGACGCTAAA	120
AAAGCCGATG	TGATCCTTAT	CAACACTTGC	GGTTTTATTG	AAAGCGCTAA	ACAAGAGAGT	180
ATCCAAACCA	TTCTCAACGC	AGCCAAAGAC	AAAAAAGAGG	GAGCGATTTT	AATTGCGAGC	240
GGGTGCTTGA	GCGAGCGCTA	TAAAGATGAA	ATCAAAGAAT	TGATCCCTGA	AGTGGATATT	300
TTTACCGGCG	TGGGGGATTA	TGACAAGATT	GATATTTTAA	TCGCTAAAAA	ACAAAACCAA	360
TTCAGCGAGC	AGGTGTTTTT	AAGCGAGCAT	TATAACGCGC	GCATTATCAC	GGGATCGAGC	420
GTGCATGCTT	ACGTTAAAAAT	TTCTGAGGGC	TGTAACCAAA	AATGCTCTTT	TTGCGCTATC	480
CCTAGCTTTA	AGGGAAAAAT	ACAAAGCAGG	GAATTAGACT	CCATTTTAAA	AGAAGTAGAA	540
GATCTAGCCC	TTAAAGGCTA	TAAAGATATG	ACTTTTATCG	CTCAAGATTC	TAGCTCATTT	600
TTATACGATA	AGGGGCAAAA	AGACGGCTTG	ATCCAGCTCA	TTAGAGCGAT	TGACAAACAG	660
CAAGCCTTAA	AGAGCGCGCG	TATTTTATAC	CTCTACCCCT	CTAGCACCAC	TTTAGAGCTG	720
ATTGGCGCGA	TTGAAGACTC	GCCTATTTTT	CAAAATTATT	TTGACATGCC	CATCCAGCAT	780
ATCAGCGACT	CCATGCTTAA	AAAAATGCGG	CGCAACTCCA	GCCAAGCACA	CCATTTAAAG	840
CTTTTAAACG	CCATGAAGCA	GGTTAAAGAA	AGCTTTATAA	GAAGCACGAT	CATTGTAGGG	900
CATCCAGAAG	AAAATGAGAG	CGAATTTGAA	GAATTGAGCG	CGTTTTTAGA	CGAGTTCCCG	960
TTTGACAGAT	TGAATATTTT	TGCTTTCAGT	GCTGAAGAAA	ACACGCATGC	CTATTCTTTA	1020
GAGAAAGTGC	CTAAAAAAAT	CATCAACGCC	CGCATTAAAG	CCTTGAATAA	AATCGCTTTA	1080
AAACACCAAA	ACCATTCTTT	TAAGGCTTTG	TTGAATAAGC	CCATTAAGGC	GTTAGTGGAA	1140
CATAAAGAGG	GCGAATATTT	TTACAAAGCA	AGGGATTTGA	GATGGGCGCC	TGAAGTGGAT	1200
GGGGAAATTT	TAATCAATGA	CAGCGAACTA	ACCACCCCTT	TAAAACCCGG	GCATTACACG	1260
ATTGTGCCTA	GCGCCTTTAA	AGACAATATT	TTACTCGCTA	AGGTTTTAAG	CCCTTTTAA	1320

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2004 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...2004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

AAAAAACCCCT	TTTACTCTCT	CTCTCTCGCT	TCATCGCTTT	TAAACGCTGA	AGACAACGGC	60
TTTTTTATCA	GCGCGGGCTA	TCAAATCGGT	GAAGCCGCTC	AAATGGTGAA	AAACACCGGC	120
GAATTGAAAA	AACTTTCAGA	CACTTATGAG	AATTTGAGCA	ACCTTTTAAC	CAATTTTAAC	180
AACCTCAATC	AGGCGGTAAC	GAACGCGAGC	AGCCCTTCAG	AAATCAATGC	TGCGATCGAT	240
AATTTAAAAG	CAAACACGCA	AGGGCTAATT	GGCGAAAAAA	CCAATTCCCC	GGCGTATCAA	300
GCGGTGTATT	TGGCGCTCAA	TGCGGCGGTA	GGGCTGTGGA	ATGTCATCGC	CTATAATGTC	360
CAATGCGGTC	CTGGTAACAG	TGGACAACAA	AGCGTAACCT	TTGAGGGCCA	ACCAGGACAT	420
AATTCAGTT	CCATTAATTG	CAATTTAACC	GGTTATAACA	ACGGGGTTAG	CGGCCCTTTA	480
TCCATTGAGA	ATTTTAAAAA	GCTTAATCAG	GCTTATCAAA	CTATCCAACA	AGCTTTAAAA	540
CAAGATAGCG	GATTTCTGT	TTTGATAGT	GCAGGAAAAC	AAGTAACTAT	AACAATAACA	600
ACGCAAACTA	ATGGAGCTAA	TAAAAGTGAA	ACTACTACTA	CTACTACTAC	TACTAATGAC	660
GCTCAAACCC	TTTTGCAAGA	AGCCAGTAAA	ATGATAAGCG	TCCTCACTAC	AAACTGCCCA	720
TGGGTCAATC	ACAATCAAGG	ACAAAACGGG	GGCGCGCCGT	GGGGTTTAGA	TACGGCAGGG	780
AATGTGTGTC	AGGTTTTTGC	CACGGAATTT	AGCGCCGTTA	CTAGCATGAT	CAAAAACGCC	840
CAAGAAATCG	TAACGCAAGC	TCAAAGCCTT	AACCAGCAAA	ACAATCAAAA	CGCGCCGCAA	900
GATTTCAATC	CTTACACCTC	TGCTGATAGG	GCTTTCGCTC	AAAACATGCT	CAATCACGCG	960
CAAGCGCAAG	CCAAGATACT	TGAGCTAGCC	GATCAAATGA	AAAAAGACCT	TAACACTATC	1020
CCAAGCCAAT	TTATCACAAA	TTACTTGGCA	GCTTGCCACA	ATGGGGGTGG	GACATTACCT	1080
GATGCGGGGG	TTACTAACAA	CACCTGGGGG	GCCGGTTGCG	CGTATGTGGA	AGAGACGATA	1140
ACGGCTTTAA	ACAACAGCCT	TGCGCATTTT	GGCACTCAAG	CTGAGCAAAT	CAAGCAATCT	1200
GAGTTGTTGG	CGCGCACCAT	ACTTGATTTT	AGAGGCAGCC	TTAGTAATTT	AAACAACACT	1260
TATAACAGCA	TCACCACGAC	CGCTTCAAAC	ACGCCTAATT	CCCCATTCTT	TAAAAATTG	1320
ATAAGCCAAT	CCACTAACCC	TAATAACCCC	GGGGGCTTAC	AGGCCGTTTA	TCAAGTCAAC	1380
CAAAGCGCTT	ATTCGCAATT	ATTAAGCGCC	ACGCAAGAA	TAGGGCATAA	CCCTTTCAGA	1440
CGCGTTGGAT	TAATCAGCTC	TCAAACCAAC	AATGGTGCCA	TGAATGGGAT	CGGTGTGCAA	1500
GTGGGCTACA	AACAATTTTT	TGGTGAAAAG	AGAAGGTGGG	GGTTAAGGTA	TTACGGCTTT	1560
TTTGACTATA	ACCATGCTTA	TATCAAATCT	AGCTTTTTCA	ATTCGGCTTC	TGATGTGTTC	1620
ACTTATGGGG	TAGGGACAGA	TGTCCTCTAT	AACTTTATCA	ATGATAAAAC	CACCAAAAAC	1680
AGCAAGATTT	CTTTTGGGGT	GTTTGGGGGG	ATTGCGTTAG	CTGGCACTTC	ATGGCTGAAT	1740
TCCAGTATG	TGAATTTAGC	GACCTTCAAT	AATTTCTATA	GCGCTAAAAT	GAATGTGGCG	1800
AATTTCCAAT	TCTTGTTCAA	TTTAGGCTTG	AGAATGAACC	TCGCTAAGAA	TAAGAAAAAA	1860
GCGAGCGATC	ATGCGGCTCA	GCATGGCGTG	GAATTAGGCG	TGAAGATCCC	CACGATCAAC	1920
ACGAATTACT	ATTCTTTGCT	AGGCACTCAA	CTCCAATACC	GAAGATTGTA	TAGCGTGTAT	1980
TTGAATTATG	TGTTGCTTA	CTAA				2004

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

ATGTTTATAC TTTTAAAGTT TGGTAGGGTT TTGGGTAAGG CTTATAGCTT ATACTTATAT	60
ATATATGAAA GCTTGATTTG TCAAGCTTTT GGGTTGTCAT TGAGTTGCAA TAACTCTATG	120
CTGTTTTCTA CTTTTTTGAT AAATCTACCA TTACCACACA ATGAGTCCTT ATGCTGTTGT	180
AGGGATATTT TAGCGTATTC TAACTCTTCA TCGCTAAAGA CATATTCATT GGAGTCAAAT	240
TTTTCTTTCA ATTCTTTATT TTGA	264

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

ATGTTTATGG CGTCAATACG GACGCTGACG CACATGACTA ACGCTGATGG TACGATCACA	60
TGCGGAGACA CGACGCCGGC GAGTTGTAAT GTGGGGATTA ACCCTAACAG CGTCTATACC	120
ACAGGAAAAT TAAACGCTAA AGTGAATCAC ACGATTTTCC AATTTT TAGT GAATGTGGGC	180
ATTAGAACC A ATATTTTGA ACACCATGGC ATTGAGTTTG GTATCAAAAT CCCACGCTC	240
CCTAATTACT TTTTCAAAGG TTCTACTACT ATAAGAGCGA AAAAACAAGG CCCACTAGAG	300
AATGGGAACC CGACTACTAT CACCGGAGCA GAAACCAATT TCAGCTTAAC CCAAACCTTA	360
CGCCGTCAGT ATTCTATGTA TTTGCGTTAT GTTTATACTT TTAA	405

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

TTGAACAAAC	TGCTTAAAAA	GGGGTTTTTA	GCGTTCCTTTT	TAAGCGTGTA	TTTAAGGGCT	60
GATGATCTGG	TTACTTATAC	GATCGCCAAA	GAAGAAGATC	TAGGGTACCA	GCGGTTTTTA	120
GCCAAGAAGT	GTTTAAGGGG	TAAAACCCAC	CCCCCATGTT	TTACCGCGTC	TAAAAAGCCC	180
AAGAGGAAAC	CTTTTAATAT	AGATAAAAGC	TCCCATTATT	ATGGCAGGAG	CGTGGTGCAA	240
ATGTCATGGC	TACAGAGTAG	GGAAAAATTT	GAAAACCATT	CAAAATACCG	AAACATTCCT	300
TTTGCTGAAG	TCAGTTTGAT	TTATGGCTAT	AAACAATTTT	TTCCTAAAAA	AGAGCACTAC	360
GGCTTCCGTT	TTTATGTCTC	TTTGGATTAC	GCTTATGGCT	TTTTTCTTAA	AAATAAAGGC	420
GCATTAGGCG	ATAGTTTGAG	GGCGAGTTCG	CAGATCCCTA	AAAGCTATAG	AGAAAAATTA	480
CAAAGAAAAG	AGACTTTTAT	TAACGCTATT	TTTTATGGCG	TGGGGGCTGA	CTTTTTTATAC	540
AAACGCGCTT	TTGGGACGCT	GATTTTAGGG	GTGAATTTTCG	TGGGAGAAAC	CTGGTTTTTAT	600
GAAACAAAGA	TTTTCAAACA	ATGGGCTAAA	GACTCTCTAA	ATACTTACCG	CCCCAACATG	660
TTTCAAGTGA	TGTTGAATGT	GGGGTATCGC	TACCGCTTTT	CAAGGTATAA	GAATTGGGCG	720
ATAGAATTTG	GCGCGCGCAT	CCCCTTTTTA	ATTAATGATT	ATTTTAAAC	CCCTTTATAC	780
ACCCTTCATT	TCAAACGCAA	TATTTCTGTC	TATCTCACTT	CAACTTATGA	TTTTTAG	837

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1497 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

ATGAAATTAA	AAAAACGAAA	AGTTGCGGCT	ACATTGCTAA	AGCGTTTGAC	CTTGCCACTA	60
TTGTTCACTA	CGGGTTCATT	AGGGGCGGTT	ACTTATGAAG	TGCATGGGGA	TTTTATCAAC	120
TTCTCCAAAG	TGGGTTTTAA	CCGTTCGCCT	ATTAACCCTG	TTAAAGGTAT	CTATCCTACA	180
GAAACTTTTG	TTAACCTTAC	GGGTAAGCTA	GAGGGGTCTG	TGCATTTAGG	TAGGGGATGG	240
ACCGTGAATG	TAGGCGGTGT	TTTGGGCGGA	CAAGTTTATG	ATAACACTAG	GTATGATAGG	300
TGGGCAAAGG	ATTTTACCCC	CCCAAGCTAT	TGGGATAAAA	CTTCTTGCGG	CACTGATTCT	360
TTGAGCCTTT	GTATGAATGC	GAATAAAATG	TGGCAACAGC	AAGGGCCAGG	TGGTATCATT	420
GACCCTAGGG	GTATTGGCTA	TATGTATATG	GGTGAGTGGA	ACGGCTTGTT	CCCTAATTAC	480

TATCCGGCTA	ACGCCTACTT	GCCCGGGCAT	TCAAGGCGCT	ATGAAGTTTA	TAAAGCGAAT	540
CTTACCTATG	ACAGCGACAG	AGTCCATATG	GTAATGGGGC	GCTTTGATGT	TACCGAGCAG	600
GAGCAAATGG	ATTGGATTTA	CCAATTGTTC	CAAGGTTTTT	ATGGGACTTT	CAAGCTTACT	660
AAGAACATGA	AATTCTTGCT	CTTTAGCTCT	TGGGGTCGTG	GTATCGCTGA	TGGTCAATGG	720
TTGTTCCCTA	TCTATCGTGA	AAAGCCTTGG	GGTATTCATA	AGGCGGGTAT	TATTTATCGC	780
CCTACAAAGA	ATCTAATGAT	CCACCCTTAT	GTGTATCTCA	TCCCAATGGT	AGGTACATTG	840
CCCGGTGCTA	AAATAGAATA	CGATACCAAT	CCTGAGTTTA	GCGGTAGAGG	TATAAGGAAT	900
AAAACGACTT	TCTATGTGTT	GTATGACTAT	CGTTGGAATA	ACGCTGAATA	CGGCCGTTAC	960
GCACCCGCTC	GTTATAACAC	TTGGGATCCG	TTCTTGATA	ATGGTAAGTG	GCGTGGCTTG	1020
CAAGGTCTTG	GTGGTGGCAG	GCTCTATTTG	CACCACCACA	TAGACATTAA	CAACTACTTT	1080
GTGGTTGGTG	GTGCTTACCT	CAACATCGGT	AACCCTAACA	TGAACTTAGG	TACTTGGGGT	1140
AACCCTGTGG	CTCTTGATGG	TATCGAACAA	TGGGTCGGTG	GCATCTACAG	CTTAGGCTTT	1200
GCGGGGATTG	ACAACATTAC	CGATGCTGAT	GCGTTCCTG	AGTATGTTAA	AGGTGGAGGT	1260
AAGCATGGTA	AGTTCAGTTG	GAGCGTTTAT	CAGCGCTTCA	CTACCGCACC	AAGGGCTTTG	1320
GAATATGGTA	TTGGTATGTA	TCTAGACTAT	CAGTTCAGCA	AGCATGTTAA	AGCGGGTCTC	1380
AAACTCGTGT	GTTTAGAGTT	CCAAATCCGT	GCGGGTTACA	ACCCTGGAAC	CGGTTTCCTT	1440
GGGCCAAACG	GTCAGCCGCT	CAACTTGAAT	AATGGTTTGT	TTGAATCTTC	GCGGTTTC	1497

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

TTGAAAGAAA	AATTTGATTT	TTTTAAAGGC	AAAAATTTTA	AAATTGTCTA	TTGTATTGGC	60
GAAGATTTAA	CGACCAGAGA	AAAGGGTTTT	AGGGCTGTAA	AGGAATTTT	AAGCGAGCAA	120
TTAGAAAATA	TTGATCTTAA	TTATTCCAAT	TTAATTGTGG	CTTATGAGCC	TATTTGGGCG	180
ATTGGCACTA	AAAAAGCGCG	CTTTTAG				207

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

ATGAGTAAGA GCGCGATTTT TGTTCTTTCT GGCTTTTCTAG CGTTCTTGCT CTATGCTTTG	60
TTATTATATG GTTTGTTGTT AGAAAGGCAT AATAAAGAAG CAGAGAAAAT CCTTTTAGAT	120
TTAAATAAAA AGGACGAACA AGCCATTGAC TTGAATTTAG AAGATCTGCC AAGCGAGAAA	180
AAGAATGAAA AAATTGAAAA AGTAACGGAA AAACAGGGCG ATTTTCTAGA GCCTAAAGAA	240
GAACCCAAAG AAGAGCCTGA AGAAAGCCTT GAAGATATTT TTTCTTCACT CAATGATTTT	300
CAAGAAAAGA CAGACAAAAA CGCTCAAAAA GACGAGCAAA AAAATGAACA AGAAGAACAA	360
AGGCGTTTAA GAGAGCAACA ACGCTTGAAA CAAAACCAAG AAAACCAAGA GATGTTGAAA	420
GGTTTGCAAC AAAATTTGAA TCAATTCACG CAAAATTAG AAAGCGTTAA AAACAAGACT	480
TTAGATTTGC AAATCCCTAA ACAAGATGGG GTTGATGAAA AGGCTTATCA AGAGTGGTAC	540
GCTCAATCT ATCAAATTTT ATATAAAGGC TGGAGGGGCG TTTTCTATCA CAAGGCTTCA	600
GTGAGCGTGC TGATTATGAT CACTAAAGAT GGAGAGTTTG ATTATACCAT TCTTAGCTAC	660
TCTGATTTTA AGGATTATAA CAAGAGCGTG ATGACCCTTT TAGATGATTT AAAGAAAGTG	720
GATTTCCCCC CATATCCTGG AGGAAACATG ATTTCTATTA AAGTTAATTT TACGACTAAG	780
GAAGAACAAT GA	792

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2355 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

ATGGAGCAGC CAGTCATTAA AGAAGGGACT TTAGCTTTAA TTGATACCTT TGCCTATTTG	60
TTTAGAAGCT ATTACATGAG CGCTAAAAAT AAGCCTTTAA CCAACGATAA GGGCTTTCCT	120
ACAGGGCTTT TAACGGGGCT TGTGGGCATG GTTAAAAAAT TTTATAAAGA CAGAAAAAAC	180
ATGCCCTTTA TCGTGTTCGC CCTAGAAAGC CAGACTAAAA CTAAAAGAGC TGAAAAACTG	240
GGCGAATACA AACAAAATCG TAAAGACGCC CCTAAAGAGA TGCTTTTACA AATCCCTATC	300
GCCTTAGAAT GGTTGCAAAA AATGGGTTTT ACTTGCGTGG AGGTGGGAGG GTTTGAAGCC	360
GATGATGTGA TCGCAAGTTT AGCCACGCTA AGCCCTTATA AAACCCGCAT TTATTCTAAA	420

GATAAGGATT	TTAACCAGCT	TTTGAGCGAT	AAAATCGCGC	TTTTTGATGG	CAAAACGGAG	480
TTTTTGCGGA	AAGATTGCGT	GGAAAAATAC	GGGATTTTGC	CGAGTCAATT	CACGGATTAT	540
CAGGGCATTG	TGGGGGATAG	CAGCGATAAT	TACAAGGGGG	TTAAAGGCAT	TGGGAGCAAG	600
AACGCTAAGG	AATTGTTGCA	GCGATTAGGG	AGCTTGGAAG	AAATCTATGA	AAATTTAGAC	660
TTGGCGAAAA	ATTTACTCAG	CCCTAAAATG	TATCAAGCCT	TGATACAAGA	CAAAGGAAGC	720
GCCTTTTTTA	GCAAAGAATT	AGCCACTTTA	GAAAGAGGAT	GCATTAAAGA	ATTTGATTTT	780
TTAAGTTGCG	CTTTTCCGAG	CGAAAACCCC	TTGTTGAAAA	TCAAAGATGA	ATTGAAAGAA	840
TATGGTTTCA	TTTCTACCTT	AAGGGATTTA	GAAAATTTCC	CTTTCATTGT	AGAAAACGTG	900
CCCATATTAA	ACAGCACGCC	TATATTAGAC	AATACCCCCG	CCTTAGACAA	CGCCCCTAAA	960
AAATCGCGCA	TGATTGTTTT	AGAAAGCGCT	GAGCCTTTGA	GCATGTTTTT	AGAAAAATTA	1020
GAAAACCCTA	ACGCTAGGGT	TTTTATGCGT	TTGGTTTTGG	ATAAGACAA	AAAAATTCTA	1080
GCCCTAGCGT	TTTTATTACA	AGATCAAGGC	TATTTTTTAC	CTTTAGAAGA	GGCGTTGTTT	1140
TCGCCCTTTT	CTTTGGAATT	TTTACAAAAC	GCTTTTTCTC	AAATGTTACA	GCATGCGTGT	1200
ATCATTGGGC	ATGATTTAAA	GCCTTTATTA	AGCTTTTTTA	AAGCCAAATA	TCAGGTGCCT	1260
TTGGAAAATA	TCCGCATCCA	AGACACTCAG	ATTTTAGCGT	TTTTAAAGAA	TCCGGAAAAA	1320
GTGGGGTTTG	ATGAGGTTTT	AAAGGAATAT	TTAAAAGAAG	ATTTAATCCC	GCATGAAAAG	1380
ATCAAAGATT	TTAAGACAAA	AAGTAAGGCG	GAAAAATCAG	AACTTTTAAG	CATGGAATTA	1440
AACGCCTTAA	AGCGTTTGTG	CGAATACTTT	GAAAAAGGGG	GGCTAGAAGA	GGATTTGCTC	1500
ACTTTAGCTA	GAGACATTGA	AACGCCGTTT	GTGAAAGTTT	TAATGGGCAT	GGAATTTCAA	1560
GGCTTTAAGA	TTGATGCGCC	TTATTTCAAG	CGCTTAGAGC	AGGAGTTTAA	GAATGAATTA	1620
AACGTTTTAG	AGCGCCAAAT	TTTGATCTA	ATCGGCGTGG	ATTTCAACCT	CAATTCGCCC	1680
AAGCAACTTG	GCGAAGTCTT	GTATGATAAA	TTAGGGCTTC	CTAAAAATAA	AAGCCACTCT	1740
ACCGATGAAA	AAAACCTGTT	AAAAATCCTA	GACAAGCACC	CAAGCATCCC	TTTGATTTTA	1800
GAATACAGGG	AATTGAATAA	GCTTTTTAAC	ACTTACACGA	CCCCCTTATT	GCGCTTAAAA	1860
GACAAAGACG	ATAAAATCCA	TACCACTTTC	ATCCAAACCG	GCACAGCTAC	CGGGCGTTTA	1920
AGCTCGCATT	CGCCTAATTT	GCAAAATATC	CCGGTGCGAT	CGCCTAAAGG	CTTACTCATT	1980
CGTAAGGGTT	TTATCGCTAG	CTCTAAAGAA	TATTGTTTAT	TAGGGGTGGA	TTATTGCGAG	2040
ATTGAATTAC	GCTTGTTGGC	CCATTTTCAGC	CAGGATAAGG	ATTTAATGGA	AGCGTTTTTA	2100
AAGGGGCGAG	ACATCCATTT	AGAAACTTCT	AAGGCGTTGT	TTGGAGAAGA	TTTAGCCAAA	2160
GAAAAACGAT	CCATCGCTAA	AAGCATTAAT	TTTGGGCTGG	TGTATGGCAT	GGGGAGTAAG	2220
AAATTGAGCG	AAACTTTAAG	CATCCCTTTA	AGTGAGGCTA	AAAGTTACAT	AGAAGCGTAT	2280
TTCAAGCGAT	TCCCTAGCAT	TAAAGATTAT	TTGAATGGCA	TGCGAGAAGA	GATTTTAAAA	2340
ACTTCTAAAG	CTTTT					2355

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

GTGAGCGAGA	GCGAAAAACA	AGAAATTGAA	AACAAGATAG	AAGAAAGAAA	ACGTGCCAAA	60
GAACAAAAAG	ATTTTTTAAA	AGCCGATAGC	ATCAGAGAAG	AGCTTTTACA	ACAAAAAATC	120
GCTTTGATGG	ACACCCACAC	AGGCACGATT	TGGGAGAAGC	TTTTTTAA		168

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

TTGCCGAGCG	TTCAAATATG	GGGGAGCTAC	ACTAACTCGT	TTAAACAAAC	CTTTAGCGCA	60
AGTAATAGCA	ATCTGGTGAT	TGGGTATAAC	GCAACATGGA	CTGATCCCAA	TGTTTCTTCT	120
AGCGACACGG	TGGCTTTTGG	GGACCCTTCA	GGGAGCGCTC	TTAATGGGCA	TTGCGGGCCT	180
TGGCCCTATT	ACCAATGCAC	AGGCACGACT	AACGGCACTT	ATAGCGCTTA	TCATGTCTAT	240
ATCACAGCGA	ATCTGCGTTC	TGGCAATCGT	ATAGGCACCG	GTGGGGCAGC	CAATCTAATC	300
TTTAATGGGG	TAGATAGTAT	CAATATCGCT	AACGCTACCA	TCACGCAACA	TAACGCCGGG	360
GCTTATTCAA	GCTCTATGAC	TTTTTCCACG	CAAAACATGG	ACAATTCGCA	GAATTTGAAT	420
GGCCTAAATT	CTAACGGCAA	GCTTTTGGTG	TATGGCACAA	CTTTCACTAA	CCAAGCCAAA	480
GACGGGAAAT	TCATTTTCAA	TGCAGGGCAA	GCGACTTTTG	AAAACACCAA	CTTTAATGGA	540
GGGAGTTACC	AATTCAGCGG	CGATAGCTTG	AATTTTTTCAA	ATAACAACCA	GTTCAATAGC	600
GGTTCGTTTG	AGATTGGCGC	AAAAAATACT	ATTTTTTAATA	ACGCTAATTT	TAACAACAGC	660
ACTTCTTTTA	ATTTCAATAA	TTCTAGCGCG	ACCACTTCGT	TTGTGGGGGA	TTTCACTAAC	720
GCTAATTCAA	ATTTGCAAAT	CGCTGGGAAC	GCTGTTTTTG	GGAACCTCTAC	TAATGGCTCT	780
CAAAATACCG	CTAATTTTAA	TAATACCGGC	TCTGTTAATA	TTGCAGGGAA	TGCAACCTTT	840
GATAACGTGG	TATTTAACAG	CCCTACGAAC	ACGAGCGTGA	AAGGGAAAAGT	TACTCTCAAT	900
AACATCACTT	TAAAAAACTT	GAACGCTCCT	TTGTCTTTTG	GCGATGGGAC	GATTGTTTTT	960
AGCGCTCATT	CGGTGATTAA	TATTGGTGAA	GCTATCACAA	ATGGCAACCC	TATCACCCCT	1020
GTAAGCTCTT	CTAAAGCAAT	TGAATACAAC	GACGCTTTCA	GTAAAAATCT	ATGGCAGCTC	1080
ATCAACTACC	AAGGGCATGG	GGCTAGCAGT	GAAAAGCTCG	TTTCTAGTGC	GGGTAATGGC	1140
GTCTATGATG	TGGTGTATTC	TCTCAACAAC	CAAACCTACA	ATTTCCAAGA	GGTTTTTTTCA	1200
CCCAACAGCA	TTTCTATCCG	GCGTTTGGGC	GTTGGCATGG	TGTTTGATTA	TGTGGATATG	1260
GAAAAATCGG	ATCGTTTGTA	TTATCAAAAC	GCTCTCGGTT	TTATGACCTA	CATGCCTAAT	1320
AGCTATAACA	ATAATTTAGG	GAATTTAAAC	AACACCATT	ACTATTACGA	CAACAGCATT	1380
GACTTTTATG	CGAGCGGGAA	AACTCTATTC	ACTAAAGCGG	AATTTTCTCA	AACGTTCACT	1440
GGGCAAAACA	GCGGATCGT	TTTTGGGGCT	AAAAATATAT	GGACGAGCGT	AAGCGATGCG	1500
CCGCAATCTA	ATGTGATCAT	TCGCTTTGGG	GACAATAAGG	GAGCAGGGAG	TAATGATGCG	1560
AGTGGGCATT	GCTGGAATTT	GCAATGCATA	GGCTTTATCA	CAGGGCATT	TGAAGCGCAA	1620
AAGATTTACA	TCACCGGCAG	TATTGAAAGC	GGGAACCGCA	TTTCTAGCGG	TGGGGCGCGA	1680
GCCTTAATTT	TAACGGGCTT	CAAGGCATTC	TTTTAA			1716

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

ATGGTTGTTT	TAGGAAGCAC	CGGCTCTATC	GGGAAAAACG	CCCTTAAAAT	CGCAAAAAAA	60
TTTGGTGTA	AAATAGAAGC	CTTAAGCTGT	GGGAAAAATA	TCGCTTTAAT	CAATGAACAA	120
ATCAAAGTTT	TCAAACCCAA	AAAAGTAGCG	ATCTTAGATC	CTAACGATTT	GAATAATTTA	180
GAGCCTTTGG	GCGCGGAAGT	GTTTGTGGGG	TTAGACGGCA	TTGATGCGAT	GATAGAGGAG	240
TGCGTTTCCA	ATTTAGTCAT	TAACGCCATT	GTGGGCGTAG	CCGGATTGAA	AGCGAGCTTT	300
AAAAGCTTAC	AAAGGAACAA	AAAAGTAGCC	CTAGCGAATA	AAGAAAGTTT	AGTGAGCGCG	360
GGGCATTTAT	TAGACATTTT	ACAAATCAGC	CCCCTTGATA	GCGAGCATTT	TGGTTTGTGG	420
GCGTTGTGTC	AAAACAAGAC	TTTAAAGCCT	AAATCTTTAA	TCATTAGCGC	GAGTGGGGGG	480
GCTTTTAGGG	ACACGCCCTT	AGATCTTATC	GCTATTCAAA	ATGCGCAAAA	CGCGCTCAAG	540
CACCTTAATT	GGAGCATGGG	GGATAAAATC	ACCATTGATT	CAGCGAGCAT	GGTCAATAAA	600
CTTTTGTAAA	TTTGTAGAAC	CTATTGGCTT	TTTGGTGCGT	CTTTAAAGAT	TGACGCGCTG	660
ATTGAAAGAA	GTCTATCGT	GCATGCTTTG	GTGGAGTTTG	AAGACAACCT	TGTCATTGCG	720
CATTTAGCGA	GTGCGGACAT	GCAATTACCC	ATAAGCTATG	CCATTAACCC	TAAATTAGCT	780
TCTTTGAGTG	CTTCCATTAA	ACCCTTAGAT	TTATACGCTT	TAAGCGCGAT	TAAATTCGAA	840
CCCATTAGCG	TGGAGCGCTA	CACTTTGTGG	CGTTATAAAG	ATTTGTTGTT	GGAAAACCCA	900
AAGCTTGGCG	TGGTGCTGAA	TGCGAGCAAT	GAAGTGGCGA	TGAAGAAGTT	CTTGAATCAA	960
GAAATCGCTT	TTGGTGGCTT	TATCCAAATC	ATCTCTCAAG	CTTTAGAATT	GTATGCTAAA	1020
AAATCTTTCA	AGCTCTCTAG	TTTAGATGAA	GTGCTAGCGT	TAGATAAGGA	AGTTAGGGAG	1080
CGTTTTGGAA	GTGTAGCGAG	AGTGTAG				1107

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

ATGAAAACGA CAGAAAACAC AGATGAAACT CACTTAAGGG AAACTAAAAA TAACTAGGA	60
CGCAAACCAA AAGCAGACGC TAATAAAAAA ACTCGCGCGG TAAGCTTGTA TTTTCTGAT	120
GAGCAATACC AAAAACTAGA GAAATGGCT AACGAAGAAG AAGAAAGCGT GGGATCTTAT	180
ATCAAACGCT ATATTTTGAA GGCTTTAAGA AAAATAGAAC AAGGTGGTGG CTTTATAGCT	240
TTTAACTTGT TTTTAATTTA A	261

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2412 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

TTGTGGCTTA AGTCAAATT CTTTCTTTTA ATGGGCGTGG GTTTGCTCTC CCATTCACTC	60
AACGCTTTAA GCCTCACGCT CACGCAAGGC AAAGAAGAAG GAGAAGATTT TTCGGTTTTA	120
ACCTTACGAA ACGATAAGGC GTTTTCTTGC TCTTATGCTA ATGAAAACC GCCGAGCGGG	180
ATTGAAGCGT CTTTATCTAT TATACACGCT AAACGCCCCA TAGAATGCGT GATAGATTCT	240
ATTCTTAAAG AGGGCTTTAC CCCTTTAGAA AACGCTTTT TCAATATCAC CTATTCCATG	300
CGCCAGCAAC AATTCATTTT ACACATCAAA CCCAAAGTGA TGCGAAGGCT CACCCTTTTT	360
TCTTTTGATA GGGATTATAA AAAAGCGATC CCCCTTTTGT TGGAAAACGA CGCTAAAGCC	420
AAGATGTGGC AATCATAGG CTATGATCAA AAAATCCCCT TTTTGAGCGA AAAAGACAAC	480
GCTCAAAAAG GCTTGAATTT CCCCATATC ATTAAAGACG CTCAAACCCC TATCATTCAA	540
GAGCTGGATG TGAATAACAA ACCCCTACTC ACCACAAAGG GCTATGATTT AAACGCCTAT	600
TTAGAAGCTA AAAAACAAAT GGATTCGCAA GCCTATTTTG ACGCCTTACG CACGATCAGC	660
CGCGCGTTTA AAAATTACCC TCAAACGATT TTTAAAAAAG ATCTGTATTT ATTAGAAATT	720
ATCGCATTAG GTAAATTAGG CATTAAAAAA TCCTTACTCA TAGATATTGG CACCCAATGG	780
ATTAAAAATT ACCCGACTGA TCCTAATATC CCTGAAGCGC TATACTATGT CGCCAAAGCT	840
TTAGATGAAA ACAACAATTA CAAACAAGCC GTGCGCTATT ACAAACGAAT CCTTTTAGAA	900
TACAAAACT CCCGCTACGC TCCCTTAGCC CAAATGCGTT TAGCCATTGA AGCGGCTGAA	960
GGCTCTGATT TGAGCAACGC TAATATGCTT TTAAAGAAG CTTTTTCTAA CGCCAAAGAC	1020
AAAGAGAGCG CGAGTGAAAT CGCGCTTAAT TGGGCTGAAG CAGAGATAAA CTATCAAAAC	1080
TTAATAACG CTAAATATCT CATTGATAAG GTGGTTCAAT CCAACCCTGA TTATCTTTCT	1140

ATGCACAGCG	AATTAGCCCT	AGAATTGCTC	AAGTTATTGA	AAAAAAACCA	AATGAATGAA	1200
AGTGCGATTG	AGATCGCTCA	CTTGCTCCTC	AATCAAGATG	ATGACTTGAA	AGCTAAAGAG	1260
CAAGCGCTCT	ATGATTTAGG	GGCGTTGTAT	GCAAGGATCA	AGGATTTTAA	AAACGCCCCAC	1320
CTTTACAATC	TGCAATATTT	GCAAGACCAT	GCGGAATTGG	AGCGGGCTTC	TGTCGTTAGA	1380
GCACGCGATG	AAAAAGCCCT	TTTTTCAATG	GAAGGGAACA	CGCAAGAAAA	AATCGCCCCAC	1440
TACGATAAAA	TCATTCAAAA	TTTCCCTAAT	TCTAATGAAG	CCCAAAAGGC	TTTAGAGTTG	1500
AAAGCCCAAC	TCTTGTTTGA	CAATAAGCAC	TATGCTGAAG	TTTtagGCAT	GCAAAAAAAT	1560
TTGCCCAAAG	ATTCTCCCTT	GATCCAAAAA	ACGCTCAATA	TCCTTGCTAA	AACCCCATTA	1620
GAGGATCATC	GTTGCAAAGA	AGCTTTAAAA	TACTTATCCC	AGATCACCGC	CTTTGCATTC	1680
AACCCCAAG	AAGAAATCCA	AGCCTTTGAT	TGCTTGATTT	TCGCATCGCT	CAAGGAAAAA	1740
GCGCAAATTA	TTGCCCTAAA	CGCTTTAAAA	GCGGCTAAAA	CCCCTAGCGA	GAAATTAACA	1800
TGGCTTTATC	GTTTGGGGCG	CAATTACTAC	CGCTTAGGGG	ATTTTAAAAA	TTCCACTCTG	1860
GCTTCTAAAG	ACGCCTTAAT	CCTCGCTCAA	AGCTTAAATA	AAAAAGAGTT	TTATGACATT	1920
GCTTTTGTGT	TATTTTCAGA	TTACATGCAA	AACAATGAAA	AAGGATTGGC	CCTCAATTTG	1980
TATGCGTTTT	TAGAAAAGCA	TTTCAAAGAC	GATAAACGCA	TGGCGTTGGT	TTATTTTAAA	2040
TTATTAGAGA	ATGAAAAAGA	CCCTAAAAGC	GTTAAAATTT	ATGCCACAAG	CTTACTCAAA	2100
CTCCAAGACG	CTTATAAGGA	TTATTCTTAC	ACGCCCTTTG	GCGAATTTGC	CCTTATTGAC	2160
GCTTACAGAA	CCACCAAAGA	TTATTCAAAA	GCGTTAGAAA	CGCTAGACAA	ACTCTTAAAC	2220
CGCAGGCTTT	CTTTAGAAGA	TCACCAAAAA	GCCTTATACT	TGCAATCCAG	CTTATTGGAT	2280
TTAACCAATC	AAAAAGCAAA	ATCTAAAGCC	AGTTTAGAAA	AATGCGTTCA	ATTAAAGCAA	2340
AAAGATCAAA	CAAACGCATG	GCAAAATTTA	TGCGAACAGG	GTTTAAATTT	ATTCAAAAAC	2400
AAGGAGTCAT	GA					2412

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

ATGATATTAA	GAGCGAGCGT	GTTGAGCGCG	TTACTTCTTG	TAGGCTTAGG	GGCAGCCCCCT	60
AAACATTCAG	TTTCAGCTAG	TGACAAACGG	ATGCAGGATA	ATTTAGTGAG	CGTGATTGAA	120
AAACAAACCA	ATAAAAAGGT	GCGTATTTTA	GAAATCAAAC	CTTTAAATC	CAGCCAGGAT	180
TTAAAAATGG	TCGTTATTGA	AGATCCGGAC	ACTAAATACA	ATATCCCGCT	TGTAGTGAGT	240
AAGGATGGTA	ATTCAATCAT	AGGGCTTAGC	AATATCTTTT	TTAGCAATAA	AAGCGATGAT	300
GTGAAATTAG	TTGCAGAAAC	CAATCAAAAA	ATCCAAGCCC	TTAACGCTAC	CCAGCAAAAC	360
AGCGCGAAAT	TGAACGCTAT	TTTTAATGAA	ATACCGGCTG	ATTATGCGAT	AGAGTTGCCC	420
TCTACTAACG	CTGAAAATAA	GGATAAAATC	CTTTACATTG	TTTCTGATCC	CATGTGCCCG	480
CATTGCCAAA	AAGAGCTCAC	TAAACTCAGG	GATCACTTAA	AAGAAAACAC	TGTGAGAATG	540
GTTGTAGTGG	GGTGGCTTGG	AGTCAATTCG	GCTAAAAAAG	CGGCTTTGAT	CCAAGAAGAA	600
ATGGCGAAAG	CTAGGGCTAG	GGGAGCGAGC	GTGGAAGATA	AAATCTCTAT	TCTTGAAAAG	660

ATTTATTCCA	CCCAATACGA	TATTAACGCT	CAAAAAGAGC	CTGAAGATTT	ACGCACTAAA	720
GTGGAAAATA	CCACTAAAAA	GATTTTTGAA	TCTGGCGTGA	TTAAGGGTGT	GCCTTTCTTG	780
TATCATTATA	AGGCATGA					798

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

TTGGATTTTA	AAGCGATAGA	GCATGGAGAG	GAAACCCTAA	AAAACGAGAC	TTTAAGAGCG	60
TTAAGCGATT	TTGCGAAGTC	TAGCGATACG	CATATCGTGG	CATGCAGTAT	TGAAAAAAT	120
AATAAAAAAC	TTTACGATAG	CGCTTATATC	ATTCCACCAA	AAGGAAAAAT	CGTTGGCAAA	180
CACCGCAAGA	TCTATTTGTG	GGGCGATGAA	AAATCGCGCT	TCAAAGGGG	TAAAAAATAC	240
GAGGTTTTTA	CGCTGGATTT	TGGGGATTTT	AGCGCGAAAG	TGGGTTTGCA	AATTTGCTAT	300
GAAACTGGCT	TTGGCGTGGG	TGCGAACCTG	CTTGTTGTTAC	AAGGGGCTGA	GGTTTTAATC	360
TATCCTAGTG	CGTTTGGCAA	AGCTAGGGCT	TATAATPGGG	ATTTGTTGAG	CAAAGCTAGA	420
GCGTTAGAAA	ATGGCTGTTT	TGTGTGCGCT	TGCAATCATA	GTGGGGAAGA	AACTAACGCT	480
AAATTAAAAAC	AAACGCTAGA	ATTTGCCGGT	GATTCAAGAA	TCATCGCACC	CAATGGGAAA	540
ATCATCGCCC	AAGCCACCAA	GCTTAATGAA	GTCATTATCG	CCGAAATGGA	TTTAAACGAA	600
GTGGCACTGC	AACGCCAAAA	AATCCCTTAT	TTACAAGATT	TTGACACCAA	ACTCACCAAA	660
AAGGGGTTTG	GAAAACTCAC	TTAA				684

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

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ATGGCAAAAG AAATTTTAGT GGCTTATGGC GTGGATATTG ATGCGGTGGC TGGTGGGCTG      60
GGGAGCTATG GTGGGGAGGA TTCGCCTGAT GATATTTTCGC GTGGGCTTTT TGCGGGGGAA      120
GTGGGGATCC CACGGCTTTT GAAATTGTTT AAAAAATACC ATCTCCCTGC GACTTGGTTT      180
GCGCCGGGGC ATTCTATTGA AACTTTTCCT GAACCAATGA AAATGATCGT GGATGCAGGG      240
CATGAAGTGG GTGCGCATGG GTATTCACAC GAAAACCCTA TCGCTATGAC GGCCAAGCAA      300
GAAGAAGACG TTTTGTTAAA AAGCGTTGAA TTGATTAAAG ATCTACCCGG CAAAGCCCCC      360
ACAGGCTATG TGGCGCCGTG GTGGGAGTTT TCTAATATCA CTAATGAATT GCTTTTAAAA      420
CACGGCTTCA AATACGACCA TTCGCTCATG CACAATGATT TCACGCCCTA TTTCGTGCGC      480
GTGGGGGATA GTTGAGCAA GATTGATTAT AGTTTGAGAG CCAAGGATTG GATGAAGCCT      540
TTAATCCGTG GGGTGAAAC AAATTTAGTG GAAATCCCTG CGAACTGGTA TTTGGACGAT      600
TTACCGCCGA TGATGTTTAT CAAAAATCC CCAATAGCT TTGGTTTTGT AAGCCCGCGC      660
GATATAGGGC AAATGTGGAT CGATCAATTT GATTGGGTTT ATCGTGAGAT GGATTATGCG      720
GTGTTTAGCA TGACAATCCA CCCTGATGTG AGCGCCCGTC CGCAAGTGTT GCTCATGCAT      780
GAAAAAATCA TTGAGCATAT CAACCAGCAC GAGGGCGTGC GTTGGGTAAC GTTCAATGAA      840
ATCGCTGATG ATTTCTTAAA ACGAAACCCT AGGAAAAAAT AG                        882

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(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

```

GTGTGCGGCG TATTATCGTT ACAAGCGCGT TTGAGCTTTG AAAATTGCTC TAAGCCCCTA      60
GACTGCTCAC TATTCGCTAC AACTTGCACC CCGCAAAACC CGATCGGCAG TTGCATGGTC      120
AGCTCTCAAG GGGGCGTGTG CGGCGTATTA TCGTTACAAG CGCGTTTGAG CTTTGAAAAT      180
TGCTCTAAGC CCCTAGACTG CTCACTATTC GCCACAACTT GCACCCCGCA AAACCCGATC      240
GGCAGTTGCA TGGTCAGCTC TCAAGGGGGC GTGCGCGGCG TATTATCGTT ACAAGCGCGT      300
TTGAGTTTTA AAAATTGCTT TTAGTGAAA TCGCTCAAAC CCTCGCAATT GACATTGATG      360
CTAACCGGTT TTTTAGGGGG GTTTTCTTTT TTGACAACCG GTTTTTGGTA A                411

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(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

ATGAATGGTT	TTTGCGCTAG	ACTACGAGCC	ATAACATTTA	ATGAAAGACT	AAAAATGAAA	60
ATAGCGGTAT	TACTCAGTGG	GGGGGTGGAT	AGCTCTTATA	GCGCTTATAG	CTTAAAAGAG	120
CAAGGGCATG	AATTAGTGGG	GATTTATTTA	AAACTCCATG	CGAGTGAAAA	AAAGCATGAT	180
TTATACATTA	AAAACGCTCA	AAAAGCGTGC	GAGTTTTTTAG	GCATTCCCTT	AGAGGTGTTG	240
GATTTTCAAA	AGGATTTTAA	AAGCGCGGTT	TATGATGAAT	TTATCAACGC	CTATGAAGAA	300
GGGCAAACCC	CTAACCCATG	CGCGTTGTGC	AACCCTTTAA	TGAAGTTTGG	GCTAGCTTTA	360
GATCACGCTT	TAAAAATTAGG	GTGTGAAAAG	ATCGCTACCG	GGCATTATGC	GAGGGTCAAA	420
GAAATTGACA	AGGTAAGTTA	TATTCAAGAG	GCTTTGGATA	AAACTAAAGA	TCAGAGCTAT	480
TTTTTATACG	CTTTAGAGCA	TGAAGTTATC	GCTAAATTGG	TGTTCCCTTT	AGGGGATTTG	540
CTAAAAAAGG	ATATTAAGCC	TTTAGCCTTG	AATGCGATGC	CCTTTTTFAGG	CACTTTAGAA	600
ACTTATAAGG	AATCTCAAGA	AATCTGCTTT	GTGGAAAAAA	GCTACATTGA	CACTTTAAAA	660
AAGCATGTTG	AAGTGGAAAA	AGAGGGCGTG	GTGAAAAACC	TACAAGGCGA	AGTCATTGGC	720
ACGCATAAAG	GCTATATGCA	ATACACGATT	GGCAAACGCA	AAGGCTTTAG	TGTTAAAGGC	780
GCGTTAGAGC	CGCATTTTGT	GGTGGGGATT	GACGCTAAAA	AGAACGAGTT	GATTGTGGGC	840
AAAAAAGAAG	ATCTCGCCAC	GCATTCGCTT	AAGGCTAAAA	ACAAATCTTT	AACGAAAGAT	900
TTTAAAGATG	GCGAATACTT	CATCAAGGCC	CGTTACAGGA	GCGTGCCTAC	TAAAGCGTTT	960
GTGAGCTTAA	AAGATGGAAT	GATTGAAGTG	GAATTTAAAG	AGCCTTTTTA	CGGCGTGGCT	1020
AAAGGGCAAG	CCTTGGTCGT	TTATAAAGAT	GATATTTTGC	TTGGCGGGGG	CGTGATTGTT	1080
TAA						1083

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

ATGAAAGCTA	GCATTTATGA	TTTCACTTTA	GATGAATTGA	GCCAACTTTT	AAAACCAAGT	60
TTTAGGGCTA	AACAGCTTTA	TTTGTGGCTC	TATGCGAAGT	ATAAAACAAG	CTTTAAAGAC	120
ATGCAAAATA	ATTTTTCAAA	AGACTTTATC	GCTTATTGG	AGCAAGAATT	TACTTTGCGC	180
ACGATAGAAA	TCGCGCATGT	GAGGGAGAGT	GTTGATGGCT	CTAAAAATA	CCTTTTTTAAA	240
TCTTTAAGGG	ACAACCACAC	TTTTGAAGCG	GTGTTGTTGA	AAATGAAAGA	CAAAAAGATT	300
GATGAAGAAA	CGAACGCCGT	TTTAGAGGGG	GAAAAATACA	CCGTGTGCGT	GTCTTGTCAA	360
ATCGGCTGTC	AAGTGGGTTG	CTCGTTTTGT	TTCACTCAAA	AAGGCGGTTT	TGTAAGGGAT	420
CTCAAAGCGA	GCGAGATTAT	CCAGCAAGCC	CTACTCATTA	AAGAGGCCAA	TAACCTCCCC	480
ATTGAAAAAG	CGCTCAACAT	TGTTTTTATG	GGAATGGGCG	AGCCTTTGAA	CAATTTAGAT	540
GAGGTGTGTA	AAGCGGTTGA	GATTTTTAAT	ACCGGCATGC	AAATTTCAAC	TAAAAGGATC	600
ACCATTTCCA	CGAGCGGCGT	GGCCGATAAA	ATCCCCATTT	TAGCGGGCAA	AAACTTAGGC	660
GTGCAATTAG	CCATATCCTT	ACACGCCGTA	GATGATAAAA	CGCGCTCGTC	TTTAATGCCC	720
TTGAATAAAA	AATACAACAT	TGAATGCGTT	TTGAATGAAG	TGAGGAAATG	GCCTTTAGAG	780
CAGCGAAAAA	GAGTGATGTT	TGAATACCTT	TTAATCAAAG	ATTTAAACGA	TAGCCTGGAT	840
TGCGCTAAAA	AACTTTTAAA	ACTTTTAAAC	GGCATTAAT	CCAAAGTGAA	TTTGATCTTA	900
TTCAACCCGC	ATGAAGGCTC	TAAGTTTGAG	CGCCCTAGCT	TAGAGAGCGC	CAGAATGTTT	960
GCGGATTTTT	TAAACGCCAA	AGGCTTATTA	TGCACCATTA	GAGAATCCAA	AGCCTTGGAT	1020
ATTGAAGCGG	CTTGCGGGCA	ATTGAGGGAG	AAAAAGCTCC	AGCAGAAAAT	TTAA	1074

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

ATGGCTGAAT	GGAAAACGGA	CACAGAAGAA	GTCAAAAAGG	TTGTTGGAAG	ATGCAGGGAA	60
TTTAAAAGAT	CCCTGCAAGA	AGAAAAATGC	AGTCCATTTA	TCAAAGACCT	TGATAGTTAC	120
GCGCTAAAAA	TCATAGTGGA	GCGCAGAAAA	ACTGAAATGC	AATTGGAAAA	AGCCATAGGA	180
GAATTAAAAA	AAGCCAAAAG	CAATGAAGAT	GACGCTAAAG	TTGCTTTAAG	AGTCTTGCAA	240
GGTGCTTCTG	TCGTCTCGTG	GATTTGGCCT	CCTGCTAGAA	TAGCTGCTAC	GGCAGCCATT	300
GTAGCCGCTG	AAGCTGTTTT	GAAATTTATG	AAAGAAGACA	CAGAAAAATG	CAAAAAGGAAT	360
GTGGAGCTAT	TAGAACGAAT	GCTTGAAATC	TACTCGAATC	AAGCCAAAGC	GAGCGCGAAT	420
CTTATGAATC	AAGCTTGGA	GGGCATTAAA	AAGAGGTTGC	ATTTTTATAC	TGATAAGCAC	480
CAGGAATTTA	TCAGGCGTTT	GAAACAAGCG	AGCGATGCGA	TAGATAACGA	ATACAACCTT	540
CCAACCTCCAG	GCGTTTTATT	GGAATACGAT	TTTGAACGGC	CTGCTATCTC	TTATACCCCT	600

441.

AAAAAAGCG	TTTTTAATGA	GCGCTTGAAG	GATTTGAGGG	AAAATTTTAG	CGCTTCTTTA	660
TACGCTGATT	TGAAAGACAA	GATCCATCAT	AACGCCCTGT	CTAACGATGA	TTTAGAACGC	720
ATGATAGCTT	TTAGAGAGCA	AGAATTTGAA	AAGAGTTTAG	AGGATTGGAT	GGGTGCATAT	780
TCTTATGATG	AAAACCTTAA	CGATGAATTA	GATCGCATGG	CAATATCTAA	AGAGCAGGAG	840
TTGGAAAAGA	GTTTAGAGGA	TTTGATGCCA	AGCGTTTTAG	GCGTGCCTTC	TTATAACGAA	900
AGCTTGACTT	TAGCCAAAAA	TCGTTGCGTT	AAAACTTTA	AGGAAGCTTT	AGAAGGTTTT	960
ACAGAAAAAA	TCAAAGAATC	CCCTAACGAT	TCAAACGCTA	TCAATGAAGC	CTTTGATAAT	1020
TTAGAAACAG	AGTTAGAGCG	CGCTACAGAA	AATTTGAGTC	AAAAAATCGA	TCCCGTTTTA	1080
GAACGGAATG	AAAATTATAC	GCAAAAAGCG	TTGGAGTATA	GGGAGTTTTT	AGAAAGCCGT	1140
AAAGAGAGCT	TTATTGTAGA	TGAAAAAAAC	CCCTATCCGG	AAGAAGTCAG	CTTTAATGAA	1200
TGGCGTTGGG	CGGAATTTGA	TAGCGTTTTT	AGCGCCATTG	TGCCTTTAGA	AGATTTAAAT	1260
AAAACCGCAT	GCGCTCATCA	TGCCCTAAAG	GCTTTACAAG	CTACGCTAAA	GACAACGATT	1320
TGGGCTTTGA	TGCGACAGAG	TTGGAACAGA	TCGCAAAAGG	ATTCATCCCT	AGGGGGTATT	1380
TGTGGCATT	TGACGCGAAT	GTTT	TAG			1407

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

ATGAAACAAA	GTTTGCGCGA	ACAAAAATTA	TTGAAAATTT	TGAAAAATGA	TGTCTTGACG	60
ATTTTGGATA	GTTTTTCTAA	TTACCTTTTT	GAAGTGAAG	AAGAATGGA	CTTCATAGAA	120
GAAGAAATGG	AAGGTGAAAT	CACTGAACAA	AACCTTACCG	CTCTTTATGA	TTTTTCTAAT	180
TTCTTAGAAG	ACCATGTCAA	TGTGTTTTAT	GAGAATGTTT	TGAATATAGA	TGATGTCAAA	240
ACAGAACACC	TTATTCAGG	TCTCATAGAT	AGTCTTAACG	CTAATCTTCA	CTTTGTCAAG	300
TCATTTCTCA	GTAATCAGGA	TTTAGACTTC	CGCTTTTTTA	AAGAAATAAA	CGATGGGCAA	360
GATCCCCAAA	AAACATTATC	AAGATTGATT	CCTCTTCAAA	GTGGGAAGAA	TGATGCAAGC	420
TCGTTTAAAG	CCAATAATTC	TTTTGTTTCA	TTAGTTTATG	TTTATGCTTA	CTTCATGCTA	480
GAAACTATCA	GGCAGTCGTA	TAGGATTCTC	AGATTACTAG	AAAAACCTAT	CAATAACAAC	540
ATAAGCGAGG	ACATGCAGAG	CGATATAGAG	AATTTTTTTG	TTCAAGCAAA	TTTTTTAGAA	600
TACTATGTTT	AGAACAAAAT	ATACCCAACC	AATCATGCCT	ATGACTTCAC	GCATTTGATC	660
ATGGACTCCA	TTATTCCTAA	TTGGATTTCAG	ATTGATATGA	GCGTTGAAGC	TAAAAAGAAA	720
GAGCTTTTTT	AAAAATATTT	TCAAAACATT	GATGAAGTAA	CAAACAAAAT	GCTCGATCAA	780
GAAAATCAAA	ACAAAAACAG	CGATTGA				807

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs

442

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

TTGCTCTCTA ATAAAACGCT CCCTAAAAGA TTCGCCACTT ATAGCTTGCA AGAAGTGGGC	60
GTTATTTTCC TGACCACTCA GATTTTATCT ATCATGCGCA AGACCCGTTG CTCTAAAACG	120
CTTTTTTTTA TCACTAGGGG CAGGGAGAGT TTCCGCTACC AGCTGTGCGA TCATTACAAA	180
CAAAAACGCC ACCAATTTGA TGAAGATTTT AGATCCCTTT TAAAAGCTCT CAAAATCGCT	240
TTAGTGGAAG AATACCCCTT AAAAAAGGG GCTAAAATCC AGGGCGAACA TTGTTTTGAA	300
TATGAAGCCG ATGATATTAT CTCTTTTAC AAAAGAAAG ACCCCAACAA TTATGTGATA	360
GCGAGCATGG ATAAGGATAT TTTGTATTCC AATAGAGGCT CTCATTTCAT TCTCAAAACG	420
AACGCTTTTT TTAATGTGAG CCAAAAAGAA GCCCATTTTT TTGCTTATTA CCAATGCGTT	480
GTGGGGGATA AAGGGGATAA TATTAAGGGG GTTAAAGGGA TTGGCGGCTT CAACTATAAA	540
GATTTTTTAA ACGAAGACGC TAAAGAGCAT GAATATGGG AGCAGATCAT TCAAGCGTTC	600
AAAATTAAAG AAGATTTGAG CGATAGCGAA GCCAAAGAAA AGGCTCTATT AAACATGCGT	660
TTAGTCAATA TGCACCAGAT GACCCACCAT GGCCTGATCA AACTATGGGA GCCTGAGTTT	720
AAAAAAGCTT TTTTCCCTAA AAAACCCCAA AGACCTGATT TTAAAAGAAT TTCTTAA	777

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

TTGTGTTTGA AACTCTTAAT TTGGAATTTT AAGGAGCATT CTTTGAAAGT CAATTTCTTT	60
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GCCACTTGTC	TAGGAGCAGC	TATTTATAGC	AACGCATCGC	TTAACGCTAT	CAAATTACTC	120
CGCAAGGAAA	ATTTGGAAGT	GGTTTTTAAA	AAAGACCAGA	CATGTTGTGG	CCAGCCAAGC	180
TACAACTCAG	GATACTATGA	AGAGACTAAA	AAAGTCGTTT	TATACAATAT	CAAACTTTAT	240
TCCAATAACG	ACTACCCTAT	TATTTTGCCT	AGCGGTTCAT	GCACAGGGAT	GATGCGGCAT	300
GATTATTTGG	AATTGTTTGA	AGGGCATGCG	GAATTTAACA	TGGTTAAAGA	TTTTTGCTCT	360
AGGGTGTATG	AATTGAGCGA	GTTTTTGGAT	AAAAAATTGC	AAGTCAAATA	CGAAGATAAG	420
GGCGAACCTC	TCAAAATCAC	ATGGCATTCT	AATTGCCATG	CCTTAAGGGT	GGCTAAAGTG	480
ATTGACTCGG	CGAAAAATCT	CATCAGACAG	CTTAAAAATG	TGGAATCAT	TGAATTGGAA	540
AAAGAAGAAG	AATGCTGCGG	GTTTGGGGGG	ACTTTTTTCAG	TTAAAGAGCC	TGAAATTTC	600
GCGGTTATGG	TCAAAGAAAA	GATTAAAGAC	ATAGAGAGCC	GTCATGTGGA	TGTGATCGTT	660
TCAGCGGATG	CTGGGTGCTT	GATGAATATC	AGCACCGCTA	TGCAAAAAAT	GGGCTCTTTG	720
ACAAAACCCA	TGCATTTTTA	TGACTTTTTA	GCCTCAAGGC	TTGACTTTTA	A	771

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

TTGAAAATAT	TCGTTCTGTT	GATGTCGGTA	ATTTTAGGAA	TATCATTAAC	AGGTTGCATA	60
GGCTATCGTA	TGGACTTAGA	ACATTTTAAC	ACGCTCTATT	ATGAAGAAAG	CCCTAAAAAA	120
GCTTATGAAT	ATTCCAAACA	ATTCACGAAG	AAAAAAAAGA	ACGCTCTTTT	ATGGGACTTG	180
CAAAACGGCT	TGAGCGCTTT	ATACGCAAGG	GATTATAAGA	CTTCTTTAGG	GGTATTGGAT	240
CAAGCCGAGC	AACGCTTTGA	TAAAACCCAA	AGCGCTTTCA	CAAGAGGGGC	TGGTTATGTG	300
GGCGCTACCA	TGATTAATGA	TAATGTACGC	GCTTATGGGG	GGAATATTTA	TGAGGGCGTT	360
TTAATCAATT	ATTACAAAGC	GATAGACTAC	ATGCTTTTAA	ACGATAGCGC	GAAAGCTAGG	420
GTGCAATTCA	ACCGCGCGAA	TGAACGCCAA	CGCAGGGCTA	AAGAATTTTA	TTATGAGGAA	480
GTGCAAAAAG	CCATTAAAGA	AATCGATTCT	AGCAAAAAGC	ACAATATTAA	TATGGAACGC	540
TCTAGGGCAG	AAGTGAGCGA	GATTTTAAAC	AACACCTATT	CTAATTTAGA	CAAATACGAA	600
GCTTATCAAG	GCTTGCTTAA	CCCGGCGGTT	TCGTATCTTT	CAGGGTTGTT	TTACGCTTTA	660
AATGGGGATA	AGAATAAGGG	ATTAGGCTAT	CTTAATGAAG	CCTATGGGAT	CAGTCAAAGC	720
CCTTTCGTGG	CTCAAGACTT	GGTTTTTTTC	AAAAACCCTA	ACAGGAGCCA	TTTCACTTGG	780
ATCATCATTG	AAGATGGTAA	AGAGCCGCAA	AAAAGCGAAT	TTAAAAATTGA	TGTGCCTATT	840
TTTATGATTG	ATTGCGTTTA	TAACGTGAGC	GTGGCCTTGC	CCAAGCTAGA	AAAAGGGGAA	900
GCGTTTTATC	AAAATTTTAC	CCTCAAGGAC	GGAGAAAAAG	TAACACCCCTT	TGACACTTTA	960
GCCTCAATAG	ATGCGGTGGT	CGCTAGCGAA	TTCAGGAAGC	AATTGCCCTA	CATTATCACT	1020
AGGGCTATTT	TATCGGCCAC	TTTTAAAGTG	GGCATGCAAG	CGGTGGCGAA	CTATTATTTA	1080
GGGTTTGTTG	GCGGGTTAGT	AACTTCGTTG	TATTCAGGTG	TGAGCACCTT	TGCAGACACC	1140
AGAAACACGA	GCATTTTTCG	CCATAAAATC	TACCTCATGC	GCATCAAAAA	CAAAGCCTTT	1200
GAAAGTTATG	AAGTTCGAGC	CGATTCCATT	GACGCTTTTT	CGTTTTTCATT	AAAGCCTTGT	1260

444

AAAAGATCGC TTGAAAGCCC TAAAATCATT GACGCTAGGG AATTGCTTTC AGGGTTTGTA	1320
ACAGCCCCAC AAGTCTTTTG CTCTAACC GC CATAATATTT TATATGTGCG CAGCTTTAAA	1380
AACGGGTTTG TTTTGAGTCA TTAAAATGA	1410

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

ATGAAACAAA TAAAAGCTTT AGCCTTATTT AGTGGGGGGT TGGATAGTTT GTTGTCCATG	60
AAATTACTCA TTGATCAAGG CATTGAAGTA ACCGCTTTAC ACTTCAATAT AGGGTTTGGA	120
GGGAATAAAG ATAAAAGAGA GTATTTTGAA AACGCCACCG CGCAAATTGG GGCTAAACTC	180
TTGGTGTGCG ATATTAGAGA GCAGTTCTTT AACGATGTGT TGTTCAAGCC CAAATACGGC	240
TATGGGAAGT ATTTCAACCC TTGCATTGAT TGCCATGCCA ACATGTTTAG GAACGCTTTT	300
TATAAAATGC TTGAATTGGA TCGGATTTT GTTTTGAGCG GGAAGTGCT AGGGCAACGC	360
CCTAAATCCC AAAGGAAAGA AGCGCTCAAT CAGGTGAGGA AATTAGTCAG AGAAGTGGGC	420
GAAGAGGCTC GTTTTGATCT TATTTTAGAC CGAACGCAAG CAAGCGGTGA AAAACCGCAA	480
TTTTTAGACG AATTGCTCTT AAGGCCCATG AGCGCTAAAC TCTTAGAGCC TACTTTTATG	540
GAAAAAAGG GTTGGGTTGA TAGGAAAAG CTTTGTAGTG TGAGTGGTAG GGGGCGTGCT	600
AGGCAATTGC AAATGATCAA AGATTATGGC TTGAAATATT ATGAAAAGCC AGGTGGGGGG	660
TGCTTGCTTA CGGACATTCA AGTGAGTAAT AAGATTGAAG ATTTGAAAGA ATACAGAGAA	720
ATGGTGTTTG AAGATGGCGT GATTGTCAA AACGGGCGTT ATTTGTCTT ACCCCATAAC	780
GCTCGTTTGG TGGTGGCAAG GAATGAAGAA GAAAACCATA AATTAGACAT TGAACACCCC	840
TTAATGGATA AGATTGAATT GCTAGGCTGT AAAGGTCCTT TGAGTTTGGT GGATAAAAAC	900
GCCAGCCAAG AAGATAAAGA ATTGGCCGGT CGTATCGCTT TAGGCTATGC TAAGACTTTA	960
AAAAATCAAG CTTACCTCAT TCAAATAGGG AATGAAAAGC GCGAACTTTA CCCTTTGGAT	1020
AAAGAGAACG CTAGGGAGTA TTTGTTTCGCT TGA	1053

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

ATGAAAAAAT	ACAGCGCTAT	CCCCACCCCT	TGCTATGCGC	TAGAGAGCGA	ACGCTTAGAA	60
AAAAACGCCA	AGATTTTAGA	AATCGTGCGC	CAGCAAAGCG	GGGCAAAGGT	TTTGCTCGCT	120
TTAAAAGGGT	ATGCGTTTTG	GCGTGAGTTT	GGGATTTTGA	GGCAAAAATT	GAACGGGTGT	180
TGCGCGAGCG	GTCTTTATGA	GGCTAAGCTC	GCTTTTGAAG	AATTTGGGGG	GCGAGAGAGC	240
CATAAGGAAA	TTTGCGTTTA	TAGCCCGGCC	TTTAAAGAGG	CTGAAATGAG	CGCGATTTTA	300
CCCCTAGCGA	CAAGCATCAT	TTTCAACTCT	TTTCACCAAT	ACGCCACCTA	CAAAGACAGG	360
ATTTTAGACA	AAAACAAGCA	GTTAGAAAAC	TTGGGCTTAA	GCCCCATTAA	AATGGGTTTG	420
AGGATTAACC	CCCTTTATAG	CGAAGTAACC	CCAGCGATCT	ATAACCCATG	CTCTAAAATG	480
AGCCGGTTAG	GGATTACGCC	TAGCGGATTT	GAAAAAGGAG	TCAAAGAGCA	TGGCTTAGAG	540
GGGGTGAGCG	GGTTGCATTT	CCATACGCAT	TGCGAGCAAA	ACGCCGACGC	TTTGTGCCGG	600
ACTTTAGAGC	ATGTGGAAAG	GCATTTCAAG	CCTTATTTAG	AAAACATGGC	GTGGGTGAAT	660
TTTGGTGGGG	GGCATCATAT	CACCAGGAGC	GATTATGATG	TGAATTTGCT	CATTCAAACG	720
ATTAAGGATT	TTAAAGAACG	CTACCACAAT	ACAGAAGTGA	TCTTAGAGCC	TGGGGAAGCC	780
ATAGGGTGGC	AATGCGGGTT	TTTAATCGCA	AGCGTGATAG	ATATCGTTCA	AAACGATCAA	840
GAAATTGCGA	TTTTAGACGC	TTCTTTTAGC	GCTCACATGC	CCGATTGCCT	AGAAATGCCT	900
TATCGCCCTA	GTATTCCTAA	GGTTTCTGTA	GAAAACGATG	AGGAAATTAT	TGAAGTTGAA	960
AAGGGCGAAA	ATCAAGGGGC	GTTTTCTTAC	TTTTTAGGCG	GCCCCACTTG	TTTGGCGGGG	1020
GATTTTATGG	GGAGTTTATG	CTTTGAAACG	CCTTTAAAAA	GGGGCGATAA	AATCGTGTTT	1080
CAAGACATGC	TCCATTATAC	GATCGTGAAA	AACAACCTCGT	TTAATGGCGT	GCCACTGCCA	1140
AGCCTGGCTA	AAATAGATTC	GCAAGGTTTT	AAGATCCTCA	AAAGCTTTTC	TTATGAAGAT	1200
TATAAAAACA	GGAATTAA					1218

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 966 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

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ATGGCTGATA GTTTAGCGGG CATTGATCAA GTTACGAGTT TACATAAAAA TAACGAGTTG      60
CAATTGTTGT GTTTCAGGCT GGGTAAAAAC AAGGATTTGT ATGCGGTCAA TGTCTTTAAG      120
ATCCGTGAAG TGGTGAAATA CCATGGCAAT CTCACTATCA TTAGCCACGA AAACAATTCTG      180
CTCGTTGAGG GCTTGATCAT TATAAGAGAG CTCACCATTC CTTTGATTGA CATGAAAAAA      240
TGGTTTTATT ATGACAGCCA AAACAAGAGC AAGGATTTAC GCCCTTACAG GATAGAAAAA      300
GAAAAAGGCG AAGACGATAT TGTCATGATT TGTGAGTTTT CTCGCTGGAC CATAGGGGTT      360
AGGATCTATG AAGCGGATAG GATTTTGAGC AAGAAATGGA CTGAAATGGA GCAAAGCGCT      420
GGGCTAGGGG GATCTGCTGG GAATAACAAA CTCGTGAGCC GCACGCGCTA TTTTGACGGG      480
CGCTTGGTGC AAGTGGTGGA TATTGAAAAA ATGCTTATAG ACGTGTTCCTC TTGGATTGAA      540
GATGAAAAAC ACAACGATTT AGAGACGCTT TCTAAAATCC ATTCTAACCA ATGCGTTTTG      600
CTCGCTGATG ATTCCCCAAG CGTCTTAAAA ACCATGCAAA TGATTTTAGA CAAGCTGGGC      660
GTCAAGCACA TTGACTTTAT CAATGGTAAA ACCTTATTAG AGCATTGTGT CAACCCAACA      720
ACCGATGTGA GTAATATTGG CCTGATTATT ACCGATTTAG AAATGCCAGA AGCGAGCGGT      780
TTTGAAGTGA TCAAACAGGT TAAAAACAAT CCTTTGACTT CAAAATCCC CATTGTGGTC      840
AATTCTTCTA TGAGCGGCAG CTCTAATGAA GACATGGCCA GGAGTTTGAA GGCCGATGAT      900
TTCATCTCCA AGTCTAACCC TAAAGACATC CAGCGGGTGG TTAAGCAATT TTTGGAATTA      960
GCATGA

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(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

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Glu Arg Ile Lys Arg Arg Ala Val Met Lys Lys Ile Val Val Ser Leu
1           5           10           15
Cys Val Ala Leu Gly Phe Leu Ser Ala Asp Pro Ala Gln Ala Asn Lys
          20           25           30
Ala Ile Ser Asp Ala Asp Leu Ile Glu Glu Ile Arg Asp Leu Lys Lys
          35           40           45
Ile Ile Ser Ala Gln Asn Thr Glu Ile Asn Gln Leu Arg Lys Val Gln
          50           55           60
Glu Val Leu Ser Gly Gln Leu Gly Asp Met Arg Lys Asp Ile Leu Ser
65           70           75           80
Thr Arg Asp Tyr Cys Ile Ser Leu Arg Pro Tyr Ile Tyr Asn Trp Arg
          85           90           95

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(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

Asn	Ala	Trp	Asn	Asp	Phe	Val	Lys	Ser	Gly	Ser	Leu	Gly	Pro	Phe	Ser	1	5	10	15
Asn	Gly	Tyr	Tyr	Glu	His	Lys	Thr	Ile	Arg	Leu	Asn	Pro	Glu	Gln	Asn	20	25	30	
Leu	Ile	Val	Leu	Ser	His	Tyr	Leu	Lys	Leu	Leu	Glu	Ile	Gln	Arg	Glu	35	40	45	
Ala	Ala	Lys	Met	Thr	Ala	Ile	Phe	Gly	Ala	Lys	Gln	Pro	His	Pro	Gln	50	55	60	
Ser	Leu	Thr	Val	Gly	Gly	Val	Thr	Ser	Val	Met	Asp	Ile	Leu	Asp	Pro	65	70	75	80
Thr	Arg	Leu	Ala	Glu	Trp	Lys	Ser	Lys	Phe	Glu	Val	Val	Ala	Asn	Phe	85	90	95	
Ile	Asn	His	Ala	Tyr	Tyr	Pro	Asp	Leu	Val	Met	Ala	Gly	Glu	Met	Phe	100	105	110	
Ala	Asn	Glu	Pro	Ser	Val	Ile	Lys	Gly	Cys	Gly	Leu	Arg	Asn	Phe	Ile	115	120	125	
Ala	Tyr	Glu	Glu	Val	Leu	Leu	Gly	Lys	Asp	Lys	Tyr	Leu	Leu	Ser	Ser	130	135	140	
Gly	Val	Val	Leu	Asp	Gly	Asp	Ile	Ser	Lys	Leu	His	Pro	Ile	Asp	Glu	145	150	155	160
Ser	Leu	Ile	Lys	Glu	Glu	Val	Thr	His	Ser	Trp	Tyr	Gln	Tyr	Glu	Asp	165	170	175	
Thr	Lys	Glu	Val	Gln	Leu	His	Pro	Tyr	Asp	Gly	Gln	Thr	Asn	Pro	His	180	185	190	
Tyr	Thr	Gly	Leu	Lys	Asp	Gly	Glu	Ser	Val	Gly	Ile	Glu	Asn	Lys	Ile	195	200	205	
Ile	Pro	Ala	Lys	Val	Leu	Asp	Thr	Lys	Asp	Lys	Tyr	Ser	Trp	Ile	Lys	210	215	220	
Ser	Pro	Arg	Tyr	Asp	Ser	Lys	Pro	Met	Glu	Val	Gly	Pro	Leu	Ser	Ser	225	230	235	240
Val	Val	Val	Gly	Leu	Ala	Ala	Lys	Asn	Pro	Tyr	Val	Thr	Glu	Val	Ala	245	250	255	
Thr	Lys	Phe	Leu	Lys	Asp	Thr	Lys	Leu	Pro	Leu	Glu	Ala	Leu	Phe	Ser	260	265	270	
Thr	Leu	Gly	Arg	Thr	Ala	Ala	Arg	Cys	Ile	Glu	Ala	Lys	Thr	Ile	Ala	275	280	285	
Asp	Asn	Gly	Leu	Leu	Ala	Phe	Asp	Ala	Leu	Val	Glu	Ile				290	295	300	

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

```

Gly Ile Asn Met Ser Lys Lys Ile Val Val Asp Pro Ile Thr Arg Ile
1           5           10           15
Glu Gly His Leu Arg Ile Glu Val Ile Val Asp Asp Asp Asn Val Ile
          20           25           30
Thr Asp Ala Phe Ser Ser Ser Thr Leu Phe Arg Gly Leu Glu Thr Ile
          35           40           45
Ile Lys Gly Arg Asp Pro Arg Asp Ala Gly Phe Ile Ala Gln Arg Ile
          50           55           60
Cys Gly Val Cys Thr Tyr Ser His Tyr Lys Ala Gly Val Thr Ala Val
65           70           75           80
Glu Asn Ala Leu Gly Ile Thr Pro Pro Leu Asn Ala Gln Leu Val Arg
          85           90           95
Ser Leu Met Asn Met Ala Leu Leu Phe His Asp His Val Val His Phe
          100          105          110
Tyr Thr Leu His Gly Leu Asp Trp Cys Asp Ile Leu Ser Thr Leu Lys
          115          120          125
Ala Asp Pro Ile Gln Ala Ala Lys Leu Ser Phe Lys Tyr Ser Pro Tyr
          130          135          140
Pro Ile Asn Thr Gly Ala Gly Arg Ile Lys Ser Gly Ser Lys Thr Leu
145          150          155          160
Gly Met Ile Ser Leu Lys Ala Asp Leu
          165

```

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

```

Trp Leu Trp Leu His Gln Arg Met Ser Gln Lys Ile Leu Ile Leu Gly
1           5           10           15
Ile Gly Asn Ile Leu Phe Gly Asp Glu Gly Ile Gly Val His Leu Ala
          20           25           30
His Tyr Leu Lys Arg Asn Phe Ser Phe Phe Pro Ser Val Asp Ile Val
          35           40           45
Asp Gly Gly Thr Met Ala Gln Gln Leu Ile Pro Leu Ile Thr Ser Tyr
          50           55           60
Glu Lys Val Leu Ile Leu Asp Cys Val Ser Ala Lys Gly Val Glu Ile
65           70           75           80
Gly Ser Val Tyr Ala Phe Asp Phe Lys Asp Ala Pro Lys Glu Ile Thr
          85           90           95
Trp Ala Gly Ser Ala His Glu Val Glu Met Leu His Thr Leu Arg Leu
          100          105          110
Thr Glu Phe Leu Gly Asp Leu Pro Lys Thr Phe Ile Val Gly Leu Val
          115          120          125
Pro Phe Val Ile Gly Ser Glu Thr Thr Phe Lys Leu Ser Ser Glu Met
          130          135          140
Leu Asn Ala Leu Glu Thr Ala Leu Lys Ala Ile Glu Thr Gln Leu Asn
145          150          155          160
Ala Trp Gly Val Lys Met Gln Arg Thr Asp His Ile Ala Leu Asp Cys
          165          170          175
Ile Ala Glu Leu Ser Tyr Lys Gly Phe
          180          185

```

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

```

Tyr Gln Ile Leu Asn Gln Arg Lys Thr Met Lys Lys Val Leu Leu Leu
1           5           10           15
Thr Leu Ser Leu Ser Leu Ser Phe Trp Leu His Ala Glu Arg Asn Gly
          20           25           30
Phe Tyr Leu Gly Leu Asn Phe Ala Glu Gly Ser Tyr Ile Gln Gly Gln
          35           40           45
Gly Ser Ile Gly Glu Lys Ala Ser Ala Glu Asn Ala Leu Asn Gln Ala
          50           55           60
Ile Asn Asn Ala Gln Asn Ser Leu Phe Pro Asn Thr Gln Ala Ile Arg
65           70           75           80

```

450

Asp Val Gln Asn Ala Leu Asn Ala Val Lys Asp Ser Asn Lys Ile Ala
 85 90 95
 Asn Arg Phe Ala Gly Asn Gly Gly Ser Gly Gly Ile
 100 105

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

Arg Val Ser Gly Asn Leu Lys Ser Asp Gln Ser Thr Cys Ala Pro Tyr
 1 5 10 15
 His Ile Asp Lys Asn Gln Glu Tyr Lys Gly Arg Tyr Ile Gly Gln Val
 20 25 30
 Pro Arg Gly Met Leu Ser His Trp Val Arg Ile Lys Asn Gly Val Val
 35 40 45
 Glu Asn Tyr Gln Ala Val Val Pro Ser Thr Trp Asn Ala Gly Pro Arg
 50 55 60
 Asp Ser Lys Asn Gln Arg Gly Ala Tyr Glu Met Ser Leu Ile Gly Thr
 65 70 75 80
 Lys Ile Ala Asp Leu Thr Gln Pro Leu Glu Ile Ile Arg Thr Ile His
 85 90 95
 Ser Phe Asp Pro Cys Ile Ala Cys Ser Val His Val Met Asp Phe Lys
 100 105 110
 Gly Gln Ser Leu Asn Glu Phe Lys Val Glu Pro Asn Phe Ala Lys Phe
 115 120 125

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

451

(A) NAME/KEY: misc_feature
(B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

```

Leu Tyr Gln Asn Asp Lys Gly Phe Lys Thr Glu Leu Arg Ile Leu Ser
1          5          10          15
Val Phe Ile Val Glu Phe Leu Val Asn Ile Leu Gly Phe Met Leu Ala
          20          25          30
His Met Leu His Phe Trp Phe Leu Arg Cys Val Lys Ala Leu Ala Trp
          35          40          45
Leu Met Lys Thr Phe Asp Arg Arg Arg Tyr Phe Asp Ala Lys Ala Asn
          50          55          60
Leu Asp Phe Val Phe Gly Asp Ser Lys Ser Glu Glu Glu Lys Lys Arg
65          70          75          80
Ile Ile Lys Lys Gly Val
          85

```

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

```

Tyr Lys Lys Gly Asn Gln Ile Met Asn Ile Gln Thr Lys Lys Arg Phe
1          5          10          15
Leu Ala Asn Leu Leu Leu Phe Ser Leu Phe Ser Cys Leu Lys Ala Glu
          20          25          30
Thr Leu Ser Glu Asp His Gln Ile Leu Leu Ser Ser Asp Ala Phe His
          35          40          45
Arg Gly Asp Phe Ala Thr Ala Gln Lys Gly Tyr Met Asn Leu Tyr Arg
50          55          60
Ala Asn Gln
65

```

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

```

Leu Cys Leu Lys Leu Leu Ile Trp Asn Phe Lys Glu His Ser Leu Lys
1           5           10           15
Val Asn Phe Phe Ala Thr Cys Leu Gly Ala Ala Ile Tyr Ser Asn Ala
          20           25           30
Ser Leu Asn Ala Ile Lys Leu Leu Arg Lys Glu Asn Leu Glu Val Val
          35           40           45
Phe Lys Lys Asp Gln Thr Cys Cys Gly Gln Pro Ser Tyr Asn Ser Gly
          50           55           60
Tyr Tyr Glu Glu Thr Lys Lys Val Val Leu Tyr Asn Ile Lys Leu Tyr
65           70           75           80
Ser Asn Asn Asp Tyr Pro Ile Ile Leu Pro Ser Gly Ser Cys Thr Gly
          85           90           95
Met Met Arg His Asp Tyr Leu Glu Leu Phe Glu Gly His Ala Glu Phe
          100          105          110
Asn Met Val Lys Asp Phe Cys Ser Arg Val Tyr Glu Leu Ser Glu Phe
          115          120          125
Leu Asp Lys Lys Leu Gln Val Lys Tyr Glu Asp Lys Gly Glu Pro Leu
130          135          140
Lys Ile Thr Trp His Ser Asn Cys His Ala Leu Arg Val Ala Lys Val
145          150          155          160
Ile Asp Ser Ala Lys Asn Leu Ile Arg Gln Leu Lys Asn Val Glu Leu
          165          170          175
Ile Glu Leu Glu Lys Glu Glu Glu Cys Cys Gly Phe Gly Gly Thr Phe
          180          185          190
Ser Val Lys Glu Pro Glu Ile Ser Ala Val Met Val Lys Glu Lys Ile
          195          200          205
Lys Asp Ile Glu Ser Arg His Val Asp Val Ile Val Ser Ala Asp Ala
210          215          220
Gly Cys Leu Met Asn Ile Ser Thr Ala Met Gln Lys Met Gly Ser Leu
225          230          235          240
Thr Lys Pro Met His Phe Tyr Asp Phe Leu Ala Ser Arg Leu Gly Leu
          245          250          255

```

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

453

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

```

Met Lys Lys Ile Phe Leu Gly Met Ala Leu Ala Phe Ser Val Ser Met
1           5           10           15
Ala Glu Lys Ser Gly Ala Phe Leu Gly Gly Gly Phe Gln Tyr Ser Asn
          20           25           30
Leu Glu Asn Gln Asn Thr Thr Arg Thr Pro Ser Ala Asn Asn Asn Thr
          35           40           45
Pro Ile Asn Thr Ser Met Phe Gly Asn Asn Gln Ala Ala Pro Ala Gln
          50           55           60
Glu Thr Pro Ser Val Ile Asn Thr Asn Asn Tyr Gly Gln Met Tyr Gly
65           70           75           80
Val Asp Ala Met Ala Gly Tyr Lys Trp Phe Phe Gly Lys Thr Lys Arg
          85           90           95
Phe Gly Phe Arg Thr Tyr Gly Tyr Tyr Ser Tyr Asn His Ala Asn Leu
          100          105          110
Ser Phe Val Gly Ser Lys Leu Gly Ile Met Asp Gly Ala Ser Gln Val
          115          120          125
Asn Asn Phe Thr Tyr Gly Val Gly Phe Asp Ala Leu Tyr Asn Phe Tyr
          130          135          140
Glu Ser Lys Glu Gly Tyr Asn Thr Ala Gly Leu Phe Val Gly Phe Gly
145          150          155          160
Leu Gly Gly Asp Ser Phe Ile Val Gln Gly Glu Ser Tyr Leu Lys Ser
          165          170          175
Gln Met Gln Ile Cys Asn Asn Thr Ala Gly Cys Ser Ala Ser Met Asn
          180          185          190
Thr Ser Tyr Phe Gln Met Pro Val Glu Phe Gly Phe Arg Ser Asn Phe
          195          200          205
Ser Lys His Ser Gly Ile Glu Val Gly Phe Lys Leu Pro Leu Phe Thr
          210          215          220
Asn Gln Phe Tyr Lys Glu Arg Gly Val Asp Gly Ser Val Asp Val Phe
225          230          235          240
Tyr Lys Arg Asn Phe Ser Ile Tyr Phe Asn Tyr Met Ile Asn Leu
          245          250          255

```

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

```

Ala Cys Glu Ile Arg Ala Trp Ala Phe Asp Arg Met Leu Arg Val Leu
1           5           10           15
Ser Val Gly Val Val Phe Ile Leu Leu Gly Cys Gln Phe Phe Asn Lys
          20           25           30
Thr Thr Leu His Leu Lys Tyr Lys Asp Tyr Pro Lys Asn Ser Pro Leu
          35           40           45
Lys Thr Ala Ser Thr Leu Thr Pro Pro Lys Ile Phe Phe Asn Ala His
          50           55           60
Phe Val Pro Pro Phe Tyr Gln Lys Glu Phe Lys Lys Ala Leu Ala Gln
65           70           75           80
Gln Ile Ala Tyr Phe Leu Lys Asp Lys Ser Ala Leu Thr Phe Asn Ile
          85           90           95
Ser Gly Asn Val Phe Phe Ser Phe Glu Glu Ser Pro Lys Asp Leu Lys
          100          105          110
Ala Ile Lys Glu Arg Leu Lys Lys Thr Ile Glu Pro Asn Thr Asp Pro
          115          120          125
Lys Ala Val Met Arg Phe Leu Asn Leu Gln Ala Ser Leu Ile Leu Glu
          130          135          140
Cys Val Pro Gln Thr Ala Cys Pro Phe Asp Thr Leu Leu Ile Pro Thr
145          150          155          160
Ala Leu Ser Val Pro Ile Asp Tyr Ala Asn Arg Leu Gly Asp Asn Pro
          165          170          175
Ser Leu Phe Pro Gln Glu Asp Lys Ser Tyr His Asn Ala Leu Ile Lys
          180          185          190
Ala Leu Asn Lys Ala Tyr Tyr Ser Leu Met Glu Gly Leu Glu Lys Arg
          195          200          205
Leu Asn Ala Ile Glu Asn Ala Ala Trp Leu
          210          215

```

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

```

Thr Ile Gln Glu Arg Leu Tyr Arg His Glu Ile Ser Arg Leu Gln Val
1           5           10           15
Lys Thr Asp Glu Thr Leu Lys Leu Ile Lys Glu Ala Lys Lys Arg Leu
          20           25           30

```

455

```

Asn Tyr Asn Asp Asp Ile Arg Asp Val Leu Gln Gly Leu Leu Asn Ile
   35           40           45
Val Pro Asp Leu Ile Thr Ile Asn Ser Ile Glu Ile Asp Gln Gln Ser
   50           55           60
Val Val Val Ser Gly Lys Thr Pro Ser Lys Glu Ala Phe Tyr Phe Leu
   65           70           75           80
Phe Gln Asn Lys Leu Asn Pro Met Phe Asp Tyr Ser Arg Ala Glu Phe
           85           90           95
Phe Pro Leu Ser Asp Gly Trp Phe Asn Phe Val Ser Thr Asn Phe Ser
           100          105          110
Asn Ser Leu Leu Ile Lys Asn Pro Glu Ser Ile Lys
   115           120

```

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

```

Ile Ser Ile Glu Gln Thr Asn Lys Val Val Tyr Ala Lys Glu Ala Ala
1           5           10           15
Ile Ser Ala Ala Ser Leu Gly Asp Ile Lys Thr Ala Met His Leu Ala
   20           25           30
Met Leu Tyr Gln Lys Ile Thr Asn Asn Arg Asn Asp Val Ser Ile Asn
   35           40           45
Lys Ile Leu Val Asp Gly Tyr Ala Gln Met Gly Gln Ile Asp Lys Ala
   50           55           60
Ile Glu Leu Leu His Lys Ile Arg Lys Glu Glu Lys Thr Ile Ala Thr
   65           70           75           80
Asp Asn Val Leu Gly Thr Leu Tyr Leu Thr Gln Lys Arg Leu Asp Lys
   85           90           95
Ala Phe Pro Leu Leu Asn Lys Phe Tyr Asn Gln Val His Asp Glu Asp
   100          105          110
Ser Leu Glu Lys Leu Ile Thr Ile Tyr Phe Leu Gln Asn Arg Lys Lys
   115          120          125
Glu Gly Leu Val Leu Leu Gln Ser His Ile Asp Arg Tyr Gly Cys Ser
   130          135          140
Glu Gln Leu Cys Gln Lys Ala Leu Asn Thr Phe Thr Gln Phe Asn Glu
   145          150          155          160
Leu Asp Leu Ala Lys Thr Thr Phe Ala Arg Leu Tyr Glu Lys Asn Pro
   165          170          175
Ile Val Gln Asn Ala Gln Phe Tyr Ile Gly Val Leu Ile Leu Leu Lys
   180          185          190

```

456

Glu Phe Asp Lys Ala Gln Gln Ile Ala Glu Leu Phe Pro Phe Asp Arg
 195 200 205
 Arg Leu Leu Leu Asp Leu Tyr Thr Ala Gln Lys Lys Phe Asp Gln Ala
 210 215 220
 Ser Lys Gln Ala Ser Leu Ile Tyr Gln Glu Arg Lys Asp Pro Lys Phe
 225 230 235 240
 Leu Gly Leu Glu Ala Ile Tyr His Tyr Glu Ser Leu Ser Ala Asn Lys
 245 250 255
 Lys Lys Leu Thr Lys Glu Glu Met Leu Pro Ile Ile Gln Lys Leu Glu
 260 265 270
 Gln Ala Thr Lys Glu Arg Gln Ala Trp Leu Ala Lys Thr Lys Asp Lys
 275 280 285
 Glu Asp Ala Gln Asp Ala Phe Phe Tyr Asn Phe Leu Gly Tyr Ser Leu
 290 295 300
 Ile Asp Tyr Asp Met Asp Val Lys Arg Gly Met Asp Leu Val Arg Lys
 305 310 315 320
 Ala Leu Ala Leu Asp Ser Asn Ser Val Leu Tyr Leu Asp Ser Leu Ala
 325 330 335
 Trp Gly Tyr Tyr Lys Leu Gly Asn Cys Leu Glu Ala Lys Lys Ile Phe
 340 345 350
 Ser Ser Ile Ala Lys Glu Leu Ile Gln Asn Glu Pro Glu Leu Lys Glu
 355 360 365
 His Asn Lys Ile Ile Gln Glu Cys Lys Lys
 370 375

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

Phe Tyr Thr Gly Lys Lys Gly Ala Cys Met Arg Lys Ile Leu Leu Met
 1 5 10 15
 Gly Leu Ile Leu Gln Ala Leu Phe Gly Glu Glu Thr Ala Gln Glu Leu
 20 25 30
 Leu Gln Cys Ser Ala Ile Phe Glu Ser Lys Lys Ala Glu Leu Lys Glu
 35 40 45
 Asp Leu Arg Gln Leu Ser Glu Lys Glu Gln Ser Leu Arg Ile Leu Gln
 50 55 60
 Thr Glu Asn Ala Arg Leu Leu Asp Glu Lys Ser Asp Leu Leu Asn Lys
 65 70 75 80
 Lys Glu Lys Glu Ile Asp Glu Lys Leu Lys Asn Leu Ala Ala Lys Glu
 85 90 95

457

Glu Ala Phe Lys Thr Leu Gln Thr Glu Glu Lys Lys Arg Leu Lys Asn
 100 105 110
 Leu Ile Glu Glu Asn Glu Gly Ile Leu Arg Glu Ile Lys Gln Ala Lys
 115 120 125
 Asp Ser Lys Ile Gly Glu Thr Tyr Ser Lys Met Lys Asp Ser Lys Ser
 130 135 140
 Ala Leu Ile Leu Glu Asn Leu Pro Thr Gln Asn Ala
 145 150 155

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

Lys Arg Leu Cys Asp Arg Leu Trp Ser Gly Gly Tyr Tyr Leu Ser Val
 1 5 10 15
 Glu Arg Arg Asn Val Met Gly Val Ala Val Val Leu Phe Leu Thr Leu
 20 25 30
 Ile Leu Leu Phe Leu Val Leu Arg Asp Phe Gly Leu Ala Ser Pro Lys
 35 40 45
 Gln Lys Ile Leu Ala Phe Leu Ile Val Gly Ile Ile Gly Ala Ser Ile
 50 55 60
 Ser Val Tyr Thr Tyr Lys Gln Asn Gln Gln Asn Gln Gln Glu Ile Ala
 65 70 75 80
 Leu Gln Arg Ala Phe Leu Arg Gly Glu Thr Leu Leu Cys Lys Gly Ile
 85 90 95
 Lys Val Asn Asn Gln Thr Phe Asn Leu Val Ser Gly Thr Leu Ser Phe
 100 105 110
 Leu Gly Lys Lys Gln Thr Pro Met Lys Asp Val Leu Val Asp Leu Asp
 115 120 125
 Ser Cys Gln Thr Leu Gln Lys Asp Pro Leu Ile Gln Pro
 130 135 140

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

```

Ala Lys Asn Thr Ile Phe Asn Asn Ala Asn Phe Asn Asn Ser Thr Ser
1          5          10          15
Phe Asn Phe Asn Asn Ser Ser Ala Thr Thr Ser Phe Val Gly Asp Phe
          20          25          30
Thr Asn Ala Asn Ser Asn Leu Gln Ile Ala Gly Asn Ala Val Phe Gly
          35          40          45
Asn Ser Thr Asn Gly Ser Gln Asn Thr Ala Asn Phe Asn Asn Thr Gly
          50          55          60
Ser Val Asn Ile Ala Gly Asn Ala Thr Phe Asp Asn Val Val Phe Asn
65          70          75          80
Ser Pro Thr Asn Thr Gly Val Lys Gly Lys Val Thr Leu Asn Asn Ile
          85          90          95
Thr Leu Lys Thr
          100

```

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

```

Trp Ala Met Asn Val Trp Val Tyr Arg Pro Leu Leu Ala Phe Met Asp
1          5          10          15
Asn Arg Gln Ala Glu Ile Lys Asp Ser Leu Ala Lys Ile Lys Thr Asp
          20          25          30
Asn Thr Gln Ser Val Glu Ile Gly His Gln Ile Glu Thr Leu Leu Lys
          35          40          45
Glu Ala Ala Glu Lys Arg Arg Glu Met Leu Ala Glu Ala Ile Gln Lys
          50          55          60
Ala Thr Glu Ser Tyr Asp Ala Val Ile Lys Gln Lys Glu Asn Glu Leu
65          70          75          80
Asn Gln Glu Phe Glu Ala Phe Ala Lys Gln Leu Gln Asn Glu Lys Gln

```


	85		90		95										
Ile	Leu	Lys	Glu	Gln	Leu	Gln	Ala	Gln	Met	Thr	Val	Phe	Glu	Asp	Glu
	100				105								110		
Leu	Asn	Lys	Arg	Val	Ala	Met	Gly	Leu	Gly	Ser					
	115					120									

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

Lys	Gly	Gly	Phe	Ile	Ser	Ala	Lys	Ser	Cys	Leu	Ser	Met	Ala	Ser	Gly
1				5					10					15	
Leu	Phe	Glu	Asn	Asp	Glu	Ile	Lys	Asn	Asn	Lys	Ala	Arg	Asp	Phe	Phe
			20					25					30		
Tyr	Ser	His	Ser	Ser	Leu	Ile	Val	Phe	Phe	Leu	Leu	Leu	Leu	Gly	Phe
			35				40						45		
Gly	Tyr	Tyr	Leu	Gly	Lys	Leu	Leu	Phe	Gly	Gly	Ser	Ser	Leu	Glu	Val
	50					55					60				
Tyr	Leu	Asp	Leu	Arg	Asp	Lys	His	Glu	Arg	Leu	Gln	Gln	Glu	Ile	Thr
65				70					75					80	
Glu	Leu	Gln	Ser	Lys	Asn	Val	Arg	Leu	Gln	Lys	Arg	Leu	Phe	Glu	Leu
				85					90					95	
Arg	Glu	Leu	Arg	Pro	Arg	Asp									
				100											

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

```

Leu Tyr Tyr Asn Ser Gln Leu Asn Trp Gly Phe Thr Asp Leu Ser Leu
1          5          10          15
Cys Glu Leu Trp Leu Ser Phe Val Arg Asn Glu Met Ile Lys Ser Trp
20          25          30
Thr Lys Lys Trp Phe Leu Ile Leu Phe Leu Met Ala Ser Cys Phe Gly
35          40          45
His Leu Val Ala Thr Thr Gly Glu Lys Tyr Phe Lys Met Ala Asn Gln
50          55          60
Ala Leu Lys Arg Gly Asp Tyr His Arg Ala Val Ala Phe Tyr Lys Arg
65          70          75          80
Ser Cys Asn Leu Arg Met Gly Val Gly Cys Thr Ser Leu Gly Ser Met
85          90          95
Tyr Glu Tyr Gly Asp Gly Val Asp Gln Asn Ile Ser Lys Ala Val Phe
100          105          110
Tyr Tyr Arg Arg Gly Cys Asn Leu Arg Asn Tyr Leu Ala Cys Ala Ser
115          120          125
Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Gln Lys Asp Phe Pro
130          135          140
Lys Ala Ile Tyr Tyr Tyr Arg Arg Gly Cys His Leu Lys Gly Gly Val
145          150          155          160
Ser Cys Gly Ser Leu Gly Phe Met Tyr Phe Asn Gly Thr Gly Val Lys
165          170          175
Gln Asn Tyr Ala Lys Ala Leu Ser Phe Ser Lys Tyr Ala Cys Ser Leu
180          185          190
Asn Tyr Gly Ile Ser Cys Asn Phe Val Gly Tyr Met Tyr Lys Ser Ala
195          200          205
Lys Gly Val Glu Lys Asp Leu Lys Lys Ala Leu Ala Asn Phe Lys Arg
210          215          220
Gly Cys His Leu Lys Asp Gly Ala Ser Cys Val Ser Leu Gly Tyr Leu
225          230          235          240
Tyr Glu Ala Gly Met Asp Val Lys Gln Asn Glu Glu Gln Ala Leu Asn
245          250          255
Leu Tyr Lys Lys Gly Cys Ser Leu Lys Glu Gly Ser Gly Cys His Asn
260          265          270
Val Ala Val Met Tyr Tyr Thr Gly Lys Gly Ala Pro Lys Asp Leu Glu
275          280          285
Lys Ala Thr Ser Tyr Tyr Lys Lys Gly Cys Ala Leu Gly Phe Ser Gly
290          295          300
Ser Cys Lys Val Leu Glu Val Ile Gly Lys Glu Ser Asp Asn Leu Gln
305          310          315          320
Asp Asp Ala Gln Asn Asp Thr Gln Asp Ser Val Gln
325          330

```

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

461

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...94

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

```

Ile Lys Val Arg Ser Val Lys Lys Thr Glu Arg Gly Leu Leu Ile Glu
1           5           10           15
Lys Phe Thr Ser Gln Gly Glu Leu Val Pro Leu Glu Ile Val Val Glu
20           25           30
Thr Ile Leu Ser Glu Ile Lys Ser Ser Ser Lys Gly Ile Ile Leu Ile
35           40           45
Asp Gly Tyr Pro Arg Ser Val Glu Gln Met Gln Ala Leu Asp Lys Glu
50           55           60
Leu Asn Ala Pro Asn Glu Val Ile Leu Lys Ser Val Ile Glu Val Glu
65           70           75           80
Val Ser Glu Asn Thr Ala Lys Glu Arg Val Leu Gly Gln Phe
85           90

```

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

```

His Phe Val Phe Arg Gly Asp Phe Cys Trp Ala Tyr Arg Tyr Tyr Ser
1           5           10           15
Ile Asp Lys Glu Arg Glu Thr Gln Arg His Asp Ser Ser Tyr Ile Val
20           25           30
Ile Asp Glu Leu Val Gly Met Cys Leu Ala Met Ala Ile Asn Gly Leu
35           40           45
Ser Leu Val Gly Val Ile Leu Ser Phe Ile Phe Leu Gly Cys Tyr Asp
50           55           60
Ile Thr Lys Pro Ser Leu Ile Gly Lys Ile Asp Lys Glu Val Lys Gly
65           70           75           80
Gly Leu Gly Val Val Ala Asp Asp Ala Leu Ala Gly Val Leu Ala Gly
85           90           95
Leu Ser Thr Leu Leu Ala Ile Asn Ile Leu Gly Phe Phe Asn Ile Lys
100          105          110

```

Phe

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

```

Met Trp Pro Val Ala Leu Lys Gln Pro Asn Arg Val Ser His His Phe
1          5          10          15
Tyr Ile Met Ala Met Leu Phe Ile Leu Phe Asp Val Glu Ile Val Phe
          20          25          30
Met Phe Pro Trp Ala Ile Asp Phe Lys Lys Leu Gly Leu Phe Gly Leu
          35          40          45
Val Glu Met Leu Gly Phe Val Phe Phe Leu Ala Ile Gly Phe Ile Tyr
          50          55          60
Ala Leu Lys Arg Asn Ala Leu Ser Trp Gln Lys Leu Glu Val Lys
65          70          75

```

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

```

Phe Asp Leu Gly Val Arg Thr Asn Phe Ala Lys Thr Asn Phe Asn Lys
1          5          10          15
His Arg Leu Asp Gln Gly Ile Glu Phe Gly Val Lys Ile Pro Val Ile

```

463

	20		25		30										
Ala	His	Lys	Tyr	Phe	Ala	Thr	Gln	Gly	Ser	Ser	Ala	Ser	Tyr	Met	Arg
	35				40				45						
Asn	Phe	Ser	Phe	Ile	Cys	Gly	Leu	Phe	Ser	Arg	Phe				
50					55					60					

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

Phe	Gly	Ser	Arg	Ala	Phe	Arg	Arg	Ile	Phe	Thr	Lys	Trp	Gly	Glu	Arg
1				5					10					15	
Asp	Phe	Arg	Lys	Gly	Ala	Val	Val	Leu	Met	Arg	Leu	Leu	Ile	Ala	Leu
			20					25					30		
Val	Leu	Phe	Leu	Trp	Trp	Leu	Asn	Leu	Gly	Ala	Lys	Glu	Ala	Asp	Phe
		35					40					45			
Ile	Ser	Asp	Trp	Glu	Tyr	Gly	Leu	Ala	Leu	Tyr	Lys	Asn	Pro	Arg	Gly
	50					55				60					
Val	Ala	Cys	Ala	Lys	Cys	His	Gly	Ile	Lys	Gly	Glu	Gln	Gln	Glu	Ile
65				70					75					80	
Thr	Phe	Tyr	Tyr	Glu	Lys	Gly	Glu	Lys	Lys	Ile	Leu	Tyr	Ala	Pro	Lys
			85					90						95	
Ile	Asn	His	Leu	Asp	Phe	Lys	Thr	Phe	Lys	Asp	Ala	Leu	Ser	Leu	Gly
		100						105					110		
Phe	Cys	Met	Met	Pro	Thr	Tyr	Asn	Leu	Asn	Leu	Glu	Glu	Ile	Gln	Ala
	115						120				125				
Ile	Tyr	Leu	Tyr	Ile	Thr	Ser	Leu	Gly	His	Lys	Asp	Glu	Arg	Lys	Asp
	130					135					140				
Pro	Ser	Lys	Pro												
145															

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

```

Lys Asn Arg His Lys Leu Leu Tyr Leu Leu Leu Lys Asn Leu Asn Phe
1           5           10           15
Leu Lys Thr Ile Ser Thr Ile Phe Thr Gln Lys Arg Val Ile Ile Arg
20           25           30
Ser Gln Gln Gly Phe Ser Cys Tyr Leu Asn Leu Lys Val Lys Thr Met
35           40           45
Lys Lys Leu Ala Ala Leu Phe Leu Val Ser Ala Leu Gly Val Met Ser
50           55           60
Leu Asn Ala Trp Glu Gln Thr Leu Lys Ala Asn Asp Leu Glu Val Lys
65           70           75           80
Ile Lys Ser Val Gly Asn Pro Ile Lys Gly Asp Asn Thr Phe Val Leu
85           90           95
Ser Pro Thr Leu Lys Gly Lys Ala Leu Glu Lys Ala Ile Val Arg Val
100          105          110
Gln Phe Met Met Pro Glu Met Pro Gly Met Pro Ala Met Lys Glu Met
115          120          125
Ala Gln Val Ser Glu Lys Asn Gly Leu Tyr Glu Ala Lys Thr Asn Leu
130          135          140
Ser Met Asn Gly Thr Trp Gln Val Arg Val Asp Ile Lys Ser Lys Glu
145          150          155          160
Gly Gln Val Tyr Arg Thr Lys Thr Ser Leu Asp Leu
165          170

```

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

```

Cys Leu Phe Val Leu Thr Lys Ser Gln Arg Ile Arg Met Lys Arg Leu
1           5           10           15
Leu Leu Leu Ala Leu Ala Leu Phe Phe Ser Leu Ser Cys Thr Asn Ala
20           25           30

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Helicobacter pylori*

(A) NAME/KEY: misc_feature
(B) LOCATION 1...293

Ile	Lys	Phe	Ala	Lys	Lys	Ile	Val	Leu	Ile	Leu	Lys	Lys	Gly	Gly	Phe
1				5					10					15	
Met	Lys	Thr	Asn	Gly	Leu	Phe	Lys	Met	Trp	Gly	Leu	Phe	Leu	Val	Leu
			20					25					30		
Ile	Ala	Leu	Val	Phe	Asn	Ala	Cys	Ser	Asp	Ser	His	Lys	Glu	Lys	Lys
		35					40					45			
Asp	Ala	Leu	Glu	Val	Ile	Lys	Gln	Arg	Gly	Val	Leu	Lys	Val	Gly	Val
	50					55					60				
Phe	Ser	Asp	Lys	Pro	Pro	Phe	Gly	Ser	Val	Asp	Ser	Lys	Gly	Asn	Tyr
65					70					75					80
Gln	Gly	Tyr	Asp	Val	Val	Ile	Ala	Lys	Arg	Met	Ala	Leu	Asp	Leu	Leu
				85					90					95	
Gly	Asp	Glu	Asn	Lys	Ile	Glu	Phe	Ile	Pro	Val	Glu	Ala	Ser	Ala	Arg
			100					105					110		
Val	Glu	Phe	Leu	Lys	Ala	Asn	Lys	Val	Asp	Ile	Ile	Met	Ala	Asn	Phe
		115					120					125			
Thr	Arg	Thr	Lys	Glu	Arg	Glu	Lys	Val	Val	Asp	Phe	Ala	Asn	Pro	Tyr
	130					135					140				
Met	Lys	Val	Ala	Leu	Gly	Val	Ile	Ser	Lys	Asp	Gly	Val	Ile	Lys	Asn
145					150					155					160
Ile	Glu	Glu	Leu	Lys	Asp	Lys	Glu	Leu	Ile	Val	Asn	Lys	Gly	Thr	Thr
				165					170					175	
Ala	Asp	Phe	Tyr	Phe	Thr	Lys	Asn	Tyr	Pro	Asn	Ile	Lys	Leu	Leu	Lys
			180					185					190		
Phe	Glu	Gln	Asn	Thr	Glu	Thr	Phe	Leu	Ala	Leu	Leu	Asn	Asn	Lys	Ala
		195					200					205			
Ile	Ala	Leu	Ala	His	Asp	Asn	Thr	Leu	Leu	Leu	Ala	Trp	Val	Lys	Gln
	210					215					220				
His	Pro	Glu	Phe	Lys	Leu	Gly	Ile	Thr	Ser	Leu	Gly	Asp	Lys	Asp	Val
225					230					235					240

466

```

Ile Ala Pro Ala Ile Lys Lys Gly Asn Pro Lys Leu Leu Glu Trp Leu
                245                250                255
Asn Asn Glu Ile Asp Ser Leu Ile Ser Ser Asp Phe Leu Lys Glu Ala
                260                265                270
Tyr Gln Glu Thr Leu Glu Pro Ile Tyr Gly Asp Gly Ile Lys Pro Glu
                275                280                285
Glu Ile Ile Phe Glu
                290

```

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

```

Ala Phe Glu Glu Leu Glu Pro Leu Ser Phe Ser Phe Asn Ser Pro Lys
1          5          10          15
Gly Ala Cys Glu Ser Cys Leu Gly Leu Gly Thr Lys Phe Ser Leu Asp
          20          25          30
Ile Ser Lys Ile Leu Asp Pro Asn Thr Pro Leu Asn Gln Gly Ala Ile
          35          40          45
Lys Val Ile Phe Gly Tyr Asn Arg Ser Tyr Tyr Ala Gln Met Phe Glu
          50          55          60
Gly Phe Cys Thr Tyr Asn Gly Ile Asp Ser Ala Leu Cys Phe Asn Glu
65          70          75          80
Leu Asn Lys Glu Gln Gln Asp Ala Leu Leu Tyr Gly Asn Gly Thr Glu
          85          90          95
Ile Ser Phe His Phe Lys Asn Ser Pro Leu Lys Arg Pro Trp Lys Gly
          100         105         110
Ile Ile Gln Ile Ala Tyr Asp Met Phe Lys Glu Gln Lys Asp Leu Ser
          115         120         125
Asp Tyr Met Ser Glu Lys Thr Cys Ser Ser Cys Asn Gly His Arg Leu
          130         135         140
Lys Ala Ser Ser Leu Ser Val Gln Val Ala Gly Leu Lys Met Ala Asp
          145         150         155         160
Phe Leu Thr Lys Pro Ile Glu Glu Val Tyr His Phe Phe Asn Asp Pro
          165         170         175
Thr His Phe Asn Tyr Leu Asn Glu Gln Glu Lys Lys Ile Ala Glu Pro
          180         185         190
Ile Leu Lys Glu Ile Leu Glu Arg Val Phe Phe Leu Tyr Asp Val Gly
          195         200         205
Leu Gly Tyr Leu Thr Leu Gly Arg Asp Ala Arg Thr Ile Ser Gly Gly
          210         215         220

```


Glu Ser Gln Arg Ile Arg Ile Ala Ser Gln Ile Gly Ser Gly Leu Thr
 225 230 235 240
 Gly Val Leu Tyr Val Leu Asp Glu Pro Ser Ile Gly Leu His Glu Lys
 245 250 255
 Asp Thr Leu Lys Leu Ile Asn Thr Leu Arg Asn Leu Gln Lys Lys Gly
 260 265 270
 Asn Thr Leu Ile Val Val Glu His Asp Lys Glu Thr Ile Lys His Ala
 275 280 285
 Asp Phe Val Val Asp Ile Gly Pro Lys Ala Gly Arg His Gly Gly Glu
 290 295 300
 Val Val Phe Ser Gly Ser Val Lys Asp Leu Leu Gln Asn Asn His Ser
 305 310 315 320
 Thr Ala Leu Tyr Leu Asn Gly Thr Lys Lys Ile Glu Arg Pro Lys Phe
 325 330 335
 Glu Pro Pro Lys Glu Lys His Phe Leu Glu Ile Lys Asn Val Asn Ile
 340 345 350
 Asn Asn Ile Lys Asn Leu Ser Val Gln Ile Pro Leu Lys Gln Leu Val
 355 360 365
 Cys Ile Thr Gly Val Ser Gly Ser Gly Lys Ser Ser Leu Ile Leu Gln
 370 375 380
 Thr Leu Leu Pro Thr Ala Gln Thr Leu Leu Asn His Ala Lys Lys Asn
 385 390 395 400
 Gln Ser Leu Asn Gly Val Glu Ile Val Gly Leu Glu Tyr Leu Asp Lys
 405 410 415
 Val Ile Tyr Leu Asp Gln Ala Pro Ile Gly Lys Thr Pro Arg Ser Asn
 420 425 430
 Pro Ala Thr Tyr Thr Gly Val Met Asp Glu Ile Arg Ile Leu Phe Ala
 435 440 445
 Glu Gln Lys Glu Ala Lys Ile Leu Gly Tyr Ser Thr Ser Arg Phe Ser
 450 455 460
 Phe Asn Val Lys Gly Gly Arg Cys Glu Lys Cys Gln Gly Asp Gly Asp
 465 470 475 480
 Ile Lys Ile Glu Met His Phe Leu Pro Asp Val Leu Val Gln Cys Asp
 485 490 495
 Ser Cys Lys Gly Ala Lys Tyr Asn Pro Gln Thr Leu Glu Ile Lys Val
 500 505 510
 Lys Gly Lys Ser Ile Ala Asp Val Leu Asn Met Ser Val Glu Glu Ala
 515 520 525
 Tyr Glu Phe Phe Ala Lys Phe Pro Lys Ile Ala Val Lys Leu Lys Thr
 530 535 540
 Leu Ile Asp Val Gly Leu Gly Tyr Ile Thr Leu Gly Gln Asn Ala Thr
 545 550 555 560
 Thr Leu Ser Gly Gly Glu Ala Gln Arg Ile Lys Leu Ala Lys Glu Leu
 565 570 575
 Ser Lys Lys Asp Thr Gly Lys Thr Leu Tyr Ile Leu Asp Glu Pro Thr
 580 585 590
 Thr Gly Leu His Phe Glu Asp Val Asn His Leu Leu Gln Val Leu His
 595 600 605
 Ser Leu Val Ala Leu Gly Asn Ser Met Leu Val Ile Glu His Asn Leu
 610 615 620
 Asp Ile Ile Lys Asn Ala Asp Tyr Ile Ile Asp Met Gly Pro Asp Gly
 625 630 635 640
 Gly Asp Lys Gly Gly Lys Val Ile Ala Ser Gly Thr Pro Leu Glu Val
 645 650 655
 Ala Gln Asn Cys Glu Lys Thr Gln Ser Tyr Thr Gly Lys Phe Leu Ala
 660 665 670
 Leu Glu Leu Lys

675

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

```

Ile Ile Ile Asp Tyr Ser Ser Gln Tyr Phe Ser Gly Arg Ala Ala Ala
1           5           10           15
Phe Tyr Gln Ala Leu Asp Asn Phe Ile Ser Arg Tyr Ala Gln Arg Leu
          20           25           30
Ile Val Thr Asn Leu Ser Gln Ala Ile Arg Ile Tyr Gly Tyr Glu Val
          35           40           45
Gly Gly Thr Phe Arg Tyr Lys Gly Val Ser Leu Asn Val Gly Ile Ser
          50           55           60
Arg Thr Trp Pro Thr Thr Arg Gly Tyr Leu Met Ala Asp Ser Tyr Glu
65           70           75           80
Leu Ala Ala Ser Thr Gly Asn Val Phe Ile Ile Lys Leu Asp Tyr Thr
          85           90           95
Ile Ser Lys Asn Arg Asp Gln Ser Cys Met Ala Leu Ala Ala Leu Leu
          100          105          110
Pro Val Trp Ile Ile Ala Gly Leu Ile Phe Thr Cys Leu Ile Met Gly
          115          120          125
Gln Leu Lys Asn Pro Lys Pro Leu Pro Ile
          130          135

```

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

```

Gln Gly Met Gly Leu Lys Asn Leu Ser Thr Leu Leu Val Phe Leu Phe
1          5          10          15
Phe Cys Leu Gly Cys Val Ser Asn Phe Asn Glu Asp Thr Tyr Thr Leu
20          25          30
Asp Leu Val Leu Glu Lys Lys Ile Gln Ala Ser Arg Lys Gly Glu Ile
35          40          45
Thr Gln Asp Asn Val Pro Ile Ile Thr Ala Ile Ala Thr His Leu Asn
50          55          60
Asp Val Asp Ser Gly Thr Tyr Tyr Asp His Glu Tyr Phe Leu Val Glu
65          70          75          80
Ile Phe Thr Gln Asn Asn Asp Trp Ile Asp Asp Gly Tyr Ile Ser Tyr
85          90          95
Glu Leu Phe Gly Thr Lys Pro Thr Gly Ser Glu Pro Leu Trp Val Arg
100         105         110
Glu Ile Thr Arg Asp Glu Phe Asp Gly Ile Leu Glu Thr Thr Asn Arg
115         120         125
Trp Ser Arg Ala Phe Leu Ile Ala Phe Asp Lys Leu Asp Tyr Leu Ala
130         135         140
Val Gln Glu Ala Lys Leu Glu Leu Asp Ala Tyr Ser Leu Gly Lys Ile
145         150         155         160
Val Phe Asn Phe Ala Tyr Gln Val Pro Leu Pro Gln Phe
165         170

```

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

```

Gln Lys Glu Val Ser Asn Tyr Glu Glu Ser Ile Leu Val Asn Thr Pro
1          5          10          15
Tyr Ala Arg Val Asn Ile Leu Ala Ile Glu Lys Asn Glu Ser Pro Ile
20          25          30
Glu Leu Leu Ala Pro Val Asp Leu Val Thr Ala Leu Ser Asp Leu Met
35          40          45
Leu Gly Gly Glu Gly Ala Ser Lys Glu Glu Met Asp Asn Asp Asp Leu
50          55          60
Asp Ala Phe Lys Glu Met Ala Ser Asn Ile Phe Gly Ala Ile Ala Thr
65          70          75          80

```

470

Ser Leu Lys Ser Gln Glu Leu Leu Pro Lys Leu Asn Phe Thr Thr Thr
 85 90 95
 Asn Ala Glu Ile Ala Lys Glu Leu Pro Lys Lys Glu Asp
 100 105

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

Ile Cys Leu Leu Lys Glu Lys Ile Met Ser Asn Ser Met Leu Asp Lys
 1 5 10 15
 Asn Lys Ala Ile Leu Thr Gly Gly Gly Ala Leu Leu Leu Gly Leu Ile
 20 25 30
 Val Leu Phe Tyr Leu Ala Tyr Arg Pro Lys Ala Glu Val Leu Gln Gly
 35 40 45
 Phe Leu Glu Ala Arg Glu Tyr Ser Val Ser Ser Lys Val Pro Gly Arg
 50 55 60
 Ile Glu Lys Val Phe Val Lys Lys Gly Asp Arg Ile Lys Lys Gly Asp
 65 70 75 80
 Leu Val Phe Ser Ile Ser Ser Pro Glu Leu Glu Ala Lys Leu Ala Gln
 85 90 95
 Ala Glu Ala Gly His Lys Ala Ala Lys Ala Val Ser Asp Glu Val Lys
 100 105 110
 Arg Gly Ser Arg Asp Glu Thr Ile Asn Ser Ala Arg Asp Val Trp Gln
 115 120 125
 Ala Ala Lys Ser Gln Ala Asn Leu Ala Lys Glu Thr Tyr Lys Arg Val
 130 135 140
 Gln Asp Leu Tyr Asp Asn Gly Val Ala Ser Leu Gln Lys Arg Asp Glu
 145 150 155 160
 Ala Tyr Ala Ala Met Lys Ala Pro Asn Thr Thr Arg Ala Arg Leu Thr
 165 170 175
 Lys Ser Ile Lys Trp Leu
 180

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

471

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

```

Met Glu Phe Leu Ser Gly Tyr Phe Leu Trp Val Lys Ala Phe His Val
1           5           10           15
Ile Ala Val Ile Ser Trp Met Ala Ala Leu Phe Tyr Leu Pro Arg Leu
20           25           30
Phe Val Tyr His Ala Glu Asn Ala His Lys Lys Glu Phe Val Gly Val
35           40           45
Val Gln Ile Gln Glu Lys Lys Leu Tyr Ser Phe Ile Ala Ser Pro Ala
50           55           60
Met Gly Phe Thr Leu Ile Thr Gly Ile Leu Met Leu Leu Ile Ala Pro
65           70           75           80
Glu Met Phe Lys Ser Gly Gly Trp Leu His Ala Lys Leu Ala Leu Val
85           90           95
Val Leu Leu Leu Ile Tyr His Phe Tyr Cys Lys Lys Cys Met Arg Glu
100          105          110
Leu Glu Lys Asp Pro Thr Gly Lys Asn Ala Arg Phe Tyr Arg Val Phe
115          120          125
Asn Glu Ile Pro Thr Ile Leu Met Ile Leu Ile Val Ile Leu Val Val
130          135          140
Val Lys Pro Phe
145

```

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 291 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

```

Gly Leu Thr Ile Arg Gln Ala Phe Asn Lys Thr Arg Ser Thr His Ser
1           5           10           15
Arg Thr Leu Leu Leu Asp Ile Asp Cys Val Ile Pro Asn Ile Val Arg

```

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEO ID NO:526:

Gly Val Tyr His Asn Lys Glu Ile Ile Val Ala Tyr Arg Lys Ile Gly

473

```

1           5           10           15
Lys Val His Ser Thr Leu Thr Thr Thr Ser Met Ile Leu Ala Phe Gly
                20           25           30
Val Gln Lys Val Leu Phe Ser Gly Val Ala Gly Ser Leu Val Lys Asp
                35           40           45
Leu Lys Ile Asn Asp Leu Leu Val Ala Thr Gln Leu Val Gln His Asp
                50           55           60
Val Asp Leu Ser Ala Phe Asp His Pro Leu Gly Phe Ile Pro Glu Ser
65           70           75           80
Ala Ile Phe Ile Glu Thr Ser Gly Ser Leu Asn Ala Leu Ala Lys Lys
                85           90           95
Ile Ala Asn Glu Gln His Ile Ala Leu Lys Glu Gly Val Ile Ala Ser
                100           105           110
Gly Asp Gln Phe Val His Ser Lys Glu Arg Lys Glu Phe Leu Val Ser
                115           120           125
Glu Phe Lys Ala Ser Ala Val Glu Met Glu Gly Ala Ser Val Ala Phe
                130           135           140
Val Cys Gln Lys Phe Gly Val Pro Cys Cys Val Leu Arg Ser Ile Ser
145           150           155           160
Asp Asn Ala Asp Glu Lys Ala Gly Met Ser Phe Asp Glu Phe Leu Glu
                165           170           175
Lys Ser Ala His Thr Ser Ala Lys Phe Leu Lys Ser Met Val Asp Glu
                180           185           190
Leu

```

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

```

Lys Leu Ala Leu Phe Lys Gln Arg Gln Leu Lys Gln Asn Lys Asn Ala
1           5           10           15
Gln Ala Asn Pro Lys Ser Pro Phe Ile Thr His Val Val Leu Pro Lys
                20           25           30
Glu Thr Leu Ser Ser Ile Ala Lys Arg Tyr Gln Val Ser Ile Ser Ser
                35           40           45
Ile Gln Leu Ala Asn Asn Leu Lys Asp Ser Asn Ile Phe Ile His Gln
                50           55           60
Arg Leu Ile Ile Pro Thr Asn Lys Lys Leu Leu Ala Thr Arg Glu Phe
65           70           75           80

```

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

```

Gly His Arg Lys Arg Ile Phe Ser Lys Pro Ala Leu Leu Arg Ala Leu
1          5          10          15
Glu Pro Asn Glu Ala Leu Ile Phe Ser Gln Thr Leu Arg Phe Asp Gly
20          25          30
Tyr Val Glu Lys Leu Tyr Ala Asn Lys Thr Tyr Thr Pro Ile Lys Lys
35          40          45
Gly Asp Arg Leu Leu Ser Val Tyr Ser Pro Glu Leu Ala Gly Val Gln
50          55          60
Ser Glu Leu Leu Ser Ser Leu Lys Phe Asn Gln Gln Val Gly Ala Ile
65          70          75          80
Lys Glu Lys Leu Lys Leu Leu Gly Leu Glu Asn Phe Ser Ile Glu Lys
85          90          95
Ile Ile Ser Ser His Lys Val Gln Asn Glu Ile Thr Ile Tyr Ser Arg
100          105          110
Phe Asn Gly Val Ile Phe Lys Lys Ser Pro Asp Leu Asn Glu Gly Ser
115          120          125
Phe Ile Lys Lys Gly Gln Glu Leu Phe Lys Ile Ile Asp Leu Ser Arg
130          135          140
Leu Trp Ala Leu Val Lys Val Asn Gln Glu Asp Leu Glu Phe Leu Lys
145          150          155          160
Asn Thr His Gln Ala Ile Leu Phe Val Glu Gly Val Lys Gly Lys Gln
165          170          175
Ala Ile Thr Leu Glu Asn Ile Asn Pro Ile Ile Asn Ala Gln Asp Lys
180          185          190
Met Leu Glu Ala Arg Phe Asn Val Pro Asn Leu Lys Leu Leu Tyr Tyr
195          200          205
Pro Asn Met Phe Ala Gln Val Glu Ile Phe His Lys Pro Gln Lys Met
210          215          220
Lys Ile Leu Pro Lys Glu Ala Val Leu Ile Lys Gly Gly Lys Ala Ile
225          230          235          240
Val Phe Lys Lys Asp
245

```

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids

475

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

```

Ser Gly Glu His Thr Met Lys Lys Tyr Ile Leu Asn Leu Ala Leu Val
1      5      10      15
Gly Ala Leu Ser Ala Ser Phe Leu Met Ala Lys Pro Ala His Asn Ala
20      25      30
Asn Asn Ser Thr His Asn Thr Lys Glu Thr Thr Asp Ala Ser Ala Gly
35      40      45
Val Leu Ala Thr Val Asp Gly Arg Pro Ile Thr Lys Ser Asp Phe Asp
50      55      60
Met Ile Lys Gln Arg Asn Pro Asn Phe Asp Phe Asp Lys Leu Lys Glu
65      70      75      80
Lys Glu Lys Glu Ala Leu Ile Glu Gln Ala Ile Arg Thr Ala Leu Val
85      90      95
Glu Asn Glu Ala Lys Ala Glu Lys Leu Asn Gln Thr Pro Glu Phe Lys
100     105     110
Ala Met Met Glu Ala Val Lys Lys Gln Ala Leu Val Glu Phe Trp Ala
115     120     125
Lys Lys Gln Ala Glu Glu Val Lys Lys Asp Pro Asn Pro Arg Lys Arg
130     135     140
Asn Ala Gly Phe Leu Gln Arg Gln
145     150

```

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

476

```

Arg Ala Leu Lys Thr His Gly Ala Leu Ala Phe Val Gln Ala Phe Leu
1          5          10          15
Glu Ser Phe Lys Gly Phe Leu Ser Gln Ala Thr Leu Ile Ser Val Leu
20          25          30
Ile Ala Ser Val Leu Ile Leu Phe Cys Ala Ile Leu Leu Leu Leu Ala
35          40          45
Leu Leu Leu Arg Asn Arg Trp Ala Ser Tyr Ile Thr Thr Ala Ala Phe
50          55          60
Leu Gly Ala Phe Leu Ser Met Pro Phe Val Leu Asn Val Leu Leu Thr
65          70          75          80
Gln Ala Ile Tyr Pro Ile Glu Thr Arg Ile Leu His Ala Asn Pro Leu
85          90          95
Ser Tyr Ser Asn Ala Phe Ser Leu Gln Val Gly Val Lys Asn Ile Ser
100         105         110
Lys Phe Ser Leu Asn Lys Cys Val Leu Arg Leu Glu Val Leu Lys Asn
115         120         125
Pro His Asn Phe Val Glu Glu Arg Ala Phe Lys Trp Phe Val Lys Lys
130         135         140
Ser Tyr Glu Lys Thr Phe Lys Glu Lys Ile Leu Pro Glu Glu Ser Lys
145         150         155         160
Val Phe Ser Phe Phe Ile Asp Asp Tyr Pro Tyr Ser Lys Thr Ala Pro
165         170         175
Tyr Gln Val Ser Leu Phe Cys Leu
180

```

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

```

Ala Met Asn Ile Lys Thr His Ser Ser Asn Glu Lys Glu Arg Phe Val
1          5          10          15
Arg Ile Glu Glu Asp Glu Lys Lys Glu Leu Phe Ala Glu Ala Thr Asn
20          25          30
Glu Asn Pro His Gly Leu Ser Leu Met Ala Leu Ile Gly Val Leu Val
35          40          45
Phe Gly Gly Ala Phe Leu Ala Leu Leu Val Pro Lys Ile Tyr Leu Ser
50          55          60
Asn Asn Ile Tyr Tyr Ile Ser Arg Lys Ile Asn Thr Leu Glu Asp Gln
65          70          75          80
Lys Arg Leu Leu Leu Glu Glu Gln Gln Ile Leu Lys Asn Glu Leu Glu
85          90          95

```

477

Lys Glu Arg Phe Lys Tyr Tyr Ile Glu Asn Ser Glu Asn Ile Gly Asp
 100 105 110
 Ile Ala Phe
 115

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

Leu Leu Leu Ile His Phe Leu Ile Leu Arg Lys Leu Leu Gln His Lys
 1 5 10 15
 Thr Ile Met Asp Lys Ile Ile Ile Gln Gly Ala Arg Glu Asn Asn Leu
 20 25 30
 Lys Asn Ile Phe Leu Glu Ile Pro Lys Asn Gln Phe Val Val Phe Thr
 35 40 45
 Gly Leu Ser Gly Ser Gly Lys Ser Thr Leu Ala Phe Asp Thr Leu Tyr
 50 55 60
 Ala Glu Gly Gln Arg Arg Tyr Leu Glu Ser Leu Ser Ser Tyr Ala Arg
 65 70 75 80
 Gln Phe Leu Asp Lys Val Gly Lys Pro Asn Val Asp Lys Ile Glu Gly
 85 90 95
 Leu Thr Pro Ala Ile Ala Ile Asp Gln Lys Thr Thr Ser Lys Asn Pro
 100 105 110
 Arg Ser Thr Val Gly Thr Ile Thr Glu Ile Tyr Asp Tyr Leu Arg Leu
 115 120 125
 Leu Leu Ala Arg Val Gly Glu Gln Phe Cys Pro Thr Cys Leu Glu Pro
 130 135 140
 Ile Ser Ser Met Ser Ala Ser Asp Ile Ile Ser Gln Ile Cys His Leu
 145 150 155 160
 Glu Glu Asn Ser Lys Ile Ile Ile Leu Ala Pro Ile Ile Lys Asp Lys
 165 170 175
 Lys Gly Ser Phe Asn Asp Lys Leu Glu Ser Leu Arg Leu Lys Gly Tyr
 180 185 190
 Val Arg Ala Phe Val Asp Gly Val Met Val Arg Leu Asp Glu Glu Ile
 195 200 205
 His Leu His Lys Thr Lys Lys His Thr Ile Glu Ala Val Val Asp Arg
 210 215 220
 Val Val Ile Asn Ser Glu Asn Ala Ser Arg Ile Ala Ser Ala
 225 230 235

(2) INFORMATION FOR SEQ ID NO:533:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...361
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

```

His Gln Ser Phe Lys Arg Ala Phe Glu Pro Arg Arg Lys Gly Arg Val
1          5          10          15
Phe Arg Ile Met Gly Phe Glu Lys Ser Ile Leu Asp Asn Leu Asn Gly
20          25          30
Ala Gln Lys Ile Ala Ala Cys His Ile Gln Gly Pro Leu Leu Ile Leu
35          40          45
Ala Gly Ala Gly Ser Gly Lys Thr Lys Thr Leu Thr Ser Arg Leu Ala
50          55          60
Tyr Leu Ile Gly Ala Cys Gly Val Pro Ser Glu Asn Thr Leu Thr Leu
65          70          75          80
Thr Phe Thr Asn Lys Ala Ser Lys Glu Met Gln Glu Arg Ala Leu Lys
85          90          95
Leu Leu Lys Asn Gln Ala Leu Ile Pro Pro Leu Leu Cys Thr Phe His
100         105         110
Arg Phe Gly Leu Leu Phe Leu Arg Gln His Met Asn Leu Leu Lys Arg
115         120         125
Ala Cys Asp Phe Ser Val Leu Asp Ser Asp Glu Val Lys Thr Leu Cys
130         135         140
Lys Gln Leu Lys Ile Ser Asn Phe Arg Ala Ser Ile Ser Gln Ile Lys
145         150         155         160
Asn Gly Met Met Asp Leu Ser Val Gln Asp Ser Glu Cys Tyr Lys Ala
165         170         175
Tyr Glu Leu Tyr Gln Asn Ala Leu Lys Lys Asp Asn Leu Val Asp Phe
180         185         190
Asp Asp Leu Leu Cys Leu Ser Leu Lys Ile Leu Gln Asp Asn Glu Lys
195         200         205
Leu Ala Lys Glu Thr Ser Glu Arg Tyr His Tyr Ile Met Val Asp Glu
210         215         220
Tyr Gln Asp Thr Asn Ala Leu Gln Leu Glu Phe Leu Lys Gln Leu Ser
225         230         235         240
Phe Thr His His Asn Leu Cys Val Val Gly Asp Asp Asp Gln Ser Ile
245         250         255
Tyr Gly Phe Arg Gly Ala Asp Ile Ser Asn Ile Leu Asn Phe Ser Lys
260         265         270
His Phe Lys Gly Ala Lys Ile Val Lys Leu Glu Thr Asn Tyr Arg Ser
275         280         285
Ser Ala Glu Ile Leu Ala Cys Ala Asn Ser Leu Ile Ser His Asn Gln
290         295         300

```

479

```

His Arg His Ile Lys Thr Leu Gln Ser Phe Lys Gly Ser His Lys Ser
305                310                315                320
Val Ile Cys Lys Glu Tyr Pro Thr Gln Lys Glu Glu Ser Leu Asp Val
                325                330                335
Ala Tyr Gln Ile Gln Ser Pro Phe Lys Glu Gly Arg Glu Phe Arg Lys
                340                345                350
Tyr Arg Tyr Phe Val Ser Phe Lys Trp
                355                360

```

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

```

Met Arg Lys Thr Ile Ser Ala Leu Phe Leu Ser Ala Cys Ile Gly Leu
1                5                10                15
Ser Ser Val His Ala Ser Asn Ala Leu Ile Leu Gln Thr Asp Phe Ser
                20                25                30
Leu Lys Asp Gly Ala Val Ser Ala Met Lys Gly Val Ala Phe Ser Val
                35                40                45
Asp Ser Asn Leu Lys Ile Phe Asp Leu Thr His Glu Ile Pro Pro Tyr
                50                55                60
Asn Ile Trp Glu Gly Ala Tyr Arg Leu Tyr Gln Thr Ala Ser Tyr Trp
65                70                75                80
Pro Lys Gly Ser Val Phe Val Ser Val Val Asp Pro Gly Val Gly Thr
                85                90                95
Asn Arg Lys Ser Val Val Leu Lys Thr Lys Asn Gly Gln Tyr Phe Val
                100                105                110
Ser Pro Asp Asn Gly Thr Leu Thr Leu Val Ala Gln Thr Leu Gly Ile
                115                120                125
Asp Ser Arg Ala Glu Ile Asp Glu Asn Ser Ile Arg Leu Lys Gly Ser
130                135                140
Lys Phe Leu Ser Ser Arg Pro Val
145                150

```

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

480

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

```

Asp Ile Phe Asn Lys Glu Glu Ile Met Ala Ile Asp Leu Ala Glu Val
1           5           10           15
Thr Gly Ala Lys Ala Ala Gln Glu Arg Lys Lys Glu Gln Pro Thr Ile
20           25           30
Ala Asn Gly Leu Asp Lys Asn Ala Phe Met Lys Leu Phe Leu Glu Gln
35           40           45
Leu Lys Asn Gln Asp Pro Thr Ala Pro Met Glu Thr Asp Lys Ile Ile
50           55           60
Thr Gln Thr Ala Gln Leu Thr Gln Val Glu Met Gln Glu Glu Asn Lys
65           70           75           80
Lys Thr Met Gln Glu Val Ala Ser Ala Met Lys Ser Asn Lys Glu Thr
85           90           95
Asn Glu Ser Leu Lys Asp Phe Gln Gly Ala Leu Lys Asp Thr Met Glu
100          105          110
Asn Leu Asn Lys Gly Met Asp Asp Ser Leu Lys Ala Asn Asn Ala Leu
115          120          125
Arg Glu Val Ser Ala Leu Asn Ser Val Ser Met Ile Gly Lys Ile Ala
130          135          140
Glu Thr Asp Val Ser Gly Ala Asn Phe Asp Gly Asn Asn Lys Leu Ser
145          150          155          160
Phe Ser Leu Phe Phe Asp Glu Lys Ile Asp Ala Ser Lys Gly Val Pro
165          170          175
Ala Ile Gln Ile Leu Asn Glu Asn Asn Glu Leu Val Lys Thr Ile Pro
180          185          190
Leu Lys Asp Tyr Asn Gly Gln Lys Gly Tyr Ile Asn Phe Glu Trp Asp
195          200          205
Gly Thr Asn Glu Lys Gly Glu Lys Val Pro Lys Gly Asn Tyr Lys Ile
210          215          220
Lys Ala Glu Tyr Asn Leu Gly Ser Pro Lys Gln Ala Val Phe Ala Asn
225          230          235          240
Ala His Trp

```

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

481

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

```

Asn Ala His Ala Phe Thr His Pro Phe Ser Ala Pro Ala Arg Phe Arg
1          5          10          15
Leu Ala Gln Lys Arg Lys Asp Asn Thr Leu Pro Phe Leu Arg Pro Asp
20          25          30
Gly Lys Ser Gln Val Ser Val Arg Tyr Glu Asn Asn Lys Pro Val Ser
35          40          45
Val Asp Thr Ile Val Ile Ser Thr Gln His Ser Pro Glu Val Ser Gln
50          55          60
Lys His Leu Lys Glu Ala Val Ile Glu Glu Ile Val Tyr Lys Val Leu
65          70          75          80
Pro Lys Glu Tyr Leu His Asp Asn Ile Lys Phe Phe Ile Asn Pro Thr
85          90          95
Gly Lys Phe Val Ile Gly Gly Pro Gln Gly Asp Ala Gly Leu Thr Gly
100          105          110
Arg Lys Ile Ile Trp Asp Thr Tyr Gly Gly Phe Cys Pro His Gly Gly
115          120          125
Gly Ala Phe Thr Gly Lys Asp Pro Tyr Lys Val Asp Met Ser Ala Ala
130          135          140
Tyr Ala Ala Arg Tyr Val Ala Lys Asn Leu Val Ala Ser Gly Val Cys
145          150          155          160
Asp Lys Ala Thr Val Gln Leu Ala Tyr Ala Ile Gly Val Ile Glu Pro
165          170          175
Val Ser Ile Tyr Val Asn Thr His Asn Thr Ser Lys His Ser Ser Ala
180          185          190
Glu Leu Glu Lys Cys Val Lys Ser Val Phe Lys Leu Thr Pro Lys Gly
195          200          205
Ile Ile Glu Ser Leu Asp Leu Leu Arg Pro Ile Tyr Ser Leu Thr Ser
210          215          220
Ala Tyr Gly His Phe Gly Arg Glu Leu Glu Glu Phe Thr Trp Glu Lys
225          230          235          240
Thr Asn Lys Val Glu Ile Lys Ala Phe Phe Lys Arg
245          250

```

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

Val	Ile	Ser	Tyr	His	Phe	Ile	Ile	Leu	Lys	Asp	Val	Phe	Ile	Met	Arg
1				5					10					15	
Ile	Lys	Ala	Tyr	Phe	Leu	Arg	Leu	Ser	His	Trp	Phe	Leu	Ser	Phe	Gly
			20					25					30		
Trp	Val	Leu	Ala	Leu	Val	Lys	Thr	Leu	Lys	Asn	Leu	Lys	Ile	Leu	Lys
		35					40					45			
Thr	Ile	Pro	Pro	Asn	Lys	Ile	Ala	Leu	Lys	Pro	Thr	Pro	Tyr	Gly	Ser
	50					55					60				
Glu															
65															

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

Lys	Gly	Ile	Ser	Met	Lys	Lys	Ser	Leu	Cys	Leu	Ser	Phe	Phe	Leu	Thr
1				5					10					15	
Phe	Ser	Asn	Pro	Leu	Gln	Ala	Leu	Val	Ile	Glu	Leu	Leu	Glu	Glu	Ile
			20					25					30		
Lys	Thr	Ser	Pro	His	Lys	Gly	Thr	Phe	Lys	Ala	Lys	Val	Leu	Asp	Ser
		35					40					45			
Lys	Glu	Pro	Arg	Gln	Val	Leu	Gly	Val	Tyr	Asn	Ile	Ser	Pro	His	Lys
	50					55					60				
Lys	Leu	Thr	Leu	Thr	Ile	Thr	His	Ile	Ser	Thr	Ala	Ile	Val	Tyr	Gln
65					70					75				80	
Pro	Leu	Asp	Glu	Lys	Leu	Ser	Leu	Glu	Thr	Thr	Leu	Ser	Pro	Asn	Arg
				85					90					95	
Pro	Thr	Ile	Pro	Arg	Asn	Thr	Gln	Ile	Val	Phe	Ser	Ser	Lys	Glu	Leu
			100					105					110		
Lys	Glu	Pro	His	Ser	Asn	Pro	Ile	Pro	Ser						
		115						120							

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

483

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

```

Lys Lys Phe His Thr Leu Ile Leu Pro Val Glu Trp Gly Thr Glu Ile
1          5          10          15
Val Leu Val Val Ser Gly Ser Leu Gln Asn Ile Val Arg Ser Phe Leu
20          25          30
Arg Arg Ile Ser Val Phe Phe Ile Ile Asp Phe Ile Asn Phe Ile Phe
35          40          45
Val Ile Asp Gln Ile Ile His Phe Phe Gly Asp Phe Phe Ile Phe Phe
50          55          60
Phe Met Leu Asn Leu Phe Tyr Ile Leu Ile Arg Leu Ile Asp Leu Ile
65          70          75          80
Val Leu Ser Gly Phe Ser Val Val Leu Val Arg Leu Gly Gln Phe Phe
85          90          95
Arg Leu Ile Phe Ala Cys Ala Gln His Ala Phe Asn Lys Val Asp Ile
100         105         110
Asp Lys Met Ser Asp Phe Arg Phe His Gln Leu Ser Phe Phe Lys Ser
115         120         125
Val Tyr Asn Leu Phe Ile Leu Ser
130         135

```

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

```

Tyr Phe Leu Leu Ser Gly Glu Leu Arg Leu Ser Trp Trp Leu Val Ala
1          5          10          15

```

484

```

Arg Cys Lys Thr Leu Phe Val Leu Phe Cys Glu Gly Ser Ala Phe Ser
      20                      25                      30
Ser Leu Leu Ile Ser Ser Ile Leu Phe Ser Leu Leu Ile Arg Ser Phe
      35                      40                      45
Thr Ser Leu Val Thr Phe Ser Ser Ser Ser Ser Cys Ser Ile Phe Phe
      50                      55                      60
Ile Ser Leu Leu Gly
65

```

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

```

Thr Leu Phe Lys Ser Ser Asp Lys Val Cys Asn Leu Met Arg Val Ile
1      5      10      15
Ile Lys Phe Met Leu Ile Ser Leu Lys Thr Phe Leu Lys Ile Leu Leu
      20      25      30
Glu Ile Phe Leu Lys Thr Phe Gln Lys Ile Trp Ile Val Cys Val Val
      35      40      45
Ile Trp Gly Leu Gly Cys Ser Phe Leu Asn Ala Asn Ser Val Gln Leu
      50      55      60
Glu Glu Thr Leu Arg Arg Asn Pro Lys Asn Leu Ile Trp Gln His Phe
      65      70      75      80
Lys Lys Lys Phe Lys Lys Ser Asn Thr Ile Pro Tyr Ala Pro Asn Ser
      85      90      95
Arg Trp Lys Tyr Leu Gly Thr Ser Ile Gly Ile Leu Gly Val Ser Leu
      100     105     110
Val Ile Gly Ile Val Gly Leu Tyr Leu Met Pro Glu Ser Val Thr Asn
      115     120     125
Trp Asp Lys Glu Lys Phe Gly Val Lys Ser Trp Phe Glu Asn Val Arg
      130     135     140
Met Gly Pro Lys Leu Asp Asn Asp Ser Phe Ile Phe Asn Glu Ile Leu
      145     150     155     160
His Pro Tyr Phe Gly Ala Met Tyr Tyr Met Gln Pro Arg Met Ala Gly
      165     170     175
Phe Ser Trp Met Thr Ser Ala Phe Phe Ser Phe Ile Thr Ser Thr Leu
      180     185     190
Phe Trp Glu Tyr Gly Leu Glu Pro Phe Val Glu Val Pro Ser Trp Gln
      195     200     205
Asp Leu Val Ile Thr Pro Leu Leu Gly Phe Ile Leu Gly Glu Gly Phe
      210     215     220

```

485

Tyr Gln Leu Thr Pro Ile Ser Asn Ala Thr Lys Ala Ser Cys Leu Ala
 225 230 235 240
 Leu Tyr Phe

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

Lys Lys Arg Lys Pro Met Phe Arg Lys Leu Ala Thr Ser Val Ser Leu
 1 5 10 15
 Ile Ser Leu Leu Ile Ser Asn Ala Leu Tyr Ala Lys Glu Ile Ser Glu
 20 25 30
 Ala Asp Lys Val Ile Lys Ala Thr Lys Glu Thr Lys Glu Thr Lys Lys
 35 40 45
 Glu Ala Lys Arg Leu Lys Lys Glu Ala Lys Gln Arg Gln Gln Ile Pro
 50 55 60
 Asp Asn Lys Lys Pro Gln Tyr Val Ser Val Asp Asp Thr Lys Thr Gln
 65 70 75 80
 Ala Leu Phe Asp Ile Tyr Asp Thr Leu Asn Val Asn Asp Lys Ser Phe
 85 90 95
 Gly Asp Trp Phe Gly Asn Ser Ala Leu Lys Asn Lys Thr Tyr Leu Tyr
 100 105 110
 Ala Met Asp Leu Leu Asp Tyr Asn Asn Tyr Leu Ser Ile Glu Asn Pro
 115 120 125
 Ile Ile Lys Thr Arg Ala Met Gly Thr Tyr Ala Asp Leu Ile Ile Ile
 130 135 140
 Thr Gly Ser Leu Glu Gln Val Asn Gly Tyr Tyr Asn Ile Leu Lys Ala
 145 150 155 160
 Leu Asn Lys Arg Asn Ala Lys Phe Val Leu Lys Ile Asn Asp Lys Ile
 165 170 175
 Pro Tyr Ala Gln Ala Thr Phe Leu Arg Val Pro Lys Arg Ser Asp Pro
 180 185 190
 Asn Ala His Thr Leu Asp Lys Gly Ala Ser Ile Asp Glu Ser Lys Leu
 195 200 205
 Phe Glu Gln Gln Lys Lys Met Tyr Phe Asn Tyr Ala Asn Asp Val Ile
 210 215 220
 Cys Arg Pro Asn Asp Glu Val Cys Ser Pro Leu Arg Asp Glu Met Val
 225 230 235 240
 Ala Met Pro Thr Asn Asp Ser Val Thr Gln Lys Pro Asn Ile Ile Ala
 245 250 255

486

```

Pro Tyr Ser*Leu Tyr Arg Leu Lys Glu Thr Asn Asn Ala Asn Glu Ala
      260                      265                      270
Gln Pro Ser Pro Tyr Ala Thr Gln Thr Ala Pro Glu Asn Ser Lys Glu
      275                      280                      285
Lys Leu Ile Glu Glu Leu Ile Ala Asn Ser Gln Leu Ile Ala Asn Glu
      290                      295                      300
Glu Glu Arg Glu Lys Lys Leu Leu Ala Glu Lys Glu Lys Gln Glu Thr
      305                      310                      315                      320
Glu Leu Ala Lys Tyr Lys Leu Lys Asp Leu Glu Asn Gln Lys Lys Leu
      325                      330                      335
Lys Ala Leu Glu Ala Glu Leu Lys Lys Lys Asn Thr Lys Lys Pro Arg
      340                      345                      350
Val Val Glu Val Pro Ile Pro Pro Lys Thr Ser Asp Ser Asp Glu Thr
      355                      360                      365
Met Arg Val Ile Lys Glu Lys Glu Asn Tyr Asn Gly Leu Leu Val Asp
      370                      375                      380
Lys Glu Thr Thr Ile Lys Arg Ser Tyr Lys Gly Thr Leu Ile Ser Glu
      385                      390                      395                      400
Asn Ser Tyr Ser Lys Lys Thr Pro Ile Asn Leu Glu Asp Leu Arg Ser
      405                      410                      415
Leu Glu Glu Glu Ile Lys Ser Tyr Tyr Val Lys Ser Asn Gly Leu Cys
      420                      425                      430
Tyr Ala Asn Gly Ile Asn Leu Tyr Val Lys Ile Lys Asn Asp Pro Tyr
      435                      440                      445
Lys Glu Gly Met Leu Cys Gly Tyr Glu Ser Val Gln Lys Leu Leu Ser
      450                      455                      460
Pro Leu Arg Asp Lys Leu Lys Tyr Asp Lys Gln Lys Leu Gln Lys Ala
      465                      470                      475                      480
Leu Leu Lys Asp Leu Lys
      485

```

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

```

Val Val Gly Thr Met Glu Asp Phe Leu Tyr Asn Thr Leu Tyr Phe Ile
1          5          10          15
Glu Asp Tyr Lys Leu Val Val Ile Phe Ser Phe Ile Gly Leu Ile Ala
      20          25          30
Leu Phe Phe Leu Tyr Lys Phe Ile Lys Thr Gln Lys Lys Val Phe Lys
      35          40          45

```

487

```

Asp Lys Ala Asn Gln Pro Gln Lys Lys Lys Ser Phe Lys Glu Ile Ile
 50          55          60
Ile Asp Gly Leu Lys Glu Arg Val Lys Thr Phe Gly Phe Trp Leu Pro
65          70          75          80
Ser Tyr Thr Ile Thr Ile Leu Phe Phe Tyr His Ile Arg Val Ile Phe
          85          90          95
Leu Asp Ser Leu Arg
          100

```

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

```

Arg Met Ala Gln Ile Val Lys Gly Ser Asp Met Phe Glu Asp Phe Tyr
 1          5          10          15
Arg Thr Thr Leu Ser Phe Leu Arg Ser Leu Leu Leu Leu Leu Gly Leu
          20          25          30
Leu Leu Pro Phe Ser Leu Cys Ile Ala Asp Glu Tyr Ile Ser Ile Ser
          35          40          45
Asp Asp Trp Asp Glu Arg Ala Arg Asn Gln Trp Asp Glu Thr Ala Arg
          50          55          60
Asn His Lys Thr Tyr Tyr Phe Glu Asn Gly Leu Asp His Phe Asn Gln
65          70          75          80
Gly Gln Tyr Lys Gln Ala Phe Lys Asp Phe Lys Leu Ala Gln Glu Tyr
          85          90          95
Ser Ile Gly Leu Gly Asn Val Tyr Leu Ala Lys Met Tyr Leu Glu Gly
          100          105          110
Lys Gly Val Lys Val Asp Tyr Lys Lys Ala Gln Phe Tyr Ala Gln Asn
          115          120          125
Ala Ile Lys Gly Tyr Gly Ser Gly Leu Leu Gly Gly Ala Leu Ile Leu
          130          135          140
Gly Arg Met Gln Ala Glu Gly Leu Gly Met Lys Lys Asp Leu Lys Gln
145          150          155          160
Ala Leu Lys Thr Tyr Arg His Val Val Arg Met Phe Ser Asn Lys Ser
          165          170          175
Ala Asn Phe Ala Asn Lys Phe Gly Ser Asn Leu Ala Glu Phe Thr Ser
          180          185          190
Met Leu Ile Gly Ser Arg Phe Ile Asp Leu Ser Gly Leu Ser Ala Asn
          195          200          205
Pro Ile Lys Phe Gly Asn Lys Phe Gly Ile Leu Val Lys Lys Ala Leu
210          215          220

```

488

Gln Ile Lys Asp Asn Thr Leu Ser Trp Glu Asp Ile Ala Glu Ile Ser
 225 230 235 240
 Ser Asn Ile Ile Leu Leu Lys Gln Gln Met Gly Glu Ile Leu Tyr Arg
 245 250 255
 Ile Gly Ile Ala Tyr Lys Glu Gly Leu Gly Thr Arg Lys Lys Lys Asp
 260 265 270
 Arg Ala Lys Lys Phe Leu Gln Lys Ser Ala Glu Phe Gly Tyr Glu Lys
 275 280 285
 Ala Met Glu Ala Leu
 290

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

Asp Phe His Asp Phe Cys Ala Asn Ile His His Arg Ile Arg Trp Arg
 1 5 10 15
 His Arg His Ile Ala Ser Leu Leu Ser Arg Ser Met Pro Lys Ile His
 20 25 30
 Ala Val Phe Lys Ala Phe Ile Pro Ile Pro Phe Ala Leu Phe Ala Ile
 35 40 45
 His Phe Val Val Leu Gly Ile Gly Ser Val Phe Asn Leu Asn Arg Ile
 50 55 60
 Lys Asp Lys Lys Phe Ile Leu Arg Ala Lys Ile Ser His Ile Ala Gln
 65 70 75 80
 Ala

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

```

Lys Ala Met Leu Ser Ser Thr Asn Asp Ile Arg Tyr Gln Asn Pro Lys
1          5          10          15
Asn Lys Ala Leu Lys Gly Glu Ile Leu Ala Asn Leu Lys Phe Ile Lys
20          25          30
Lys Leu Leu Gly Ile Gly Cys Lys Asp Pro Ser Ala Tyr Val Gln Leu
35          40          45
Gly Val Ser Lys Ser Glu Lys Gln Glu Ile Glu Asn Lys Ile Glu Glu
50          55          60
Arg Lys Arg Ala Lys Glu Gln Lys Asp Phe Leu Lys Ala Asp Ser Ile
65          70          75          80
Arg Glu Glu Leu Leu Gln Gln Lys Ile Ala Leu Met Asp Thr Pro Gln
85          90          95
Gly Thr Ile Trp Glu Lys Leu Phe
100

```

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

```

Met Arg Lys Val Ile Ile Met Asn Gly Tyr Leu Arg Val Lys Thr Pro
1          5          10          15
Tyr Phe Leu Ala Ser Val Val Leu Thr Phe Trp Thr Phe Asn Ser Phe
20          25          30
Met Ser Ala Lys Asp Lys His His Phe Leu Lys Lys Val Thr Thr Thr
35          40          45
Glu Gln Lys Phe Ser Ser Ser Ala Pro Ile Ser Trp Gln Ser Glu Glu
50          55          60
Val Arg Asn Ser Thr Ser Ser Arg Thr Val Ile Ser Asn Lys Glu Leu
65          70          75          80
Lys Lys Thr Gly Asn Leu Asn Ile Glu Asn Ala Leu Gln Asn Val Pro
85          90          95
Gly Ile Gln Ile Arg Asp Ala Thr Gly Thr Gly Val Leu Pro Lys Ile
100          105          110
Ser Val Arg Gly Phe Gly Gly Gly Gly Asn Gly His Ser Asn Thr Asn

```

490

115	120	125
Met Ile Leu Val Asn Gly Ile Pro Ile Tyr Gly Ala Pro Tyr Ser Asn		
130	135	140
Ile Glu Leu Ala Ile Phe Pro Val Thr Phe Gln Ser Val Asp Arg Ile		
145	150	155
Asp Val Ile Lys Gly Gly Thr Ser Val Gln Tyr Gly Pro Asn Thr Phe		160
	165	170
		175
Gly Gly Val Val Asn Val Ile Thr Lys Glu Ile Pro Lys Glu Trp Glu		
	180	185
		190
Asn Gln Ala Ala Glu Arg Ile Thr Phe Trp Gly Arg Ser Ser Asn Gly		
	195	200
		205
Asn Phe Val Asp Pro Lys Glu Lys Gly Lys Pro Leu Ala Gln Thr Leu		
	210	215
		220
Gly Asn Gln Met Leu Phe Asn Thr Tyr Gly Arg Thr Ala Gly Met Leu		
225	230	235
		240
Gly Lys Tyr Ile Gly Ile Ser Ala Gln Gly Asn Trp Ile Asn Gly Gln		
	245	250
		255
Gly Phe Arg Gln Asn Ser Pro Thr Lys Val Gln Asn Tyr Leu Leu Asp		
	260	265
		270
Ala Ile Tyr Lys Ile Asn Ala Thr Asn Thr Phe Lys Ala Tyr Tyr Gln		
	275	280
		285
Tyr Tyr Gln Tyr Asn Ser Tyr His Pro Gly Thr Leu Ser Ala Gln Asp		
	290	295
		300
Tyr Ala Tyr Asn Arg Phe Ile Asn Glu Arg Pro Asp Asn Gln Asp Gly		
305	310	315
		320
Gly Arg Ala Lys Arg Phe Gly Ile Val Tyr Gln Asn Tyr Phe Gly Asp		
	325	330
		335
Pro Asp Arg Lys Val Gly Gly Asp Phe Lys Phe Thr Tyr Phe Thr His		
	340	345
		350
Asp Met Ser Arg Asp Phe Gly Phe Ser Asn Gln Tyr Gln Ser Val Tyr		
	355	360
		365
Met Ser Gly Gln Asn Lys Ile Leu Pro Phe Lys Gly Lys Gly Glu Ile		
	370	375
		380
Ser Ala Lys Asn Pro Asn Cys Gly Leu Tyr Ser Tyr Ser Asp Thr Asn		
385	390	395
		400
Ser Pro Cys Trp Gln Phe Phe Asp Asn Ile Arg Arg Ser Val Val Asn		
	405	410
		415
Ala Phe Glu Pro Lys Leu Asn Leu Ile Val Asn Thr Gly Lys Val Lys		
	420	425
		430
Gln Thr Phe Asn Met Gly Met Arg Phe Leu Thr Glu Asp Leu Tyr Arg		
	435	440
		445
Arg Ser Thr Thr Arg Lys Asn Pro Ser Met Pro Asn Asn Gly Ser Gly		
	450	455
		460
Phe Asp Ala Gly Thr Ser Leu Asn Asn Phe Asn Asn Tyr Thr Ala Val		
465	470	475
		480
Tyr Ala Ser Asp Glu Ile Asn Phe Asn Asn Gly Met Leu Thr Ile Thr		
	485	490
		495
Pro Gly Leu Arg Tyr Thr Phe Leu Asn Tyr Glu Lys Lys Asp Ala Pro		
	500	505
		510
Pro Phe Lys Val Gly Gln Thr Pro Lys Thr Thr Lys Glu Arg Tyr Asn		
	515	520
		525
Gln		

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

491

(A) LENGTH: 194 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

Arg	Val	Gly	Phe	Arg	Ser	Phe	Ser	Gly	Gly	His	Cys	Ala	Glu	Ile	Phe	1	5	10	15
Arg	Phe	Asn	Pro	His	Pro	Met	Ala	Phe	Cys	Ala	Arg	Gln	Lys	Pro	Leu	20	25	30	
Lys	Glu	Ile	Met	Arg	Phe	Phe	Ile	Leu	Phe	Phe	Met	Gly	Met	Leu	Gly	35	40	45	
Val	Gly	Phe	Ser	Gln	Thr	Glu	Leu	Asp	Leu	Lys	Asp	Leu	Glu	Lys	Lys	50	55	60	
Pro	Ala	Gly	Ile	Val	Arg	Asp	Tyr	Tyr	Leu	Trp	Arg	Tyr	Ile	Ser	Asp	65	70	75	80
Lys	Lys	Thr	Ser	Leu	Glu	Asn	Ala	Lys	Lys	Ala	Tyr	Glu	Leu	Thr	Gln	85	90	95	
Asn	Lys	Asn	Ser	Ala	Leu	Gln	Lys	Ala	Met	Gln	Glu	Lys	Gly	Val	Glu	100	105	110	
Asn	Ser	Asp	Lys	Ser	Pro	Asp	Ala	Lys	Met	Pro	Glu	Asp	Ile	Tyr	Cys	115	120	125	
Lys	Gln	Ile	Thr	Leu	Glu	Ser	Met	Leu	Glu	Thr	Thr	Asp	Ala	Phe	Gln	130	135	140	
Ala	Ser	Cys	Ile	Ala	Ile	Ala	Leu	Lys	Ser	Lys	Ile	Arg	Asp	Phe	Asp	145	150	155	160
Lys	Ile	Pro	Ile	Gln	Thr	Phe	Lys	Pro	Leu	Gln	Glu	Lys	Ile	Lys	Glu	165	170	175	
Ala	Tyr	Pro	Ile	Leu	Tyr	Glu	Glu	Leu	Glu	Ile	Leu	Gln	Ser	Lys	Asn	180	185	190	
Val	Ser																		

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

```

His Ala Leu Tyr Ser Pro Ile Lys Ile Ala Phe Glu Lys Ala Leu Lys
1           5           10           15
Asn Ala Lys Glu Ser Val Phe Ile Ala Ser Ser Tyr Phe Ile Pro Gly
          20           25           30
Lys Lys Ile Met Lys Ile Phe Lys Asn Gln Ile Ser Lys Gly Ile Glu
          35           40           45
Leu Asn Ile Leu Thr Asn Ser Leu Ser Ser Thr Asp Ala Ile Val Val
          50           55           60
Tyr Gly Ala Trp Glu Arg Tyr Arg Asn Lys Leu Val Arg Met Gly Ala
65           70           75           80
Asn Val Tyr Glu Ile Arg Asn Asp Phe Phe Asn Arg Gln Ile Lys Gly
          85           90           95
Arg Phe Ser Thr Lys His Ser Leu His Gly Lys Thr Ile Val Phe Asp
          100          105          110
Asp Ala Leu Thr Leu Leu Gly Ser Phe Asn Ile Asp Pro Arg Ser Ala
          115          120          125
Tyr Ile Asn Thr Glu Ser Ala Val Leu Phe Asp Asn Pro Ser Phe Ala
          130          135          140
Lys Arg Val Arg Leu Ser Leu Lys Asp His Ala Gln Gln Ser Trp His
145          150          155          160
Leu Val Leu Tyr Arg His Arg Val Ile Trp Glu Ala Thr Glu Glu Gly
          165          170          175
Ile Leu Ile His Glu Lys Asn Ser Pro Asp Thr Ser Phe Phe Leu Arg
          180          185          190
Leu Ile Lys Glu Trp Ser Lys Val Leu Pro Glu Arg Glu Leu
          195          200          205

```

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

```

Gly Lys Ile Lys Gly Val Met Met Lys Phe Phe Leu Leu Lys Lys Phe
1           5           10           15
Ser Glu Phe Leu Asn Thr Gln Thr His Phe Asn Leu Lys Arg Leu Asn

```

			20					25					30		
Ala	Ser	Ser	Phe	Leu	Leu	Glu	Thr	Phe	Ser	Lys	Glu	Lys	His	Ala	Phe
		35					40					45			
Val	Val	Asp	Leu	Ser	Ala	Pro	Tyr	Ile	Gly	Leu	Ser	Lys	Lys	Pro	Pro
	50					55					60				
Glu	Ser	Val	Leu	Lys	Asn	Thr	Leu	Ala	Leu	Asp	Phe	Cys	Leu	Asn	Lys
65					70					75					80
Phe	Thr	Lys	Asn	Ala	Lys	Ile	Leu	Gln	Ala	Asn	Val	Ile	Asp	Asn	Asp
			85						90					95	
Arg	Ile	Leu	Glu	Ile	Lys	Gly	Ala	Lys	Asp	Leu	Ala	Tyr	Lys	Ser	Glu
			100					105					110		
Thr	Phe	Ile	Leu	Arg	Leu	Glu	Met	Ile	Pro	Lys	Lys	Ala	Asn	Leu	Met
		115					120					125			
Ile	Leu	Asp	Gln	Glu	Lys	Cys	Val	Ile	Glu	Ala	Phe	Arg	Phe	Asn	Asp
	130					135				140					
Arg	Val	Ala	Lys	Asn	Asp	Ile	Leu	Gly	Ala	Leu	Pro	Pro	Asn	Ile	Tyr
145					150					155					160
Glu	His	Gln	Glu	Glu	Asp	Leu	Asp	Phe	Lys	Gly	Leu	Leu	Asp	Ile	Leu
				165					170					175	
Glu	Lys	Asp	Phe	Leu	Ser	Tyr	Gln	His	Lys	Glu	Leu	Glu	His	Lys	Lys
			180					185					190		
Asn	Gln	Ile	Ile	Lys	Arg	Leu	Asn	Ala	Gln	Lys	Glu	Arg	Leu	Lys	Glu
		195					200					205			
Lys	Leu	Glu	Lys	Leu	Glu	Asp	Pro	Lys	Thr	Leu	Gln	Leu	Glu	Ala	Lys
	210					215					220				
Glu	Leu	Gln	Thr	Gln	Ala	Ser	Leu	Leu	Leu	Thr	Tyr	Gln	His	Leu	Ile
225					230					235					240
Asn	Arg	Arg	Glu	Asn	Arg	Val	Ile	Leu	Lys	Asp	Phe	Glu	Asp	Lys	Glu
				245					250					255	
Cys	Met	Ile	Glu	Ile	Asp	Lys	Ser	Met	Pro	Leu	Asn	Ala	Phe	Ile	Asn
			260					265					270		
Lys	Lys	Phe	Thr	Leu	Ser	Lys	Lys	Lys	Lys	Gln	Lys	Ser	Gln	Phe	Leu
		275					280					285			
Tyr	Leu	Glu	Glu	Glu	Asn	Leu	Lys	Glu	Lys	Ile	Ala	Phe	Lys	Glu	Asn
	290					295					300				
Gln	Ile	Asn	Tyr	Val	Arg	Asp	Ala	Ala	Glu	Glu	Ser	Val	Leu	Glu	Met
305					310					315					320
Phe	Met	Pro	Val	Lys	Asn	Ser	Lys	Ile	Lys	Arg	Pro	Met	Asn	Gly	Tyr
				325					330					335	
Glu	Val	Leu	Tyr	Tyr	Lys	Asp	Phe	Lys	Ile	Gly	Leu	Gly	Lys	Asn	Gln
			340					345					350		
Lys	Glu	Asn	Ile	Lys	Leu	Leu	Gln	Asp	Ala	Arg	Ala	Asn	Asp	Leu	Trp
		355					360					365			
Met	His	Val	Arg	Asp	Ile	Pro	Gly	Ser	His	Leu	Ile				

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

Gly	Phe	Met	Met	Ile	Phe	Ile	Asp	Ala	Cys	Phe	Arg	Lys	Glu	Thr	Pro	1	5	10	15
Tyr	Thr	Pro	Ile	Trp	Met	Met	Arg	Gln	Ala	Gly	Arg	Tyr	Leu	Ser	Glu	20	25	30	
Tyr	Gln	Glu	Ser	Arg	Lys	Lys	Ala	Gly	Ser	Leu	Leu	Glu	Leu	Cys	Lys	35	40	45	
Asn	Ser	Asp	Leu	Ala	Thr	Glu	Val	Thr	Leu	Gln	Pro	Val	Glu	Ile	Leu	50	55	60	
Gly	Val	Asp	Ala	Ala	Ile	Leu	Phe	Ser	Asp	Ile	Leu	Val	Val	Pro	Leu	65	70	75	80
Glu	Met	Gly	Leu	Asn	Leu	Glu	Phe	Ile	Pro	Lys	Lys	Gly	Pro	His	Phe	85	90	95	
Leu	Glu	Thr	Ile	Thr	Asp	Leu	Lys	Ser	Val	Glu	Ser	Leu	Lys	Val	Gly	100	105	110	
Val	Tyr	Lys	Gln	Leu	Asn	Tyr	Val	Tyr	Asp	Thr	Ile	Ser	Gln	Thr	Arg	115	120	125	
Gln	Lys	Leu	Ser	Lys	Glu	Lys	Ala	Leu	Ile	Gly	Phe	Cys	Gly	Ser	Pro	130	135	140	
Trp	Thr	Leu	Ala	Thr	Tyr	Met	Ile	Glu	Gly	Glu	Gly	Ser	Lys	Ser	Tyr	145	150	155	160
Ala	Lys	Ser	Lys	Lys	Met	Leu	Tyr	Ser	Glu	Pro	Glu	Val	Leu	Lys	Ala	165	170	175	
Leu	Leu	Glu	Lys	Leu	Ser	Leu	Glu	Leu	Ile	Glu	Tyr	Leu	Ser	Leu	Gln	180	185	190	
Ile	Gln	Ala	Gly	Val	Asn	Ala	Val	Met	Ile	Phe	Asp	Ser	Trp	Ala	Ser	195	200	205	
Ala	Leu	Glu	Lys	Glu	Ala	Tyr	Leu	Glu	Phe	Ser	Trp	Asp	Tyr	Leu	Lys	210	215	220	
Lys	Ile	Ser	Lys	Glu	Leu	Lys	Lys	Arg	Tyr	Ala	His	Ile	Pro	Val	Ile	225	230	235	240
Leu	Phe	Pro	Lys	Gly	Ile	Gly	Ala	Tyr	Leu	Asp	Ser	Ile	Asp	Gly	Glu	245	250	255	
Phe	Asp	Leu	Phe	Gly	Leu	Asp	Gly	Gly	Thr	Pro	Leu	Thr	Ala	Ala	Lys	260	265	270	
Lys	Lys	Leu	Ala	Val	Ile	Ile	Phe	Leu	Gln	Gly	Ile	Tyr	Asn	Pro	Pro	275	280	285	
Ala	Phe	Met	Ile	Lys												290			

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

```

Arg Val Phe Leu Thr Lys Lys Phe Met Ser Trp Met Val Val Ile Gly
1          5          10          15
Ala Leu Ile Cys Val Leu Leu Gly Val Phe Ile Phe Phe Thr Ser Met
20          25          30
Ser Val Lys Lys Ser Leu Thr Ala Tyr Leu Asn Ala Tyr Leu Glu Gln
35          40          45
Arg Pro Asn Ile Glu Gly Met Gly Ile Ile Gly Val Pro Phe Lys Cys
50          55          60
Glu Arg Phe Phe Lys Ile Ala Cys Val Ser Lys Glu Leu Arg Phe Leu
65          70          75          80
Asn Pro Gln Asn Ser Pro Ile Met Asp Phe Lys Asn Leu Glu Ile Lys
85          90          95
Leu His Ser Leu Asp Lys Ser Ser Leu Thr Leu Ser Ile His Ser Gln
100         105         110
Ile Gln Ser Pro Ile Leu Glu Gln Ser Ile Gln Gln Lys Ile Ser Gln
115         120         125
Ile Pro Leu Lys Asn Leu Asn Ala Leu Leu Glu Lys Phe Lys Pro Thr
130         135         140
Arg Leu Asn Cys Ser Leu Thr Phe Asn Ala Leu Asp Glu Lys Thr Leu
145         150         155         160
Asn Asp Asn Leu Lys Cys Asp Leu Thr Asn Ala Glu Asn Leu Leu Leu
165         170         175
His Phe Phe Ser Arg Gly Phe Asn Gly Gly Ala Arg Lys Ser Leu Pro
180         185         190

```

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

Gln Asp Gln Pro Met Gln Phe Gln Lys Thr Leu Leu Ser Leu Ser Leu
 1 5 10 15
 Leu Phe Leu Ser Tyr Cys Ile Ala Glu Glu Asn Gly Ala Tyr Ala Ser
 20 25 30
 Val Gly Phe Glu Tyr Ser Ile Ser His Ala Val Glu His Asn Asn Pro
 35 40 45
 Phe Leu Asn Gln Glu Arg Ile Gln Thr Ile Ser Asn Ala Gln Asn Lys
 50 55 60
 Ile Tyr Lys Leu Asn Gln Val Lys Asn Glu Ile Thr Asn Met Pro Asn
 65 70 75 80
 Thr Phe Asn Tyr Ile Asn Asn Ala Leu Lys Asn Asn Ala Lys Leu Thr
 85 90 95
 Pro Thr Glu Lys Gln Ala Glu Thr Tyr Tyr Leu Gln Ser Thr Leu Gln
 100 105 110
 Asn Ile Glu Lys Ile Val Met Leu Ser Gly Gly Val Ala Ser Asn Pro
 115 120 125
 Lys Leu Ala Gln Ala Leu Glu Lys Met Gln Glu Pro Ile Thr Asn Pro
 130 135 140
 Leu Glu Leu Val Glu Asn Leu Lys Asn Leu Glu Leu Gln Phe Ser Gln
 145 150 155 160
 Ser Gln Asn Ser Met Leu Ser Ser Leu Ser Ser Gln Ile Ala Gln Ile
 165 170 175
 Ser Asn Ser Leu Asn Ala Leu Asp Pro Ser Ser Tyr Ser Lys Asn Val
 180 185 190
 Ser Ser Met Tyr Gly Val Gly Leu Ser Val Gly Tyr Lys His Phe Phe
 195 200 205
 Thr Lys Lys Lys Asn Gln Gly Phe Arg Tyr Tyr Leu Phe Tyr Asp Tyr
 210 215 220
 Gly Tyr Thr Asn Phe Gly Phe Val Gly Asn Gly Phe Asp Gly Leu Gly
 225 230 235 240
 Lys Met Asn Asn His Leu Tyr Gly Leu Gly Ile Asp Tyr Leu Phe Asn
 245 250 255
 Phe Ile Asp Asn Ala Gln Lys His Ser Ser Val Gly Phe Tyr Val Gly
 260 265 270
 Phe Ala Leu Ala Gly Ser Ser Trp Val Gly Ser Gly Leu Gly Met Trp
 275 280 285
 Val Ser Gln Met Asp Phe Ile Asn Asn Tyr Leu Thr Asp Tyr Arg Ala
 290 295 300
 Lys Met His Thr Ser Phe Phe Gln Ile Pro Leu Asn Phe Gly Val Arg
 305 310 315 320
 Val Asn Val Asp Arg His Asn Gly Phe Glu Met Gly Leu Lys Ile Pro
 325 330 335
 Leu Ala Val Asn Ser Phe Tyr Glu Thr His Gly Lys Gly Leu Asn Ala
 340 345 350
 Ser Leu Phe Phe Lys Arg Leu Val Met Phe Asn Val Ser Tyr Val Tyr
 355 360 365
 Ser Phe
 370

(2) INFORMATION FOR SEQ ID NO:554:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 243 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...243
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

Glu	Pro	Met	Pro	Met	Gly	Lys	Ala	Leu	Lys	Glu	Tyr	Gln	Ile	Lys	Lys	1	5	10	15
Thr	Arg	Asp	Val	Gly	Ile	Gly	Ala	Lys	Asn	Ser	Glu	Ile	Met	Thr	Ser	20	25	30	
Ala	Gln	Val	Glu	Leu	Gly	Lys	Met	Leu	Tyr	Phe	Asp	Pro	Arg	Ile	Ser	35	40	45	
Thr	Ser	Tyr	Leu	Val	Ser	Cys	Asn	Thr	Cys	His	Asn	Leu	Gly	Leu	Gly	50	55	60	
Gly	Val	Asp	Leu	Ile	Pro	Ser	Ala	Ile	Gly	Ser	Gln	Trp	Lys	Lys	Asn	65	70	75	80
Pro	His	Leu	Leu	Ser	Ser	Pro	Thr	Val	Tyr	Asn	Ser	Val	Phe	Asn	Asp	85	90	95	
Val	Gln	Phe	Trp	Asp	Gly	Arg	Val	Thr	His	Leu	Asn	Glu	Gln	Ala	Gln	100	105	110	
Gly	Pro	Ile	Gln	Ser	Ser	Phe	Glu	Met	Gly	Ala	Asp	Pro	Lys	Val	Val	115	120	125	
Val	Glu	Lys	Ile	Asn	Ser	Ile	Pro	Gly	Tyr	Val	Lys	Leu	Phe	Arg	Lys	130	135	140	
Ala	Tyr	Gly	Ser	Lys	Val	Lys	Ile	Asp	Phe	Lys	Leu	Ile	Ala	Asp	Ser	145	150	155	160
Ile	Ala	Met	Phe	Glu	Ala	Thr	Leu	Ile	Thr	Pro	Ser	Arg	Tyr	Asp	Asp	165	170	175	
Phe	Leu	Arg	Gly	Asn	Pro	Lys	Ala	Leu	Ser	Lys	Ala	Glu	Lys	Glu	Gly	180	185	190	
Leu	Asp	Leu	Phe	Ile	Ser	Lys	Gly	Cys	Val	Ala	Cys	His	Asn	Gly	Ile	195	200	205	
Asn	Leu	Gly	Gly	Thr	Met	Gln	Pro	Phe	Gly	Val	Val	Lys	Pro	Tyr	Lys	210	215	220	
Phe	Ala	Asn	Val	Gly	Asp	Phe	Lys	Gly	Asp	Lys	Asn	Gly	Leu	Val	Lys	225	230	235	240
Val	Pro	Thr																	

(2) INFORMATION FOR SEQ ID NO:555:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 amino acids
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

```

Asn Asp Phe Trp Arg Lys Glu Ile Thr Met Arg Ala Thr Ala Ile Lys
1           5           10           15
Ile Phe Ser Phe Ser Ser Ala Leu Ala Leu Leu Gln Gly Cys Leu
          20           25           30
Ser Ile Asn Leu Lys Gln Met Leu Pro Glu Ile Arg Thr Tyr Asp Leu
          35           40           45
Asn Ala Ser Ser Phe Glu Met Thr Gln Cys Pro Lys Pro Leu Thr Glu
          50           55           60
Val Arg Leu Ile Ile Ile Leu Ser Ala Asp Leu Phe Asn Thr Lys Glu
65           70           75           80
Ile Val Phe Lys Ala Gln Asp Gly Gln Ile Thr His Gly Lys His Gln
          85           90           95
Lys Trp Ile Asp Leu Pro Arg Asn Met Leu Lys Thr Met Phe Met Gln
          100          105          110
Glu Ala Gln Lys Ala Cys Leu Gly Val Ala Leu Pro Pro Tyr Gly Ala
          115          120          125
Gly Ala Pro Thr Tyr Ala Val Arg Phe Thr Ile Leu Ser Phe Ser Leu
          130          135          140
Leu Glu Lys Glu Asn Ser Thr Tyr Arg Ala Glu Phe Ala Leu Gly Tyr
145          150          155          160
Asp Ile Ser Val Lys Gly Asp Ser His Ser Gly Val Ile Ile Lys His
          165          170          175
Glu Asn Ile Ser Ser Leu Glu Asn Lys Thr Thr Lys Thr Ser Lys Asn
          180          185          190
Gly Ser Gln Asp Phe Gln Glu Ser Ala Ile Gln Ser Leu Gln His Val
          195          200          205
Ser Thr Gln Ala Met Gln Glu Ala Ile Ser Leu Ile Lys Lys Ala Val
          210          215          220
Glu Ala Gln Ser Val Ser Pro Leu Lys Lys
225          230

```

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 283 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

```

Arg Gln Phe Ile Gln Phe Asn Thr Arg Arg Glu Ile Leu Glu Arg His
1           5           10           15
Val Asn Tyr Thr Leu Ile Gly Gly Leu Phe Phe Leu Cys Leu Val Cys
20           25           30
Met Val Gly Phe Ile Leu Trp Leu Gly His Leu Gly Leu Asp Asp Gly
35           40           45
Lys Tyr Tyr Glu Tyr Val Val Tyr Thr Asp Lys Asp Leu Gly Gly Ile
50           55           60
Ala Thr Asn Ser Pro Ile Asn Tyr Lys Gly Ile Gln Val Gly Asn Val
65           70           75           80
Ile Lys Val Gly Phe Ala Lys Asp Lys Val Gly Val Val Arg Leu Asp
85           90           95
Leu Met Ile Lys Ser Ser Val Lys Ile Arg Lys Asp Ser Lys Val Ala
100          105          110
Val Ser Ser Arg Gly Phe Met Gly Leu Lys Phe Leu Ala Leu Glu Gln
115          120          125
Ser His Asn Glu Glu Phe Tyr Gly Ser Gly Asp Lys Gly Glu Arg Ile
130          135          140
Leu Ile Phe Lys Glu Gly Leu Met Asp Arg Leu Ser Gly Asp Ala Asn
145          150          155          160
Gln Val Val Gln Glu Val Met Lys Ala Ile Arg Asn Val Asn Arg Ile
165          170          175
Leu Asp Asp Glu Asn Val Glu Lys Phe Lys His Ile Leu Ala Ser Val
180          185          190
Asp Asp Leu Ile Ala Asn Leu Asp Ser Arg Lys Thr Gln Phe Asp Ser
195          200          205
Leu Ile Asn Asn Ala Asn Asn Leu Val Ser Asn Val Asn Asn Val Ala
210          215          220
Leu Asp Val Asp Lys Arg Val Lys Gln Gly Gln Tyr Asp Phe Lys Ala
225          230          235          240
Met Phe Thr Pro Leu Ile Met Gln Ala Gln Leu Ser Leu Arg Asn Ile
245          250          255
Asp Asn Phe Val Glu Lys Gly Ser Ala Leu Ile Asp Lys Phe Asp Ala
260          265          270
Asn Pro Tyr Lys Thr Ile Phe Gly Glu Arg Lys
275          280

```

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

500

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

```

Ser Ser Ser Gln Ser Ile Ala Leu Leu Ile Gly Leu Trp Phe Gly Phe
1           5           10           15
Gln Lys Arg Ile Ala Leu Gly Val Trp Phe Phe Phe Ser Ile Leu Leu
          20           25           30
Gly Glu Phe Thr Leu Lys Ser Leu Lys Leu Leu Val Ala Arg Pro Arg
          35           40           45
Pro Val Thr Asn Gly Glu Leu Val Phe Ala His Gly Phe Ser Phe Pro
          50           55           60
Ser Gly His Ala Leu Ala Ser Ala Leu Phe Tyr Gly Ser Leu Ala Leu
65           70           75           80
Leu Leu Cys Tyr Ser Asn Ala Asn Asn Arg Ile Lys Thr Ile Gly Ala
          85           90           95
Ile Ile Leu Leu Phe Trp Ile Phe Leu Met Ala Tyr Asp Arg Val Tyr
          100          105          110
Leu Gly Val His Tyr Pro Ser Asp Val Leu Gly Gly Phe Leu Leu Gly
          115          120          125
Ile Ala Trp Ser Cys Cys Ser Leu Ala Leu Tyr Leu Gly Phe Leu Lys
130          135          140
Arg Pro Tyr Lys Ala Ala
145          150

```

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

```

Met Met Asp Leu Glu Ser Leu Arg Gly Phe Ala Tyr Ala Phe Phe Thr
1           5           10           15
Ile Leu Phe Thr Leu Phe Leu Tyr Ala Tyr Ile Phe Ser Met Tyr Arg
          20           25           30
Lys Gln Lys Lys Gly Ile Val Asp Tyr Glu Arg Tyr Gly Tyr Leu Ala
          35           40           45
Leu Asn Asp Ala Leu Glu Asp Glu Leu Ile Glu Pro Arg His Lys Glu

```

501

50 55 60
Val His Asp Lys Gly Ile Lys Glu Ser
65 70

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

[illegible]

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

```

Met Lys Leu Phe Asn Pro Arg Leu Ile Val Phe Ile Phe Ala Leu Leu
1           5           10           15
Leu Gly Val Gly Phe Ser Val Pro Ser Leu Leu Glu Thr Lys Gly Pro
          20           25           30
Lys Ile Thr Leu Gly Leu Asp Leu Arg Gly Gly Leu Asn Met Leu Leu
          35           40           45
Gly Val Gln Thr Asp Glu Ala Leu Lys Asn Lys Tyr Leu Ser Leu Ala
          50           55           60
Ser Ala Leu Glu Tyr Asn Ala Lys Lys Gln Asn Ile Leu Leu Lys Asp
65           70           75           80
Ile Lys Ser Ser Leu Glu Gly Ile Ser Phe Glu Leu Leu Asp Glu Asp
          85           90           95
Glu Ala Lys Lys Leu Asp Ala Leu Leu Leu Glu Leu Gln Gly His Ser
          100          105          110
Gln Phe Glu Ile Lys Lys Glu Ala Glu Phe Tyr Ser Val Lys Leu Thr
          115          120          125
Pro Leu Glu Gln Glu Glu Leu Arg Lys Asn Thr Ile Leu Gln Val Ile
          130          135          140
Gly Ile Ile Arg Ile Arg Leu Asp His Leu Ala Trp Gln Ser Leu
145          150          155

```

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

```

Gly Asn Val Lys Val Asn Lys Lys His Arg Leu Ala Phe Leu Gly Leu
1           5           10           15
Ile Val Gly Val Leu Phe Phe Phe Ser Ala Cys Gln His Arg Leu His
          20           25           30
Met Gly Tyr Tyr Ser Glu Val Thr Gly Asp Tyr Leu Phe Asn Tyr Asn
          35           40           45
Ser Thr Ile Val Val Ala Tyr Asp Arg Ser Asp Ala Met Thr Ser Tyr
          50           55           60
Tyr Ile Asn Val Ile Val Tyr Glu Leu Gln Lys Leu Gly Phe Tyr Asn
65           70           75           80
Val Phe Thr Gln Ala Asn Ser Arg
          85

```

(2) INFORMATION FOR SEQ ID NO:562:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 165 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...165
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

```

Lys Ala Leu Met Val Gly Met Lys Thr Gly Ala Trp Thr Gly Leu Lys
1           5           10           15
Leu Phe Ala Gln Pro Leu Leu Val Val Leu Ala Phe Met Leu Leu Tyr
          20           25           30
Ala Leu Ala His Ala Val Leu Gly Phe Tyr Val Lys Lys Asp Ser Ala
          35           40           45
Pro Met Ser Pro Asn Val Glu Lys Ser Glu Thr Glu Arg Gln Asn Ser
          50           55           60
Thr Phe Ser Pro Lys Glu Glu Ala Asn Ala Thr Thr Thr Ala Thr Glu
65           70           75           80
Gln Asn Pro Thr Lys Asp Thr Val Pro Pro Leu Asp Thr Ala Thr Gln
          85           90           95
Lys Gln Glu Ile Lys Gln Glu Ile Lys Gln Glu Ile Lys Gln Glu Ile
          100          105          110
Lys Gln Glu Ile Lys Gln Glu Ile Lys Gln Glu Ile Lys Gln Glu Thr
          115          120          125
Lys Gln Glu Gln Glu Lys Glu Asn Lys Pro Lys Gln Asn Ser Val Ser
          130          135          140
Pro Val Gln Asn Asp Gln Lys Thr Pro Thr Thr Pro Leu Met Gly Lys
145          150          155          160
Lys Thr Ser Arg Val
          165

```

(2) INFORMATION FOR SEQ ID NO:563:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

```

Met Leu Tyr Ala Ser Lys Ala Arg Leu Phe Leu Gln Ile Lys Gly Lys
1      5      10      15
Phe Met Leu Arg Ile Leu Ile Pro Leu Leu Ile Ile Val Trp Val Leu
      20      25      30
Trp Arg Leu Phe Leu Arg Gln Lys Pro His Lys Asp Asp His Arg Asp
      35      40      45
Asn His Ser Tyr Thr Gln Gln Thr Pro Lys Glu Leu Glu Asp His Met
      50      55      60
Ile Val Cys Ser Lys Cys Gln Thr Tyr Val Ser Ser Lys Asp Ala Ile
65      70      75      80
Tyr Ser Gly Ala Val Ala Tyr Cys Ser Glu Thr Cys Leu Lys Asp Lys
      85      90      95
Gly

```

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

```

Lys Thr Ile Asn Lys Leu Arg Ile Ile Met Lys Pro Thr Asn Glu Pro
1      5      10      15
Lys Lys Pro Phe Phe Gln Ser Pro Ile Val Leu Ala Val Leu Gly Gly
      20      25      30
Ile Leu Leu Ile Phe Phe Leu Arg Ser Phe Asn Ser Asp Gly Ser Phe
      35      40      45
Ser Asp Asn Phe Leu Ala Ser Ser Thr Lys Asn Val Ser Tyr His Glu
      50      55      60
Ile Lys Gln Leu Ile Ser Asn Asn Glu Val Glu Asn Val Ser Ile Gly
65      70      75      80
Gln Thr Leu Ile

```

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 amino acids

505

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

```

Phe Lys Asn Asn Lys Thr Pro Leu Thr Phe Glu Arg Asp Lys Gly Ser
1      5      10      15
Leu Asp Gly Leu Lys Lys Glu Arg Gln Gly Phe Tyr Lys Gln Val His
      20      25      30
Tyr Leu Arg Ile Leu Ile Leu Ser Met Ser Phe Leu Asn Ile Leu Asn
      35      40      45
Ala Glu Asn Leu Ser Tyr Met Ser Ser Ser Tyr Gln Ile Gly Thr Val
      50      55      60
Phe Met Arg Pro Leu Asn Thr Asn Lys Leu Leu Gln Gly Ala Ser Ile
65      70      75      80
Leu Gln Gly Tyr Glu Val Asn Pro Lys Asn Asp Trp Ala Tyr Ser Arg
      85      90      95
Tyr Tyr Phe Phe Ile Asp Tyr Gly Asn Val Leu Phe Asn Asn Asp Ser
      100     105     110
Thr Leu Gln Ala Asn Met Phe Thr Tyr Gly Val Gly Gly Asp Phe Met
      115     120     125
Val Ala Tyr Ala Lys Asn Pro Ile Asn Arg Trp Ala Phe Phe Phe Gly
      130     135     140
Leu Gln Leu Ala Ala Asn Thr Trp Ile Leu Asn Asn Lys Val Lys Asp
145     150     155     160
Leu Val Val Asn Thr Trp Asp Ser Leu Lys Asp Phe Asn Phe His Asn
      165     170     175
Thr Tyr Phe Arg Ala Ile Gly Lys Phe Gly Val Gln Phe Arg Thr Ile
      180     185     190
Val Leu Tyr His Lys Val Asp Val Glu Ile Gly Met Lys Ile Phe Leu
      195     200     205
Thr Pro Glu Arg Arg Ser Leu Phe Glu Arg Ser Phe Leu Phe Phe Val
      210     215     220
Ser His Ser Trp His Phe
225      230

```

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

```

Gly Ile Cys Leu Lys Phe Gln Ile Val Ser Leu Leu Leu Ala Phe Leu
1           5           10           15
Leu Ala Ser Cys Leu Pro Pro Lys Gly His His Ser Gly Leu Val Asn
20           25           30
Met Tyr Ile Ala His Gln Gly Gln Ser Val Arg Thr Tyr Trp Arg Lys
35           40           45
Val Asp Arg Gly Val Val Ala Lys His Asn Glu Thr Leu Lys Glu Asn
50           55           60
Pro Lys Ile Lys Leu Lys Asp Pro Lys Gly Pro Leu Phe Met Leu Gly
65           70           75           80
Ser Asn Arg Phe Met Leu Leu Trp Lys Asn Arg Tyr Thr Leu Ala Lys
85           90           95
Val Gln Ser Phe Lys Leu Glu Pro Gly Phe Tyr Tyr Leu Asp Ser Phe
100          105          110
Ser Val Glu Thr Gln Lys Gly Ile Leu Gln Ser Ala Pro Gly Tyr Ser
115          120          125
Tyr Thr Lys Asn Gly Tyr Asp Phe Lys Asn Asn Arg Pro Phe Phe Leu
130          135          140
Ala Phe Glu Val Lys Pro Asp Ser Lys Ile Val Leu Pro Ser Val Glu
145          150          155          160
Leu Ser Leu Ile Lys Thr Pro Arg Gly Phe Leu Gly Val Phe Leu Phe
165          170          175
Asp Asn Asn Glu Lys Gly Ala Asn Thr Pro Trp Ile Glu Gly Ser Leu
180          185          190
Asn Leu Lys Leu Lys Asn Ala Ser Phe Lys Asp Ala Trp Glu Leu Glu
195          200          205
Arg

```

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

```

Lys Pro Phe Gly Tyr Leu Gly Leu Leu Tyr Lys Gln Gly Thr Gln Lys
1      5      10      15
Asn Pro His Ser Tyr Val Gly Ala Pro Ala Arg Leu Gly Val Asp Phe
20     25     30
Ser Tyr Ser Asn Gly Trp Ser Phe Gly Ile Gly Ala Ile Gly Ala Trp
35     40     45
Asn Ile Tyr Asn Lys Gln Arg Leu Ala Asn Leu Tyr Ile Ser Leu Gly
50     55     60
Asn Phe Phe Gly Asn Pro Asn Asn Val Lys Pro Tyr Leu Ser Ala Gly
65     70     75     80
Asp Val Ser Asp Ala Tyr Leu Gln Tyr Ala Asn Gln Arg Phe Lys Ile
85     90     95
Ala Leu Gly Arg Phe Asn Thr Asp Phe Val Asp Phe Asp Trp Ile Gly
100    105    110
Gly Asn Ile Gln Gly Val Ser Val Ala Phe Lys Gln Asn Ser Met Arg
115    120    125
Tyr Phe Gly Ile Phe Met Asp Ser Met Leu Tyr Asn Gly His Gln Ile
130    135    140
Asn Lys Glu Gln Gly Asn Arg Ile Ala Thr Phe Leu Asn Ala Leu Ala
145    150    155    160
Leu Met Ile Leu Cys Leu Asn Ala Cys Met
165    170

```

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

```

Leu Gly Ser Pro Met Gln Phe Gln Lys Thr Leu Ser Ser Leu Ser Leu
1      5      10      15
Phe Leu Ser Leu Ser Leu Phe Leu Ser Phe Ser Ile Ala Glu Asn
20     25     30
Gly Ala Tyr Ala Ser Val Gly Phe Glu Tyr Ser Ile Ser His Ala Val
35     40     45
Glu His Asn Asn Pro Phe Leu Asn Gln Glu Arg Ile Gln Thr Ile Ser
50     55     60
Asn Ala Gln Asn Gln Ile Tyr Lys Leu Asn Gln Ile Glu Asn Glu Ile
65     70     75     80
Thr Asn Met Gln Asn Thr Phe Asn Tyr Thr Asn Asn Ala Leu Lys Asn
85     90     95

```

508

```

Asn Ala Lys Leu Thr Pro Thr Glu Met Gln Ala Glu Gln Tyr Tyr Leu
      100                      105                      110
Gln Ser Thr Leu Gln Asn Ile Glu Lys Ile Val Met Leu Ser Gly Gly
      115                      120                      125
Val Ala Ser Asn Pro Lys Leu Val Gln Ala Leu Glu Lys Met Gln Glu
      130                      135                      140
Pro Ile Thr Asn Pro Leu Glu Leu Val Glu Asn Leu Lys Asn Leu Glu
      145                      150                      155                      160
Leu Gln Phe Ser Gln Ser Gln Asn Ser Met Leu Ser Ser Leu Ser Ser
      165                      170                      175
Gln Ile Ala Gln Ile Ser Asn Ser Leu Asn Ala Leu Asp Pro Ser Ser
      180                      185                      190
Tyr Ser Lys
      195

```

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

```

Lys Gly Lys Val Met Asn Ser Ser Asn Leu Lys Asn Trp Leu Phe Pro
1      5      10      15
Thr Ile Cys Phe Phe Leu Phe Cys Tyr Ile Leu Ile Phe Leu Ile Phe
      20      25      30
Phe Met Phe Lys Asn Leu Gln Ser Gln Ser Phe Gly Ser Val Ala Glu
      35      40      45
Thr Gly Lys Lys Pro Ile Thr Thr Thr Lys Lys Phe Gly Lys Glu Leu
      50      55      60
Gln Lys Gln Ile Ser Lys Ile His
65      70

```

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

```

Leu Met Arg Lys Val Leu Tyr Ala Leu Met Gly Phe Leu Leu Val Phe
1           5           10           15
Ser Ala Leu Lys Ala Asp Asp Phe Leu Glu Glu Ala Asn Glu Thr Ala
20           25           30
Pro Ala Asn Leu Asn His Pro Met Gln Asp Leu Asn Ala Ile Gln Gly
35           40           45
Ser Phe Phe Asp Lys Asn Arg Ser Lys Met Ser Asn Thr Leu Asn Ile
50           55           60
Asp Tyr Phe Gln Gly Gln Thr Tyr Lys Ile Arg Leu Arg Tyr Ala Met
65           70           75           80
Ala Thr Leu Leu Phe Phe Ser Lys Pro Ile Ser Asp Phe Val Leu Gly
85           90           95
Asp Lys Val Gly Phe Asp Ala Lys Ile Leu Glu Ser Asn Asp Arg Ile
100          105          110
Leu Leu Ile Lys Pro Leu Gln Ile Gly Val Asp Ser Asn Ile Ser Val
115          120          125
Ile Asp Ser Glu Gly Lys Ile Phe Ser Phe Tyr Val Phe Ser Thr Thr
130          135          140
Phe Thr Ser Ser Lys His Pro Asn Leu Gln Val Phe Ile Glu Asp Lys
145          150          155          160
Asn Tyr Tyr Thr Asn Ala Phe Ile Lys Pro Gln Lys Glu Asn Gln Glu
165          170          175
Asn Met Ser Glu Asn Ala Pro Lys Asp Ala Gln Lys Asn Asn Lys Pro
180          185          190
Leu Lys Glu Glu Lys Glu Glu Thr Lys Glu Lys Glu Glu Glu Thr Ile
195          200          205
Ile Ile Gly Asp Asn Thr Asn Ala Met Lys Ile Ile Lys Lys Asp Ile
210          215          220
Gln Lys Gly Tyr Lys Ala Leu Lys Ser Ser Gln Arg Lys Trp Tyr Cys
225          230          235          240
Leu Trp Ala Cys Ser Lys Lys Ser Lys Leu Ser Leu Met Pro Lys Glu
245          250          255
Ile Phe Asn Asp Lys Gln Phe Thr Tyr Phe Lys Phe Asp Lys Arg Leu
260          265          270
Ala Leu Ser Lys Ser Arg
275

```

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

```

Tyr Arg Glu Met Asp Tyr Ala Val Phe Ser Met Thr Ile His Pro Asp
1           5           10           15
Val Ser Ala Arg Pro Gln Val Leu Leu Met His Glu Lys Ile Ile Glu
          20           25           30
His Ile Asn Gln His Glu Gly Val Ala Trp Val Thr Phe Asn Glu Ile
        35           40           45
Ala Asp Asp Phe Leu Lys Arg Asn Pro Arg Lys Lys
       50           55           60

```

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

```

Leu Val Leu Gln Gly Ala Glu Val Leu Ile Tyr Pro Ser Ala Phe Gly
1           5           10           15
Lys Ala Arg Ala Tyr Asn Trp Asp Leu Leu Ser Lys Ala Arg Ala Leu
          20           25           30
Glu Asn Gly Cys Phe Val Cys Ala Cys Asn His Ser Gly Glu Glu Thr
        35           40           45
Asn Ala Lys Leu Lys Gln Thr Leu Glu Phe Ala Gly Asp Ser Arg Asn
       50           55           60
His Arg Thr Gln Trp Glu Asn His Arg Pro Ser His Gln Ala
       65           70           75

```

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

511

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

```

Asn Leu Pro Val Ile Gln Gly Ile Ile Ala Pro Asn Gly Lys Ile Ile
1           5           10           15
Ala Gln Ala Thr Lys Leu Asn Glu Val Ile Ile Ala Glu Met Asp Leu
          20           25           30
Asn Glu Val Ala Leu Gln Arg Gln Lys Ile Pro Tyr Leu Gln Asp Phe
          35           40           45
Asp Thr Lys Leu Thr Lys Lys Gly Phe Gly Lys Leu Thr
          50           55           60

```

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

```

Ile Ile Met Phe Gly Met Gly Phe Phe Glu Ile Leu Val Val Leu Ile
1           5           10           15
Val Ala Ile Ile Phe Leu Gly Pro Glu Lys Phe Pro Gln Ala Val Val
          20           25           30
Asp Ile Val Lys Phe Phe Arg Ala Val Lys Lys Thr Leu Asn Asp Ala
          35           40           45
Lys Asp Thr Leu Asp Lys Glu Ile Asn Ile Glu Glu Ile Lys Lys Glu
          50           55           60
Thr Leu Glu Tyr Gln Lys Leu Phe Glu Asn Lys Val Glu Ser Leu Lys
          65           70           75           80
Gly Val Lys Ile Glu Glu Leu Glu Asp Ala Lys Val Thr Ala Glu Asn
          85           90           95
Glu Ile Lys Ser Ile Gln Asp Leu Met Gln Asp Tyr Lys Arg Ser Leu
          100          105          110
Glu Thr Asn Thr Ile Pro Asn His Leu Asn Glu Glu Val Ser Asn Glu
          115          120          125

```

512

Glu Ala Leu Asn Lys Glu Val Ser Ser Asp Glu Ser Pro Lys Glu Val
 130 135 140
 Gln Leu Thr Thr Asp Asn Asn Ala Lys Glu His Asp Lys Glu Lys Glu
 145 150 155 160
 His Val

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

Arg Tyr Arg Ser Phe Ser Arg Asn Gln Ser Asn Phe Arg Arg Cys Glu
 1 5 10 15
 Gln Pro Tyr Gly Ser Thr Leu Asn Ser Val Pro Leu Trp Ile Met Val
 20 25 30
 Val Gly Ala Ala Gly Ile Ala Leu Gly Leu Ser Leu Tyr Gly Pro Lys
 35 40 45
 Leu Ile Lys Thr Val Gly Ser Glu Ile Thr Glu Leu Asp Lys Met Gln
 50 55 60
 Ala Phe Cys Ile Ala Leu Ser Ala Val Ile Thr Val Leu Leu Ala Ser
 65 70 75 80
 Gln Leu Gly Leu Pro Val Ser Ser Thr His Ile Val Val Gly Ala Val
 85 90 95
 Phe Gly Val Gly Phe Leu Arg Glu Arg Leu Arg Glu Gln Ser Arg Arg
 100 105 110
 Arg Phe Ala Arg Ile Arg Asp Asn Ile Val Ala Ala His Phe Gly Glu
 115 120 125
 Asp Leu Glu Glu Ile Glu Gly Phe Leu Glu Arg Phe Asp Lys Ala Asn
 130 135 140
 Leu Lys Glu Lys Ser Leu Met Leu Glu Ser Leu Lys Lys Ser Lys Asn
 145 150 155 160
 Thr Ala Ile Ala Leu Glu Leu Lys Lys Lys Asp Lys Lys Ser Leu Lys
 165 170 175
 Lys Val Tyr Lys Glu Glu Val Ile Lys
 180 185

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid

513

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

```

Ala Gln Ile Phe Val Arg Phe Asn Tyr Val Leu Gly Ala Ile Gly Phe
1           5           10           15
Val Val Leu Leu Tyr Glu Ile Ile Ser Phe Ile Tyr Tyr Lys Arg Ser
20           25           30
Leu Val Tyr Leu Ile Leu Gly Val Ala Ile Gly Ala Leu Cys Leu Leu
35           40           45
Phe Val Phe Tyr Tyr Thr Pro Tyr Ile Leu Asn Ala Gln Lys Val Gly
50           55           60
Glu Val Ala Leu Gln Ser Ala Glu Phe Ala Arg Ser His Ala Gln Ser
65           70           75           80
Glu Trp Leu Phe Lys Glu Leu Phe Val Leu Val Cys Ala Leu Phe Phe
85           90           95
Trp Arg Leu Phe Gly Lys Asn Ala Leu
100           105

```

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

```

Lys Ala Cys Lys Met Lys Cys Ser Ser Phe Thr Ser Asn Ser Val Leu
1           5           10           15
Asn Phe Phe Val Val Leu Ser Phe Ile Thr Ile Gly Leu Val Phe Phe
20           25           30
Phe Leu Arg Ser Gln Pro Thr Ser Val Val Ser Lys Glu Asn Ile Pro
35           40           45
Lys Ile Glu Leu Glu Asn Phe Lys Ala Phe Gln Ile Asn Asp Lys Ile

```

514

```

      50              55              60
Leu Asp Leu Ser Ile Glu Gly Lys Lys Ala Leu Gln Tyr Asp Asp His
65              70              75              80
Glu Ile Phe Phe Asp Ser Lys Ile Lys Arg Tyr Asp Glu Asp Thr Ile
      85              90              95
Glu Ser Val Glu Ser Pro Glu Ala Lys Arg Gln Gln Asp Leu Tyr Phe
      100              105              110
Phe Pro Asn Gly
      115

```

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

```

Asn Gln Thr Lys Pro Glu Arg Lys Glu Lys Ile Pro His Phe Gln Arg
1              5              10              15
Arg Val Leu Met Arg Trp Trp Cys Phe Leu Val Cys Cys Leu Ser Val
      20              25              30
Leu Ser Val Met Asp Ala Lys Lys Leu Glu Asn Lys Gly Leu Lys Lys
      35              40              45
Glu Arg Glu Leu Leu Glu Ile Thr Gly Asn Gln Phe Val Ala Asn Asp
      50              55              60
Lys Thr Lys Thr Ala Val Ile Gln Gly Asn Val Gln Ile Lys Lys Gly
65              70              75              80
Lys Asp Arg Leu Phe Ala Asp Lys Val Ser Val Phe Leu Asn Asp Lys
      85              90              95
Arg Lys Pro Glu Arg Tyr Glu Ala Ala
      100              105

```

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

```

Lys Glu Ser Asn Ser Met Asp Leu Asp Lys Leu Lys Asp Tyr Arg Ala
1           5           10           15
Leu Arg Asn Ala Ile Leu Arg Leu Leu Pro Tyr Leu Asp Ser Gly Ile
20           25           30
Thr Glu Leu Ile Met Asn Lys Glu Lys Glu Ile Trp Leu Tyr Lys Leu
35           40           45
Asn Gly Val Arg Glu Lys Val Phe Asp Glu Asn Leu Asp Lys Ala Phe
50           55           60
Ile Leu Gly Phe Gly Glu Gln Leu Ala Ser Phe Arg Asp Leu Phe Phe
65           70           75           80
Asn Ala Asn Tyr Pro Thr Leu Asn Thr Ser Ile Pro Thr Ser Arg Tyr
85           90           95
Arg Val Ser Met Asn His Phe Ala Ile Ser Ala Asp Asn Glu Leu Ser
100          105          110
Leu Asn Ile Arg Val Pro Ser Asp Lys Lys Phe Asp Leu Lys Ala Phe
115          120          125
Lys Leu Ser Ser Ile Cys Gln Tyr Asp Tyr Glu Tyr Leu Lys Asn Leu
130          135          140
Met Ile Asp Gly Lys Asn Leu Leu Ile Ser Gly Gly Thr Gly Ser Gly
145          150          155          160
Lys Thr Ser Phe Leu Asn Ala Leu Ile Glu Phe Ile Pro Lys His Thr
165          170          175
Arg Ile Val Ser Val Glu Asp Ser Glu Glu Leu Asp Leu Arg Ala Phe
180          185          190
Glu Asn His Lys Ser Leu Leu Val Asp Lys Thr Glu Ser Ser Lys Phe
195          200          205
Thr Tyr Glu Asn Ala Leu Asn Met Ala Met Arg Met Ser Pro Asp Arg
210          215          220
Leu Met Val Gly Glu Ile Asp Thr Arg Asn Ser Met Leu Phe Leu Arg
225          230          235          240
Phe Gly Asn Thr Gly His Lys Gly Met Val Ser Thr Leu His Ala Asp
245          250          255
Ser Val-His Gly Val Ile Glu Ala Ile Ala Leu Asn Leu Gln Met Asn
260          265          270
Lys Ser Gly Leu Asp Val Asn Val Ala Lys Lys Phe Phe Lys Ser Ser
275          280          285
Val Asp Val Val Val Gln Ile Val Leu Asp Lys Ala Thr Asn Thr Arg
290          295          300
Tyr Ile Gln Glu Ile Leu Pro Ala Lys Asp Leu Arg Asp Ser Leu
305          310          315

```

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...87

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

```

Gly Val Lys Ala Met Asn Tyr Asp Val Leu Met Gly Phe Leu Ala Leu
1          5          10          15
Ile Leu Leu Ile Leu Trp Tyr Ala Tyr Gly Leu Arg Gln Tyr Leu Lys
          20          25          30
Leu Lys Asp Lys Asn Lys Arg Leu Lys Glu Lys Leu Gln Arg Cys Asn
          35          40          45
Cys Asn Ile Lys Ile Pro Ser Ile Leu Glu Met Ala His Lys Pro Ile
          50          55          60
Ile Met Asp Ile Lys Gly Glu Leu Leu Pro His Leu Thr Glu Ser Tyr
65          70          75          80
Arg Lys Ser Lys Phe Lys Glu
          85

```

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

```

Leu Ser Arg Asn Gly Val Val Ser Ser Val Ser Ser Asp Gly Ser Lys
1          5          10          15
Ile Leu Met Ser Leu Ala Pro Asp Gly Gln Pro Asp Val Tyr Leu Tyr
          20          25          30
Asp Thr His Lys Lys Thr Lys Thr Lys Ile Thr Arg Tyr Pro Gly Ile
          35          40          45
Asp Val Ser Gly Val Phe Leu Glu Asp Asp Lys Ser Met Ala Phe Val
          50          55          60
Ser Asp Arg Ser Gly Tyr Pro Asn Ile Tyr Met Lys Lys Leu Gly Leu
65          70          75          80
Lys Glu Arg Arg Ser Asn Ser Phe Met Lys Glu Glu Ala Met Asn
          85          90          95

```

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

```

Gly Asp Lys Met Leu Lys Lys Leu Leu Leu Ile Ser Leu Phe Leu Gly
1          5          10          15
Phe Leu Arg Ala Glu Gly Glu His Tyr Glu Ile Ile Ala Glu Leu Ser
20          25          30
Lys Ala Phe Leu Lys Ala Lys Glu Val Leu Thr Ala Ile Asn Lys Thr
35          40          45
Tyr Lys Thr Cys Ile Glu Thr Gly His Asp Arg Thr Gln Ile Arg Leu
50          55          60
Gln Asn Asp Phe Leu Glu Asn Leu Ser Gln Thr Glu Gln Gln Phe Asp
65          70          75          80
Asp Tyr Phe Glu Lys Asp Phe Lys Ser Val Gly Val Leu Lys Thr Leu
85          90          95
Leu Lys Asp Ile Gln Ser Leu Glu Lys Thr Ser Asn Lys Leu Val Cys
100         105         110
Val Ala Pro Lys Asn Ala Lys Asn Phe Glu Ile Leu Glu Gly Ala Ile
115         120         125
Thr Gln Ile Ile Gly Leu Glu Glu Gln Met Asn Gln Phe Ile Asn Gly
130         135         140
Ala Lys
145

```

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

518

(A) NAME/KEY: misc_feature

(B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

```

Ile Gln Arg Leu Lys Glu Met Leu Arg Asn Gln Phe Arg Ile Val Phe
1      5      10      15
Val Thr Cys Ile Val Ala Ser Ser Leu Gln Ala Gln Glu Asn Thr Pro
      20      25      30
Thr Leu Gly Lys Val Thr Thr Lys Gly Glu Arg Thr Phe Glu Tyr Asn
      35      40      45
His Gln Met Tyr Thr Asp Arg Lys Glu Leu Gln Gln Arg Gln Ser Asn
      50      55      60
Gln Thr Arg Asp Ile Phe Arg Thr Arg Ala Asp Val Asn Ala Ala Ser
65      70      75      80
Gly Gly Leu Met Ala Gln Lys Ile Tyr Ala Arg Gly Ile Glu Ser Arg
      85      90      95
Leu Leu Arg Val Thr Ile Asp Gly Val Ala Gln Asn Gly Asn Ile Phe
      100      105      110
His His Asp
      115

```

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

```

Ala Val Ser Trp Ile Met Ala Cys Trp His Lys Arg Leu Ala Val Gly
1      5      10      15
Cys Cys Ile Val Leu Leu Ser Cys Val Met Ser Ala Asn Asn Val Ser
      20      25      30
Ile Val Arg Asp Asp Pro Pro Leu Asp Pro Thr Leu Pro Ala Trp Ile
      35      40      45
Tyr Ser Val Ala Leu Leu Lys Val Tyr Phe Ser Asp Gly Thr Tyr Lys
      50      55      60
Glu Gly Tyr Ala Thr Leu Leu Glu Asn Gly Arg Tyr Ile Ala Ser Ser
65      70      75      80
Glu Thr Leu Tyr Ser Asn Gly Leu Tyr Pro Lys Met Ile Leu Ala Lys
      85      90      95
Met Gln Asp Ser Ser Ala Lys Glu Leu Ile Cys Ile Ala Ser Leu His
      100      105      110
Leu Glu Ala Met Asp Arg Asp Gln Gly Leu Ser Leu Leu Lys Thr Ala

```

519

```

      115              120              125
Asp Phe Arg Asp Asp Tyr Cys His Lys Arg Glu Glu Ser Tyr Tyr His
  130              135              140
Ala Arg Ile Tyr Ala Lys Tyr Ala Gln Thr Phe His Ser Asn Pro Tyr
  145              150              155              160
Thr Asn Gln Lys Thr Pro Thr Ser Asp Leu Tyr Tyr Pro Ala Leu Asn
      165              170              175
Glu Gly Asn Ser Phe Ser Ile Gln Thr Thr Asp Ile Ser Val Ala Glu
      180              185              190
Leu Leu Lys Ser Lys Lys Phe Leu Ser Leu Asp Ala Ser Phe Lys Lys
      195              200              205
Gly Ser Val Leu Trp Gly Gly Arg Pro Tyr Phe Ser Glu Val Gly Glu
      210              215              220
Phe Met Gly Met Thr Ser Ser Thr Leu Glu Asn Gln Glu Ser Leu Val
  225              230              235              240
Ile Ile Pro Lys Glu Lys Ile Ala Arg Phe Leu Ser Ala Leu Lys Asn
      245              250              255
Gln Asn Ile Phe Pro Asn Ile Pro
      260

```

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

```

Leu Gly Gly Leu Asp Met Tyr Lys Leu Gly Ile Phe Leu Leu Ala Thr
  1              5              10              15
Leu Leu Ser Ala Asn Thr Gln Lys Val Ser Asp Ile Ala Lys Asp Ile
      20              25              30
Gln His Lys Glu Thr Leu Leu Lys Lys Thr His Glu Glu Lys Asn Gln
      35              40              45
Leu Asn Ser Arg Leu Ser Ser Leu Gly Glu Ala Ile Arg Ser Lys Glu
      50              55              60
Leu Gln Lys Val Glu Ile Glu Arg Gln Met Val Ala Leu Lys Lys Ser
      65              70              75              80
Leu Glu Lys Asn Arg Asn Glu Ser Leu Val Gln Glu Lys Val Leu Thr
      85              90              95
Asn Tyr Arg Lys Ser Leu Asp His Leu Gln Lys Gln Arg Ser Phe Leu
      100              105              110
Gln Lys Arg Val Phe Asp Thr Leu Leu Glu Asp Phe Leu Phe Ser Gln
      115              120              125
Ala Leu Lys Gly Gln Asn Leu Ala Ser Ser Asn Asp Val Ile Leu Leu

```

520

130 135 140
 Ser Gly Val
 145

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 523 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

Tyr	Ile	Pro	Phe	Asn	Leu	Phe	Gln	Gly	Gln	Thr	Asn	Met	Lys	Lys	Leu	1	5	10	15
Leu	Tyr	Thr	Met	Leu	Ala	Leu	Leu	Leu	Ile	Gly	Leu	Leu	Thr	Ala	Tyr	20	25	30	
Leu	Ile	Leu	Phe	Thr	Glu	Trp	Gly	Asn	Lys	Ile	Ile	Ala	Ser	Tyr	Ile	35	40	45	
Glu	Lys	Lys	Ile	Asn	Pro	Asn	Glu	Arg	Tyr	Leu	Ser	Val	Lys	Thr	Phe	50	55	60	
Lys	Leu	Arg	Phe	Asn	Ser	Leu	Asp	Phe	Lys	Ala	Gln	Ala	Asn	Asp	Asp	65	70	75	80
Ser	Thr	Leu	Ile	Leu	Lys	Gly	Asp	Phe	Ser	Leu	Leu	Thr	Gln	Ser	Val	85	90	95	
Asn	Leu	Asp	Tyr	His	Ile	Asp	Ile	Lys	Asn	Leu	Arg	Ser	Phe	Lys	Asp	100	105	110	
Leu	Ile	Pro	Tyr	Pro	Leu	Arg	Gly	Ala	Ile	Val	Thr	Ser	Gly	Asn	Ile	115	120	125	
Lys	Gly	His	Arg	Lys	Ala	Leu	Val	Val	Gln	Gly	Val	Ser	Asn	Val	Ala	130	135	140	
Gln	Ser	His	Thr	Ala	Tyr	Asn	Ala	Leu	Leu	Asp	Asp	Phe	Lys	Leu	Ser	145	150	155	160
His	Leu	Ser	Leu	Asn	Ala	Lys	Asp	Ala	Asn	Leu	Glu	Asp	Leu	Leu	Tyr	165	170	175	
Leu	Ile	Asn	Arg	Pro	Ala	Tyr	Ala	Asn	Ala	Lys	Val	Ser	Leu	Gln	Ala	180	185	190	
Asp	Phe	Asn	Ser	Leu	Lys	Pro	Leu	Glu	Gly	His	Leu	Ile	Leu	Thr	Ala	195	200	205	
Asn	Asn	Ala	Leu	Ile	Asn	Asn	Ala	Leu	Ile	Asn	Gln	Ile	Phe	His	Leu	210	215	220	
Asn	Leu	Lys	Asp	Thr	Leu	Val	Phe	Asn	Leu	Ser	His	Ser	Ser	Asp	Phe	225	230	235	240
Lys	Gly	Asn	Lys	Ala	Ile	Ser	Asp	Thr	Thr	Leu	Thr	Ser	Pro	Leu	Val	245	250	255	
Asn	Phe	Thr	Ala	Leu	Lys	Ser	Glu	Tyr	Ser	Phe	Pro	Ala	Leu	Lys	Leu				

521

	260		265		270										
Asn	Ala	Pro	Tyr	Thr	Leu	Glu	Ile	Pro	His	Leu	Ala	Lys	Leu	Gln	Asn
	275						280					285			
Ile	Thr	Asn	His	Pro	Leu	Lys	Gly	Ser	Leu	Thr	Leu	Lys	Gly	Asp	Ile
	290					295					300				
Glu	Gln	Ser	Pro	Lys	Leu	Lys	Val	Ser	Gly	His	Ser	Asn	Leu	Leu	
305					310				315					320	
Asp	Gly	Ala	Leu	Asp	Phe	Thr	Leu	Leu	Asn	Lys	Asp	Leu	Lys	Ala	Arg
			325						330					335	
Phe	Ser	Asn	Ile	Ser	Thr	Ser	Lys	Ala	Leu	Asp	Leu	Phe	His	Tyr	Pro
		340						345				350			
Lys	Phe	Phe	Gln	Ser	Ile	Ala	Asp	Ala	Asn	Leu	Asp	Tyr	Asp	Leu	Ile
	355					360					365				
Ser	Lys	Gln	Gly	Val	Leu	Lys	Ala	Asn	Leu	Lys	Asn	Ala	Arg	Phe	Leu
	370					375					380				
Lys	Asn	Ala	Phe	Ser	Asp	Phe	Leu	Tyr	Ser	Ile	Ser	Arg	Phe	Asp	Ile
385					390					395				400	
Thr	Lys	Glu	Ile	Tyr	His	Asp	Ala	Asn	Leu	Val	Ser	Gln	Ile	Asn	Gln
			405						410					415	
Gln	Arg	Leu	Leu	Ser	Asp	Leu	Ser	Leu	Lys	Ser	Pro	Lys	Thr	Gln	Leu
		420						425					430		
Lys	Ile	His	Asn	Gly	Leu	Leu	Asp	Leu	Asn	Thr	Lys	Gln	Met	Asp	Ile
	435					440					445				
Leu	Met	Asp	Ala	Glu	Ile	Leu	Lys	Phe	Ile	Phe	Lys	Met	Lys	Leu	Gln
	450					455					460				
Gly	Ser	Met	His	Gln	Pro	Lys	Phe	Ser	Leu	Ile	Leu	Asn	Glu	Lys	Ala
465				470						475				480	
Ile	Gln	Gln	Asn	Leu	Gln	Gln	Gly	Leu	Lys	Glu	Ile	Leu	Lys	Asn	Asp
			485						490					495	
Thr	Leu	Lys	Lys	Gly	Leu	Asp	His	Leu	Leu	Lys	Asp	Asp	Lys	Leu	Lys
		500						505					510		
Glu	Lys	Leu	Glu	Lys	Gly	Leu	Lys	Gly	Leu	Phe					
	515						520								

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

Ala	Phe	Leu	Tyr	Ile	His	Ser	Ile	Ala	Leu	Ala	Arg	Val	Ile	Leu	Gln
1				5				10					15		
Leu	Lys	Pro	Leu	Leu	Thr	Ile	His	Leu	Asn	Ala	Lys	Ser	Gln	Ser	Ser

522

	20		25		30
Leu Lys Asn Lys Ile Thr Leu Lys Asn Lys Leu Asn His Ala Arg Ile					
35			40		45
Ile Leu Glu Phe Ile Pro Ser Leu Ile Tyr Phe Leu Ile Gln Lys Val					
50			55		60
Ser Val Leu Lys His Leu Ala Pro Leu Ile His Ile Pro Phe Lys Ala					
65			70		75
Leu Trp Leu Gly Thr Ala Leu Ser Met Phe Leu Ser Leu Asn Leu Asn					
	85		90		95
Ala Glu Glu Asn Pro Thr Lys Thr Glu Pro Lys Pro Ala Lys Gly Val					
	100		105		110
Lys Asn Lys Pro Lys Ser Pro Val Thr Asn Val Met Met Thr Asn Cys					
	115		120		125
Asp Asn Leu Lys Asp Phe Asn Ala Lys Gln Lys Glu Val Leu Lys Ala					
	130		135		140
Ala Tyr Gln Phe Gly Ser Thr Glu Asn Leu Gly Tyr Glu Met Ala Gly					
145			150		155
Ile Ala Trp Lys Glu Ser Cys Ala Gly Thr Tyr Lys Ile Asn Phe Ser					
	165		170		175
Asn Pro Ser Ala Gly Ile Tyr His Ala Tyr Ile Pro Ser Val Leu Lys					
	180		185		190
Ser Tyr Gly His Asn Asn Ser Pro Phe Leu Arg Asn Val Met Gly Arg					
	195		200		205
Ile Ala Thr Leu Lys Thr Met Arg Leu Leu Leu Lys Trp Pro					
210			215		220

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

Leu Val Ile Ile Ser Leu Leu Thr Thr Leu Lys Leu Lys Ser Ile Lys					
1		5		10	15
Glu Ile Ser Ile Lys Lys Phe Ile Leu Ser Ser Leu Val Phe Ala Cys					
	20		25		30
Ile Asn Thr Gly Val Glu Ala Leu Glu Asn Asp Gly Ser Lys Pro Asn					
	35		40		45
Asp Leu Ala Ser Pro Lys Glu Thr Pro Lys Glu Ala Gln Lys Asn Glu					
	50		55		60
Ala Gln Asn Glu Thr Ser Gln Ser Asn Gln Thr Pro Lys Glu Met Lys					
65			70		75
Val Lys Ser Ile Ser Tyr Val Gly Leu Ser Tyr Met Ser Asp Met Leu					

523

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

Glu	Phe	Gly	Val	Lys	Arg	Ile	Leu	Phe	Phe	Leu	Ala	Ala	Thr	Thr	Phe
1				5					10					15	
Leu	Leu	Arg	Ala	Glu	Thr	Ala	Ser	Ala	Thr	Ile	Asn	Thr	Thr	Val	Asp
			20					25					30		
Pro	Asn	Val	Met	Phe	Ser	Glu	Ser	Ser	Thr	Gly	Asn	Val	Lys	Lys	Asp
		35					40					45			
Arg	Lys	Arg	Val	Leu	Lys	Ser	Met	Val	Asp	Leu	Glu	Lys	Glu	Arg	Val
	50					55					60				
Lys	Asn	Phe	Asn	Gln	Tyr	Ser	Glu	Thr	Lys	Met	Ser	Lys	Gly	Asp	Leu

524

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

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

Ser	Arg	Thr	Leu	Cys	Ala	Lys	Ile	Val	Leu	Gln	Lys	Glu	Arg	Lys	Lys
1				5					10					15	
Met	Glu	Ile	Gln	Gln	Thr	His	Arg	Lys	Ile	Asn	Arg	Pro	Leu	Val	Ser
			20					25					30		
Leu	Val	Leu	Ala	Gly	Ala	Leu	Ile	Ser	Ala	Ile	Pro	Gln	Glu	Ser	His
		35					40					45			
Ala	Ala	Phe	Phe	Thr	Thr	Val	Ile	Ile	Pro	Ala	Ile	Val	Gly	Gly	Ile
		50				55					60				
Ala	Thr	Gly	Thr	Ala	Val	Gly	Thr	Val	Ser	Gly	Leu	Leu	Ser	Trp	Gly

525

65					70					75				80	
Leu	Lys	Gln	Ala	Glu	Glu	Ala	Asn	Lys	Thr	Pro	Asp	Lys	Pro	Asp	Lys
				85					90					95	
Val	Trp	Arg	Ile	Gln	Ala	Gly	Lys	Gly	Phe	Asn	Glu	Phe	Pro	Asn	Lys
			100					105					110		
Glu	Tyr	Asp	Leu	Tyr	Lys	Ser	Leu	Leu	Ser	Ser	Lys	Ile	Asp	Gly	Gly
		115					120					125			
Trp	Asp	Trp	Gly	Asn	Ala	Ala	Arg	His	Tyr	Trp	Val	Lys	Gly	Gly	Gln
		130				135					140				
Trp	Asn	Lys	Leu	Glu	Val	Asp	Met	Lys	Asp	Ala	Val	Gly	Thr	Tyr	Lys
145					150					155					160
Leu	Ser	Gly	Leu	Arg	Asn	Phe	Thr	Gly	Gly	Asp	Leu	Asp	Val	Asn	Met
				165					170					175	
Gln	Lys	Ala	Thr	Leu	Arg	Leu	Gly	Gln	Phe	Asn	Gly	Asn	Ser	Phe	Thr
			180				185						190		
Ser	Tyr	Lys	Asp	Ser	Ala	Asp	Arg	Thr	Thr	Arg	Val	Asn	Phe	Asn	Ala
		195					200					205			
Lys	Asn	Ile	Ser	Ile	Asp	Asn	Phe	Val	Glu	Ile	Asn	Asn	Arg	Val	Gly
		210				215					220				
Ser	Gly	Ala	Gly	Arg	Lys	Ala	Ser	Ser	Thr	Val	Leu	Thr	Leu	Gln	Ala
225					230					235					240
Ser	Glu	Gly	Ile	Thr	Ser	Ser	Lys	Asn	Ala	Glu	Ile	Ser	Leu	Tyr	Asp
			245						250					255	
Gly	Ala	Thr	Leu	Asn	Leu	Ala	Ser	Asn	Ser	Val	Lys	Leu	Asn	Gly	Asn
			260					265					270		
Val	Trp	Met	Gly	Arg	Leu	Gln	Tyr	Val	Gly	Ala	Tyr	Leu	Ala	Pro	Ser
		275					280						285		
Tyr	Ser	Thr	Ile	Asn	Thr	Ser	Lys	Val	Gln	Gly	Glu	Val	Asp	Phe	Asn
		290				295					300				
His	Leu	Thr	Val	Gly	Asp	Gln	Asn	Ala	Ala	Gln	Ala	Gly	Ile	Ile	Ala
305					310					315					320
Ser	Asn	Lys	Thr	His	Ile	Gly	Thr	Leu	Asp	Leu	Trp	Gln	Ser	Ala	Gly
			325						330					335	
Leu	Asn	Ile	Ile	Ala	Pro	Pro	Glu	Gly	Gly	Tyr	Lys	Asp	Lys	Pro	Asn
			340					345					350		
Ser	Thr	Thr	Ser	Gln	Ser	Gly	Thr	Lys	Asn	Asp	Lys	Lys	Glu	Ile	Ser
		355					360					365			
Gln	Asn	Asn	Asn	Ser	Asn	Thr	Glu	Val	Ile	Asn	Pro	Pro	Asn	Asn	Thr
		370				375					380				
Gln	Lys	Thr	Glu	Thr	Glu	Pro	Thr	Lys	Ser	Leu	Met	Gly	Leu	Leu	Leu
385					390					395					400
Lys	Ala	Lys	Thr	Arg	Leu	Ser									
					405										

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

```

Gln Ile Phe Cys Ser Thr Gln Ser Ser Lys Leu Pro Leu Lys Lys Ala
1           5           10           15
Pro Lys Ala Asp Lys Ser Pro Leu Leu Ile Leu Val Ser Glu Tyr Trp
          20           25           30
Leu Lys Phe Phe Thr Arg Ser Phe Ser Lys Ser Thr Met Leu Phe Lys
          35           40           45
Thr Leu Leu Arg Ser Phe Phe Thr Phe Pro Val Glu Leu Ser Glu Asn
          50           55           60
Ile Thr Leu Gly Ser Thr Val Val Leu Ile Val Ala Glu Ala Val Ser
65           70           75           80
Ala Leu Asn Lys Lys Val Val Ala Ala Lys Lys Asn Lys Ile Arg Phe
          85           90           95
Thr Pro Asn Ser Tyr Ile His Asn Arg Asn Lys Asn Arg Arg Tyr Ser
          100          105          110
Ser Leu Ser Pro Leu Leu Lys Ser Ser Ser Ile Cys Lys Asn Pro Pro
          115          120          125
Arg Ile Gln Ala Ile Leu Ile Ile Leu Lys Tyr Arg Leu Ser Lys Gly
          130          135          140
Phe Asn Pro Val Val Val Ile Leu Arg Ile Gln Lys Met Arg Thr Leu
145          150          155          160
Gln Lys Leu

```

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

```

Gly Leu Ile Thr Met Asp Lys Asn Asn Asn Asn Asn Leu Arg Leu Ile
1           5           10           15
Leu Ala Ile Ala Leu Ser Phe Leu Leu Ile Ala Leu Asn Ser Tyr Phe
          20           25           30
Phe Gln Glu Pro Asn Lys Thr Thr Thr Glu Thr Thr Lys Gln Glu Thr
          35           40           45
Thr Asn Asn His Thr Ala Thr Ser Pro Thr Ala Ser Asn Thr Ile Thr

```

527

50		55		60
Gln Asp Phe Ser Val Thr	Gln Thr Ile Pro	Gln Glu Ser Leu Leu Ser		
65	70	75	80	
Thr Ile Ser Phe Glu His Ala Lys Ile	Glu Ile Asp Ser Leu Gly Arg			
	85	90	95	
Ile Lys Gln Val Tyr Leu Lys Asp Lys Lys Tyr Leu Thr Pro Lys Glu				
	100	105	110	
Lys Gly Phe Leu Glu His Val Ser His Leu Phe Ser Ser Lys Glu Asn				
	115	120	125	
Ser Gln Pro Ser Leu Lys Glu Leu Pro Leu Leu Ala Ala Asp Lys Leu				
	130	135	140	
Lys Pro Leu Glu Val Arg Phe Leu Asp Pro Thr Leu Asn Asn Lys Ala				
145	150	155	160	
Phe Asn Thr Pro Tyr Ser Ala Ser Lys Thr Thr Leu Gly Pro Asn Glu				
	165	170	175	
Gln Leu Val Leu Thr Gln Asp Leu Gly Thr Leu Ser Ile Ile Lys Thr				
	180	185	190	
Leu Thr Phe Tyr Asp Asp Leu His Tyr				
	195	200		

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

Gly Val Ser Ile Ile Met Val Leu Lys Thr Lys Leu Lys Ile Ile Ser	
1	5 10 15
Ser Val Ile Leu Ser Thr Leu Leu Trp Val Gly Cys Ser Ser Glu Met	
	20 25 30
Ala Thr Tyr Gln Asn Val Asn Asp Ala Thr Lys Asn Thr Thr Ala Ser	
	35 40 45
Ile Asn Ser Thr Asp Leu Leu Leu Thr Ala Asn Ala Met Leu Asp Ser	
	50 55 60
Met Leu Gly Thr	
65	

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

Ala	Met	Lys	Asn	Gln	Val	Lys	Lys	Ile	Leu	Gly	Met	Ser	Val	Val	Ala	1	5	10	15
Ala	Met	Val	Ile	Val	Gly	Cys	Ser	His	Ala	Pro	Lys	Ser	Gly	Ile	Ser	20	25	30	
Lys	Ser	Asn	Lys	Ala	Tyr	Lys	Glu	Ala	Thr	Lys	Gly	Ala	Pro	Asp	Trp	35	40	45	
Val	Val	Gly	Asp	Leu	Glu	Lys	Val	Ala	Lys	Tyr	Glu	Lys	Tyr	Ser	Gly	50	55	60	
Val	Phe	Leu	Gly	Arg	Ala	Glu	Asp	Leu	Ile	Thr	Asn	Asn	Asp	Val	Asp	65	70	75	80
Tyr	Ser	Thr	Asn	Gln	Ala	Thr	Ala	Lys	Ala	Arg	Ala	Asn	Leu	Ala	Ala	85	90	95	
Asn	Leu	Lys	Ser	Thr	Leu	Gln	Lys	Asp	Leu	Glu	Asn	Glu	Lys	Thr	Arg	100	105	110	
Thr	Val	Asp	Ala	Ser	Gly	Lys	Arg	Ser	Ile	Ser	Gly	Thr	Asp	Thr	Glu	115	120	125	
Lys	Ile	Ser	Gln	Leu	Val	Asp	Lys	Glu	Leu	Ile	Thr	Ser	Lys	Met	Leu	130	135	140	
Ala	Arg	Tyr	Val	Gly	Lys	Asp	Arg	Val	Phe	Val	Leu	Val	Gly	Leu	Asp	145	150	155	160
Lys	Gln	Ile	Val	Asp	Lys	Val	Arg	Glu	Glu	Leu	Gly	Met	Val	Lys	Lys	165	170	175	

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

529

```

Pro Lys Pro Tyr Ala Val Ser Ile Leu Cys Ile Cys Val Met Phe Ile
1           5           10           15
Leu Phe Lys Phe Gly Arg Val Leu Gly Lys Ala Tyr Ser Leu Tyr Leu
          20           25           30
Tyr Ile Tyr Glu Ser Leu Ile Cys Gln Ala Phe Gly Leu Ser Leu Ser
          35           40           45
Cys Asn Asn Ser Met Leu Phe Ser Thr Phe Leu Ile Asn Leu Pro Leu
          50           55           60
Pro His Asn Glu Ser Leu Cys Cys Cys Arg Asp Ile Leu Ala Tyr Ser
65           70           75           80
Asn Ser Ser Ser Leu Lys Thr Tyr Ser Leu Glu Ser Asn Phe Ser Phe
          85           90           95
Asn Ser Leu Phe
          100

```

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*.

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

```

Thr Ala Arg Met Asn Arg Met Lys Pro Ile Phe Leu Leu Ile Phe Leu
1           5           10           15
Leu Leu Ala Ser Leu Ile Ala Arg Glu Lys Asp Ala Ser Ser Asn Leu
          20           25           30
Phe Asp Leu Ile Asp Lys Gly Ile Asn Arg Glu Gln Glu Leu Lys Glu
          35           40           45
Gln Glu Gln Lys Thr Arg Leu Lys Leu Ala Gln Ser Pro Leu Val Ala
          50           55           60
Leu Glu Ile Val Pro Gln Glu Thr Pro Tyr Leu Glu Trp Gln Gly Ala
65           70           75           80
Arg Glu Ser Tyr Tyr Leu Lys Val Glu Arg Cys Ser Gly Glu Arg Gly
          85           90           95
Tyr Phe Lys Asp
          100

```

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

530

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

```

Val Ala Arg Ala Phe Ile Ala Leu Tyr Ala Ile Ser Ala Val Asn Lys
1           5           10           15
Ser Lys Val Glu Ala Leu Lys Thr Glu Phe Ile Lys Ile Phe Asn Tyr
          20          25          30
Ala Pro Lys Pro Glu Ala Met Gln Pro Val Val Val Ile Pro Pro Asp
          35          40          45
Ser Gly Lys Glu Glu Glu Gln Met Ala Ser Glu Ser Ser Lys Pro Ala
          50          55          60
Ser Gln Asn Thr Glu Thr Lys Ala Thr Ile Ala Arg Lys Gly Glu Gly
          65          70          75          80
Ser Val Leu Glu Gln Ile Asp Gln Gly Ser Val Leu Lys Leu Pro Ser
          85          90          95
Ser Leu Leu Phe Glu Asn Ala Thr Ser Asp Ala Ile Asn Gln Asp Met
          100         105         110
Met Leu Tyr Ile Glu Arg Ile Ala Lys Ile Ile Gln Lys Leu Pro Lys
          115         120         125
Arg Val His Ile Asn Val Arg Gly Phe Thr Asp Asn Thr Pro Leu Asn
          130         135         140
Lys Thr Arg Phe Lys Ser His Tyr Glu Leu Ala Ala Asn Arg Ala Tyr
          145         150         155         160
Arg Val Met Lys Val Leu Ile Gln Tyr Gly Val Asp Pro Asn Gln Leu
          165         170         175
Ser Phe Ser Ser Tyr Gly Ser Thr Asn Pro Ile Ala Pro Asn Asp Ser
          180         185         190
Leu Glu Asn Arg Met Lys Asn Asn Arg Val Glu Ile Phe Phe Ser Thr
          195         200         205
Asp Ala Asn Asp Leu Ser Lys Ile His Ser Ile Leu Asp Glu Glu Phe
          210         215         220
Asn Pro His Lys Gln Gln Glu
          225         230

```

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...98

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

```

Gln Arg Leu Tyr Leu Gly Lys Leu Asn Ala Lys Val Asn His Thr Ile
1           5           10           15
Phe Gln Phe Leu Val Asn Val Gly Ile Arg Thr Asn Ile Phe Glu His
          20           25           30
His Gly Ile Glu Phe Gly Ile Lys Ile Pro Thr Leu Pro Asn Tyr Phe
          35           40           45
Phe Lys Gly Ser Thr Thr Ile Arg Ala Lys Lys Gln Gly Pro Leu Glu
          50           55           60
Asn Gly Asn Pro Thr Thr Ile Thr Gly Ala Glu Thr Asn Phe Ser Leu
65           70           75           80
Thr Gln Thr Leu Arg Arg Gln Tyr Ser Met Tyr Leu Arg Tyr Val Tyr
          85           90           95
Thr Phe

```

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

```

Phe His Phe Tyr Cys Leu Tyr Phe Leu Asn Gly Gly Tyr Asn Arg Leu
1           5           10           15
His Lys Ser Tyr Glu Arg Ile Val Met Leu Ile Ala Arg Phe Lys Lys
          20           25           30
Ala Leu Ile Ser Tyr Ser Leu Gly Val Leu Leu Val Ser Ser Leu Leu
          35           40           45
Gly Val Ala Asn Ala Ser Asn Gln Glu Ile Gln Val Lys Asp Tyr Phe
          50           55           60
Gly Glu Gln Thr Ile Lys Leu Pro Val Ser Lys Ile Ile Tyr Leu Gly
65           70           75           80
Ser Phe Ala Glu Val Pro Ala Met Phe Asn Thr Trp Asp Arg Val Val
          85           90           95
Gly Ile Ser Asp Tyr Ala Phe Lys Ser Asp Ile Val Lys Ala Thr Leu
          100          105          110
Lys Asp Leu Glu Arg Ile Lys Pro Met Ser Ser Asp His Val Ala Ala

```

532

```

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

```

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

```

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

```

	35		40		45							
Asp	Lys	Lys	Asp	Ala	Lys	Lys	Pro	Lys	Asn	Ser	Val	Ala
50						55					60	

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

Arg	Ile	Ile	Lys	Gly	Asn	Ile	Met	Ser	Ser	Gly	Leu	Ile	Tyr	Ile	Ser
1			5					10					15		
Leu	Glu	Val	Leu	Val	Ala	Cys	Leu	Ile	Thr	Ala	Leu	Ile	Met	Tyr	Tyr
		20					25					30			
Val	Met	Lys	Lys	Ile	Tyr	Tyr	Ala	Arg	Gly	Gln	Ala	Ile	Leu	Lys	Gly
	35					40					45				
Ala	Ser	Ala	Lys	Ala	Lys	Leu	Met	Glu	Phe	Gln	Ala	Lys	Ser	Phe	Val
	50				55					60					
Glu	Ala	Glu	Glu	Met	Arg	Met	Lys	Ser	Gln	Glu	Cys	Lys	Leu	Gln	Gln
65				70					75				80		
Gln	Tyr	Glu	Asn	Lys	Asn	Leu	Gln	Leu	Gln	Thr	His	Phe	Asp	Lys	Lys
			85				90					95			
Glu	Ala	His	Leu	Lys	His	Leu	Glu	Ala	Gln	His	Lys	Glu	Phe	Val	Arg
		100					105					110			
Asp	Glu	Lys	Arg	Tyr	Leu	Glu	Lys	Glu	Lys	Lys	Glu	Leu	Glu	Lys	Glu
	115					120					125				
Arg	Gln	Ile	Leu	Glu	Gln	Glu	Arg	Glu	Asn	Phe	Lys	Lys	Gln	Arg	Ala
	130					135					140				
Ile	Cys	Lys	Glu	Ala	Gln	Ala	Lys	Ala	Leu	Asp	Ala	Met	Leu	Asn	Tyr
145				150					155				160		
Met	Ala	Tyr	Thr	Lys	Asp	Glu	Ile	Lys	Ser	Met	Ile	Leu	Glu	Gln	Leu
			165				170					175			
Glu	Gln	Glu	Leu	Glu	Ala	Gln	Lys	Ser	Ala	Leu	Ile	Arg	Arg	Tyr	Glu
		180					185					190			
Glu	Glu	Ala	Phe	Ile	Met	Cys	Leu								
	195					200									

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...167
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

```

Gly Arg Ala Phe Met Met Arg Glu Ile Leu Thr Asn Arg Phe Phe Pro
1           5           10           15
Ser Leu Phe Lys Lys Arg Leu Asp Phe Ser Asn Arg Val Val Leu Gly
          20           25           30
Leu Gly Ser Asn Leu Lys Asn Pro Leu Lys Ile Leu Lys Ser Cys Phe
          35           40           45
Leu Tyr Phe Lys Asn His Ser Lys Ile Gly Lys Ile Phe Ser Ser Pro
          50           55           60
Ile Tyr Ile Asn Pro Pro Phe Gly Tyr Thr Asn Gln Pro Asn Phe Tyr
          65           70           75           80
Asn Ala Thr Ile Ile Leu Lys Thr Ser Leu Gly Leu Arg His Phe Phe
          85           90           95
Ala Leu Val Phe Tyr Ile Glu Arg Arg Phe Gly Arg Ala Arg Lys Arg
          100          105          110
Asp Phe Lys Asp Ala Pro Arg Thr Leu Asp Ile Asp Ile Ile Ala Phe
          115          120          125
Asn Gln Val Ile Leu Arg Gln Asn Asp Leu Thr Leu Pro His Pro Lys
          130          135          140
Trp Ser Glu Arg Asp Ser Val Leu Val Pro Leu Thr Leu Gln Gln Ile
          145          150          155          160
Leu Phe Lys Arg Glu Glu Trp
          165

```

(2) INFORMATION FOR SEQ ID NO:603:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 171 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...171
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

535

```

Ile Ile Glu Ile Leu Val Ile Gln Gly Pro Asn Leu Asn Met Leu Gly
1           5           10           15
His Arg Asp Pro Arg Leu Tyr Gly Met Val Thr Leu Asp Gln Ile His
          20           25           30
Glu Ile Met Gln Thr Phe Val Lys Gln Gly Asn Leu Asp Val Glu Leu
          35           40           45
Glu Phe Phe Gln Thr Asn Phe Glu Gly Glu Ile Ile Asp Lys Ile Gln
          50           55           60
Glu Ser Val Gly Ser Asp Tyr Glu Gly Ile Ile Ile Asn Pro Gly Ala
65           70           75           80
Phe Ser His Thr Ser Ile Ala Ile Ala Asp Ala Ile Met Leu Ala Gly
          85           90           95
Lys Pro Val Ile Glu Val His Leu Thr Asn Ile Gln Ala Arg Glu Glu
          100          105          110
Phe Arg Lys Asn Ser Tyr Thr Gly Ala Ala Cys Gly Gly Val Ile Met
          115          120          125
Gly Phe Gly Pro Leu Gly Tyr Asn Met Ala Leu Met Ala Met Val Asn
          130          135          140
Ile Leu Ala Glu Met Lys Ala Phe Gln Glu Ala Gln Lys Asn Asn Pro
145          150          155          160
Asn Asn Pro Asn Asn Pro Ile Asn Asn Gln Lys
          165          170

```

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

```

Pro Arg Ile Ile Ala Phe Phe Trp Ile Trp Gly Ser Asn Thr Asn Ala
1           5           10           15
Ile Ala Leu Ile Gly Leu Ala Arg Leu Phe Leu Asn Pro Lys Asp Phe
          20           25           30
Val Phe Lys Arg Glu Gln Ser Phe Lys Asp Lys Glu Arg Gln Lys Ile
          35           40           45
Tyr Asp Ile Val Lys Glu Ala Gln Glu Lys Ala Ile Gln Ala Leu Glu
          50           55           60
Arg Gly
65

```

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

536

(A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

Arg	Leu	Trp	Leu	Trp	Ala	Val	Phe	Thr	His	Ser	Thr	Gly	His	Gly	Ile
1				5					10					15	
Asp	Leu	Asp	Ile	His	Glu	Leu	Pro	Tyr	Ile	Ser	Ser	Arg	Ser	Glu	Thr
			20					25					30		
Ile	Leu	Glu	Gly	Met	Val	Phe	Ser	Val	Glu	Pro	Gly	Ile	Tyr	Ile	
		35				40					45				
Pro	Gly	Phe	Phe	Gly	Val	Arg	Ile	Glu	Asp	Leu	Val	Val	Ile	Lys	Asn
	50					55					60				
Ser	Arg	Ala	Glu	Leu	Leu										
65					70										

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

Tyr	Gln	Tyr	Ile	Gln	Gln	Gly	Gly	Gly	Phe	Gly	Val	Asn	Val	Gly	Arg
1				5					10					15	
Thr	Leu	Gly	Asn	Arg	Thr	His	Val	Ser	Leu	Gly	Tyr	Asn	Leu	Asn	Val
			20					25					30		
Thr	Lys	Leu	Leu	Gly	Phe	Ser	Ser	Pro	Leu	Tyr	Asn	Arg	Tyr	Tyr	Ser
		35				40						45			
Ser	Val	Asn	Glu	Val	Ala	Ser	Pro	Arg	Gln	Cys	Ser	Thr	Pro	Ala	Ser
	50					55					60				
Val	Ile	Ile	Asn	Arg	Leu	Ser	Gly	Gly	Arg	Thr	Pro	Leu	Val	Pro	Glu

537

[illegible]

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) **FEATURE:**

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

Met	Ala	Cys	Glu	Phe	Leu	Lys	Lys	Pro	Lys	Tyr	Tyr	Lys	Phe	Ile	Glu
1				5					10					15	
Gly	Ala	Asn	Tyr	Leu	Ser	Leu	Gly	Leu	Ser	Met	Val	Val	Ala	Ile	Leu
			20					25					30		
Met	Gly	Val	Ala	Ile	Gly	Tyr	Gly	Leu	Lys	Lys	Leu	Thr	His	Ile	Ser
		35					40					45			
Trp	Leu	Phe	Trp	Leu	Gly	Val	Ile	Trp	Gly	Val	Leu	Ala	Ser	Phe	Leu
	50					55					60				
Asn	Val	Tyr	Lys	Ala	Tyr	Lys	Asn	Met	Gln	Lys	Asp	Tyr	Glu	Glu	Leu
65					70					75					80
Ala	Lys	Asp	Pro	Lys	Tyr	Thr	Gln	Asn	Lys	Thr	Lys				
				85					90						

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...89

538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

```

Arg Asn Leu Met Lys Thr Thr Glu Asn Thr Asp Glu Thr His Leu Arg
1          5          10          15
Glu Thr Lys Asn Lys Leu Gly Arg Lys Pro Lys Ala Asp Ala Asn Lys
20          25          30
Lys Thr Arg Ala Val Ser Leu Tyr Phe Ser Asp Glu Gln Tyr Gln Lys
35          40          45
Leu Glu Lys Met Ala Asn Glu Glu Glu Ser Val Gly Ser Tyr Ile
50          55          60
Lys Arg Tyr Ile Leu Lys Ala Leu Arg Lys Ile Glu Gln Gly Gly Gly
65          70          75          80
Phe Ile Ala Phe Asn Leu Phe Leu Ile
85

```

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

```

Ile Leu Lys Gly Gly Phe Leu Gly Phe Phe Ile Val Ala Leu Ser Ser
1          5          10          15
Tyr Tyr Gly Val Lys Lys Arg Leu Asp Leu Arg Lys Gln Asp Ser Lys
20          25          30
Glu Lys Glu Glu Lys Gln Lys Phe Gln Lys Phe Ala Leu Gly Leu Glu
35          40          45
Met Ser Phe Asn Val Trp Arg Leu Gly Gly Tyr Gly Val Leu Leu Gly
50          55          60
Ile Leu Gly Val Leu Leu Phe Leu His Leu Phe Asn Gly Leu Pro Phe
65          70          75          80
Leu Ile Gly Val Phe Val Ser Ser Leu Ser Ser Ala Leu Leu Arg Phe
85          90          95
Leu Asn Asn Asn Gly Lys Phe
100

```

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

```

Ala Leu Thr Pro Asn Pro Met Lys Leu Pro Val Val Glu Ser Phe Phe
1           5           10           15
Ser Leu Gln Gly Glu Gly Lys Arg Ile Gly Lys Pro Ser Leu Phe Leu
20           25           30
Arg Leu Gly Gly Cys Asn Leu Ser Cys Lys Gly Phe Asn Cys Lys Thr
35           40           45
Leu Phe Asn Asp Glu Ile Leu Thr Gly Cys Asp Ser Leu Tyr Ala Val
50           55           60
His Pro Lys Phe Lys Thr Ser Trp Asp Tyr Tyr Asn Glu Pro Lys Pro
65           70           75           80
Leu Ile Glu Arg Leu Val Asn Leu Ala Pro Asn Tyr Lys Asp Phe Asp
85           90           95
Phe Ile Leu Thr Gly Gly Glu Pro Ser Leu Tyr Phe Asn Asn Pro Ile
100          105          110
Leu Leu Ser Val Leu Glu His Phe Tyr His Lys Lys Ile Pro Leu Phe
115          120          125
Val Glu Ser Asn Gly Ser Ile Phe Phe Glu Phe Ser Pro Ile Leu Lys
130          135          140
Glu Leu His Phe Thr Leu Ser Val Lys Leu Ser Phe Ser Leu Glu Gln
145          150          155          160
Glu Ser Lys Arg Ile Asn Leu Lys Ala Leu Gln Asn Ile Leu Asn Asn
165          170          175
Ala Lys Ser Val His Phe Lys Phe Val Leu Glu Ser Gln Asn Ala Ala
180          185          190
His Ser Ile Ala Glu Ile Gln Ser Leu Leu Lys Gln Leu Ser Leu Lys
195          200          205
Asn Asn Glu Ile Phe Leu Met Pro Leu Gly Thr Thr Asn Asn Glu Leu
210          215          220
Asp Lys Asn Leu Lys Thr Leu Ala Pro Leu Ala Ile Glu His Gly Phe
225          230          235          240
Arg Leu Ser Asp Arg Leu His Ile Arg Leu Trp Asp Asn Lys Lys Gly
245          250          255
Phe

```

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

Phe	Lys	Asp	Gln	Gly	Met	Asn	Leu	Asn	Phe	Met	Pro	Leu	Leu	His	Ala	1	5	10	15
Tyr	Asn	His	Val	Ser	Ile	Asp	Phe	His	Phe	Asn	Ser	Ser	Ala	Arg	Asp	20	25	30	
Phe	Cys	Val	His	Glu	Val	Pro	Leu	Tyr	Glu	Phe	Ser	Asn	Thr	Gly	Glu	35	40	45	
His	Ala	Val	Ile	Gln	Val	Arg	Lys	Ser	Gly	Leu	Ser	Thr	Leu	Glu	Met	50	55	60	
Leu	Gln	Ile	Phe	Ser	Gln	Ile	Leu	Gly	Val	Lys	Ile	Ala	Glu	Leu	Gly	65	70	75	80
Tyr	Ala	Gly	Leu	Lys	Asp	Lys	Asn	Ala	Leu	Thr	Thr	Gln	Phe	Ile	Ser	85	90	95	
Leu	Pro	Lys	Lys	Tyr	Ala	Pro	Leu	Leu	Glu	Lys	Asn	Thr	Ser	Asn	Phe	100	105	110	
Gln	Glu	Arg	Asn	Leu	Lys	Ile	Leu	Ser	Leu	Asn	Tyr	His	His	Asn	Lys	115	120	125	
Ile	Lys	Leu	Gly	His	Leu	Lys	Gly	Asn	Arg	Phe	Phe	Met	Arg	Phe	Lys	130	135	140	
Lys	Met	Thr	Pro	Leu	Asn	Ala	Gln	Lys	Thr	Glu	Gln	Val	Leu	Glu	Gln	145	150	155	160
Ile	Ala	Gln	Phe	Gly	Met	Pro	Asn	Tyr	Phe	Gly	Ser	Gln	Arg	Phe	Gly	165	170	175	
Lys	Phe	Asn	Asp	Asn	His	Lys	Glu	Gly	Leu	Lys	Ile	Leu	Gln	Asn	Glu	180	185	190	
Thr	Lys	Phe	Ala	His	Gln	Lys	Leu	Asn	Ala	Phe	Leu	Ile	Ser	Ser	Tyr	195	200	205	
Gln	Ser	Tyr	Leu	Phe	Asn	Ser	Leu	Leu	Ser	Lys	Arg	Leu	Glu	Ile	Ser	210	215	220	
Lys	Ile	Ile	Ser	Ala	Phe	Ser	Val	Lys	Glu	Ser	Leu	Glu	Phe	Phe	Lys	225	230	235	240
Gln	Lys	Asn	Leu	Ser	Val	His	Ser	Asn	Ala	Leu	Lys	Ala	Leu	Lys	Asn	245	250	255	
Gln	Ala	His	Pro	Phe	Lys	Ile	Leu	Glu	Gly	Asp	Val	Met	Arg	His	Tyr	260	265	270	
Pro	Tyr	Gly	Lys	Phe	Phe	Asp	Ala	Leu	Glu	Leu	Glu	Lys	Glu	Ser	Glu	275	280	285	
Arg	Phe	Leu	Asn	Lys	Glu	Ala	Val	Pro	Thr	Gly	Leu	Leu	Asp	Gly	Lys	290	295	300	
Lys	Ala	Leu	Tyr	Ala	Lys	Asn	Leu	Ser	Leu	Glu	Ile	Glu	Lys	Gly	Phe	305	310	315	320
Gln	His	Asn	Leu	Leu	Ser	Gly	His	Ala	Lys	Thr	Leu	Gly	Ser	Arg	Arg	325	330	335	
Phe	Phe	Trp	Val	Phe	Val	Glu	Asn	Ile	Thr	Ser	Gln	Tyr	Ile	Lys	Glu	340	345	350	
Lys	Ala	Gln	Phe	Glu	Leu	Glu	Phe	Tyr	Leu	Pro	Lys	Gly	Ser	Tyr	Ala	355	360	365	

541

Ser Ala Leu Leu Lys Glu Ile Lys His Glu Lys Gly Glu Asn Asn Asp
 370 375 380
 Glu Phe
 385

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

Lys Ile Lys Gly Lys Glu Met Lys Phe Leu Asn Gly Leu Ala Gly Asn
 1 5 10 15
 Leu Leu Ile Val Val Ile Leu Leu Cys Val Val Val Phe Phe Ala Leu
 20 25 30
 Lys Ala Ile His Ile Gln Lys Glu Gln Ala Thr Asn Tyr Tyr Arg Tyr
 35 40 45
 Lys Asp Ile Asn Ala Leu Glu Ala Lys Asn Thr Gln Asn His Ala
 50 55 60

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

Met Leu Glu Ile Glu Leu Lys Lys Lys Phe Thr Lys Asp Leu Lys Lys
 1 5 10 15
 His Ile Leu Asn Gln Lys Ile Glu Leu Glu Val Phe Asp Leu Val Val

542

```

      20      25      30
Glu Asn Leu Arg Asn Gln Ile Pro Leu Asp Lys Arg Phe Lys Asp His
      35      40      45
Ala Leu Ser Gly Thr Tyr Lys Gly Cys Arg Glu Arg His Ile Lys Pro
      50      55      60
Asp Val Leu Leu Val Tyr Arg Val Lys Gly Asn Val Leu Thr Leu Val
      65      70      75      80
Arg Leu Gly Ser His Ser Glu Leu Phe Cys Lys Pro Pro Thr Pro Leu
      85      90      95
Ile Thr Leu Lys
      100

```

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 646 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

```

Ser Asn Tyr Asn Asn Leu Asn Thr Leu Val Ser Leu Ser Ser Asp Pro
1      5      10      15
Ser Ala Val Asn Asp Ala Arg Asp Asn Leu Gly Ser Ser Ala Arg Asn
      20      25      30
Leu Leu Asp Val Lys Ala Asn Ser Pro Ala Tyr Gln Ala Val Leu Leu
      35      40      45
Ala Leu Asn Ala Ala Val Gly Leu Trp Gln Val Thr Ser Tyr Ala Phe
      50      55      60
Thr Ala Cys Gly Pro Gly Ser Asn Glu Asn Ala Asn Gly Gly Ile Gln
      65      70      75      80
Thr Phe Asn Asn Val Pro Gly Gln Asn Thr Thr Thr Ile Thr Cys Asn
      85      90      95
Ser Tyr Tyr Glu Pro Gly His Gly Gly Pro Ile Ser Thr Glu Asn Tyr
      100      105      110
Ala Ile Ile Asn Lys Ala Tyr Gln Ile Ile Gln Lys Ala Leu Thr Ala
      115      120      125
Asn Gly Glu Gly Ile Pro Val Leu Ser Asn Thr Thr Thr Lys Leu Asp
      130      135      140
Phe Thr Ile Asn Gly Asp Lys Arg Thr Gly Gly Glu Pro Asn Lys Lys
      145      150      155      160
Leu Val Tyr Pro Trp Ser His Gly Lys Ala Ile Ser Thr Ser Trp Asn
      165      170      175
Ala Thr Ile Thr Val Pro Thr Thr Glu Asn Ile Asn Thr Thr Asn Ser
      180      185      190
Ala Gln Glu Leu Leu Lys Gln Ala Ser Ile Ile Ile Thr Thr Leu Asn

```

195	200	205
Ser Ala Cys Pro Asn Phe Gln Asn Gly Gly Ser Gly Tyr Trp Ala Gly		
210	215	220
Ile Ser Gly Asn Gly Thr Met Cys Gly Met Phe Lys Asn Glu Ile Ser		
225	230	235
Ala Ile Gln Gly Met Ile Ala Asn Ala Gln Glu Ala Val Ala Gln Ala		
245	250	255
Lys Ile Val Ser Glu Asn Thr Gln Asn Gln Asn Ser Leu Asp Ala Gly		
260	265	270
Lys Pro Phe Asn Pro Tyr Thr Asp Ala Ser Phe Ala Glu Ser Met Leu		
275	280	285
Lys Asn Ala Gln Ala Gln Ala Glu Ile Leu Asn Gln Ala Glu Gln Val		
290	295	300
Val Lys Asn Phe Glu Lys Ile Pro Thr Ala Phe Val Asn Asp Ser Leu		
305	310	315
Gly Val Cys Tyr Glu Val Gln Gly Gly Glu Arg Arg Gly Thr Asn Pro		
325	330	335
Gly Gln Thr Thr Ser Asn Thr Trp Gly Ala Gly Cys Ala Tyr Val Gly		
340	345	350
Gln Thr Ile Thr Asn Leu Lys Asn Ser Ile Ala His Phe Gly Thr Gln		
355	360	365
Glu Gln Gln Ile Gln Gln Ala Glu Asn Ile Ala Asp Thr Leu Val Asn		
370	375	380
Phe Lys Ser Arg Tyr Ser Glu Leu Gly Asn Thr Tyr Asn Ser Ile Thr		
385	390	395
Thr Ala Leu Ser Asn Ile Pro Asn Ala Gln Ser Leu Gln Asn Ala Val		
405	410	415
Ser Lys Lys Asn Asn Pro Tyr Ser Pro Gln Gly Ile Asp Thr Asn Tyr		
420	425	430
Tyr Leu Asn Gln Asn Ser Tyr Asn Gln Ile Gln Thr Ile Asn Gln Glu		
435	440	445
Leu Gly Arg Asn Pro Phe Arg Lys Val Gly Ile Val Ser Ser Gln Thr		
450	455	460
Asn Asn Gly Ala Met Asn Gly Ile Gly Ile Gln Val Gly Tyr Lys Gln		
465	470	475
Phe Phe Gly Gln Lys Arg Lys Trp Gly Ala Arg Tyr Tyr Gly Phe Phe		
485	490	495
Asp Tyr Asn His Ala Phe Ile Lys Ser Ser Phe Phe Asn Ser Ala Ser		
500	505	510
Asp Val Trp Thr Tyr Gly Phe Gly Ala Asp Ala Leu Tyr Asn Phe Ile		
515	520	525
Asn Asp Lys Ala Thr Asn Phe Leu Gly Lys Asn Asn Lys Leu Ser Val		
530	535	540
Gly Leu Phe Gly Gly Ile Ala Leu Ala Gly Thr Ser Trp Leu Asn Ser		
545	550	555
Glu Tyr Val Asn Leu Ala Thr Met Asn Asn Val Tyr Asn Ala Lys Met		
565	570	575
Asn Val Ala Asn Phe Gln Phe Leu Phe Asn Met Gly Val Arg Met Asn		
580	585	590
Leu Ala Arg Pro Lys Lys Lys Asp Ser Asp His Ala Ala Gln His Gly		
595	600	605
Ile Glu Leu Gly Leu Lys Ile Pro Thr Ile Asn Thr Asn Tyr Tyr Ser		
610	615	620
Phe Met Gly Ala Glu Leu Lys Tyr Arg Arg Leu Tyr Ser Val Tyr Leu		
625	630	635
Asn Tyr Val Phe Ala Tyr		
645		

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

```

Asp Leu Lys Met Leu Thr Ile Glu Thr Ser Lys Lys Phe Asp Lys Asp
1          5          10          15
Leu Lys Ile Leu Val Lys Asn Gly Phe Asp Leu Lys Leu Leu Tyr Lys
          20          25          30
Val Val Gly Asn Leu Ala Thr Glu Gln Pro Leu Glu Pro Lys Tyr Lys
          35          40          45
Asp His Pro Leu Lys Gly Ala Leu Lys Asp Phe Arg Glu Cys His Leu
          50          55          60
Lys Pro Asp Leu Leu Leu Val Tyr Gln Ile Lys Lys Gln Glu Asn Thr
          65          70          75          80
Leu Phe Leu Val Arg Leu Gly Ser His Ser Glu Leu Phe
          85          90

```

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

```

Arg Ala Trp Arg Met Lys Ser Met Arg Phe Ser Tyr Ile Glu Pro Arg
1          5          10          15
Ala Lys Tyr Leu Ile Ser Lys Leu Ser Lys Ile Trp Val Phe Tyr Ile

```

545

	20		25		30										
Phe	Leu	Ser	Phe	Val	Leu	Ile	Gly	Gly	Leu	Val	Trp	Phe	Met	His	Asn
	35						40					45			
Ala	Ile	Lys	Arg	Ala	Gln	Asp	Asn	Ala	Ser	Ser	Leu	Thr	Ile	Gln	Glu
	50					55					60				
Glu	Leu	Tyr	Arg	Cys	Tyr	Ile	Thr	Arg	Leu	Ser	Val	Lys	Met	Ile	Ile
65					70				75						80
Leu															

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

Val	Lys	Phe	Pro	Tyr	Leu	Leu	Asn	Ile	Arg	Ile	Met	Leu	Tyr	Leu	Arg
1			5						10					15	
Lys	Glu	Asn	Gly	Val	Arg	Thr	Leu	Ile	Ser	Leu	Gly	Ile	Leu	Leu	Ser
			20					25					30		
Val	Leu	Asn	Gly	Asp	Asp	Leu	Arg	Leu	Tyr	Ser	Lys	Pro	Leu	Val	Tyr
	35					40					45				
Ser	Ala	Gly	Ser	Gly	Ile	Ile	Gly	Ile	Asp	Ile	Asp	Lys	Arg	Thr	Phe
	50					55				60					
Tyr	Lys	Arg	Ala	Phe	Ala	Phe	Thr	Met	Lys	Ser	Leu	Phe	Gly	Glu	Asn
65					70				75					80	
Leu	Leu	Leu	Phe	Val	Lys	Leu	Lys	His	Ser	Ala	Leu	Met	Ser	Lys	His
			85					90					95		
Met	Lys	Gly	Pro	Leu	Glu	Asn	Arg	His	His	His	Ser	Phe	Ala	Lys	Asn
			100					105					110		
Tyr	Glu	Lys	Ala	Val	Asn	Gly	Cys	Gln	Lys	Tyr	Val	His	Ile	Lys	Leu
	115					120						125			
Pro	Glu	Gly	Pro	Pro	Ser	Asn	Phe	Gln	Ser	Gly	Ser	Tyr	Met	Ala	Thr
	130					135					140				
Met	Val	Met	Arg	Phe											
145															

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

```

Val Ile Thr Asn Gln Gln Asn Glu Val Lys Thr Phe Thr Pro Ile Glu
1           5           10           15
Thr Lys Lys Ile Thr Ser Lys Glu Gln Ala Phe Leu Thr Leu Ser Ala
20           25           30
Leu Met Asp Ala Val Glu Asn Gly Thr Gly Ser Leu Ala Arg Ile Lys
35           40           45
Gly Leu Glu Ile Ala Gly Lys Thr Gly Thr Ser Asn Asn Asn Ile Asp
50           55           60
Ala Trp Phe Ile Gly Phe Thr Pro Thr Leu Gln Ser Val Ile Trp Phe
65           70           75           80
Gly Arg Asp Asp Asn Thr Pro Ile Gly Lys Gly Ala Thr Gly Gly Val
85           90           95
Val Ser Ala Pro Val Tyr Ser Tyr Phe Met Arg Asn Ile Leu Ala Ile
100          105          110
Glu Pro Ser Leu Lys Arg Lys Phe Asp Val Pro Lys Gly Leu Arg Lys
115          120          125
Glu Ile Val Asp Lys Ile Pro Tyr Tyr Ser Ser Pro Asn Ser Ile Thr
130          135          140
Pro Thr Pro Lys Lys Thr Asp Asp Ser Glu Glu Arg Leu Leu Phe
145          150          155

```

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

```

Leu Leu Leu Asn Leu Lys Ile Tyr Val Thr Leu Cys Lys Ile Gln Gly
1           5           10           15

```


547

```

Asp Ser Val Leu Glu Lys Ser Phe Leu Lys Ser Lys Gln Leu Val Leu
      20                      25                      30
Cys Gly Leu Gly Val Phe Met Leu Gln Ala Leu His Phe Ala Gln Thr
      35                      40                      45
Leu His Lys Glu Ile Leu Phe Tyr Lys Met Cys Leu Ile Gly Cys Cys
      50                      55                      60
Lys Ile Ala Ala Ser Ile Ser Arg Lys Gly Trp Ile Ala Arg Thr Leu
      65                      70                      75                      80

```

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

```

Val Lys Cys Gly Lys Lys Gly Ile Leu Val Ser Thr Arg Lys Ala Met
1      5      10      15
Phe Leu Cys Lys Ile Pro Leu Ser Leu Thr Leu Met Glu Ala Arg Ser
      20      25      30
Val Leu Thr Gln Glu Ile Arg Ser Phe Leu Pro Glu Thr Thr Ser
      35      40      45
Leu Ser Leu Thr Ile Leu Glu Arg Ser Ile Cys Cys Leu Ile Lys Phe
      50      55      60
Leu Thr Leu Thr Ser Pro Cys Leu Thr Gln Gln Arg Pro Lys Ile Asn
      65      70      75      80
Ala Thr Asn Asn Asn Val Ser Val Ser Gln Gly Asn Leu Phe Ile Asn
      85      90      95
Ala Ser Cys Val Gln Gln Ser Asp Pro Thr Thr Ala Ser Ala Thr Asn
      100     105     110
Pro Cys Thr Thr Ala Gln Asn Asn Ala Ser Ser Ser Asn Ala Ser Asn
      115     120     125
Asn Ala Pro Ile Ala Leu Asn Asn Asn Asp Glu Ser Leu Val Val Thr
      130     135     140
Ala Asn Gly Phe Asn Phe Ser Gly Asn Ile Tyr Ala Asn Gly Val Val
      145     150     155     160
Asp Phe Ser Lys Ile Lys Gly Ser Ala Asn Val Lys Asn Leu Tyr Leu
      165     170     175
Tyr Asn Asn Ala Gln Phe Gln Ala Asn Asn Leu Thr Ile Ser Asn Gln
      180     185     190
Ala Val Leu Glu Lys Asn Ala Ser Phe Val Thr Asn Asn Leu Asn Ile
      195     200     205
Gln Gly Ala Phe Asn Asn Asn Ala Thr Gln Lys Ile Glu Val Leu Gln
      210     215     220

```

548

```

Asn Leu Val Ile Ala Ser Asn Ala Ser Leu Ser Thr Gly Ile Tyr Gly
225                230                235                240
Leu Glu Val Gly Gly Ala Leu Asn Asn Leu Gly Ala Ile His Phe Asn
                245                250                255
Leu Glu Asn Ser Gln Thr Pro Val Asn Pro Leu Ile Gln Val Gly Gly
                260                265                270
Ile Ile Asn Leu Asn Thr Thr Gln Thr Pro Phe Met Asn Val Ser Val
                275                280                285
Ala Asn Gly Gly Thr Tyr Thr Leu Leu Lys Ser Ser Arg Tyr Ile Asp
                290                295                300
Tyr Asn Ile Asn Pro Asn Ser Leu Gln Ser Tyr Leu Lys Leu Tyr Thr
305                310                315                320
Leu Ile Asn Ile Asn Gly Asn His Ile Glu Glu Lys Asn Gly Val Leu
                325                330                335
Thr Tyr Leu Gly Gln Arg Val Leu
                340

```

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

```

Leu Leu Ala Arg Thr Ile Leu Asp Phe Arg Gly Ser Leu Ser Asn Leu
1                5                10                15
Asn Asn Thr Tyr Asn Ser Ile Thr Thr Thr Ala Ser Asn Thr Pro Asn
                20                25                30
Ser Pro Phe Leu Lys Asn Leu Ile Ser Gln Ser Thr Asn Pro Asn Asn
                35                40                45
Pro Gly Gly Leu Gln Ala Val Tyr Gln Val Asn Gln Ser Ala Tyr Ser
50                55                60
Gln Leu Leu Ser Ala Thr Gln Glu Leu Gly His Asn Pro Phe Arg Arg
65                70                75                80
Val Gly Leu Ile Ser Ser Gln Thr Asn Asn Gly Ala Met Asn Gly Ile
                85                90                95
Gly Val Gln Val Gly Tyr Lys Gln Phe Phe Gly Glu Lys Arg Arg Trp
                100                105                110
Gly Leu Arg Tyr Tyr Gly Phe Phe Asp Tyr Asn His Ala Tyr Ile Lys
                115                120                125
Ser Ser Phe Phe Asn Ser Ala Ser Asp Val Phe Thr Tyr Gly Val Gly
130                135                140
Thr Asp Val Leu Tyr Asn Phe Ile Asn Asp Lys Thr Thr Lys Asn Ser
145                150                155                160

```

549

```

Lys Ile Ser Phe Gly Val Phe Gly Gly Ile Ala Leu Ala Gly Thr Ser
      165                      170                      175
Trp Leu Asn Ser Gln Tyr Val Asn Leu Ala Thr Phe Asn Asn Phe Tyr
      180                      185                      190
Ser Ala Lys Met Asn Val Ala Asn Phe Gln Phe Leu Phe Asn Leu Gly
      195                      200                      205
Leu Arg Met Asn Leu Ala Lys Asn Lys Lys Lys Asp Ser Asp His Ala
      210                      215                      220
Ala Gln His Gly Val Glu Leu Gly Val Lys Ile Pro Thr Ile Asn Thr
225                      230                      235                      240
Asn Tyr Tyr Ser Phe Leu Gly Thr Lys Leu Glu Tyr Arg Arg Leu Tyr
      245                      250                      255
Ser Val Tyr Leu Asn Tyr Val Phe Ala Tyr
      260                      265

```

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

```

Arg Asn Val Glu Ala Arg Tyr Tyr Tyr Gly Asp Thr Ser Tyr Phe Tyr
1      5      10      15
Leu His Ala Gly Val Leu Gln Glu Phe Ala His Phe Gly Ser Asn Asp
      20      25      30
Val Ala Ser Leu Asn Thr Phe Lys Ile Asn Ala Ala Arg Ser Pro Leu
      35      40      45
Ser Thr Tyr Ala Arg Ala Met Met Gly Gly Glu Leu Gln Leu Ala Lys
      50      55      60
Glu Val Phe Leu Asn Leu Gly Val Val Tyr Leu His Asn Leu Ile Ser
65      70      75      80
Asn Ala Ser His Phe Ala Ser Asn Leu Gly Met Arg Tyr Ser Phe
      85      90      95

```

(2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

550

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

```

Arg Leu Pro Lys Lys Glu Asp Tyr Ala Lys Ala Met Val Phe Ser Phe
1          5          10          15
Lys Met Glu Ala Ile Lys Glu Ser Gln Ile Val Leu Leu Ile Thr Ser
20          25          30
Ala Phe Glu Gly Gln Phe Glu Lys Thr His Lys Glu Glu Lys Glu Glu
35          40          45
Thr Thr Lys Ser Ala Thr Glu Glu Thr Lys Thr His Asp Ala Ser Leu
50          55          60
Glu Asn Ile Glu Ile Arg Asn Ile Ser Met Leu Leu Asp Val Lys Leu
65          70          75          80
Asn Val Lys Val Arg Ile Gly Gln Lys Lys Met Ile Leu Lys Asp Val
85          90          95
Val Ser Met Asp Ile Gly Ser Val Val Glu Leu Asp Gln Leu Val Asn
100         105         110
Asp Pro Leu Glu Ile Leu Val Asp Asp Lys Val Ile Ala Lys Gly Glu
115         120         125
Val Val Ile Val Asp Gly Asn Phe Gly Ile Gln Ile Thr Asp Ile Gly
130         135         140
Thr Lys Lys Glu Arg Leu Glu Gln Leu Lys Asn
145         150         155

```

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

```

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

```

551

```

      35              40              45
Gly Tyr Ser Ser Phe Ser Asn Gln Ala Asn Ser Leu Asn Ser Gly Ala
  50              55              60
Asn Asn Ala Asn Phe Gly Val Tyr Ser Arg Phe Phe Ala Asn His Pro
  65              70              75              80
Glu Phe Asp Phe Glu Ala Gln Gly Ala Leu Gly Ser Asp Gln Ser Ser
      85              90              95
Leu Asn Phe Lys Ser Thr Leu Leu Gln Asp Leu Asn Gln Ser Tyr Asn
      100              105              110
Tyr Leu Ala Tyr Ser Ala Thr Ala Arg Ala Ser Tyr Gly Tyr Asp Phe
      115              120              125
Ala Phe Phe Arg Asn Ala Leu Val Leu Lys Pro Ser Val Gly Val Ser
      130              135              140
Tyr Asn His Leu Gly Ser Thr Asn Phe Lys Ser Asn Ser Gln Ser Gln
  145              150              155              160
Val Ala Leu Lys Asn Gly Ala Ser Ser Gln His Leu Phe Asn Ala Asn
      165              170              175
Ala Thr Trp Lys Arg Val Ile Ile Met Gly Thr Leu His Thr Phe Ile
      180              185              190
Cys Met Arg Glu Phe Tyr Lys Ser Ser Leu Thr Leu Asp Arg Met Met
      195              200              205
Trp Arg Leu
      210

```

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

```

His Ala Arg Glu Phe Cys Gln Val Val Met Phe His Lys Ala Leu Ile
  1              5              10              15
Thr Phe Ile Val Leu Trp Phe Phe Leu Asn Gly Leu Gly Ala Tyr Asp
      20              25              30
Phe Lys His Cys Gln Ala Phe Phe Lys Lys Ala Ser Leu Gln Lys Gly
      35              40              45
Gly Val Ala Leu Lys Glu Leu Pro Lys Gly Val Tyr Leu Tyr Tyr Ser
      50              55              60
Lys Thr Tyr Pro Lys His Ala Lys Val Ile Lys Ser Asp Pro Phe Ile
  65              70              75              80
Gly Leu Tyr Leu Leu Gln Ser Ala Pro Ser Glu Tyr Val Tyr Thr Leu
      85              90              95
Arg Asp Leu Asp Lys Asp Ala Leu Ile Arg Pro Met Ala Ser Ile Gly

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Helicobacter pylori*

(A) NAME/KEY: misc_feature
(B) LOCATION 1...165

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

```

      35              40              45
Ser  Gln  Leu  Lys  Asn  Glu  Glu  Leu  Leu  Lys  Leu  Ala  Gly  Thr  Leu  Pro
      50              55              60
Ser  Asn  Glu  Ala  Ile  Asp  Tyr  Arg  Met  Glu  Val  Ser  Lys  Arg  Leu  Ile
      65              70              75              80
Ala  Leu  Ser  Ala  Glu  Asp  Ala  Lys  Asn  Phe  Arg  Ala  Asn  Phe  Ser  Arg
      85              90              95
Ile  Ala  Arg  Lys  Asn  Leu  Ser  Lys  Met  Ser  Glu  Glu  Asp  Phe  Lys  Lys
      100             105             110
Met  Arg  Glu  Glu  Val  Arg  Lys  Glu  Leu  Glu  Glu  Lys  Thr  Lys  Gly  Leu
      115             120             125
Ser  Ala  Glu  Glu  Ile  Lys  Ala  Lys  Gly  Leu  Asn  Val  Ser  Val  Cys  Ser
      130             135             140
Gly  Asp  Thr  Arg  Lys  Val  Trp  Cys  Arg  Ala  Val  Lys  Lys  Lys  Asp  Glu
      145             150             155             160
His  Cys  Ser  Pro  Lys
      165

```

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

```

Phe  Lys  Arg  Lys  Asn  Met  Lys  Lys  Ala  Leu  Lys  Ile  Leu  Ser  Val  Gly
1              5              10              15
Ala  Leu  Leu  Phe  Val  Ala  Leu  Asn  Ala  Lys  Asp  Phe  Ser  Lys  Thr  Ser
      20              25              30
Asp  Glu  Asp  Leu  Ala  Lys  Met  Ala  Gly  Val  Val  Ala  Pro  Gln  Asp  Ile
      35              40              45
Val  Asp  Tyr  Thr  Lys  Glu  Leu  Lys  Lys  Arg  Met  Glu  Lys  Met  Pro  Glu
      50              55              60
Asp  Lys  Arg  Lys  Ala  Phe  His  Lys  Gln  Leu  His  Glu  Tyr  Ala  Thr  Lys
      65              70              75              80
Asn  Thr  Asp  Lys  Met  Thr  Val  Ala  Asp  Phe  Glu  Ala  Arg  Gln  Lys  Ala
      85              90              95
Ile  Lys  Glu  Ala  Leu  Lys  Lys  Gly  Asn  Met  Glu  Asp  Met  Asp  Asp  Asp
      100             105             110
Phe  Gly  Leu  Arg  Ser  Cys  Lys  His  Gly  Lys  Lys  His  Lys  His  Asp  Lys
      115             120             125
His  Gly  Lys  Lys  His  Gly  Lys  Lys  His  Asp  Lys  Asp  His  Asp  Asp  Lys
      130             135             140
Asp  His  Asp  His  His  Asp  Glu  Asp  His  Ser  Asp  Lys  His

```

554

145

150

155

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

```

Ile Gln Arg Tyr Trp Asn Gly Ala Leu Met Lys Asn Gln His Lys Asn
1      5      10      15
Pro Leu Thr Lys Ala Leu Met Lys Thr Tyr Pro Tyr Asn His Phe Leu
20      25      30
Phe Phe Cys Phe Ile Leu Gly Ala Phe Leu Leu Gly Leu Leu Ser Pro
35      40      45
Ala Tyr Ala Leu Ser Ile Ile Thr Thr Lys Glu Ile Asp Ala Asn Leu
50      55      60
Leu Asn Gly Ala Ile Glu Ser Arg Val Val Leu Gly Lys Arg Val Phe
65      70      75      80
Lys Val Glu Ala His Gly Phe Tyr Phe Arg Asn Asn Ala Thr Asn Ser
85      90      95
Ile Asp Ile Glu Ile Thr Ser Leu Leu Arg Asp Asn Gln Ser Phe Pro
100     105     110
Leu Thr Ser Ser Ala Lys Thr Ser Leu Lys Ile Pro Pro Asn Ala Lys
115     120     125
Ile Lys Lys Ser Thr Ile Leu Val Leu Lys Gly Glu Asn Ala Glu Glu
130     135     140
Val Ala Lys Ile Leu Gly Val Ser Lys Glu Glu Tyr Gln Lys Leu Glu
145     150     155     160
Asn Ile Ala Gln Thr Lys Ala Ala Asn Asp Pro Met Tyr Ala Asn Thr
165     170     175
Pro Phe Ser Asn Gly Ser Asp Ser Ser Phe Tyr Asp Asn Asn Pro Asn
180     185     190
Ser Pro Ser Asn Asn Ala Ile Asn Gly Lys Asp Gly Ala Asn Gly Ser
195     200     205
Asn Gly Tyr Gly Ala Asn Gly Asn Asp Gly Val Asn Gly Ile Ser Gly
210     215     220
Ser Asn Gly Ala Asn Gly Ser His Ser Asn Asn Asn Ala Ile Gly Ser
225     230     235     240
Gly Ile Asp Thr Asp Gly Val Leu Gly Val Asp Gly Val Asn Gly Ser
245     250     255
Ser Ser Ser Ser Gly Gly Ser Val Gly Gly Tyr Glu Asn Asn Phe Thr
260     265     270
Asn His Gly Ser Thr Asn Asn Asn Thr Gly Gly Tyr Asp Asn Phe Asn

```


555

275										280					285				
Asn	Gly	Ser	Ser	Ser	Gly	Gly	Ser	Leu	Gly	Asn	Gly	Gly	Leu	Phe	Pro				
290						295					300								
Ile	Pro	Phe	Gly	Asn	Gly	Asp	Thr	Asn	Asn	Ser	Asn	Asn	Ser	Thr	Asn				
305					310					315					320				
Thr	Thr	Ser	Pro	Thr	Asn	Gly	Ser	Ser	Ser	Asn	Asn	Ala	Thr	Asn	Pro				
					325					330					335				
Ser	Ser	Gln	Glu	Asn	Asn	Tyr	Ser	Ser	Gln	Tyr	Cys	Lys	Val	Pro	Glu				
			340					345					350						
Leu	Ser	Pro	Asn	Asn	Thr	Met	Lys	Leu	Asp	Val	Ile	Ala	Lys	Asp	Gly				
		355					360					365							
Ser	Cys	Ile	Ser	Met	Asn	Ala	Leu	Arg	Asp	Asp	Thr	Lys	Cys	Ala	Tyr				
	370					375					380								
Arg	Tyr	Asp	Phe	Glu	Ala	Gly	Lys	Ala	Ile	Lys	Gln	Thr	Gln	Tyr	Tyr				
385					390					395					400				
Tyr	Val	Asp	Arg	Glu	Asn	Lys	Thr	Gln	Asn	Ile	Gly	Gly	Cys	Val	Asp				
				405					410					415					
Leu	Gln	Gly	Ala	Gln	Tyr	Ala	Met	Gln	Leu	Tyr	Lys	Asp	Asp	Ser	Lys				
			420					425					430						
Cys	Ala	Leu	Gln	Thr	Thr	Ser	Asp	Lys	Gly	Tyr	Gly	Met	Gly	Lys	Thr				
		435					440					445							
Gln	Thr	Phe	Gln	Thr	Glu	Ile	Val	Phe	Arg	Gly	Met	Asp	Asn	Leu	Ile				
	450					455					460								
His	Val	Ala	Val	Pro	Cys	Ser	Asp	Tyr	Ala	Arg	Val	Gln	Asp	Arg	Ile				
465					470					475					480				
Val	Arg	Tyr	Glu	Lys	Asn	Asp	Lys	Thr	Gln	Thr	Leu	Thr	Pro	Ile	Val				
				485					490					495					
Asp	Gln	Tyr	Tyr	Asn	Asp	Pro	Asn	Asn	Pro	Asn	Lys	Gln	Glu	Ile	Leu				
			500					505					510						
Asn	Arg	Gly	Ile	Ala	Thr	Gln	Leu	Ser	Ser	Gln	Tyr	Gln	Glu	Phe	Ala				
		515					520					525							
Cys	Gly	Gln	Trp	Glu	Tyr	Asn	Asp	Ala	Lys	Leu	Glu	Ala	Lys	Arg	Pro				
	530					535					540								
Thr	Met	Leu	Lys	Ser	Tyr	Asn	Lys	Leu	Asn	Gly	Glu	Trp	Val	Glu	Val				
545					550					555					560				
Thr	Pro	Cys	Asn	Phe	Glu	Ala	Gly	Ile	Lys	Ser	Gly	Ala	Val	Val	Ser				
				565					570					575					
Pro	Tyr	Val	Met	Gly	Val	Pro	Ser	Ser	Lys	Val	Leu	Ser	Asp	Ile	Thr				
			580					585					590						
Thr	Ser	His	Tyr	Phe	Arg	Ile	Glu	Arg	Lys	Asn	Tyr	Gly	Glu	Arg	Glu				
		595					600					605							
Gln	Cys	Gln	Lys	Leu	Tyr	Gly	Val	Asn	Arg	Cys	Gln	Pro	Gln	Tyr	Ser				
	610					615					620		</						

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...113
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

```

Met Ala Lys Met Asn Ala Pro Asp Gly Val Ala Val Trp Val Asn Glu
1           5           10           15
Asp Arg Cys Lys Gly Cys Asp Ile Cys Val Ser Val Cys Pro Ala Gly
          20           25           30
Val Leu Gly Met Gly Ile Glu Lys Glu Arg Val Leu Gly Lys Val Ala
          35           40           45
Lys Val Ala Tyr Pro Glu Ser Cys Ile Gly Cys Val Gln Cys Glu Leu
          50           55           60
His Cys Pro Asp Phe Ala Ile Tyr Val Ala Asp Arg Lys Asp Phe Lys
65           70           75           80
Phe Ala Lys Val Ser Lys Glu Ala Gln Glu Arg Ser Glu Lys Val Lys
          85           90           95
Ala Asn Lys Tyr Met Leu Leu Glu Glu Thr Ile Leu Glu Gly Arg Gly
          100          105          110
Lys

```

(2) INFORMATION FOR SEQ ID NO:630:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...329
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

```

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

```

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

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Helicobacter pylori*

(A) NAME/KEY: misc_feature
(B) LOCATION 1...148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

558

```

Lys Phe Met Arg Leu Leu Phe Leu Leu Leu Ser Ala Thr Leu Met Leu
1           5           10           15
Leu Ala Glu Glu Lys Ile Pro Leu Ser Asp Asp Ala Pro Ile Lys Leu
           20           25           30
Val His Trp Gln Asn Ala Leu Lys Glu Val Gln Pro Asp Ser Asn Ala
           35           40           45
Pro Ala Thr Pro Pro Ile Lys Ala Val Gln Thr Thr Leu Thr Phe Glu
           50           55           60
Thr Pro Phe Asn Lys Thr Pro Lys Ile Met Glu Val Glu Gly Gln Lys
65           70           75           80
Val Ile Val Leu Lys Asn Ala Gln Leu Asp Ser Lys Lys Thr Met Asp
           85           90           95
Phe Lys Glu Ala Ser Leu Asn Ala Leu Glu Met Phe Ser Tyr Gln Asn
           100          105          110
Asp Ile Tyr Leu Leu Ser Lys Lys Ala Lys Ala Gly Leu Glu Ile Gln
           115          120          125
Ala Ser Ser Ser Lys Asp Lys Lys Gln Leu Ala Phe Phe Phe Tyr Pro
           130          135          140
Lys Val Phe Ile
145

```

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

```

Glu Leu Ile Leu Lys Lys Lys Lys Glu Arg Asn Leu Met Lys Lys Gly
1           5           10           15
Ser Leu Ala Ile Val Leu Gly Ser Leu Leu Ala Ser Gly Thr Phe Tyr
           20           25           30
Thr Ala Leu Ala Asp Gly Met Pro Met Lys Gln Gln His Asn Asn Met
           35           40           45
Gly Glu Ser Val Glu Leu His Phe His Tyr Pro Ile Lys Gly Lys Gln
           50           55           60
Glu Pro Lys Asn Asn His Leu Val Val Leu Ile Asp Pro Lys Ile Glu
65           70           75           80
Ala Asn Lys Val Ile Pro Glu Asn Tyr Gln Lys Glu Phe Glu Lys Ser
           85           90           95
Leu Phe Leu Gln Leu Ser Asn Phe Leu Glu Arg Lys Gly Tyr Ser Val
           100          105          110
Ser Gln Phe Lys Asp Val Ser Glu Ile Pro Gln Asp Ile Lys Glu Lys

```

115	120	125
Ala Leu Leu Val Leu Arg Met Asp Gly Asn Val Ala Ile Leu Glu Asp		
130	135	140
Ile Val Glu Glu Ser Asp Ala Leu Ser Glu Glu Lys Val Ile Asp Met		
145	150	155
Ser Ser Gly Tyr Leu Asn Leu Asn Phe Val Glu Pro Lys Ser Glu Asp		
165	170	175
Ile Ile His Ser Phe Gly Ile Asp Val Ser Lys Ile Lys Ala Val Ile		
180	185	190
Glu Arg Val Glu Leu Arg Arg Thr Asn Ser Gly Gly Phe Val Pro Lys		
195	200	205
Thr Phe Val His Arg Ile Lys Glu Thr Asp His Asp Arg Ala Ile Lys		
210	215	220
Lys Ile Met Asn Gln Ala Tyr His Lys Val Met Ala His Ile Thr Lys		
225	230	235
Glu Leu Ser Lys Lys His Met Glu Arg Tyr Glu Lys Val Ser Ser Glu		
245	250	255
Met Lys Lys Arg Lys		
260		

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

Asp Gln Lys Phe Lys Gly Ile Ile Leu Ala Met Lys Ile Ser Val Ser	
1	5 10 15
Lys Asn Asp Leu Glu Asn Thr Leu Arg Tyr Leu Gln Ala Phe Leu Asp	
20	25 30
Lys Lys Asp Ala Ser Ser Ile Ala Ser His Ile His Leu Glu Val Ile	
35	40 45
Lys Glu Lys Leu Phe Leu Lys Ala Ser Asp Ser Asp Ile Gly Leu Lys	
50	55 60
Ser Tyr Ile Ser Thr Gln Ser Thr Asp Lys Glu Gly Val Gly Thr Ile	
65	70 75 80
Asn Gly Lys Lys Phe Leu Asp Ile Ile Ser Cys Leu Lys Asp Ser Asn	
85	90 95
Ile Val Leu Glu Thr Lys Asp Asp Ser Leu Val Ile Lys Gln Asn Lys	
100	105 110
Ser Ser Phe Lys Leu Pro Met Phe Asp Ala Asp Glu Phe Pro Glu Phe	
115	120 125
Pro Val Ile Asp Pro Lys Val Ser Leu Glu Ile Asn Ala Pro Phe Leu	

560

```

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

```

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

```

Asn Pro Leu Ile Gln Lys Asn Lys Ser Leu Ser Ile Phe Leu Ile Ser
1      5      10      15
Asn Ser Val Val Phe Leu Gly Lys Ile Ile Leu His Lys Val Phe Ile
      20      25      30
Met Glu Ala Leu Glu Cys Leu Lys Arg Ile Glu Lys Glu Ser Ile Gln
      35      40      45
Thr Ile Tyr Ile Asp Pro Pro Tyr Asn Thr Lys Ser Ser Asn Phe Glu
      50      55      60
Tyr Glu Asp Ala His Ala Asp Tyr Glu Lys Trp Ile Glu Glu His Leu
      65      70      75      80
Ile Leu Ala Lys Ala Val Leu Lys Gln Ser Gly Cys Ile Phe Ile Ser
      85      90      95
Met Asp Asp Asn Lys Met Ala Glu Val Lys Ile Ile Ala Asn Glu Ile
      100     105     110
Phe Gly Thr Arg Asn Phe Leu Gly Thr Phe Ile Thr Lys Gln Ala Thr
      115     120     125
Arg Ser Asn Ala Lys His Ile Asn Ile Thr His Glu Tyr Val Leu Ser
      130     135     140
Tyr Ala Lys Asn Lys Ala Phe Ala Pro Gly Phe Lys Ile Leu Arg Thr

```

561

```

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

```

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

```

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

```


(2) INFORMATION FOR SEQ ID NO:637:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...107
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

Gly	Gly	Val	Cys	Gly	Val	Leu	Ser	Leu	Gln	Ala	His	Leu	Ser	Phe	Glu
1				5				10						15	
Asn	Cys	Ser	Lys	Pro	Leu	Asp	Cys	Ser	Leu	Phe	Ala	Thr	Thr	Cys	Thr
			20					25					30		
Pro	Gln	Asn	Pro	Ile	Gly	Ser	Cys	Met	Val	Ser	Ser	Gln	Gly	Gly	Val
		35					40					45			
Cys	Gly	Val	Leu	Ser	Leu	Gln	Ala	His	Leu	Ser	Phe	Glu	Asn	Cys	Ser
	50					55					60				
Lys	Pro	Leu	Asp	Cys	Ser	Leu	Phe	Ala	Thr	Thr	Cys	Thr	Pro	Gln	Asn
65					70				75					80	
Pro	Ile	Gly	Ser	Tyr	Met	Val	Ser	Ser	Gln	Gly	Gly	Val	Arg	Gly	Val
				85					90				95		
Leu	Ser	Leu	Gln	Ala	Arg	Leu	Ser	Phe	Lys	Asn					
			100					105							

(2) INFORMATION FOR SEQ ID NO:638:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...384
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

Asn	Tyr	Ser	Asn	Lys	Asp	Asn	Pro	Met	Arg	Phe	Phe	Cys	Phe	Phe	Leu
1				5				10							15

564

```

Phe Phe Leu Thr Phe Ser Asn Ala Gln Ile Met Met Thr Phe Asp Ser
    20                25                30
Gln Thr Asn Ala Lys Leu Ser Arg Ser Asn Glu Gln Leu Ser Asp Met
    35                40                45
Leu Tyr Lys Leu Asn Glu Ser Leu Arg Ile Tyr Gln Asn Val Leu Ser
    50                55                60
Asn Asn Gln Asp Gln Leu Lys Glu Ile Lys Lys Ala Asn Ser Thr Leu
    65                70                75                80
Thr Ser Gln Arg Arg Phe Phe Asn Ala Ser Gln Ile Arg Leu Met Asp
    85                90                95
Thr Asp Ala Leu Leu Lys Gln Ser Ala Leu Glu Leu Glu Lys Leu Gln
    100               105               110
Ala Leu Glu Lys His Leu Lys Glu Ser Met Glu His Glu Arg Leu Ile
    115               120               125
Lys Glu Ser Gln Ala Leu Phe Leu Gln Glu His Cys Pro Tyr Leu Ser
    130               135               140
Gly Val Lys Asn Leu Glu Ala Ser Asn Ala Leu Glu Val Gln Glu
    145               150               155               160
Lys Asn Asn Ala Leu Phe Leu Leu Lys Glu Pro Lys Leu Phe His Leu
    165               170               175
Leu Ser Arg Leu Asp Leu Met Ser Ala Leu Asn Ala Leu Cys Asp Gln
    180               185               190
Val Leu Glu Asn Glu Ile Gln Asp Gln Gln Ser His Asn Lys Thr Leu
    195               200               205
Glu Tyr Asn Ala Leu Met Asn His Asp Phe Gln Ala Tyr Lys Ala Met
    210               215               220
Arg Leu Lys Lys Ile Lys Asn Lys Leu Gln Ser Gln Ile Gln Ala Lys
    225               230               235               240
Glu Asp Ala Leu Lys Thr Phe Leu Pro Leu Glu Lys Arg Pro Glu Thr
    245               250               255
Leu Gly Ser Ser Asp Cys Cys Asp Lys Glu Asn Leu Lys Ser Cys Ala
    260               265               270
Asn Gln Leu Gln Gln Arg Tyr Gln Asn Ala Leu Ile Glu Arg Asp Lys
    275               280               285
Glu Leu Lys Asn Ala Lys Asn Asn Lys Glu Lys His Ala Leu Ile Leu
    290               295               300
Ala Asn Tyr Glu His Thr Leu Lys Thr Leu Asn Ile Glu Phe Leu Ser
    305               310               315               320
Glu Leu Ser Glu Gln Met Ala Phe Leu Asn Glu Thr Met Ala Leu Asn
    325               330               335
Ala Gln Val Leu Ala Leu Leu Ala Gln Gln Gln Thr Lys Lys Pro Phe
    340               345               350
Asn Val Ser Asp Gly Leu Ser Gly Gly Lys Ala Leu Ile Lys Asn Ile
    355               360               365
Arg Leu Asp Pro His Gly Phe Pro Ser Phe Lys Asn Phe Lys Gln Glu
    370               375               380

```

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

```

Leu Val Phe Lys Lys Pro Phe Phe Lys Asn Arg Leu Leu Asn Val Thr
1          5          10          15
Asn Lys Leu Lys Phe Val Lys Ile Thr Ile Met Ile Lys Asp Phe Asn
20          25          30
His Tyr Cys Arg Lys Ile Thr Arg Gly Phe Val Lys Ile Pro Thr Lys
35          40          45
Lys Gln Gly Ala Lys Lys Met Lys Lys Ala Gly Phe Leu Phe Leu Ala
50          55          60
Ala Met Ala Ile Ile Val Val Ser Leu Asn Ala Lys Asp Pro Asn Val
65          70          75          80
Leu Arg Lys Ile Val Phe Glu Lys Cys Leu Pro Asn Tyr Glu Lys Asn
85          90          95
Gln Asn Pro Ser Pro Cys Ile Glu Val Lys Pro Asp Ala Gly Tyr Val
100         105         110
Val Leu Lys Asp Ile Asn Gly Pro Leu Gln Tyr Leu Leu Met Pro Thr
115         120         125
Thr His Ile Ser Gly Ile Glu Asn Pro Leu Leu Leu Asp Pro Ser Thr
130         135         140
Pro Asn Phe Phe Tyr Leu Ser Trp Gln Ala Arg Asp Phe Met Ser Lys
145         150         155         160
Lys Tyr Gly Lys Pro Ile Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn
165         170         175
Ser Lys Lys Gly Arg Ser Gln Asn His Phe His Ile His Ile Ser Cys
180         185         190
Ile Ser Leu Asp Val Arg Lys Gln Leu Asp Asn Asn Leu Lys Asn Ile
195         200         205
Asn Ser Arg Trp Ser Pro Leu Ser Gly Gly Leu Asn Gly His Lys Tyr
210         215         220
Leu Ala Arg Arg Val Thr Glu Ser Glu Leu Ala Gln Lys Ser Pro Phe
225         230         235         240
Val Met Leu Ala Lys Glu Val Pro Asn Ala His Lys Arg Met Gly Asp
245         250         255
Tyr Gly Leu Ala Val Val Gln Gln Ser Asp Asn Ser Phe Val Leu Leu
260         265         270
Ala Thr Gln Phe Asn Pro Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu
275         280         285
Ile Gln Asp His Glu Cys Ala Ile Leu Arg
290         295

```

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

```

Leu Arg Arg Leu Ala Leu Asn Thr Met Asn Ser Val Leu Glu Cys Lys
1          5          10          15
Glu Leu Ala Leu Tyr Gly Gly Ser Phe Asp Pro Leu His Lys Ala His
20          25          30
Leu Ala Ile Ile Glu Gln Thr Leu Leu Pro Phe Val Gln Leu
35          40          45
Ile Val Leu Pro Ala Tyr Gln Asn Pro Phe Lys Lys Pro Cys Phe Leu
50          55          60
Asp Ala Lys Thr Arg Phe Lys Glu Leu Glu Arg Ala Leu Lys Gly Met
65          70          75          80
Pro Arg Val Leu Leu Ser Asp Phe Glu Ile Lys Gln Glu Arg Ala Val
85          90          95
Pro Thr Ile Glu Ser Val Leu His Phe Gln Lys Leu Tyr Arg Pro Lys
100         105         110
Thr Leu Tyr Leu Val Ile Gly Ala Asp Cys Leu Arg His Leu Ser Ser
115         120         125
Trp Thr Asn Ala Lys Glu Leu Leu Lys Arg Val Glu Leu Val Val Phe
130         135         140
Glu Arg Ile Gly Tyr Glu Lys Ile Gln Phe Lys Gly Arg Tyr His Pro
145         150         155         160
Leu Lys Gly Ile Asp Ala Pro Ile Ser Ser Ser Ala Ile Arg Ala Ser
165         170         175
Leu Gly Val

```

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 269 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

567

```

Ser Ser Ile Phe Asp Tyr Asn Tyr Lys Gly Leu His Phe Ser Asn Lys
1      5      10      15
Arg Tyr Ile Met Leu Gly Ser Val Lys Lys Thr Leu Phe Gly Val Leu
      20      25      30
Cys Leu Gly Ala Leu Cys Leu Arg Gly Leu Met Ala Glu Pro Asp Ala
      35      40      45
Lys Glu Leu Val Ser Leu Gly Ile Glu Ser Val Lys Lys Gln Asp Phe
      50      55      60
Ala Gln Ala Lys Ala His Phe Glu Lys Ala Cys Glu Leu Lys Glu Gly
65      70      75      80
Phe Gly Cys Val Phe Leu Gly Ala Phe Tyr Glu Glu Gly Lys Gly Val
      85      90      95
Gly Lys Asp Leu Lys Lys Ala Ile Gln Phe Tyr Thr Lys Gly Cys Glu
      100      105      110
Leu Asn Asp Gly Tyr Gly Cys Arg Leu Leu Gly Asn Leu Tyr Tyr Asn
      115      120      125
Gly Gln Gly Val Ser Lys Asp Ala Lys Lys Ala Ser Gln Tyr Tyr Ser
      130      135      140
Lys Ser Cys Glu Leu Asn His Ala Glu Gly Cys Thr Val Leu Gly Ser
145      150      155      160
Leu His His Tyr Gly Val Gly Thr Pro Lys Asp Leu Arg Lys Ala Leu
      165      170      175
Asp Leu Tyr Glu Lys Ala Cys Asp Leu Lys Asp Ser Pro Gly Cys Ile
      180      185      190
Asn Ala Gly Tyr Met Tyr Gly Val Ala Lys Asn Phe Lys Glu Ala Ile
      195      200      205
Val Arg Tyr Ser Lys Ala Cys Glu Leu Lys Asp Gly Arg Gly Cys Tyr
      210      215      220
Asn Leu Gly Val Met Gln Tyr Asn Ala Gln Gly Thr Ala Lys Asp Glu
225      230      235      240
Lys Gln Ala Val Glu Asn Phe Lys Lys Gly Cys Lys Ser Ser Val Lys
      245      250      255
Glu Ala Cys Asp Ala Leu Lys Glu Leu Lys Ile Glu Leu
      260      265

```

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

```

His Phe Asn Ile Phe Thr Glu Asp Asn Arg Glu Ile Ser Gly Ser Thr
1      5      10      15

```

568

Asp Lys Leu Ser Tyr Asn Ala Leu Asn Gly Glu Tyr Lys Leu Leu Gln
 20 25 30
 Asn Ala Val Val Arg Glu Val Gly Lys Ser Asn Val Ile Thr Gly Asp
 35 40 45
 Glu Ile Ile Leu Asn Lys Thr Lys Gly Tyr Ala Asp Val Leu Gly Ser
 50 55 60
 Ala Lys Arg Pro Leu Asn Leu Cys Leu Ile Trp Lys Thr Leu Met Lys
 65 70 75 80
 Lys Ile Val Arg Leu Asn
 85

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

Pro Lys Ser Pro Lys Lys Ile Val Lys Arg Tyr Glu Lys Ser Ala Trp
 1 5 10 15
 Lys Met Pro Lys Glu Asn Thr Thr His Glu Asp Ala Leu Ala Lys Cys
 20 25 30
 Phe Ala Pro Ala Ile Phe Lys Ala Ile Met Leu Asn Lys Leu Ile Leu
 35 40 45
 Ala Val Val Ala Ala Pro Ile Ile Lys Met Leu Lys Leu Ser Lys Glu
 50 55 60
 Ile Trp Trp Lys Lys Met Gly Lys Lys His Ala Ile Asp Phe Lys Met
 65 70 75 80
 Arg Ile Lys Ile Leu Ala Ser Leu Ala Pro Ser Phe
 85 90

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

```

Asn Lys Asp His Leu Met Leu Asn Lys Phe Lys Lys Ile Val Gly Val
1           5           10           15
Gly Val Leu Val Gly Cys Leu Gly Val Leu Gln Ala Lys Asn Ser Leu
          20           25           30
Phe Val Leu Pro Tyr Glu Gln Arg Asp Ala Leu Asn Ser Leu Ile Ser
          35           40           45
Gly Ile Ser Ser Ala Arg Glu Asn Val Lys Ile Ala Ile Tyr Ser Phe
          50           55           60
Thr His Arg Asp Ile Ala Arg Ala Ile Lys Ser Val Ala Ser Arg Gly
65           70           75           80
Ile Lys Val Gln Ile Ile Tyr Asp Tyr Glu Ser Asn His Asn Asn Lys
          85           90           95
Gln Ser Thr Ile Gly Tyr Leu Asp Lys Tyr Pro Asn Thr Lys Val Cys
          100          105          110
Leu Leu Lys Gly Leu Lys Ala Lys Asn Gly Asn Tyr Tyr Gly Ile Met
          115          120          125
His Gln Lys Val Ala Ile Ile Asp Asp Lys Ile Val Phe Leu Gly Ser
          130          135          140
Ala Asn Trp Ser Lys Asn Ala Phe Glu Asn Asn Tyr Glu Val Phe Leu
145          150          155          160
Lys Arg Asp Asp Thr Glu Thr Ile Phe Lys Ala Lys Ser Tyr Tyr Gln
          165          170          175
Lys Met Leu Glu Gly Cys Val Gly Phe
          180          185

```

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

```

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

```

570

```

      35              40              45
Ala Leu Lys Leu His Glu Val Leu Ala Asn Asp Leu Lys Thr Ser Gln
  50              55              60
His Phe Asp Val Ser Gln Asn Lys Glu Gln Gly Ala Ile Asn Tyr Ala
  65              70              75              80
Glu Leu Lys Asp Lys Lys Val His Leu Val Ala Leu Val Ser Val Ala
      85              90              95
Val Glu Asn Gly Asn Lys Ile Ser Arg Leu Lys Leu Tyr Asp Val Asp
      100              105              110
Thr Gly Thr Leu Lys Lys Thr Phe Asp Tyr Pro Ile Val Ser Leu Asp
      115              120              125
Leu Tyr Pro Phe Ala Ala His Asn Met Ala Ile Val Val Asn Asp Tyr
      130              135              140
Leu Lys Ala Pro Ser Ile Ala Trp Met Lys Arg Leu Ile Val Phe Ser
  145              150              155              160
Lys Tyr Ile Gly Pro Gly Ile Thr Asn Ile Ala Leu Ala Asp Tyr Thr
      165              170              175
Met Arg Tyr Gln Lys Glu Ile Ile Lys Asn Asn Arg Leu Asn Ile Phe
      180              185              190
Pro Lys Trp Ala Asn Ala Glu Gln Thr Glu Phe Tyr Tyr Thr Gln Met
      195              200              205
Ala Glu Lys Arg Pro Trp Phe
      210              215

```

(2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

```

Ala Ala Met Met Phe Asn Asn Asp Ile Asp Ser Ala Thr Gly Phe Tyr
  1              5              10              15
Lys Pro Leu Ile Lys Ile Asn Ser Ala Gln Asp Leu Ile Lys Asn Thr
      20              25              30
Glu His Val Leu Leu Lys Ala Lys Ile Ile Gly Tyr Gly Asn Val Ser
      35              40              45
Thr Gly Thr Asn Gly Ile Ser Asn Val Asn Leu Glu Glu Gln Phe Lys
      50              55              60
Glu Arg Leu Ala Leu Tyr Asn Asn Asn Asn Arg Met Asp Thr Cys Val
  65              70              75              80
Val Arg Asn Thr Asp Asp Ile Lys Ala Cys Gly Met Ala Ile Gly Asn
      85              90              95
Gln Ser Met Val Asn Asn Pro Asp Asn Tyr Lys Tyr Leu Ile Gly Lys

```


571

	100		105		110										
Ala	Trp	Arg	Asn	Ile	Gly	Ile	Ser	Lys	Thr	Ala	Asn	Gly	Ser	Lys	Ile
	115						120					125			
Ser	Val	Tyr	Tyr	Leu	Gly	Asn	Ser	Thr	Pro	Thr	Glu	Asn	Gly	Gly	Asn
	130					135					140				
Thr	Thr	Asn	Leu	Pro	Thr	Asn	Thr	Thr	Asn	Asn	Ala	His	Ser	Ala	Asn
145					150				155						160
Tyr	Ala	Leu	Val	Lys	Asn	Ala	Pro	Phe	Ala	His	Asn	Thr	Thr	Pro	Asn
			165					170						175	

(2) INFORMATION FOR SEQ ID NO:647:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

Ile	Phe	Arg	Ala	Phe	Arg	Arg	Gly	Phe	Phe	Arg	Lys	Thr	Phe	Ala	Tyr
1			5					10						15	
Arg	Phe	Thr	Ala	His	His	Asp	Phe	Met	Leu	Glu	Arg	Met	Asn	Arg	Arg
		20					25					30			
Asn	Arg	Thr	Lys	Ser	Asp	Arg	Glu	Leu	Leu	Glu	Ile	Ile	Ala	Ser	Lys
	35					40					45				
Asn	Phe	Ala	Ile	Gly	Thr	Asp	Phe	Ile	Val	Gly	His	Pro	Gly	Glu	Ser
	50				55			60							
Glu	Ser	Val	Phe	Glu	Lys	Ala	Phe	Lys	Asn	Leu	Glu	Ser	Leu	Pro	Leu
65				70				75						80	
Thr	His	Ile	His	Pro	Phe	Ile	Tyr	Ser	Lys	Arg	Lys	Asp	Thr	Pro	Ser
		85					90					95			
Ser	Leu	Met	Arg	Asp	Ser	Val	Ser	Leu	Glu	Asp	Ser	Lys	Lys	Arg	Leu
		100				105						110			
Asn	Ala	Ile	Lys	Asp	Leu	Ile	Phe	His	Lys	Asn	Lys	Ala	Phe	Arg	Gln
	115				120							125			
Leu	Gln	Leu	Lys	Leu	Asn	Thr	Pro	Leu	Lys	Ala	Leu	Val	Glu	Ala	Gln
	130				135						140				
Lys	Asp	Gly	Glu	Phe	Lys	Ala	Leu	Asp	Gln	Phe	Phe	Asn	Pro	Ile	Lys
145				150				155						160	
Ile	Lys	Ser	Asp	Lys	Pro	Leu	Arg	Ala	Ser	Phe	Leu	Glu	Ile	Lys	Glu
			165				170						175		
Tyr	Glu	Ile	Lys	Glu	Arg	Glu	Asn	His	Ala	Val	Phe				
		180					185								

(2) INFORMATION FOR SEQ ID NO:648:

572

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 79 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

```

Lys Ala Leu Pro Gln Gly Arg Asn Arg Met Arg Ser Asp Val Glu Val
1           5           10           15
Leu Ser Pro Leu His Lys Ile Asp Glu Lys Tyr Leu Phe His Leu Lys
          20           25           30
Ile Ala Gly Glu Leu Ala Ser Met Gly Lys Ile Leu Ser Val Tyr Leu
          35           40           45
Ala His Lys His Ser Ala Tyr Phe Ile Leu Asn Ala Leu Ser Tyr Gly
          50           55           60
Phe Ser His Gln Asp Arg Ala Ile Ile Cys Leu Leu Gly Ala Ile
65           70           75

```

(2) INFORMATION FOR SEQ ID NO:649:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

```

Lys Gly Thr Lys Met Lys Lys Val Tyr Phe Lys Thr Phe Gly Cys Arg
1           5           10           15
Thr Asn Leu Phe Asp Thr Gln Val Met Gly Glu Asn Leu Lys Asp Phe
          20           25           30
Ser Ala Thr Leu Glu Glu Gln Glu Ala Asp Ile Ile Ile Asn Ser
          35           40           45
Cys Thr Val Thr Asn Gly Thr Asp Ser Ala Val Arg Ser Tyr Ala Arg
          50           55           60

```

573

```

Lys Met Ala Arg Leu Asp Lys Glu Val Leu Phe Thr Gly Cys Gly Val
65          70          75          80
Lys Thr Gln Gly Lys Glu Leu Phe Glu Lys Gly Leu Leu Lys Gly Val
          85          90          95
Phe Gly His Asp Asn Lys Glu Lys Ile Asn Ala Leu Leu Gln Glu Lys
          100          105          110
Lys Arg Phe Phe Ile Asp Asp Asn Leu Glu Asn Lys His Leu Asp Thr
          115          120          125
Thr Met Val Ser Glu Phe Val Gly Lys Thr Arg Ala Phe Ile Lys Ile
          130          135          140
Gln Glu Gly Cys Asp Phe Asp Cys Asn Tyr Cys Ile Ile Pro Ser Val
145          150          155          160
Arg Gly Arg Ala Arg Ser Phe Glu Lys Arg Lys Ile Leu Glu Gln Val
          165          170          175
Gly Leu Leu Cys Ser Gln Gly Val Gln Glu Val Val Leu Thr Gly Thr
          180          185          190
Asn Val Gly Ser Tyr Gly Lys Asp Arg Gly Ser Asn Ile Ala Arg Leu
          195          200          205
Ile Lys Lys Leu Ser Gln Ile Thr Gly Leu Lys Arg Ile Arg Ile Gly
          210          215          220
Ser Leu Asp Leu Ile Lys Ser Thr Met Asn Phe
225          230          235

```

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

```

Val Thr Ala Leu Ala Thr Arg Ile Gly Arg Ser Phe Ala Tyr Trp Ala
1          5          10          15
Gln Phe Ser His Lys Lys Ile Leu Lys Asp Tyr Val Ile Ala His Met
          20          25          30
Ser Ala Met Met Pro Ser Leu Leu Thr Leu Gln Trp Leu Ser Phe Ile
          35          40          45
Leu Ser Leu Ala Glu Asn Leu Cys Leu Thr Asp Ser His His Leu Lys
          50          55          60
Tyr Thr Leu Glu Lys Asn Lys Leu Val Ile His Ser Asn Asp Ala Leu
65          70          75          80
Tyr Leu Ala Lys Glu Met Leu Pro Lys Leu Ile Lys Pro Ile Pro Trp
          85          90          95
Thr Ile Glu Phe Ala
          100

```

(2) INFORMATION FOR SEQ ID NO:651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

```

Ser Asp Ala Phe Leu Ile Ile Gln Asp Phe Lys Glu Gln Arg Ile Ile
1          5          10          15
His Lys Ile Ile Gln Thr His Phe Lys Arg Met Arg Val Val Leu Ser
20          25          30
Val Lys Arg Asp Ser Glu Lys Thr Leu Glu Asn Asn Glu Glu Asn Lys
35          40          45
Asp Glu Lys Leu Ile Leu Ile Asp Glu Phe Glu Val Leu Ala Asn Lys
50          55          60
Phe Ile Ser Arg Leu Pro Asn Ile Pro Ser Thr Pro Arg Glu Phe Gly
65          70          75          80
Leu Gly Lys Gly Glu Ile Met Glu Ile Asp Val Pro Phe Gly Ser Ile
85          90          95
Phe Ala Tyr Arg His Ile Gly Ser Ile Arg Gln Lys Glu Tyr Arg Ile
100         105         110
Val Gly Leu Tyr Arg Asn Asp Val Leu Leu Leu Ser Thr Lys Ser Leu
115         120         125
Val Ile Gln Pro Arg Asp Ile Leu Leu Val Ala Gly Asn Pro Glu Ile
130         135         140
Leu Asn Ala Val Tyr His Gln Val Lys Ser Asn Val Gly Gln Phe Pro
145         150         155         160
Ala Pro Phe Gly Lys Ser Ile Tyr Leu Tyr Ile Asp Met Arg Leu Gln
165         170         175
Ser Arg Lys Ala Met Met Arg Asp Val Tyr Gln Ala Leu Phe Leu His
180         185         190
Lys Arg Leu Lys Ser Tyr Lys Leu Tyr Ile Gln Val Leu His Pro Thr
195         200         205
Ser Pro Lys Phe Tyr His Lys Phe Leu Ser Leu Glu Thr Glu Ser Ile
210         215         220
Glu Val Asn Phe Asp Phe Tyr Gly Lys Ser Phe Ile Gln Lys Leu His
225         230         235         240
Glu Asp His Gln Lys Lys Met Gly Leu Ile Val Val Gly Arg Glu Leu
245         250         255
Phe Phe Leu Lys Lys His Arg Arg Ala Leu His Lys Thr Ala Thr Pro
260         265         270
Val Tyr Lys Thr Asn Thr Ser Gly Leu Ser Lys Thr Thr Gln Ser Ile
275         280         285

```

575

```

Val Val Leu Asn Glu Ser Leu Ser Ile Asn Glu Asp Met Ser Ser Val
 290                               295                               300
Ile Phe Asp Val Ser Met Gln Met Asp Leu Gly Leu Leu Leu Tyr Asp
305                               310                               315                               320
Phe Asp Pro Asn Lys His Tyr Lys Asn Glu Ile Val Asn His Tyr Glu
                               325                               330                               335
Asn Leu Ala Asn Thr Phe Asn Arg Lys Ile Glu Ile Phe Gln Thr Asp
                               340                               345                               350
Ile Lys Asn Pro Ile Met Tyr Leu Asn Ser Leu Arg Asn Pro Ile Leu
                               355                               360                               365
His Phe Met Pro Phe Glu Glu Cys Ile Thr Gln Thr Arg Tyr Leu Trp
                               370                               375                               380
Phe Leu Ser Thr Lys Val Glu Lys Leu Ala Phe Leu Asn Asp Asp His
385                               390                               395                               400
Pro Gln Ile Phe Ile Pro Val Ala Glu
                               405

```

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...64

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

```

Pro Asn Glu Ala Ser Ala Ala Val Asn Val Gly Tyr Lys Ile Ser Lys
 1                               5                               10                               15
Ser Leu Thr Ala Ser Val Lys Leu Glu Tyr Leu Gly Val Met Thr His
                               20                               25                               30
Ser Gly Phe Thr Val Gly Ser Tyr Arg Pro Thr Pro Gly Ser Lys Ala
                               35                               40                               45
Leu Tyr Ser Asp Arg Ser His Leu Met Thr Thr Leu Ser Ala Lys Val
50                               55                               60

```

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

```

Ser Ile Val Tyr Gly Lys Asn Lys Leu Phe Ser Asp Glu Phe Tyr Glu
1           5           10           15
Lys Ile Glu Asp Ile Leu Thr Asn Asn Asn Pro Arg Tyr Lys Gln Val
          20           25           30
Cys Ile Ile Phe Asp Ala Asp Ile Lys Lys Glu Asn Gln Glu Ser Asp
          35           40           45
Ala Gly Phe Asp Asn Lys Leu Lys His Ile Arg Glu Lys Phe Lys Glu
          50           55           60
Lys Gly Thr Asp Phe Pro Lys Glu Gln Ile Phe Tyr Ser Leu Thr Ile
65           70           75           80
Lys Met Met Ala Ile
          85

```

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

```

Val Gln Ala Phe Asp Tyr Lys Ile Glu Val Leu Ala Glu Ser Phe Ser
1           5           10           15
Lys Val Gly Phe Asn Lys Lys Lys Ile Asp Ile Ala Arg Gly Ile Tyr
          20           25           30
Pro Thr Glu Thr Phe Val Thr Ala Val Gly Gln Gly Asn Ile Tyr Ala
          35           40           45
Asp Phe Leu Ser Lys Ser Leu Lys Asp Gln Gly His Val Leu Glu Gly
          50           55           60
Lys Val Gly Gly Thr Ile Gly Gly Ile Ala Tyr Asp Ser Thr Lys Phe
65           70           75           80
Asn Gln Gly Gly Ser Val Ile Tyr Asn Tyr Ile Gly Tyr Trp Asp Gly
          85           90           95
Tyr Leu Gly Gly Lys Arg Ala Leu Leu Asp Gly Thr Ser Ile His Glu
          100          105          110
Cys Ala Leu Gly Ser Asp Gly Lys Val Ile Asp Ser Ile Ala Cys Gly

```


245

(2) INFORMATION FOR SEQ ID NO:656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

```

Phe Ser Gln Arg Thr Asn Leu Leu Phe Pro Asn Asn Gln Asp Asp Gly
1          5          10          15
Asp Leu Glu Thr Leu Leu Leu Glu Ile Ala Lys His Asp Glu Phe Leu
          20          25          30
Lys Cys Phe Glu Gly Tyr Leu Glu Cys Ile Lys Ser Lys Glu His Tyr
          35          40          45
Lys Pro Ile Lys Asn Ile Arg Lys Asn Met Leu Tyr Ala Tyr Leu Glu
          50          55          60
Ala Leu Gly Leu Glu Asn Leu Thr Lys Thr Asn Ile Asp Val Phe Asp
65          70          75          80
Ser Lys Gly Lys Ile Lys Ser Arg Tyr Glu Glu Asn Tyr Lys Lys Leu
          85          90          95
Thr Glu Glu Val Ile Asp Phe Ser Ser Asn Ser Leu Ile Pro Leu Lys
          100          105          110
Asn Phe Leu Gly Gln Phe Ala Glu Asn Lys Gln Lys Thr Asn Pro Lys
          115          120          125
Ile Phe
          130

```

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

```

Ile Tyr Phe Ser Ala Lys Arg Phe Asn Thr Lys Asn Thr His Gly Thr
1           5           10           15
Gly Cys Thr Leu Ser Ser Leu Ile Val Gly Leu Leu Ala Gln Gly Leu
          20           25           30
Asp Leu Lys Asn Ala Ile Thr Lys Ala Lys Glu Leu Leu Thr Ile Ile
          35           40           45
Ile Gln Asn Pro Leu Asn Ile Gly His Gly His Gly Pro Leu Asn Leu
          50           55           60
Trp Ser Ile Lys Lys His Val
65           70

```

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

```

Arg Pro Ser Phe Gln Lys Arg Cys Ala His Phe Asn Ala Thr Leu Pro
1           5           10           15
Ile Leu Leu Lys Val Leu Glu Lys Gln Asp Lys Asp Leu Phe Leu Leu
          20           25           30
Gln Val Gly Asn Arg Ile Ile Pro Thr Lys Ser Glu Gln Glu Leu Lys
          35           40           45
Ile Asn Gln Pro Tyr Phe Ala Thr Met Gln Arg Asn Gln Leu Gly Asp
          50           55           60
Ile Val Leu Lys Asn Leu Val Pro Ala Pro Lys Ile Leu Asp Ala Leu
65           70           75           80
Asp Asp Leu Pro Val Ile Glu Met Lys Lys Leu Lys Glu Ile Leu Ser
          85           90           95
Ala Lys Asp Asn Thr Pro Leu Lys Glu Tyr Lys Glu Leu Leu Ser Glu
          100          105          110
Lys Leu Ile His Ala Lys Ser Ser Gln Glu Phe Leu Asn Thr Ala Asn
          115          120          125
Met Leu Leu Ser Leu Gln Ser Gln Val Leu Ser Phe Val Val Glu Asn
          130          135          140
Glu Arg Lys Lys Ala Phe Leu Gln Met Lys Ala Lys Lys Gln Ser Val
145          150          155          160
Asp Phe Tyr Ala Leu Tyr Pro Asn Leu Gly Glu Ile Gly Gly Val Ile
          165          170          175

```

580

Tyr Leu Lys Glu Lys Glu Lys Gln Leu Phe Leu Lys Thr Thr Leu Gln
 180 185 190
 Arg Thr Lys Glu Val Leu Lys Glu Ala Gln Asn Thr Leu Leu Gly Phe
 195 200 205
 Ser Phe Val Glu Ile Val Cys Glu Lys Thr Pro Met Leu Phe Ala Phe
 210 215 220
 Glu Asp Arg Leu Leu Asp Thr Leu Gly
 225 230

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

Leu Leu Glu Met Ile Phe Arg Ser Arg Arg Ser Lys Trp Gly Ala Leu
 1 5 10 15
 Cys Asn Ala Gln Ile Ile Glu Cys Val Ala Asn Ala Leu Glu Thr Cys
 20 25 30
 Asp Phe Gly Leu Cys Val Leu Asp Pro Val Met Val Ala Lys Asn Gly
 35 40 45
 Ala Leu Leu Leu Glu Glu Glu Ala Ile Leu Ser Leu Lys Lys Arg Leu
 50 55 60
 Leu Pro Lys Thr Asn Leu Leu Thr Pro Asn Leu Pro Glu Val Tyr Ala
 65 70 75 80
 Leu Thr Gly Val Gln Ala Arg Asp Asp Lys Ser Ala Ser Lys Ala Met
 85 90 95
 Gly Val Leu Arg Asp Leu Gly Val Lys Asn Ala Val Ile Lys Gly Gly
 100 105 110
 His Thr Glu His Phe Gln Gly Glu Phe Ser Asn Asp Trp Val Phe Leu
 115 120 125
 Glu Asp Ala Glu Phe Thr Leu Ala Pro Ser Asp Ser Thr Pro Lys Thr
 130 135 140
 Arg Met Ala Arg Val Val Leu Cys Leu Ala
 145 150

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

```

Trp Leu Gln Ser Arg Cys Phe Arg Asp Ser Ala Phe Cys Leu Ser Ser
1           5           10           15
Glu Lys Leu Phe Gly Lys Asn Leu Asn Lys Val Val Ile Leu Ala Leu
20           25           30
Arg Asp Ile Ile His Glu Tyr Gly His Thr Leu Gly Tyr Thr His Asn
35           40           45
Gly Asn Met Thr Tyr Gln Arg Val Arg Leu Cys Gln Glu Gly Asn Gly
50           55           60
Pro Glu Ala Arg Cys Glu Gly Gly His Glu Val Glu Lys Asn Gly Lys
65           70           75           80
Glu Glu Leu Glu Phe Ser Asn Gly His Glu Val Arg Asp His Asp Gly
85           90           95
Tyr Thr Tyr Asp Val Cys Ser Arg Phe Gly Gly Lys Asn Gln Pro Ala
100          105          110
Phe Pro Ser Asn Tyr Pro Asn Ser Ile Tyr Thr Asn Cys Ala Gln Val
115          120          125
Pro Ala Gly Leu Ile Gly Val Thr Thr Ala Val Trp Gln Gln Leu Ile
130          135          140
Asn Gln Asn Ala Leu Pro Ile Asn Phe Ala Asn Leu Asn Ser Gln Thr
145          150          155          160
Ser His Leu Asn Ala Gly Leu Asn Ala Gln Asn Phe Ala Thr Ser Met
165          170          175
Val Ser Ala Ile Ala Gln Asn Phe Ser Thr Thr Ser Thr Thr Thr Tyr
180          185          190
Arg Ser Ser Ser Lys Asn Phe Arg Ser Pro Ile Leu Gly Val Asn Val
195          200          205
Lys Ile Gly Tyr Gln His Tyr Phe Asn Asp Tyr Ile Gly Leu Ala Tyr
210          215          220
Tyr Gly Ile Ile Gln Tyr Asn Tyr Ala Gln Ala Asn Asp Glu Lys Ile
225          230          235          240
Gln Gln Leu Ser Tyr Gly Gly Gly Met Asp Val Leu Phe Asp Phe Ile
245          250          255
Thr Thr Tyr Thr Asn Lys Lys Gln Asp His Pro Thr Lys Lys Val Phe
260          265          270
Ala Ser Ser Phe Gly Val Phe Gly Gly Leu Arg Gly Leu Tyr Asn Ser
275          280          285
Tyr Tyr Val Phe Asn Gln Val Lys Gly Ser Gly Asn Leu Asp Ile Val
290          295          300
Thr Gly Phe Asn Tyr Arg Tyr Lys His Ser Lys Tyr Ser Ile Ala Leu
305          310          315          320
Ala Phe Leu

```

(2) INFORMATION FOR SEQ ID NO:661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

```

Tyr Asp Phe Leu Gly Val Ser Leu His Ala Leu Ser Pro Leu Glu Glu
1          5          10          15
Gln Glu Phe Leu Ile Ser Tyr Arg Leu Lys Ile Val Asp Ser Arg Val
20          25          30
Met Gly Glu Glu Tyr Ser Val Ser Lys Pro Ile Val Ser Arg Ile Lys
35          40          45
Thr Ala Pro Tyr Val Leu Asp Tyr His Cys Ser Ile Ile Thr Arg Asn
50          55          60
Leu Pro Asp Leu Lys Asn Pro Leu Leu Gln Ile Lys Leu Glu Arg Phe
65          70          75          80
Leu Leu Glu Ile Ala Leu Lys Lys Glu Lys Glu Arg Val Ile Asp Cys
85          90          95
Leu Leu Lys Ser Gln Val Ala Ile Thr His Tyr Asp His Ser Tyr Lys
100         105         110
Asn Gly Thr Thr Thr Thr Ser Ile Leu Asn Leu Lys Ala Leu Ser Val
115         120         125
Lys Ala Ser Leu Asp Gly Arg Tyr Ala Val Phe Arg Tyr Phe
130         135         140

```

(2) INFORMATION FOR SEQ ID NO:662:

(i)- SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

Glu Trp Leu Met Leu Lys Lys Ile Phe Tyr Gly Phe Ile Val Leu Phe
 1 5 10 15
 Leu Ile Ile Val Gly Leu Leu Ala Val Leu Val Ala Gln Val Trp Val
 20 25 30
 Thr Thr Asp Lys Asp Ile Ala Lys Ile Lys Asp Tyr Arg Pro Ser Val
 35 40 45
 Ala Ser Gln Ile Leu Asp Arg Lys Gly Arg Leu Ile Ala Asn Ile Tyr
 50 55 60
 Asp Lys Glu Phe Arg Phe Tyr Ala Arg Phe Glu Glu Ile Pro Pro Arg
 65 70 75 80
 Phe Val Glu Ser Leu Leu Ala Val Glu Asp Thr Leu Phe Phe Glu His
 85 90 95
 Gly Gly Ile Asn Leu Asp Ala Val Met Arg Ala Met Ile Lys Asn Ala
 100 105 110
 Lys Ser Gly Arg Tyr Thr Glu Gly Ser Thr Leu Thr Gln Gln Leu
 115 120 125
 Val Lys Asn Met Val Leu Thr Arg Glu Lys Thr Leu Thr Arg Lys Leu
 130 135 140
 Lys Glu Ala Ile Ile Ser Ile Arg Ile Glu Lys Val Leu Ser Lys Glu
 145 150 155 160
 Glu Ile Leu Glu Arg Tyr Leu Asn Gln Thr Phe Phe Gly His Gly Tyr
 165 170 175
 Tyr Gly Val Lys Thr Ala Ser Leu Gly Tyr Phe Lys Lys Pro Leu Asp
 180 185 190
 Lys Leu Thr Leu Lys Glu Ile Thr Met Leu Val Ala Leu Pro Arg Ala
 195 200 205
 Pro Ser Phe Tyr Asp Pro Thr Lys Asn Leu Glu Phe Ser Leu Ser Arg
 210 215 220
 Ala Asn Asp Ile Leu Arg Arg Leu Tyr Ser Leu Gly Trp Ile Ser Ser
 225 230 235 240
 Asn Glu Leu Lys Ser Ala Leu Asn Glu Val Pro Ile Val Tyr Asn Gln
 245 250 255
 Thr Ser Thr Gln Asn Ile Ala Pro Tyr Val Val Asp Glu Val Leu Lys
 260 265 270
 Gln Leu Asp Gln Leu Asp Gly Leu Lys Thr Gln Gly Tyr Thr Ile Lys
 275 280 285
 Leu Thr Ile Asp Leu Asp Tyr Gln Arg Leu Ala Leu Glu Ser Leu Arg
 290 295 300
 Phe Gly His Gln Lys Ile Leu Glu Lys Ile Ala Lys Glu Lys Pro Lys
 305 310 315 320
 Thr Asn Ala Ser Asn Asp Lys Asp Glu Asp Asn Leu Asn Ala Gln His
 325 330 335
 Asp Ser Tyr Arg Asn Glu His Arg
 340

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

```

Thr Pro Ser Met Ile Val Thr Glu Thr Ser Thr Gly Lys Ile Leu Ala
1          5          10          15
Leu Val Gly Gly Ile Asp Tyr Lys Lys Ser Ala Phe Asn Arg Ala Thr
          20          25          30
Gln Ala Lys Arg Gln Phe Gly Ser Ala Ile Lys Pro Phe Val Tyr Gln
          35          40          45
Ile Ala Phe Asp Asn Gly Tyr Ser Thr Thr Ser Lys Ile Pro Asp Thr
          50          55          60
Ala Arg Asn Phe Glu Asn Gly Asn Tyr Ser Lys Asn Ser Val Gln Asn
65          70          75          80
His Ala Trp His Pro Ser Asn Tyr Thr Arg Lys Phe Leu Gly Leu Val
          85          90          95
Thr Leu Gln Glu Ala Leu Ser His Ser Leu Asn Leu Ala Thr Ile Asn
          100          105          110
Leu Ala Ile Ala Trp
          115

```

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix)- FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

```

Pro Arg Asp His Thr Tyr Ser Leu Glu Asp Ser Thr Pro His Gly Ser
1          5          10          15
Leu Leu Gly Arg Asn Gly Val Thr Leu Asn Ile Arg Gln Val Phe Trp
          20          25          30
Trp Asp Asn Phe Asn Trp Ser Ile Gly Phe Tyr Asn Thr Phe Gly Asn
          35          40          45
Ser Asp Ala Phe Leu Gly Ser His Thr Met Pro Arg Gly Asn Asn Thr
          50          55          60
Ser Tyr Ile Ser Asn Glu Ile Ser Val Thr Thr Arg His Ala Gly Met
65          70          75          80
Ile Gly Tyr Asp Phe Trp Asp Asn Thr Ala Tyr Asp Gly Leu Ala Asp

```

										85					90					95				
Ala	Ile	Thr		Asn	Ala	Asn	Thr	Phe	Thr	Phe	Tyr	Thr	Ser	Val	Gly	Gly								
				100						105						110								
Ile	His	Lys	Arg	Phe	Ala	Trp	His	Val	Phe	Gly	Arg	Val	Ser	His	Ala									
				115						120						125								
Asn	Lys	Asn	Ala	Leu	Gly	Gln	Val	Gly	Arg	Ala	Asn	Glu	Tyr	Ser	Leu									
				130						135						140								
Gln	Phe	Asn	Ala	Ser	Tyr	Ala	Ser	Thr	Glu	Ser	Val	Leu	Leu	Asn	Phe									
				145						150						155								
Arg	Ile	Thr	Tyr	Tyr	Gly	Ala	Arg	Ile	Asn	Lys	Gly	Tyr	Gln	Ala	Gly									
				165						170						175								
Tyr	Phe	Gly	Ala	Pro	Lys	Phe	Asn	Asn	Pro	Asp	Gly	Asp	Phe	Ser	Ala									
				180						185						190								
Asn	Tyr	Gln	Asp	Arg	Ser	Tyr	Met	Met	Thr	Asn	Leu	Thr	Leu	Lys	Phe									
				195						200						205								

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

[illegible]

(2) INFORMATION FOR SEQ ID NO:666:

586

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...122
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

```

Arg Arg Ser Leu Tyr Tyr Val Phe Ile Lys Ser Tyr Ala Ile Leu Ala
1           5           10           15
Glu Ala Thr Ala Arg Phe Ala Gly Asp Tyr Ala Thr Glu Asn Leu Thr
          20           25           30
Ser Arg Ile Ala Leu Pro Cys Ser Asp Tyr Val Gly Arg Val Ile Gly
          35           40           45
Lys Asp Gly Lys Asn Ile Glu Ala Phe Lys Lys Ile Ser Gly Val Asp
          50           55           60
Ile Glu Phe Ser Glu Asp Ser Ser Glu Leu Cys Leu Ser Ser Phe Asn
65           70           75           80
Ile Tyr Arg Arg Glu Val Ala Ser Glu Thr Ile Lys Ile Leu Ile Glu
          85           90           95
Asp Gly Arg Ile Gln Pro Asn Arg Ile Glu Glu Val Tyr Pro Lys Ile
          100          105          110
His Pro Gln His Gly Lys Arg Ile Ala Phe
          115          120

```

(2) INFORMATION FOR SEQ ID NO:667:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...250
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

```

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

```


587

```

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

```

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

```

Ser Leu Trp Leu Lys Ser Lys Phe Phe Leu Leu Met Gly Val Gly Leu
1              5              10              15
Leu Ser His Ser Leu Asn Ala Leu Ser Leu Thr Leu Thr Gln Gly Lys
      20              25              30
Glu Glu Gly Glu Asp Phe Ser Val Leu Thr Leu Arg Asn Asp Lys Ala
      35              40              45

```

Phe Ser Cys Ser Tyr Ala Asn Glu Lys Pro Pro Ser Gly Ile Glu Ala
 50 55 60
 Ser Leu Ser Ile Ile His Ala Lys Arg Pro Ile Glu Cys Val Ile Asp
 65 70 75 80
 Ser Ile Pro Lys Glu Gly Phe Thr Pro Leu Glu Asn Ala Phe Phe Asn
 85 90 95
 Ile Thr Tyr Ser Met Arg Gln Gln Gln Phe Ile Leu His Ile Lys Pro
 100 105 110
 Lys Val Met Arg Arg Leu Thr Leu Phe Ser Phe Asp Arg Asp Tyr Lys
 115 120 125
 Lys Ala Ile Pro Leu Phe Val Glu Asn Asp Ala Lys Ala Lys Met Trp
 130 135 140
 Gln Ile Ile Gly Tyr Asp Gln Lys Ile Pro Phe Leu Ser Glu Lys Asp
 145 150 155 160
 Asn Ala Gln Lys Gly Leu Asn Phe Pro Ile Ile Ile Lys Asp Ala Gln
 165 170 175
 Thr Pro Ile Ile Gln Glu Leu Asp Val Asn Asn Lys Pro Leu Leu Thr
 180 185 190
 Thr Lys Gly Tyr Asp Leu Asn Ala Tyr Leu Glu Ala Lys Lys Gln Met
 195 200 205
 Asp Ser Gln Ala Tyr Phe Asp Ala Leu Arg Thr Ile Ser Arg Ala Phe
 210 215 220
 Lys Asn Tyr Pro Gln Thr Ile Phe Lys Lys Asp Leu Tyr Leu Leu Glu
 225 230 235 240
 Ile Ile Ala Leu Gly Lys Leu Gly Ile Lys Lys Ser Leu Leu Ile Asp
 245 250 255
 Ile Gly Thr Gln Trp Ile Lys Asn Tyr Pro Thr Asp Pro Asn Ile Pro
 260 265 270
 Glu Ala Leu Tyr Tyr Val Ala Lys Ala Leu Asp Glu Asn Asn Asn Tyr
 275 280 285
 Lys Gln Ala Val Arg Tyr Tyr Lys Arg Ile Leu Leu Glu Tyr Lys Asn
 290 295 300
 Ser Arg Tyr Ala Pro Leu Ala Gln Met Arg Leu Ala Ile Glu Ala Ala
 305 310 315 320
 Glu Gly Ser Asp Leu Ser Asn Ala Asn Met Leu Phe Lys Glu Ala Phe
 325 330 335
 Ser Asn Ala Lys Asp Lys Glu Ser Ala Ser Glu Ile Ala Leu Asn Trp
 340 345 350
 Ala Glu Ala Glu Ile Asn Tyr Gln Asn Phe Asn Asn Ala Lys Tyr Leu
 355 360 365
 Ile Asp Lys Val Val Gln Ser Asn Pro Asp Tyr Leu Ser Met His Ser
 370 375 380
 Glu Leu Ala Leu Glu Leu Leu Lys Leu Leu Lys Lys Asn Gln Met Asn
 385 390 395 400
 Glu Ser Ala Ile Glu Ile Ala His Leu Leu Leu Asn Gln Asp Asp Asp
 405 410 415
 Leu Lys Ala Lys Glu Gln Ala Leu Tyr Asp Leu Gly Ala Leu Tyr Ala
 420 425 430
 Arg Ile Lys Asp Phe Lys Asn Ala His Leu Tyr Asn Leu Gln Tyr Leu
 435 440 445
 Gln Asp His Ala Glu Leu Glu Arg Ala Ser Val Val Arg Ala Arg Asp
 450 455 460
 Glu Lys Ala Leu Phe Ser Met Glu Gly Asn Thr Gln Glu Lys Ile Ala
 465 470 475 480
 His Tyr Asp Lys Ile Ile Gln Asn Phe Pro Asn Ser Asn Glu Ala Gln
 485 490 495
 Lys Ala Leu Glu Leu Lys Ala Gln Leu Leu Phe Asp Asn Lys His Tyr

589

	500		505		510
Ala	Glu Val Leu Gly Met Gln Lys Asn Leu Pro Lys Asp Ser Pro Leu				
	515		520		525
Ile	Gln Lys Thr Leu Asn Ile Leu Ala Lys Thr Pro Leu Glu Asp His				
	530		535		540
Arg	Cys Lys Glu Ala Leu Lys Tyr Leu Ser Gln Ile Thr Ala Phe Ala				
545		550		555	560
Phe	Asn Pro Gln Glu Ile Gln Ala Phe Asp Cys Leu Tyr Phe Ala				
	565		570		575
Ser	Leu Lys Glu Lys Ala Gln Ile Ile Ala Leu Asn Ala Leu Lys Ala				
	580		585		590
Ala	Lys Thr Pro Ser Glu Lys Leu Thr Trp Leu Tyr Arg Leu Gly Arg				
	595		600		605
Asn	Tyr Tyr Arg Leu Gly Asp Phe Lys Asn Ser Thr Leu Ala Ser Lys				
610		615		620	
Asp	Ala Leu Ile Leu Ala Gln Ser Leu Asn Lys Lys Glu Phe Tyr Asp				
625		630		635	640
Ile	Ala Phe Val Leu Phe Ser Asp Tyr Met Gln Asn Asn Glu Lys Gly				
	645		650		655
Leu	Ala Leu Asn Leu Tyr Ala Phe Leu Glu Lys His Phe Lys Asp Asp				
	660		665		670
Lys	Arg Met Ala Leu Val Tyr Phe Lys Leu Leu Glu Asn Glu Lys Asp				
	675		680		685
Pro	Lys Ser Val Lys Ile Tyr Ala Thr Ser Leu Leu Lys Leu Gln Asp				
	690		695		700
Ala	Tyr Lys Asp Tyr Ser Tyr Thr Pro Phe Gly Glu Phe Ala Leu Ile				
705		710		715	720
Asp	Ala Tyr Arg Thr Thr Lys Asp Tyr Ser Lys Ala Leu Glu Thr Leu				
	725		730		735
Asp	Lys Leu Leu Asn Arg Arg Leu Ser Leu Glu Asp His Gln Lys Ala				
	740		745		750
Leu	Tyr Leu Gln Ser Ser Leu Leu Asp Leu Thr Asn Gln Lys Ala Lys				
	755		760		765
Ser	Lys Ala Ser Leu Glu Lys Cys Val Gln Leu Lys Gln Lys Asp Gln				
	770		775		780
Thr	Asn Ala Trp Gln Asn Leu Cys Glu Gln Gly Leu Asn Leu Phe Lys				
785		790		795	800
Asn	Lys Glu Ser				

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

Lys	His	Pro	Asn	Arg	Phe	Phe	Phe	Lys	Arg	Ile	Glu	Arg	Thr	Ala	Leu	1	5	10	15
Lys	Pro	Asn	Thr	Phe	Leu	Asn	Ala	Pro	Met	Gln	Lys	Pro	Gln	Asn	Lys	20	25	30	
Pro	Ser	Ser	Ser	Gln	Gln	Ser	Pro	Gln	Asn	Phe	Ser	Tyr	Pro	Glu	Ser	35	40	45	
Lys	Leu	Gly	Ser	Lys	Asn	Ser	Lys	Asn	Ser	Leu	Leu	Gln	Pro	Leu	Val	50	55	60	
Thr	Pro	Ser	Lys	Val	Ser	Pro	Thr	Asn	Glu	Val	Lys	Thr	Pro	Thr	Asn	65	70	75	80
Asp	Ala	Asn	Pro	Pro	Leu	Lys	His	Ser	Ser	Gln	Asp	Gln	Glu	Asn	Asn	85	90	95	
Leu	Phe	Val	Ala	Pro	Pro	Thr	Glu	Lys	Thr	Leu	Pro	Asn	Asn	Thr	Ser	100	105	110	
Ser	Ala	Asp	Ala	Ser	Glu	Asn	Asn	Glu	Ser	Asn	Glu	Asn	Arg	Asp	Asn	115	120	125	
Val	Glu	Lys	Gln	Ala	Ile	Arg	Asp	Pro	Asn	Ile	Lys	Glu	Phe	Ala	Cys	130	135	140	
Gly	Lys	Trp	Val	Tyr	Asp	Asp	Glu	Asn	Leu	Gln	Ala	Tyr	Arg	Pro	Ser	145	150	155	160
Ile	Leu	Lys	Arg	Val	Asp	Lys	Asp	Lys	Glu	Ile	Thr	Thr	Asp	Ile	Thr	165	170	175	
Pro	Cys	Asp	Tyr	Ser	Thr	Ala	Glu	Asn	Lys	Ser	Gly	Lys	Ile	Ile	Thr	180	185	190	
Pro	Tyr	Thr	Lys	Ile	Ser	Val	His	Lys	Thr	Glu	Pro	Leu	Glu	Asp	Pro	195	200	205	
Gln	Thr	Phe	Glu	Ala	Lys	Asn	Asn	Phe	Ala	Ile	Leu	Gln	Ala	Arg	Ser	210	215	220	
Ser	Thr	Glu	Lys	Cys	Lys	Arg	Ala	Arg	Ala	Arg	Lys	Asp	Gly	Thr	Thr	225	230	235	240
Arg	Gln	Cys	Tyr	Leu	Ile	Glu	Glu	Pro	Leu	Lys	Gln	Ala	Trp	Glu	Ser	245	250	255	
Glu	Tyr	Glu	Ile	Thr	Thr	Gln	Leu	Val	Lys	Ala	Ile	Tyr	Glu	Arg	Pro	260	265	270	
Lys	Gln	Asp	Asp	Gln	Val	Glu	Pro	Thr	Phe	Tyr	Glu	Thr	Ser	Glu	Leu	275	280	285	
Ala	Tyr	Ser	Ser	Thr	Arg	Lys	Ser	Glu	Ile	Thr	Arg	Asn	Glu	Leu	Asn	290	295	300	
Leu	Asn	Glu	Lys	Phe	Met	Glu	Phe	Val	Glu	Val	Tyr	Glu	Gly	His	Tyr	305	310	315	320
Leu	Asn	Asp	Ile	Ile	Lys	Glu	Ser	Ser	Glu	Tyr	Lys	Glu	Trp	Val	Lys	325	330	335	
Asn	His	Val	Arg	Phe	Lys	Glu	Arg	Val	Cys	Met	Ala	Leu	Lys	Ile	Lys	340	345	350	
Lys	Gln	Pro	Arg	Ala	Lys	Ser	Thr	Pro	Leu	Ser	Ile	Glu	Asn	Ser	Arg	355	360	365	
Val	Val	Cys	Val	Lys	Lys	Gly	Asn	Tyr	Leu	Phe	Asn	Glu	Val	370	375	380			

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid

591

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

```

Thr Lys Lys Leu Asn Asn Thr Leu Phe Asn Lys Gly Leu Ile Ile Phe
1           5           10           15
Lys Met Phe Lys Lys Ile Ile Phe Leu Cys Val Phe Leu Ile Gly Gly
20           25           30
Phe Val Ile Pro Pro Leu Glu Ala Met Pro Ile Leu Arg Asn Lys Thr
35           40           45
Pro Lys Lys Asn Tyr Gln Glu Ala His Glu Lys Leu Tyr Arg Ser Ile
50           55           60
Ile Asn Arg Gln Lys Leu Thr Arg Lys Lys Ser Gly Trp Tyr Phe Leu
65           70           75           80
Gly Gly Val Gly Ala Val Glu Ala Ile Lys Asp Tyr Gln Gly Lys Glu
85           90           95
Met Lys Asp Trp Met Pro Arg Ser Ile
100           105

```

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

```

Ser Lys Thr Ser Tyr Cys Asn Ser Tyr Lys Arg Lys Leu Leu Pro Tyr
1           5           10           15
His Phe Leu Leu Phe Pro Leu Trp Ala Cys Phe His Asn Val Ser Arg
20           25           30
Pro Phe Ser Leu Ser His Leu Phe Leu Val Lys Arg Pro Tyr Ser Arg
35           40           45
Leu Tyr Leu His Asn Gln Ser Asn His Lys Met Arg His His Ser Ile

```

50
Leu Phe Val Ser Phe
65

55

60

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

Gln	Asp	Lys	Gly	Leu	Leu	Leu	Ser	Val	Ala	Leu	Pro	Asn	Ser	Asn	Asn	1	5	10	15
Ala	Ser	Gln	Asn	Asn	Ile	Leu	Ser	Leu	Ser	Val	Leu	His	Asn	Gln	Ile	20	25	30	
Lys	Met	Ser	Tyr	Gly	Asn	Lys	Val	Met	Asp	Phe	Thr	Pro	Pro	Thr	Leu	35	40	45	
Gln	Asp	Tyr	Ile	Val	Gly	Ile	Gln	Gly	Gln	Ser	Ala	Leu	Asn	Gln	Ile	50	55	60	
Glu	Ala	Val	Gly	Gly	Asn	Asn	Ala	Ile	Lys	Trp	Leu	Ser	Thr	Leu	Met	65	70	75	80
Met	Glu	Thr	Lys	Glu	Asn	Pro	Leu	Phe	Ala	Pro	Ile	Tyr	Leu	Glu	Asn	85	90	95	
His	Ser	Leu	Asn	Glu	Ile	Leu	Gly	Val	Thr	Lys	Asp	Leu	Gln	Asn	Thr	100	105	110	
Ala	Ser	Leu	Ile	Ser	Asn	Pro	Asn	Phe	Arg	Asn	Asn	Ala	Thr	Ser	Leu	115	120	125	
Leu	Glu	Met	Ala	Ser	Tyr	Thr	Gln	Gln	Thr	Ser	Arg	Leu	Thr	Lys	Leu	130	135	140	
Ser	Asp	Phe	Arg	Ala	Arg	Glu	Gly	Glu	Ser	Asn	Phe	Ser	Glu	Arg	Leu	145	150	155	160
Leu	Glu	Leu	Lys	Asn	Lys	Arg	Phe	Ser	Asp	Pro	Asn	Pro	Ser	Glu	Val	165	170	175	
Phe	Val	Lys	Tyr	Ser	Gln	Leu	Ser	Lys	His	Pro	Asn	Asn	Leu	Trp	Ile	180	185	190	
Gln	Gly	Val	Gly	Gly	Ala	Ser	Phe	Ile	Ser	Gly	Gly	Asn	Gly	Thr	Leu	195	200	205	
Tyr	Gly	Leu	Asn	Val	Gly	Tyr	Asp	Arg	Leu	Val	Lys	Ser	Val	Ile	Leu	210	215	220	
Gly	Gly	Tyr	Val	Ala	Tyr	Gly	Tyr	Ser	Gly	Phe	Asn	Gly	Asn	Ile	Met	225	230	235	240
His	Ser	Leu	Ala	Asn	Asn	Val	Asp	Val	Gly	Met	Tyr	Ala	Arg	Ala	Phe	245	250	255	
Leu	Lys	Arg	Asn	Glu	Phe	Thr	Leu	Ser	Ala	Asn	Glu	Thr	Tyr	Gly	Gly				

```

                260                265                270
Asn Ala Ser His Ile Asn Ser Ser Asn Ser Leu Leu Ser Val Leu Asn
      275                280                285
Gln Arg Tyr Asn Tyr Asn Thr Trp Thr Thr Ser Val Asn Gly Asn Tyr
      290                295                300
Gly Tyr Asp Phe Met Phe Lys Gln Lys Ser Val Val Leu Lys Pro Gln
      305                310                315                320
Val Gly Leu Ser Tyr His Phe Ile Gly Leu Ser Gly Met Lys Gly Lys
      325                330                335
Met Gln Asn Pro Ala Tyr Gln Gln Phe Val Met His Ser Asn Pro Ser
      340                345                350
Asn Glu Ser Val Leu Thr Leu Asn Met Gly Leu Glu Ser Arg Lys Tyr
      355                360                365
Phe Gly Lys Asn Ser Tyr Tyr Phe Val Thr Ala Arg Leu Gly Arg Asp
      370                375                380
Leu Leu Ile Lys Ala Lys Gly Asp Asn Val Val Arg Phe Val Gly Glu
      385                390                395                400
Asn Thr Leu Leu Tyr Arg Lys Gly Glu Ile Phe Asn Thr Phe Ala Ser
      405                410                415
Val Ile Thr Gly Gly Glu Met His Leu Trp Arg Leu Met Tyr Val Asn
      420                425                430
Ala Gly Val Gly Leu Lys Met Gly Leu Gln Tyr Gln Asp Leu Asn Ile
      435                440                445
Thr Gly Asn Val Gly Met Arg Val Ala Phe
      450                455

```

(2) INFORMATION FOR SEQ ID NO:673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

```

Pro Phe Glu Ala Leu Asn Phe Tyr Ser Lys Lys Ala Leu Asn Glu Ile
1           5           10           15
Phe Ala Asn Ala Arg Lys Ile Cys Gly Asn Lys Pro Leu Gly Ala Asn
      20           25           30
Ile Leu Tyr Ala Ile Asn Asp Tyr Gly Arg Val Leu Arg Asp Ser Cys
      35           40           45
Glu Ala Gly Ala Asn Ile Ile Ile Thr Gly Ala Gly Leu Pro Thr Asn
      50           55           60
Met Pro Glu Phe Ala Lys Asp Phe Ser Asp Val Ala Leu Ile Pro Ile
      65           70           75           80
Ile Ser Ser Ala Lys Ala Leu Lys Ile Leu Cys Lys Arg Trp Ser Asp

```

594

				85						90					95				
Arg	Tyr	Lys	Arg	Ile	Pro	Asp	Ala	Phe	Ile	Val	Glu	Gly	Pro	Leu	Ser				
			100					105					110						
Gly	Gly	His	Gln	Gly	Phe	Lys	Tyr	Glu	Asp	Cys	Phe	Lys	Glu	Glu	Phe				
		115					120					125							
Gln	Leu	Glu	Asn	Leu	Val	Pro	Lys	Val	Val	Glu	Ala	Ser	Lys	Glu	Trp				
	130					135					140								
Gly	Asn	Ile	Pro	Ile	Ile	Ala	Ala	Gly	Gly	Ile	Trp	Asp	Arg	Lys	Asp				
145				150						155					160				
Ile	Asp	Thr	Met	Leu	Ser	Leu	Gly	Ala	Ser	Gly	Val	Gln	Met	Ala	Ile				
			165						170					175					
Ser	Phe	Phe	Arg	His	Glu	Arg	Met	Arg	Arg										
			180					185											

(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

Ala	Ile	Arg	Leu	Arg	Leu	Ser	Ile	Arg	Gly	Leu	Ile	Lys	Arg	Ile	Glu				
1				5					10					15					
Glu	Gly	Asn	Ala	Pro	Lys	Ile	Ala	Cys	Val	Ser	Asn	Cys	Val	Thr	Pro				
			20					25					30						
Cys	Asn	Arg	Gly	Glu	Glu	Thr	Lys	Lys	Val	Gly	Tyr	Cys	Ile	Ala	Asp				
	35					40					45								
Gly	Leu	Gly	Arg	Ser	Tyr	Leu	Gly	Asn	Arg	Glu	Glu	Gly	Leu	Tyr	Phe				
	50					55				60									
Thr	Gly	Ala	Asn	Gly	Tyr	Arg	Val	Asp	Lys	Ile	Ile	Ser	Val	His	Glu				
65				70					75					80					
Leu	Ile	Lys	Glu	Leu	Thr	Glu	Gly												
				85															

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

595

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

```

Asn Phe Asn Gln Arg Ala Phe Leu Lys Arg Ala Leu Trp Leu Ile Leu
1           5           10           15
Gly Leu Phe Tyr Ala Leu Asn Ala Glu Ser Phe Lys Asp Val Leu Thr
          20           25           30
Lys Gly Asp Tyr Thr Phe Phe Asn Lys Lys Val Val Ser Pro Ile Lys
          35           40           45
Arg Tyr Ala Asp Arg Ser Ala Phe Tyr Leu Gly Leu Gly Tyr Gln Leu
          50           55           60
Gly Ser Ile Gln His Asn Ser Ser Asn Leu Asn Leu Ser Gln Arg Phe
65           70           75           80
Asn Lys Ser Gln Ile Ile Phe Ser Asp Ser Leu Ser Pro Val Phe Lys
          85           90           95
Asn Ser Tyr Val Ser Asn Gly Leu Gly Val Gln Val Gly Tyr Lys Trp
          100          105          110
Val Gly Lys His Glu Glu Thr Lys Trp Phe Gly Phe Arg Trp Gly Leu
          115          120          125
Phe Tyr Asp Leu Ser Ala Ser Leu Tyr Gly Ser Gln Glu Ser Gln Ser
130          135          140
Ile Ile Ile Ser Thr Tyr Gly Thr Tyr Met Asp Leu Leu Leu Asn Ala
145          150          155          160
Tyr Asn Gly Asp Lys Phe Phe Ala Gly Phe Asn Leu Gly Ile Ala Phe
          165          170          175
Ala Gly Val Tyr Asp Arg Leu Ser Asp Ala Leu Leu Tyr Gln Thr Leu
          180          185          190
Leu Gln Asn Thr Phe Gly Gly Lys Val Asn Leu Asn Gly Phe Gln Phe
          195          200          205
Leu Val Asp Leu Gly Val Arg Leu Gly Asn Glu His Asn Gln Phe Gly
          210          215          220
Phe Gly Ile Lys Ile Pro Thr Tyr Tyr Phe Asn His Tyr Tyr Ser Met
225          230          235          240
Asn Asn Ile Ser Asn Asn Ser Glu Asn Val Leu Lys Val Leu Arg Phe
          245          250          255
Leu Glu Tyr Gly Ile Asn Ser Leu Leu Tyr Gln Val Asp Phe Arg Arg
          260          265          270
Asn Tyr Ser Val Tyr Phe Asn Tyr Thr Tyr Ser Phe
          275          280

```

(2) INFORMATION FOR SEQ ID NO:676:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

```

Lys Met His Thr Ser Phe Phe Gln Ile Pro Leu Asn Phe Gly Val Arg
1           5           10           15
Val Asn Val Asp Arg His Asn Gly Phe Glu Met Gly Leu Lys Ile Pro
          20           25           30
Leu Ala Val Asn Ser Phe Tyr Glu Thr His Gly Lys Gly Leu Asn Ala
          35           40           45
Ser Leu Phe Phe Lys Arg Leu Val Met Phe Asn Val Ser Tyr Val Tyr
          50           55           60
Ser Phe
65

```

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

```

Ile Lys Arg Ile Ile Lys Ser Asn Ala Ser Leu Asn Gln Leu Asn Thr
1           5           10           15
Thr Arg Tyr Asn Thr Pro Ser His Leu Phe Phe Lys Lys Gly Val Gly
          20           25           30
Met Ala Thr Ile Gln Pro Phe Asn His Ser Thr Ile Gln Pro Phe Asn
          35           40           45
His Ser Thr Ile Gln Pro Phe Asn His Ser Ile Ile Gln Ser Phe Asn
          50           55           60
His Ser Thr Ile Gln Ala Thr Leu Pro Tyr Phe Tyr Asn Tyr Leu Ser
65           70           75           80
Phe Tyr Lys Asn Leu Phe Lys Asn Pro Leu Phe Phe Ile Ile Pro Pro
          85           90           95
Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro
          100          105          110
Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro
          115          120          125

```

Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile
130 135

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

```

Arg Tyr His His Phe Ser Gly Leu Ser Ser Cys Gly Phe Ser Ala Gln
1          5          10          15
Cys Gly Cys Gly His Val Ala Ser His Ser Leu Trp His Gln Leu Trp
20          25          30
Pro Trp Pro Asn Leu Gly Pro Glu His Leu Glu Asn Gly Gly Val Arg
35          40          45
Ser Phe Asp Asn Thr Pro Asn Tyr Ser Tyr Asn Thr Gly Ser Gly Thr
50          55          60
Thr Thr Thr Thr Cys Asn Gly Ala Ser Asn Val Gly Pro Asn Gly Ile
65          70          75          80
Leu Ser Ser Ser Glu Tyr Gln Val Leu Asn Thr Ala Tyr Gln Thr Ile
85          90          95
Gln Thr Ala Leu Asn Gln Asn Gln Gly Gly Met Pro Ala Leu Asn
100         105         110
Ser Ser Lys Asn Met Val Val Asn Ile Asn Gln Thr Phe Thr Lys Asn
115         120         125
Pro Thr Thr Glu Tyr Thr Tyr Pro Asp Gly Asn Gly Asn Tyr Tyr Ser
130         135         140
Gly Gly Ser Ser Ile Pro Ile Gln Leu Lys Ile Ser Ser Val Asn Asp
145         150         155         160
Ala Glu Asn Leu Leu Gln Gln Ala Ala Thr Ile Ile Asn Val Leu Thr
165         170         175
Thr Gln Asn Pro His Val Asn Gly Gly Gly Gly Val Met Gly Val Trp
180         185         190
Arg

```

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

598

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

```

Met Val Val Val Gly Ser Trp Gly Phe Gly Gly Lys Thr Gly Asn Val
1      5      10      15
Met Asp Ile Phe Gly Asp Ser Phe Asn Ala Ile Asn Glu Met Ile Lys
20     25     30
Asn Ala Gln Ala Val Leu Glu Lys Thr Gln Gln Leu Asn Ala Asn Glu
35     40     45
Asn Thr Gln Ile Thr Gln Pro Asp Asn Phe Asn Pro Tyr Thr Ser Lys
50     55     60
Asp Thr Gln Phe Ala Gln Glu Met Leu Asn Arg Ala Asn Ala Gln Ala
65     70     75     80
Glu Ile Leu Ser Leu Ala Gln Gln Val Ala Asp Asn Phe His Ser Ile
85     90     95
Gln Gly Pro Ile Gln Gln Asp Leu Glu Glu Cys Thr Ala Gly Ser Ala
100    105    110
Gly Val Ile Asn Asp Asn Thr Tyr Gly Ser Gly Cys Ala Phe Val Lys
115    120    125
Glu Thr Leu Asn Ser Leu Glu Gln His Thr Ala Tyr Tyr Gly Asn Gln
130    135    140
Val Asn Gln Asp Arg Ala Leu Ser Gln Thr Ile Leu Asn Phe Lys Glu
145    150    155    160
Ala Leu Ser Thr Leu Gly Asn Asp Ser Lys Ala Ile Asn Ser Gly Ile
165    170    175
Ser Asn Leu Pro Asn Ala Lys Ser Leu Gln Asn Met Thr His Ala Thr
180    185    190
Gln Asn Pro Asn Ser Pro Glu Gly Leu Leu Thr Tyr Ser Leu Asp Thr
195    200    205
Ser Lys Tyr Asn Gln Leu Gln Thr Val Ala Gln Glu Leu Gly Lys Asn
210    215    220
Pro Phe Arg Arg Ile Gly Val Ile Asn Tyr Gln Asn Asn Asn Gly Ala
225    230    235    240
Met Asn Gly Ile Gly Val Gln Ala Gly Tyr Lys Gln Phe Phe Gly Lys
245    250    255
Lys Arg Asn Trp Gly Leu Arg Tyr Tyr Gly Phe Phe Asp Tyr Asn His
260    265    270
Ala Tyr Ile Lys Ser Asn Phe Phe Asn Ser Ala Ser Asp Val Trp Thr
275    280    285
Tyr Gly Val Gly Met Asp Ala Leu Tyr Asn Phe Ile Asn Asp Lys Asn
290    295    300
Thr Asn Phe Leu Gly Lys Asn Asn Lys Leu Ser Val Gly Leu Phe Gly
305    310    315    320
Gly Phe Ala Leu Ala Gly Thr Ser Trp Leu Asn Ser Gln Gln Val Asn
325    330    335
Leu Thr Met Met Asn Gly Ile Tyr Asn Ala Asn Val Ser Ala Ser Asn
340    345    350

```

599

```

Phe Gln Phe Leu Phe Asp Leu Gly Leu Arg Met Asn Leu Ala Arg Pro
    355                      360                      365
Lys Lys Lys Asp Ser Asp His Ala Ala Gln His Gly Met Glu Leu Gly
    370                      375                      380
Val Lys Ile Pro Thr Ile Asn Thr Asp Tyr Tyr Ser Phe Met Gly Ala
    385                      390                      395                      400
Glu Leu Lys Tyr Arg Arg Leu Tyr Ser Val Tyr Leu Asn Tyr Val Phe
    405                      410                      415
Ala Tyr

```

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

```

Ala Leu Ser Arg Cys Leu Ser Asp Arg Phe Asn Gln Tyr Pro Ala Leu
1      5      10      15
Gln Lys Thr Glu His His Phe Val Asp Phe Leu Asn Gln Asp Lys His
    20      25      30
Tyr Ala Ile Ile Gln Arg Ala Asp Lys Ser Ile Ser Ser Asn Glu Ala
    35      40      45
Leu Ala Arg Ser Leu Ile Gly Ala Tyr Val Leu Asn Arg Glu Ser Ile
    50      55      60
Asn Arg Ile Asp Asp Lys Ser Arg Tyr Glu Leu Val Arg Leu Gln Ser
    65      70      75      80
Ser Ser Lys Val Trp Gln Arg Phe Glu Asp Leu Ile Lys Ala Gln Asn
    85      90      95
Ser Ile Tyr Val Gln Ser His Leu Glu Arg Glu Val His Ile Val Asn
    100     105     110
Ile Ala Ile Tyr Gln Gln Asp Asn Asn Pro Ile Ala Ser Val Ser Ile
    115     120     125
Ala Ala Lys Leu Leu Asn Glu Asn Lys Leu Val Tyr Glu Lys Arg Tyr
    130     135     140
Lys Ile Val Leu Ser Tyr Leu Phe Asp Thr Pro Asp Phe Asp Tyr Ala
    145     150     155     160
Ser Met Pro

```

(2) INFORMATION FOR SEQ ID NO:681:

(i) SEQUENCE CHARACTERISTICS:

- 600

(A) LENGTH: 194 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

```

Ser Phe Lys Lys Asn Glu Arg Leu Leu Leu Val Ser Arg Phe Leu
1           5           10           15
Asn Ala Ile Asp Pro Phe Asn Leu Gly Val Leu Leu Ser Arg Phe Gln
20           25           30
Ile Lys Asn Gly Cys Ile Tyr Gly Val Cys Ser Tyr Lys Val Ser Lys
35           40           45
Phe Thr Pro Gly Tyr Glu Glu Ser Lys Ala Arg Val Leu Asn Ala Leu
50           55           60
Asn Ile Leu Ser Lys His Gln Ile Trp Gln Ser Asn Gln Glu Ser Val
65           70           75           80
Thr Lys Val Lys Gly Thr Phe Val Phe Ile Leu Glu Asn Asp Leu His
85           90           95
Leu Asp Glu Asn Ser Phe Tyr Lys Lys Leu Leu Asn Leu Ile Ile Asp
100          105          110
Asn Asp Phe Phe Asn Arg Ser His Leu Val Thr Pro Ser Asn Gly Thr
115          120          125
Asn Ser His Pro Glu Leu His Arg Ser Ile Thr Pro Arg Glu Ala Ala
130          135          140
Arg Ile Gln Ser Phe Ser Asp Asp Tyr Ile Phe Tyr Gly Asn Lys Thr
145          150          155          160
Ser Val Cys Lys Gln Ile Gly Asn Ala Val Pro Pro Leu Leu Ala Leu
165          170          175
Ala Leu Gly Lys Ala Ile Leu Lys Ser Ala Arg Asn Asp Thr Asn Pro
180          185          190
Ser Arg

```

(2) INFORMATION FOR SEQ ID NO:682:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

601

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

```

Met Gln Asp Asn Leu Val Ser Val Ile Glu Lys Gln Thr Asn Lys Lys
1           5           10           15
Val Arg Met Leu Glu Ile Lys Pro Leu Lys Ser Ser Gln Asp Leu Lys
          20           25           30
Met Val Val Ile Glu Asp Pro Asp Thr Lys Tyr Asn Ile Pro Leu Val
          35           40           45
Val Ser Lys Asp Gly Asn Ser Val Ile Gly Leu Ser Asn Ile Phe Phe
          50           55           60
Ser Asn Lys Ser Asp Asp Val Lys Leu Val Ala Glu Thr Asn Gln Lys
65           70           75           80
Ile Gln Ala Leu Asn Ala Thr Gln Gln Asn Ser Ala Lys Leu Asn Ala
          85           90           95
Ile Phe Asn Glu Ile Pro Ala Asp Tyr Ala Ile Glu Leu Pro Ser Thr
          100          105          110
Asn Ala Glu Asn Lys Asp Lys Ile Leu Tyr Ile Val Ser Asp Pro Met
          115          120          125
Cys Pro His Cys Gln Lys Glu Leu Thr Lys Leu Arg Asp His Leu Lys
          130          135          140
Glu Asn Thr Val Arg Met Val Val Val Gly Trp Leu Glu Ala Ile Arg
145          150          155          160
Leu Lys Lys Arg Leu
          165

```

(2) INFORMATION FOR SEQ ID NO:683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

```

Thr Gly Ala Ile Met Leu Ser Ser Asn Asp Leu Phe Met Val Val Leu
1           5           10           15
Gly Ala Ile Leu Leu Val Leu Val Cys Leu Val Gly Tyr Leu Tyr Leu
          20           25           30
Lys Glu Lys Glu Phe Tyr His Lys Met Arg Arg Leu Glu Lys Thr Leu
          35           40           45
Asp Glu Ser Tyr Gln Glu Asn Tyr Leu Tyr Ser Lys Arg Leu Arg Glu

```

602

```

      50              55              60
Leu Glu Gly Arg Leu Glu Gly Leu Ser Leu Glu Lys Ser Ala Lys Glu
65              70              75              80
Asp Ser Ser Leu Lys Thr Thr Leu Ser His Leu Tyr Asn Gln Leu Gln
      85              90              95
Glu Ile Gln Lys Ser Met Asp Lys Glu Arg Asp Tyr Leu Glu Glu Lys
      100              105              110
Ile Ile Thr
      115

```

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

```

Glu Arg Lys Lys Met Asn Thr Asn Leu Lys Lys Ala Leu Phe Leu Thr
1              5              10              15
Thr Leu Gly Tyr Leu Gln Ala Asn Glu Gly Phe Leu Ala Ile Met Pro
      20              25              30
Asp Glu Asn Lys Gln Glu Asp Ile Ser Gln Glu Gln Lys Leu Glu His
      35              40              45
Lys Met Glu Gln Lys Ile Ala Pro Gln Asn Thr Leu Lys Lys Gln Gln
      50              55              60
Ser Ala Pro Leu Gln Ser Ala Glu Leu Leu Gln Ser Gln Val Lys Arg
65              70              75              80
Glu Val Lys Glu Gln Lys Lys Ser Gln Lys His Leu Val Ala Met Gln
      85              90              95
Thr Lys Asn Gly Phe Phe Leu Gly Ser Glu Ile Ala Ile Thr Gly Thr
      100              105              110
Ser Leu Lys Gln Ser Leu Ser Leu Ile Ser Asn Ala Thr Asp Asp Leu
      115              120              125
Leu Thr Tyr Ser Lys Thr Ser Lys Asn Ala Asn Phe Asn Met Gly Leu
      130              135              140
Leu Ile Gly Tyr Gln His Tyr Phe Gly Ala Ser Lys Arg His Gly Ile
145              150              155              160
Lys Ile Ser Ser His Leu Tyr Gly Gly Thr Pro Ser Asp Val Ser Thr
      165              170              175
Asp Ile Lys Ile Tyr Lys Ser Lys Val Ser Thr Asn Tyr Thr Pro Leu
      180              185              190
Asn Phe Gly Ile Asp Val Lys Tyr Leu Phe Asp Phe Leu Asn Val Ile
      195              200              205
Lys Lys Asn Arg His Thr Leu Gly Leu Ser Val Gly Phe Gly Trp Arg

```


603

210	215	220
Met Gln Tyr Tyr Phe Ala Lys Ile Asp Pro Ile Lys Thr Ser His Ser		
225	230	235
Glu Phe Ile Thr Asn Lys Pro Lys Asp Ile Phe Asn His Gly Phe Tyr		240
	245	250
Pro Thr Ile Gly Leu His Tyr Tyr Leu Asn His His Gln Phe Glu Val		255
	260	265
Asn Tyr Arg Phe Gly Gly Ala Ile Asn Tyr Gln Ser Val Val Pro Ser		270
	275	280
Lys Ile Val Val Gln Asn Gly Asn Phe Lys Gly Glu Val Leu Phe Ser		285
	290	295
Asn Phe Leu Thr Lys Ala Thr Asn Ser Ser Tyr Ile Ala Phe Asn Tyr		300
305	310	315
Ala Tyr Leu Phe		320

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

Ala Asn Glu Lys Met Glu Leu Ile Lys Lys Leu Glu Lys Glu Ser Glu		
1	5	10
Val Leu Lys Lys Asp Leu Gln Gln His Ser Asn Glu Leu Phe Lys Met		15
	20	25
Leu Ile Ile Asp Asn Glu Asp Leu Phe Lys Glu Gln Phe Glu Ile Met		30
	35	40
Phe Lys Ala Trp Val Glu Ile Val Lys Met Met Phe Glu Leu Thr Lys		45
	50	55
Lys Thr Lys Phe Asp Gly Glu Met Ile Gly Tyr Thr Glu Glu Leu Leu		60
65	70	75
Thr Phe Leu Val Arg Asp Phe Phe Asn Gly Ile Phe Lys Ser Lys Val		80
	85	90
Ile Pro Lys Met Pro Ile Phe Cys Gly Asp Val Lys Cys Glu Asp Phe		95
	100	105
Asn Ala Leu Arg Ser Leu Val Tyr Leu Ser Val Leu Glu Leu Glu Glu		110
	115	120
Thr Ile Asn Pro Asn Lys Ile Pro Phe		125
130	135	

(2) INFORMATION FOR SEQ ID NO:686:

604

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

```

Asn Lys Glu Asn Asn Ile Thr Ile Cys Val Ala Asn Glu Lys Gly Gly
1           5           10           15
Ser Gly Lys Ser Thr Leu Cys Leu Asn Leu Ala Val Gln Leu Leu Lys
          20           25           30
Asp Asn Lys Glu Val Val Val Leu Asp Thr Asp Ser Gln Lys Ser Met
          35           40           45
Glu Thr Phe Ala Thr Ile Arg Ala Glu Lys Glu Arg Pro Thr Phe Ser
          50           55           60
Leu Phe Asn Arg Ser Ser Gly Phe Ser Asp Thr Leu Lys Gln Met Val
65           70           75           80
Ser Lys Tyr Glu Asn Ile Leu Ile Asp Thr Lys Gly Glu Tyr Ser Lys
          85           90           95
Glu Thr Gln Lys Ala Met Leu Leu Ser Asn Ile Val Leu Val Pro Thr
          100          105          110
Thr Pro Ser Gln Leu Asp Thr Glu Val Leu Ala Asn Met Leu Glu Arg
          115          120          125
Ile Glu Gln Leu Gln Glu Leu Asn Glu Asn Leu Arg Ala Leu Ile Val
          130          135          140
Ile Asn Arg Met Pro Thr Ile Pro Thr Leu Lys Glu Arg Gln Ala Leu
145          150          155          160
Ile Glu Phe Ile Lys Glu Asn Asn Pro Ser Asp Arg Ile Thr Leu Leu
          165          170          175
Glu Ser Ser Leu Ser Glu Arg Ile Val Tyr Lys Arg Ser Val Ser Glu
          180          185          190
Gly Leu Gly Val Ile Glu Tyr Ser Asp Lys Lys Ala Ile Asn Glu Trp
          195          200          205
Val Asn Phe Tyr Asn Glu Leu Lys Ser His Leu Glu Lys Glu Lys Ile
          210          215          220
His Ala Phe
225

```

(2) INFORMATION FOR SEQ ID NO:687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

```

Arg Ser Thr Thr Leu Ile Tyr Phe Asn Phe Lys Glu Pro Met Met Ser
1          5          10          15
Asp Glu Ile Thr Gln Glu Asn Glu Leu Glu Ile Asn Ser Asn Asn Gln
          20          25          30
Asn Gln Glu Pro Lys Glu Val Glu Lys Met Pro Leu Asn Asn Ile Gln
          35          40          45
Lys Ala Lys Lys Leu Lys Asn His Ala Asn Leu Ile Val Arg Arg Thr
          50          55          60
Asp Glu Leu Asp Lys Val Ile Asn Lys Arg Glu Ser Leu Gln Arg Glu
65          70          75          80
Phe Lys Arg Arg Ile Lys His Leu Asp Asn Lys Ile Glu Thr Leu Ser
          85          90          95
Asn Asn Ile Glu Glu Leu Lys Arg Lys
          100          105

```

(2) INFORMATION FOR SEQ ID NO:688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

```

Ser Met Lys Lys Tyr Gln Asn Lys Arg Lys Leu Gly Lys Arg Ile Asn
1          5          10          15
Cys Phe Ile Ser Asn Glu Cys Lys Asp Ile Leu Glu Asn Tyr Leu Lys
          20          25          30
Val Lys Lys Ile Ser Val Thr Glu Cys Ile Glu Ser Leu Leu Leu Ala
          35          40          45
Leu Asp Pro Ser Lys Glu Thr Leu Arg Ala Arg Asp Phe Tyr Glu Ser
          50          55          60
Leu Phe Lys Val Ile Ser Leu Asn Gln His Val Tyr Lys Glu Leu Met
65          70          75          80

```

606

```

Ala Asn Gly Asn Asn Ile Asn Gln Ile Ala Lys Asn Thr Asn Ile Ala
      85                      90                      95
Ile Lys Tyr Asn Lys Pro Phe Tyr Leu Gln Asn Leu Ala Phe Leu Glu
      100                      105                      110
Glu Ile Phe Lys Val Met Asp Thr Leu Asn Lys Asn Val Glu Glu Cys
      115                      120                      125
Lys Lys Ile Ser Leu Glu Leu Leu Leu Gln Ile Tyr Lys Glu Gln Lys
      130                      135                      140
Ser Gln Thr Glu Phe Asn Ala Ile Ser Lys Ile Leu Asn Ala Leu Asn
      145                      150                      155                      160
Glu Lys Gln Ser Thr Thr Glu Pro Lys Lys Asp Asn Ala
      165                      170

```

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

```

Lys Ser Pro Tyr Arg His Ser Ile Ser Ser Gln Val Ser Val Glu Asn
1      5      10      15
Asp Glu Glu Ile Ile Glu Val Glu Lys Gly Glu Asn Gln Gly Ala Phe
      20      25      30
Ser Tyr Phe Leu Gly Gly Pro Thr Cys Leu Ala Gly Asp Phe Met Gly
      35      40      45
Ser Phe Ser Phe Glu Thr Pro Leu Lys Arg Gly Asp Lys Ile Val Phe
      50      55      60
Gln Asp Met Leu His Tyr Thr Ile Val Lys Asn Asn Ser Phe Asn Gly
      65      70      75      80
Val Pro Leu Pro Ser Leu Ala Lys Ile Asp Ser Gln Gly Phe Lys Ile
      85      90      95
Leu Lys Ser Phe Ser Tyr Glu Asp Tyr Lys Asn Arg Asn
      100      105

```

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

607

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

```

Ala Leu Glu Lys Asn Gly Thr Ala Thr Ala Asn Ser Thr Ser Ser Thr
1           5           10           15
Ser Gly Ala Thr Gly Ser Asp Gly Gln Thr Tyr Ser Gln Gln Ala Ile
          20           25           30
Gln Tyr Leu Gln Gly Gln Gln Asn Ile Leu Asn Asn Ala Ala Asn Leu
          35           40           45
Leu Lys Gln Asp Glu Leu Leu Leu Glu Ala Phe Asn Ser Ala Val Ala
          50           55           60
Ala Asn Ile Gly Asn Lys Glu Phe Asn Ser Ala Ala Phe Thr Gly Leu
65           70           75           80
Val Gln Gly Ile Ile Asp Gln Ser Gln Leu Val Tyr Asn Glu Leu Thr
          85           90           95
Lys Asn Thr Ile Ser Gly Ser Ala Val Asn Asn Ala Gly Ile Asn Ser
          100          105          110
Asn Gln Ala Asn Ala Cys Lys Gly Val Leu Val Ser Ser Leu Thr Leu
          115          120          125
Phe Thr Thr Cys Lys
          130

```

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

```

Leu Ile Lys Glu Ala Met Ile Pro Val Phe Gly Ser Glu Thr Gly Ile
1           5           10           15
Tyr Asn His Lys Glu Gln Asn Phe Lys Gly Lys Gly Arg Phe Ile Leu
          20           25           30
Thr Ser Lys Asp Ser Lys Val Glu Gly Leu Asp Ile Ser Tyr Ser His
          35           40           45
Ala Leu Ala Ile Ile Glu Ala Gln Ser Ile Gln Ala Asn Leu Phe Leu

```

608

50		55		60
Asp Glu Ile Lys Gln Ser Gln Lys Glu Lys Lys Lys Phe Pro Thr Phe				
65		70		75
Lys Gly Gly Phe				80

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

Pro	Phe	Leu	Lys	Lys	Asn	Lys	Phe	Leu	Gln	Ile	Cys	Gln	Tyr	Phe	Ser
1			5					10						15	
Ala	His	Phe	Lys	Gln	Val	Leu	Lys	Asn	Glu	Lys	Pro	Leu	Val	Tyr	Tyr
			20					25					30		
Gly	Val	Leu	Lys	Ala	Lys	Ala	Pro	Asn	Trp	Ala	Leu	Trp	Val	Tyr	Glu
			35				40					45			
Lys	Pro	Leu	Lys	Lys	Glu	Ile	Tyr	Met	Asn	Asp	Lys	Glu	Val	Val	Val
	50				55				60						
Tyr	Glu	Pro	Asn	Leu	Phe	Gln	Ala	Thr	Ile	Thr	Pro	Leu	Lys	Asp	Lys
65				70					75					80	
Thr	Asp	Phe	Phe	Thr	Ile	Leu	Lys	Gln	Leu	Lys	Lys	Gln	Thr	Asp	Gly
				85				90					95		
Ser	Phe	Lys	Thr	Thr	Ile	Asn	Lys	Thr	Thr	Tyr	Arg	Leu	Val	Phe	Lys
			100					105					110		
Asp	Gly	Lys	Pro	Phe	Ser	Leu	Glu	Phe	Lys	Asp	Asp	Met	Asn	Asn	Leu
		115				120						125			
Val	Thr	Ile	Thr	Phe	Ser	Gln	Ala	Glu	Ile	Asn	Pro	Lys	Ile	Pro	Asn
	130					135					140				
Glu	Ile	Phe	Val	Phe	Asn	Pro	Lys	Asp	Glu	Asn	Ile	Asp	Ile	Val	Arg
145					150				155					160	
Gln															

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

```

Pro Ser Phe Leu Lys Glu Lys Phe Asp Phe Phe Lys Gly Lys Asn Phe
1           5           10           15
Lys Ile Val Tyr Cys Ile Gly Glu Asp Leu Thr Thr Arg Glu Lys Gly
20           25           30
Phe Arg Ala Val Lys Glu Phe Leu Ser Glu Gln Leu Glu Asn Ile Asp
35           40           45
Leu Asn Tyr Ser Asn Leu Ile Val Ala Tyr Glu Pro Ile Trp Ala Ile
50           55           60
Gly Thr Lys Lys Ala Arg Phe
65           70

```

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

```

Arg Asp Val Arg Phe His Val Arg Asp Leu Val Arg Gln Leu Lys Gly
1           5           10           15
Lys His Leu Ile Glu Val Ser Asp Val Ile Asn Asp Thr Thr Gln Pro
20           25           30
Asn Leu Asp Met Asn Leu Leu Thr Thr Glu Ile Ala Arg Gln Leu Arg
35           40           45
Leu Arg Ser Asn Gly Arg Phe Asn Ile Thr Arg Ala Ser Gly Gly Ser
50           55           60
Gly Ile Glu Ala Asp Ser Arg Met Val Lys Gln Arg Glu Lys Glu Arg
65           70           75           80
Glu Ser Glu Glu Tyr Asn Gln Asp Thr Thr Val Glu Lys Gly Thr Leu
85           90           95
Lys Ala Ala Asp Leu Ser Leu Ser Gly Lys Val Ser Ser Ile Ala Ala
100          105          110

```

.610

```

Ser Ile Ser Ser Ser Arg Gln Arg Leu Asp Tyr Asp Phe Thr Leu Ser
    115                      120                      125
Leu Thr Asn Arg Lys Thr Gly Glu Glu Val Trp Ser Asp Val Lys Pro
    130                      135                      140
Ile Val Lys Asn Ala Ser Asn Lys Arg Met Phe
145                      150                      155

```

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

```

Ile Lys Ser Val Leu Gly Leu Ile Leu Ile Gln Gln Asn Phe Lys Thr
1      5      10      15
Leu Lys Glu Leu Tyr Met Leu Val Thr Lys Leu Ala Pro Asp Phe Lys
    20      25      30
Ala Pro Ala Val Leu Gly Asn Asn Glu Val Asp Glu His Phe Glu Leu
    35      40      45
Ser Lys Asn Leu Gly Lys Asn Gly Val Ile Leu Phe Phe Trp Pro Lys
    50      55      60
Asp Phe Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Asp Lys Arg
65      70      75      80
Val Lys Asp Phe His Glu Lys Gly Phe Asn Val Ile Gly Val Ser Ile
    85      90      95
Asp Ser Glu Gln Val His Phe Ala Trp Lys Asn Thr Pro Val Glu Lys
    100     105     110
Gly Gly Ile Gly Gln Val Ser Phe Pro Met Val Ala Asp Ile Thr Lys
    115     120     125
Ser Ile Ser Arg Asp Tyr Asp Val Leu Phe Glu Glu Ala Ile Ala Leu
    130     135     140
Arg Gly Ala Phe Leu Ile Asp Lys Asn Met Lys Val Arg His Ala Val
145     150     155     160
Ile Asn Asp Leu Pro Leu Gly Arg Asn Ala Asp Glu Met Leu Arg Met
    165     170     175
Val Asp Ala Leu Leu His Phe Glu Glu His Gly Glu Val Cys Pro Ala
    180     185     190
Gly Trp Arg Lys Gly Asp Lys Gly Met Lys Ala Thr His Gln Gly Val
    195     200     205
Ala Glu Tyr Leu Lys Glu Asn Ser Ile Lys Leu
    210     215

```

(2) INFORMATION FOR SEQ ID NO:696:

611

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...113
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

```

Gly Val Ile Met Glu His His Lys Ala His Thr Thr Ile Gln Ala Leu
1           5           10           15
Gln Ala Lys Arg Lys Arg Leu Leu Thr Glu Leu Ala Glu Leu Glu Ala
20           25           30
Glu Ile Lys Val Ser Ser Glu Arg Arg Ser Ser Phe Asn Val Ser Leu
35           40           45
Ser Pro Ser Leu Leu Ala Glu Ile Glu Glu Ile Glu Tyr Glu Glu Lys
50           55           60
Met Ser Lys Glu Arg Arg Ile His His Asn Leu Leu Leu Ser Pro Ser
65           70           75           80
Phe Met Ala Lys Val Asp Glu Tyr Met Lys Glu Lys Gly Phe Pro Asn
85           90           95
Arg Ser Leu Leu Phe Glu Lys Ala Leu Glu Phe Tyr Met Leu Lys His
100          105          110
Pro

```

(2) INFORMATION FOR SEQ ID NO:697:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 187 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...187
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

```

Gly Phe Val Cys Gly Ser Val Leu Phe Gln Leu Gly Val Phe Met Gly

```

612

```

1           5           10           15
Leu Lys Asn Lys Ile Lys Gly Phe Val Lys Glu Arg Met Pro Phe Val
      20           25           30
Met Arg Cys Val Arg Gly Leu Lys Gly Ala Lys Asp Thr His Glu Asn
      35           40           45
Ala His Asp Arg Asp Ala Tyr Cys Gly Ile Asn Arg Glu Ile Lys Glu
      50           55           60
Met Leu Glu Ala Lys Lys Leu His Phe Leu Gln Glu Lys Ala Leu Phe
      65           70           75           80
Asn His Asp His Gln Glu Ser Val Phe Leu Ala Ile Ala Ser Leu Asn
      85           90           95
Asn Glu Ser Phe Ile Glu Tyr Asn Lys Ser Ile Tyr Lys Asn Ser Ser
      100          105          110
Leu Asn Tyr Asn Tyr Gly Gly His Leu Glu Asp Arg Val Ile His Pro
      115          120          125
Thr Leu Thr Leu Pro Asn Pro Thr His Ser Gly Tyr Phe Asp Tyr Asp
      130          135          140
Lys Lys Ser Gln Asn Pro Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile
      145          150          155          160
Arg Val Lys Asn Glu Ile Val Thr Leu Glu Ser Leu Phe Ser Met
      165          170          175
Leu Pro Ala Val Gln Arg Gly Gly His Trp Phe
      180          185

```

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

```

Lys Arg Val Cys Phe Leu Cys Phe Leu Pro Phe Lys Gly Gly Val Ile
1           5           10           15
Gly Phe Asn Asp Cys Asp Asp Gly Ser Lys Glu Val Val Leu Glu Phe
      20           25           30
Cys Lys Lys Phe Pro Ser Phe Ile Pro Ile Ser Tyr Pro Tyr Glu Val
      35           40           45
Ile Leu Lys Asp Cys Pro Ser Leu Trp His Gln Leu Tyr His Tyr Cys
      50           55           60
Asn Tyr Thr Leu Ser Phe Ile Pro Lys Asn Glu Trp Val Val Lys Ile
      65           70           75           80
Asp Cys Asp His Ile Tyr Asp Ala Lys Lys Leu Tyr Lys Ser Phe Tyr
      85           90           95
Ile Pro Lys Asn Ile Lys Glu Val Val Met Tyr Ser Arg Ile Asn Phe

```

100						105						110					
Val	Val	Arg	Asp	Phe	Glu	Val	Phe	Val	Arg	Asn	Asp	Gly	Asp'	Phe	Gly		
115						120						125					
Phe	Leu	Asp	Ala	Trp	Gly	Asp	His	Trp	Leu	Leu	Tyr	Asn	Asp	Cys	Glu		
130						135						140					
Pro	Phe	Glu	Ile	Trp	Arg	Tyr	Asn	Asp	Glu	Ser	Tyr	Glu	Val	Leu	Lys		
145						150						155					
Leu	Lys	Asp	Lys	His	His	Ile	Lys	Asp	Lys	Glu	Met	Val	Gln	Trp	His		
165						170						175					
Phe	Pro	Leu	Ala	Lys	Lys	Arg	Arg	Asn	Ala	Ile	Val	Tyr	Asp	Asp	Leu		
180						185						190					
Ile	Pro	Leu	Glu	Glu	Phe	Lys	Lys	Arg	His	Ala	Asp	Leu	Ile	Gly	Thr		
195						200						205					
Arg	Ile	Glu	Glu	Ser	Met	Leu	Asp	Glu	Lys	Arg	Ile	Leu	Glu	Val	Tyr		
210						215						220					
Gln	Lys	Phe	Arg	Leu	Pro												
225						230											

(2) INFORMATION FOR SEQ ID NO:699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEO ID NO:699:

[illegible]

(2) INFORMATION FOR SEQ ID NO:700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

614

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

Phe	Ser	Arg	Lys	Thr	Asp	Lys	Asn	Ala	Gln	Lys	Asp	Glu	Gln	Lys	Asn
1				5					10					15	
Glu	Gln	Glu	Glu	Gln	Arg	Arg	Leu	Arg	Glu	Gln	Gln	Arg	Leu	Lys	Gln
			20					25					30		
Asn	Gln	Glu	Asn	Gln	Glu	Met	Leu	Lys	Gly	Leu	Gln	Gln	Asn	Leu	Asn
			35				40					45			
Gln	Phe	Thr	Gln	Lys	Leu	Glu	Ser	Val	Lys	Asn	Lys	Thr	Leu	Asp	Leu
	50					55				60					
Gln	Ile	Pro	Lys	Gln	Asp	Gly	Val	Asp	Glu	Lys	Ala	Tyr	Gln	Glu	Trp
65				70					75					80	
Tyr	Ala	Gln	Ile	Tyr	Gln	Ile	Leu	Tyr	Lys	Gly	Trp	Arg	Gly	Val	Phe
			85					90					95		
Tyr	His	Lys	Ala	Ser	Val	Ser	Val	Leu	Ile	Met	Ile	Thr	Lys	Asp	Gly
			100					105					110		
Glu	Phe	Asp	Tyr	Thr	Ile	Leu	Ser	Tyr	Ser	Asp	Phe	Lys	Asp	Tyr	Asn
		115					120					125			
Lys	Ser	Val	Met	Thr	Leu	Leu	Asp	Asp	Leu	Lys	Lys	Val	Asp	Phe	Pro
	130					135					140				
Pro	Tyr	Pro	Gly	Gly	Asn	Met	Ile	Ser	Ile	Lys	Val	Asn	Phe	Thr	Thr
145					150					155					160
Lys	Glu	Glu	Gln												

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

615

Arg Ala Arg Leu Leu Arg Arg Lys Asn His Tyr Leu Glu Asn Lys Phe
 1 5 10 15
 Lys Asp Met Gly His Tyr Ala Ala Ser Asp Glu Val Asn Glu Lys Gln
 20 25 30
 Val Leu Lys Met Tyr Gln Glu Gly Tyr Ser Val Asp Ser Ile Ser Lys
 35 40 45
 Glu Phe Lys Val Ser Lys Gly Glu Val Glu Phe Ile Leu Asn Met Ala
 50 55 60
 Gly Leu Lys Trp
 65

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

Thr Lys Leu Asp Thr Ile Ser Leu Lys Arg Ile Gln Met Glu Lys Leu
 1 5 10 15
 Pro Lys Lys Arg Val Ser Lys Thr Lys Ser Gln Lys Leu Ile His Ser
 20 25 30
 Leu Thr Thr Gln Lys Asn Arg Ala Phe Leu Lys Lys Ile Ser Ala Asn
 35 40 45
 Glu Met Leu Leu Glu Leu Glu Lys Gly Ala Phe Lys Lys Asn Glu Ala
 50 55 60
 Tyr Phe Ile Ser Asp Glu Glu Asp Lys Asn Tyr Val Leu Val Pro Asp
 65 70 75 80
 Asn Val Ile Ser Leu Leu Ala Glu Asn Ala Arg Lys Ala Phe Glu Ala
 85 90 95
 Arg

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

Arg	Ser	Ile	Lys	Met	Lys	Gln	Ser	Leu	Arg	Glu	Gln	Lys	Leu	Leu	Lys
1				5				10					15		
Ile	Leu	Glu	Asn	Asp	Val	Leu	Thr	Ile	Leu	Asp	Ser	Phe	Ser	Asn	Tyr
			20					25					30		
Leu	Phe	Glu	Leu	Arg	Glu	Glu	Leu	Asp	Phe	Ile	Glu	Glu	Glu	Met	Glu
			35					40					45		
Gly	Glu	Ile	Thr	Glu	Gln	Asn	Leu	Thr	Ala	Leu	Tyr	Asp	Phe	Ser	Asn
			50			55					60				
Phe	Leu	Glu	Asp	His	Val	Asn	Val	Phe	Tyr	Glu	Asn	Val	Leu	Asn	Ile
65				70				75						80	
Asp	Asp	Val	Lys	Thr	Glu	His	Leu	Tyr	Ser	Gly	Leu	Ile	Asp	Ser	Leu
			85					90					95		
Asn	Ala	Asn	Leu	His	Phe	Val	Lys	Ser	Phe	Leu	Ser	Asn	Gln	Asp	Leu
			100					105					110		
Asp	Phe	Arg	Phe	Phe	Lys	Glu	Ile	Asn	Asp	Gly	Gln	Asp	Pro	Gln	Lys
			115					120					125		
Thr	Leu	Ser	Arg	Leu	Ile	Pro	Leu	Gln	Ser	Gly	Lys	Asn	Asp	Ala	Ser
			130					135				140			
Ser	Phe	Lys	Ala	Asn	Asn	Ser	Phe	Val	Ser	Leu	Val	Tyr	Val	Tyr	Ala
145				150				155						160	
Tyr	Phe	Met	Leu	Glu	Thr	Ile	Arg	Gln	Ser	Tyr	Arg	Ile	Leu	Arg	Leu
			165					170					175		
Leu	Glu	Lys	Pro	Ile	Asn	Asn	Asn	Ile	Ser	Glu	Asp	Met	Gln	Ser	Asp
			180					185					190		
Ile	Glu	Asn	Phe	Phe	Val	Gln	Ala	Asn	Phe	Leu	Glu	Tyr	Tyr	Val	Gln
			195					200					205		
Asn	Lys	Ile	Tyr	Pro	Thr	Asn	His	Ala	Tyr	Asp	Phe	Thr	His	Leu	Ile
			210					215				220			
Met	Asp	Ser	Ile	Ile	Pro	Asn	Trp	Ile	Gln	Ile	Asp	Met	Ser	Val	Glu
225				230				235						240	
Ala	Lys	Lys	Lys	Glu	Leu	Phe	Glu	Lys	Tyr	Phe	Gln	Asn	Ile	Asp	Glu
			245					250					255		
Val	Thr	Asn	Lys	Met	Leu	Ala	Gln	Glu	Asn	Gln	Asn	Lys	Asn	Ser	Asp
			260					265					270		

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

```

Val Lys Gly Glu Lys Asn Ala Trp Tyr Leu Gly Ile Ser Tyr Gln Val
1          5          10          15
Gly Gln Ala Ser Gln Ser Val Lys Asn Pro Pro Lys Ser Ser Glu Phe
          20          25          30
Asn Tyr Pro Lys Phe Pro Val Gly Lys Thr Asp Tyr Leu Ala Val Met
          35          40          45
Gln Gly Leu Gly Leu Thr Val Gly Tyr Lys Gln Phe Phe Gly Glu Lys
          50          55          60
Arg Trp Phe Gly Ala Arg Tyr Tyr Gly Phe Met Asp Tyr Gly His Ala
65          70          75          80
Val Phe Gly Ala Asn Ala Leu Thr Ser Asp Asn Gly Gly Val Cys Lys
          85          90          95
Leu Asn Glu Pro Cys Ala Thr Lys Val Gly Thr Met Gly Asn Leu Ser
          100         105         110
Asp Met Phe Thr Tyr Gly Val Gly Ile Asp Thr Leu Tyr Asn Val Ile
          115         120         125
Asn Lys Glu Asp Ala Ser Phe Gly Phe Phe Phe Gly Ala Gln Ile Ala
          130         135         140
Gly Asn Ser Trp Gly Asn Thr Thr Gly Ala Phe Leu Glu Thr Lys Ser
145          150         155         160
Pro Tyr Lys His Thr Ser Tyr Ser Leu Asp Pro Ala Ile Phe Gln Phe
          165         170         175
Leu Phe Asn Leu Gly Ile Arg Thr His Ile Gly Gln His Gln Glu Phe
          180         185         190
Asp Phe Gly Val Lys Ile Pro Thr Ile Asn Val Tyr Tyr Phe Asn His
          195         200         205
Gly Asn Leu Ser Phe Thr Tyr Arg Arg Gln Tyr Ser Leu Tyr Val Gly
          210         215         220
Tyr Arg Tyr Asn Phe
225

```

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

```

Ser Ala Val Val Glu Ser Val Val Ile Leu Lys Ile Asp Ile Asn Gln
1           5           10           15
Gly Arg Ser Cys Ser Leu Tyr Pro Thr Pro Lys Ser Val Ser Leu Val
          20           25           30
Arg Asn Gln Ser Val Ala Tyr Glu Ile Leu Cys Glu Asn Gln Pro Leu
          35           40           45
Trp Ile Glu Val Ser Thr Asn Leu Gly Gln Thr Leu Pro Phe Ser Leu
          50           55           60
Ile
65

```

(2) INFORMATION FOR SEQ ID NO:706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

```

Arg Phe Lys His Phe Arg Gly Gly Gly Phe Pro His His Asn Leu Asn
1           5           10           15
Ala Cys Gly Ala Lys Pro Thr Gly Gln Val Val Phe Tyr Pro Thr Asn
          20           25           30
Ser Leu Leu Gly Ser Thr Ser Ser Asn Ser Asn Asn Gln Gln Tyr
          35           40           45
Asn Asn Thr Leu Leu Met Asn Thr Leu Gln Gly Glu Leu Ser Thr Asn
          50           55           60
Asn Gln Asn Asn Pro Asn Gly Cys Ala Asn Gln Ile Gln Cys Leu Glu
65           70           75           80
Gln Phe Ile Gln Asn Leu Thr Pro Leu Ala Ala Thr Pro Thr Ser Thr
          85           90           95
Asn Gln Ala Asn Gln Gln Val Gln Ala Ile Ala Gln Lys Leu Gln Ser
          100          105          110
Val Ala Ile Asn Ala Leu Asp Asn Asn Ala Ile Asn Asn Thr Thr Tyr
          115          120          125
Asn Leu Asn Asn Leu His Asn Ala Leu Asn Phe Gln Ala Tyr Gln Ser
          130          135          140
Thr Ile Glu Gln Tyr Asn Asn Ala Leu Lys Gln Ile Ser Trp Ile Ser
145          150          155          160
Phe Ser Glu Pro Lys Asn Leu Leu Lys Asn Thr Ser Asn Asn Tyr Gln
          165          170          175
Ile Gly Thr Val Thr Asn Asp Gln Gly Gln Asn Ile Ser Ala Tyr Asp
          180          185          190
Cys Thr Ser Ala Thr Gly Ser Leu Ser Ser Asp Ala Ser Ser Gly Ile

```



```

      195              200              205
Ser Cys Ser Ala Thr Ser Ser Thr Ser Asn Thr Asn Ser Phe Asp Asn
  210              215              220
Ser Leu Val Ala Thr Ser Lys Val Gln Thr Ile Asn Gly Lys Glu Gln
  225              230              235              240
Ile Gly Val Asn Ser Phe Asn Leu Val Ser Gln Val Trp Ser Val Tyr
      245              250              255
Asn Ser Leu Lys Thr Ser Glu Glu Asn Leu Gln Lys Asn Ala Lys Ile
      260              265              270
Leu Cys Asn Asn Gly Ser Gln Ser Gly Thr Ser Pro Cys Asn Ser Ser
      275              280              285
Ser Gly Gly Leu Ser Ile Ser Gly Asn Ala Gln Leu Gln Asn Ile Leu
      290              295              300
Ser Pro Thr Asn Gly Thr Thr Thr Asn Thr Gln Ala Lys Ser Asn Ala
  305              310              315              320
Ser Lys Leu Lys Ala Met Val Met Val Asn Asn Glu Glu Glu Ala Lys
      325              330              335
Thr Thr Asn Phe Asn Gln Ser Ser Gly Pro Thr Thr Gln Ser Ser Asn
      340              345              350
Ser Thr Val Met Gly Ala Leu Asn Thr Val Leu Gln Asn
      355              360              365

```

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

```

Asn Pro Phe Phe Thr Ile Thr Ala Lys Leu Leu Ser Asn Thr Gln Ser
1           5           10           15
Ala Phe Asp Gln Gly Ile Ala Leu Ser Ser Asn Ile Ile Ser Ala Val
      20           25           30
Asn Ser Leu Asn Pro Ser Asn Asn Ser Gln Glu Val Lys Ala Gln Leu
      35           40           45
Gln Asn Thr Ala Gln Ser Met Thr Glu Leu Leu Gln Ile Glu His
      50           55           60
Ser Ile Thr Lys Thr Thr Ser Thr Thr Tyr Ala Gln Ser Leu Leu Ser
  65           70           75           80
Asn Leu Thr Asp Ala Val Asn Ala Ser Ser Asn Asn Thr Thr Tyr Val
      85           90           95
Ser Ala Leu Val Asn Ala Leu Asn Thr Leu Gly Val Gly Val Phe Pro
      100          105          110
Thr Thr Thr Ser Thr His Val Val Leu Asn Pro Pro Asp Lys Ser Tyr

```

620

	115		120		125
Ser	Ile	Gln	Leu	Ile	Pro
				Phe	
	130			135	

(2) INFORMATION FOR SEQ ID NO:708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

Gly	Arg	Gly	Met	Lys	Leu	Lys	Lys	Arg	Lys	Val	Ala	Ala	Thr	Leu	Leu
1				5					10					15	
Lys	Arg	Leu	Thr	Leu	Pro	Leu	Leu	Phe	Thr	Thr	Gly	Ser	Leu	Gly	Ala
		20						25					30		
Val	Thr	Tyr	Glu	Val	His	Gly	Asp	Phe	Ile	Asn	Phe	Ser	Lys	Val	Gly
		35					40					45			
Phe	Asn	Arg	Ser	Pro	Ile	Asn	Pro	Val	Lys	Gly	Ile	Tyr	Pro	Thr	Glu
	50					55					60				
Thr	Phe	Val	Asn	Leu	Thr	Gly	Lys	Leu	Glu	Gly	Ser	Val	His	Leu	Gly
65				70					75					80	
Arg	Gly	Trp	Thr	Val	Asn	Val	Gly	Gly	Val	Leu					
				85					90						

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

Met Glu Gln Pro Val Ile Lys Glu Gly Thr Leu Ala Leu Ile Asp Thr
 1 5 10 15
 Phe Ala Tyr Leu Phe Arg Ser Tyr Tyr Met Ser Ala Lys Asn Lys Pro
 20 25 30
 Leu Thr Asn Asp Lys Gly Phe Pro Thr Gly Leu Leu Thr Gly Leu Val
 35 40 45
 Gly Met Val Lys Lys Phe Tyr Lys Asp Arg Lys Asn Met Pro Phe Ile
 50 55 60
 Val Phe Ala Leu Glu Ser Gln Thr Lys Thr Lys Arg Ala Glu Lys Leu
 65 70 75 80
 Gly Glu Tyr Lys Gln Asn Arg Lys Asp Ala Pro Lys Glu Met Leu Leu
 85 90 95
 Gln Ile Pro Ile Ala Leu Glu Trp Leu Gln Lys Met Gly Phe Thr Cys
 100 105 110
 Val Glu Val Gly Gly Phe Glu Ala Asp Asp Val Ile Ala Ser Leu Ala
 115 120 125
 Thr Leu Ser Pro Tyr Lys Thr Arg Ile Tyr Ser Lys Asp Lys Asp Phe
 130 135 140
 Asn Gln Leu Leu Ser Asp Lys Ile Ala Leu Phe Asp Gly Lys Thr Glu
 145 150 155 160
 Phe Leu Ala Lys Asp Cys Val Glu Lys Tyr Gly Ile Leu Pro Ser Gln
 165 170 175
 Phe Thr Asp Tyr Gln Gly Ile Val Gly Asp Ser Ser Asp Asn Tyr Lys
 180 185 190
 Gly Val Lys Gly Ile Gly Ser Lys Asn Ala Lys Glu Leu Leu Gln Arg
 195 200 205
 Leu Gly Ser Leu Glu Lys Ile Tyr Glu Asn Leu Asp Leu Ala Lys Asn
 210 215 220
 Leu Leu Ser Pro Lys Met Tyr Gln Ala Leu Ile Gln Asp Lys Gly Ser
 225 230 235 240
 Ala Phe Leu Ser Lys Glu Leu Ala Thr Leu Glu Arg Gly Cys Ile Lys
 245 250 255
 Glu Phe Asp Phe Leu Ser Cys Ala Phe Pro Ser Glu Asn Pro Leu Leu
 260 265 270
 Lys Ile Lys Asp Glu Leu Lys Glu Tyr Gly Phe Ile Ser Thr Leu Arg
 275 280 285
 Asp Leu Glu Asn Ser Pro Phe Ile Val Glu Asn Val Pro Ile Leu Asn
 290 295 300
 Ser Thr Pro Ile Leu Asp Asn Thr Pro Ala Leu Asp Asn Ala Pro Lys
 305 310 315 320
 Lys Ser Arg Met Ile Val Leu Glu Ser Ala Glu Pro Leu Ser Met Phe
 325 330 335
 Leu Glu Lys Leu Glu Asn Pro Asn Ala Arg Val Phe Met Arg Leu Val
 340 345 350
 Leu Asp Lys Asp Lys Lys Ile Leu Ala Leu Ala Phe Leu Leu Gln Asp
 355 360 365
 Gln Gly Tyr Phe Leu Pro Leu Glu Glu Ala Leu Phe Ser Pro Phe Ser
 370 375 380
 Leu Glu Phe Leu Gln Asn Ala Phe Ser Gln Met Leu Gln His Ala Cys
 385 390 395 400
 Ile Ile Gly His Asp Leu Lys Pro Leu Leu Ser Phe Leu Lys Ala Lys
 405 410 415
 Tyr Gln Val Pro Leu Glu Asn Ile Arg Ile Gln Asp Thr Gln Ile Leu
 420 425 430
 Ala Phe Leu Lys Asn Pro Glu Lys Val Gly Phe Asp Glu Val Leu Lys
 435 440 445
 Glu Tyr Leu Lys Glu Asp Leu Ile Pro His Glu Lys Ile Lys Asp Phe

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

```
(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...76
```

Thr Ser Leu Ser Leu Phe Gly Glu Asp Leu Ala Lys Glu Lys Arg Ser

623

```

1           5           10           15
Ile Ala Lys Ser Ile Asn Phe Gly Leu Val Tyr Gly Met Gly Ser Lys
                20           25           30
Lys Leu Ser Glu Thr Leu Ser Ile Pro Leu Ser Glu Ala Lys Ser Tyr
                35           40           45
Ile Glu Ala Tyr Phe Lys Arg Phe Pro Ser Ile Lys Asp Tyr Leu Asn
                50           55           60
Gly Met Arg Glu Glu Ile Leu Lys Thr Ser Lys Ala
65           70           75

```

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

```

Lys Glu Lys Asp Asn Pro Leu Gln Asn Phe Val Phe Asn Lys Lys Trp
1           5           10           15
Leu Ile Tyr Ser Ser Leu Leu Pro Leu Phe Phe Leu Asn Pro Leu Met
                20           25           30
Ala Glu Asp Asp Gly Phe Phe Met Gly Val Ser Tyr Gln Thr Ser Leu
                35           40           45
Ala Val Gln Arg Val Asp Asn Ser Gly Leu Asn Ala Ser Gln Asp Ala
                50           55           60
Ser Thr Tyr Ile Arg Gln Asn Ala Ile Ala Leu Glu Ser Ala Ala Val
65           70           75           80
Pro Leu Ala Tyr Tyr Leu Glu Ala Met Gly Gln Gln Thr Arg Val Leu
                85           90           95
Met Gln Met Leu Cys Pro Asp Pro Ser Lys Arg Cys Leu Leu Tyr Ala
                100           105           110
Gly Gly Tyr Gln Asn Gly Gln Asn Asn Asn Gly Asp Thr Gly Asn Asn
                115           120           125
Pro Pro Arg Gly Asn Val Asn Ala Thr Phe Asp Met Gln Ser Leu Val
                130           135           140
Asn Asn Leu Asn Lys Leu Thr Gln Leu Ile Gly Glu Thr Leu Ile Arg
145           150           155           160
Asn Pro Glu Asn Leu Pro Asn Ser Lys Val Phe Asn Val Lys Phe Gly
                165           170           175
Asn Gln Ser Thr Val Ile Ala Leu Pro Glu Gly Leu Ala Asn Thr Met
                180           185           190
Asp Ala Leu Asn Asn Asp Ile Thr Asn Ala Leu Thr Thr Leu Trp Tyr
                195           200           205
Asn Gln Thr Leu Thr Asn Lys Ser Phe Ser Thr Pro Ser Asn Thr Ser

```

210	215	220
Val Asn Phe Ser Pro Gln Val Leu Gln His Leu Leu Gln Asp Gly Leu		
225	230	235
Ala Thr Ala Asn Asn Asn Gln Thr Ile Cys Ser Thr Gln Asn Gln Cys		240
	245	250
Thr Ala Thr Asn Glu Ala Lys Ser Ile Ala Gln Asn Ala Gln Asn Ile		255
	260	265
Phe Gln Ala Leu Met Gln Ala Gly Ile Leu Gly Gly Leu Ala Asn Glu		270
	275	280
Lys Gln Phe Gly Phe Thr Tyr Asn Lys Ala Pro Asn Gly Gly Asp Ser		285
	290	295
Gln Gln Gly Tyr Ser Lys Leu Cys Gly Pro Gly Ile Thr Pro Lys Arg		300
305	310	315
Gln His His Ala Ser		320
	325	

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

Tyr Asn Gln Met Gln Asp Val Ile Asn Tyr Gly Glu Ser Leu Leu Ser		
1	5	10
Asn Thr Val Ala Tyr Gly Asp Phe Ile Thr Asn Trp Val Ala Pro Tyr		
	20	25
Leu Asp Leu Asn Asn Lys Gly Leu Asn Phe Leu Pro Asn Tyr Gly Gly		
	35	40
Gln Leu Asn Gly Ala Asn Asn Gln Thr Pro Gln Leu Thr Pro Gln Gln		
	50	55
Ala Gln Gln Glu Gln Lys Val Ile Met Asn Gln Leu Glu Gln Ala Thr		
65	70	75
Asn Ala Pro Thr Pro Ala Gln Ile Asn Arg Ile Leu Ala Asn Pro Tyr		
	85	90
Ser Pro Thr Ala Lys Thr Leu Met Ala Tyr Gly Leu Tyr Arg Ser Lys		
	100	105
Ala Val Ile Gly Gly Val Ile Asp Glu Met Gln Thr Lys Val Asn Gln		
	115	120
Val Tyr Gln Met Gly Phe Ala Arg Asn Phe Leu Glu His Thr Leu Tyr		
	130	135
Ile Leu Ile Thr Leu Asn Gly Phe Gly Val Lys Met Gly Tyr Lys Gln		
145	150	155
Phe Phe Gly Lys Lys Arg Met Phe Gly Leu Arg Tyr Tyr Gly Phe Tyr		

625

				165					170					175					
Asp	Phe	Gly	Tyr	Ala	Gln	Phe	Gly	Thr	Glu	Ser	Ser	Leu	Val	Lys	Ala				
				180					185					190					
Thr	Leu	Ser	Ser	Tyr	Gly	Ala	Gly	Thr	Asp	Phe	Leu	Tyr	Asn	Val	Phe				
				195					200					205					
Thr	Arg	Lys	Arg	Gly	Thr	Glu	Ala	Ile	Asp	Ile	Gly	Phe	Phe	Ala	Gly				
				210				215						220					
Ile	Gln	Leu	Ala	Gly	Gln	Thr	Trp	Lys	Thr	Asn	Phe	Leu	Asp	Gln	Val				
				225				230						235					
Asp	Gly	Asn	His	Leu	Lys	Pro	Lys	Asp	Thr	Ser	Phe	Gln	Phe	Leu	Phe				
				245					250					255					
Asp	Leu	Gly	Ile	Met	Asp	Gln	Ile	Phe	Pro	Lys	Ser	Leu	Ile	Ser	Lys				
				260				265						270					
Lys	Asn	Leu	Val	Phe	Leu	Lys	Gly												
				275				280											

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

Gln	Pro	His	Lys	Gln	Arg	Asn	Ile	Ala	His	Leu	Gln	His	Ala	Gln	Ala				
1				5				10					15						
Val	Ile	Thr	Ser	Val	Leu	Ala	Phe	Trp	Ser	Leu	Tyr	Ala	Gly	Asn	Ala				
				20				25					30						
Leu	Ser	Phe	His	Val	Thr	Gly	Leu	Asn	Asp	Gly	Ser	Asn	Ser	Pro	Leu				
				35				40					45						
Gly	Arg	Ile	His	Arg	Asp	Gly	Asn	Cys	Thr	Gly	Leu	Gln	Gln	Cys	Phe				
				50				55				60							
Met	Ser	Lys	Glu	Thr	Tyr	Asp	Lys	Met	Lys	Thr	Leu	Ala	Glu	Asn	Leu				
				65				70				75			80				
Gln	Lys	Ala	Gln	Gly	Asn	Leu	Cys	Ala	Leu	Ser	Glu	Cys	Ser	Ser	Asn				
				85				90					95						
Gln	Asp	Ser	Gly	Phe	Pro	Val	Leu	Asp	Ser	Ala	Gly	Lys	Gln	Val	Thr				
				100				105					110						
Ile	Thr	Ile	Thr	Thr	Gln	Thr	Asn	Gly	Ala	Asn	Lys	Ser	Glu	Thr	Thr				
				115				120					125						
Thr	Thr	Thr	Thr	Thr	Thr	Asn													
				130				135											

(2) INFORMATION FOR SEQ ID NO:714:

626

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

Gly	Leu	Ser	Arg	Gln	Gly	Asn	Glu	Arg	Leu	Asp	Ala	Thr	Leu	Asn	Leu
1				5					10					15	
Lys	Thr	Gly	Val	Gln	Ser	Phe	Phe	Lys	Lys	Tyr	Ile	Gly	Ile	Arg	Gly
			20					25					30		
Val	Phe	Ala	Trp	Asp	Leu	Gly	Ser	Gly	Lys	Val	Asn	Tyr	Gln	Ser	Tyr
		35				40					45				
Lys	Asp	Pro	Thr	Asn	Ser	Phe	Phe	Thr	Met	Leu	Ala	Val	Gly	Leu	Asp
	50				55						60				
Val	Ile	Met	Glu	Phe	Pro	Leu	Gly	Ser	Tyr	Lys	His	Tyr	Leu	Gly	Ala
65				70					75					80	
Phe	Gly	Gly	Ala	Arg	Gly	Ala	Leu	Val	Val	Tyr	Thr	Asp	Lys	Gln	Asn
			85					90					95		
Phe	Lys	Phe	Phe	Lys	His	Ser	Val	Val	Ser	Gly	Gly	Leu	Ala	Ile	Ser
			100				105						110		
Gly	Gly	Trp	Leu	Ile	Leu	Leu	Arg	Thr	Pro	His	Phe				
			115				120								

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

Pro	Val	Gly	Leu	Tyr	Pro	Leu	Glu	Ser	Pro	Leu	Ile	Tyr	Glu	Glu	Asn
1				5					10					15	

627

```

His Leu Leu Pro Met Gly Phe Ile His Leu Ala Phe Arg Gly Gly Gly
      20              25              30
Ser Leu Ser Asp Lys Asn Gln Leu Gly Leu Ala Lys Leu Phe Ala Gln
      35              40              45
Val Leu Asn Glu Gly Thr Lys Glu Leu Gly Ala Val Gly Phe Ala Gln
      50              55              60
Leu Leu Glu Gln Lys Ala Ile Ser Leu Asn Val Asp Thr Ser Ala Glu
      65              70              75              80
Asp Leu Gln Ile Thr Leu Glu Phe Leu Lys Glu Tyr Glu Asp Glu Ala
      85              90              95
Ile Met Arg Leu Lys Glu Leu
      100

```

(2) INFORMATION FOR SEQ ID NO:716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

```

Tyr Ser Val Tyr Ile Arg Ser Asn Phe Ser Lys Val Ala His Phe Ala
1              5              10              15
Ser Gly Tyr Leu Gln Thr Lys Leu Ser Thr Gln Ala Lys Ser Val Ala
      20              25              30
Leu Ala Lys Lys Thr Thr Lys Glu Phe Ile Glu Lys Gly Met Thr Gln
      35              40              45
Gln Glu Leu Asp Asp Ala Lys Lys Phe Leu Leu Gly Ser Glu Pro Leu
      50              55              60
Arg Asn Glu Thr Ile Ser Ser Arg Leu Asn Thr Thr Tyr Asn Tyr Phe
      65              70              75              80
Ile Trp Val Cys Leu
      85

```

(2) INFORMATION FOR SEQ ID NO:717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

628

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

```

Arg Arg Ala Trp Ile Leu Leu Gly Leu Lys Asn Leu Lys Gly Val Trp
1          5          10          15
Val Leu Lys Gly Leu Lys Lys Ala Phe Lys Glu Arg Phe Cys Ser Gln
20          25          30
Val Tyr Ile Ser Phe Asn Val Asp His Asn Leu Leu Ser Ala Gln Val
35          40          45
Leu Arg Val Lys Asn His Arg Ile Lys Glu Lys Phe Phe Lys Thr Phe
50          55          60
Glu Thr Lys Val Glu Thr Lys Asn Gly Glu Val Pro Ile Gln Ala Leu
65          70          75          80
Lys Ile Ala Arg Thr Tyr Ser Gln Lys Tyr Pro Tyr Thr Tyr Phe Ser
85          90          95
Ala Met Ser Lys Ala Lys Glu Val Leu Cys Glu Lys Gln Ala Phe Glu
100         105         110
Gln Ile Lys Gln Glu Asn Gln Asp Tyr Gln Ala Cys Glu Val Asn Gln
115         120         125
Lys Tyr Cys Val Tyr Val Glu Ser Lys Asp Phe Leu Lys Asp Phe Lys
130         135         140
Arg Phe Lys Ile Gln Asp Val Asp Phe Leu Phe Ser Pro Phe Ser Leu
145         150         155         160
Ile Tyr Asp Phe Val Arg Asp Asn Leu Glu Asn Lys Pro Leu Leu Tyr
165         170         175
Leu Leu Leu Glu Arg Ser Arg Phe Tyr Phe Leu Ile Ala Asp Lys Lys
180         185         190
Glu Ile Phe Leu Ala Lys Ser Val Phe Leu Glu Glu Gln Pro Glu Glu
195         200         205
Phe Ile Glu Ser Lys Glu Glu Asp Ser Met Gly Met Asp Asn Glu Ala
210         215         220
Val Asp Leu Phe Leu Ser Glu Ile Gln Glu Asp Ile Asp Ser Leu Glu
225         230         235         240
Glu Ala Ile Gly Leu Asp Ser Ser Lys Asp Asn Ser Glu Lys Ile Thr
245         250         255
Glu Asp Ala Tyr Ser Leu Ile Glu Gly Met Thr Asn Ile Pro Leu Ile
260         265         270
Ala Asp Val Leu Gln Glu Gly Leu Arg Gly Val Tyr His Ser Arg Glu
275         280         285
Ile Asp Phe Val Glu Lys Val Val Val Leu Asp Ser Cys Gln Ile His
290         295         300
His Lys Ala Leu Met His Leu Gln Glu Thr Leu Met Ile Glu Val Asp
305         310         315         320
Arg Leu Asp Phe Ser Leu Val Glu Arg Leu Asn Val Leu Ala Arg Met
325         330         335
Glu Asn Glu Lys His Ala Phe
340

```

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:

629

- (A) LENGTH: 420 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

```

Met Ile Phe Gly Asp Phe Lys Tyr Gln Lys Ser Val Lys Lys Leu Thr
1           5           10           15
Ala Thr Asn Leu Asn Glu Leu Lys Asn Ala Leu Asp Phe Ile Ser Gln
20           25           30
Asn Arg Gly Lys Gly Tyr Phe Val Gly Tyr Leu Leu Tyr Glu Ala Arg
35           40           45
Leu Ala Phe Leu Asp Glu Asn Phe Gln Ser Gln Thr Pro Phe Leu Tyr
50           55           60
Phe Glu Gln Phe Leu Glu Arg Lys Lys Tyr Leu Val Glu His Leu Lys
65           70           75           80
Glu His Ala Phe Tyr Pro Lys Ile His Ser Ser Leu Asp Gln Lys Thr
85           90           95
Tyr Phe Lys Gln Phe Lys Ala Val Lys Glu His Leu Lys Asn Gly Asp
100          105          110
Thr Tyr Gln Val Asn Leu Thr Met Asp Leu Leu Leu Asn Thr Lys Ala
115          120          125
Lys Pro Lys Arg Val Phe Lys Glu Val Ile His Asn Gln Asn Thr Pro
130          135          140
Phe Lys Ala Phe Ile Glu Asn Glu Phe Gly Ser Val Leu Ser Phe Ser
145          150          155          160
Pro Glu Leu Phe Phe Glu Leu Glu Phe Leu Asp Thr Ala Ile Lys Ile
165          170          175
Ile Thr Lys Pro Met Lys Gly Thr Ile Ala Arg Ser Asn Asn Pro Leu
180          185          190
Ile Asp Glu Lys Asn Arg Leu Phe Leu Gln Asn Asp Asp Lys Asn Arg
195          200          205
Ser Glu Asn Val Met Ile Val Asp Leu Leu Arg Asn Asp Leu Ser Arg
210          215          220
Leu Ala Leu Lys Asn Ser Val Lys Val Asn Gln Leu Phe Glu Ile Ile
225          230          235          240
Ser Leu Pro Ser Val Tyr Gln Met Ile Ser Glu Ile Glu Ala Gln Leu
245          250          255
Pro Leu Lys Thr Ser Leu Phe Glu Ile Phe Lys Ala Leu Phe Pro Cys
260          265          270
Gly Ser Val Thr Gly Cys Pro Lys Ile Lys Thr Met Gln Ile Ile Glu
275          280          285
Ser Leu Glu Lys Arg Pro Arg Gly Val Tyr Cys Gly Ala Ile Gly Met
290          295          300
Val Gly Gly Lys Lys Ala Leu Phe Ser Val Pro Ile Arg Thr Leu Glu
305          310          315          320

```

630

(2) INFORMATION FOR SEQ ID NO:719:

(A) LENGTH: 285 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Helicobacter pylori*

(A) NAME/KEY: misc_feature
(B) LOCATION 1...285

Lys	Gln	Ile	Arg	Lys	Glu	Arg	Leu	Asn	Lys	Leu	Leu	Lys	Lys	Gly	Phe
1				5					10					15	
Leu	Ala	Phe	Phe	Leu	Ser	Val	Tyr	Leu	Arg	Ala	Asp	Asp	Leu	Val	Thr
		20						25					30		
Tyr	Thr	Ile	Ala	Lys	Glu	Glu	Asp	Leu	Gly	Tyr	Gln	Arg	Phe	Leu	Ala
		35					40					45			
Lys	Lys	Cys	Leu	Arg	Gly	Lys	Thr	His	Pro	Pro	Cys	Phe	Thr	Ala	Ser
	50					55					60				
Lys	Lys	Pro	Lys	Arg	Lys	Pro	Phe	Asn	Ile	Asp	Lys	Ser	Ser	His	Tyr
65					70					75				80	
Tyr	Gly	Thr	Ser	Val	Val	Gln	Met	Ser	Trp	Leu	Gln	Ser	Arg	Glu	Lys
				85					90					95	
Phe	Glu	Asn	His	Ser	Lys	Tyr	Arg	Asn	Ile	Pro	Phe	Ala	Glu	Val	Ser
		100						105					110		
Leu	Ile	Tyr	Gly	Tyr	Lys	Gln	Phe	Phe	Pro	Lys	Lys	Glu	His	Tyr	Gly
		115					120					125			
Phe	Arg	Phe	Tyr	Val	Ser	Leu	Asp	Tyr	Ala	Tyr	Gly	Phe	Phe	Leu	Lys
	130					135					140				
Asn	Lys	Gly	Ala	Leu	Gly	Asp	Ser	Leu	Arg	Ala	Ser	Ser	Gln	Ile	Pro
145					150					155					160
Lys	Ser	Tyr	Arg	Glu	Lys	Leu	Gln	Arg	Lys	Glu	Thr	Phe	Ile	Asn	Ala
				165					170					175	

631.

```

Ile Phe Tyr Gly Val Gly Ala Asp Phe Leu Tyr Lys Arg Ala Phe Gly
      180      185      190
Thr Leu Ile Leu Gly Val Asn Phe Val Gly Glu Thr Trp Phe Tyr Glu
      195      200      205
Thr Lys Ile Phe Lys Gln Trp Ala Lys Asp Ser Leu Asn Thr Tyr Arg
      210      215      220
Pro Asn Met Phe Gln Val Met Leu Asn Val Gly Tyr Arg Tyr Arg Phe
      225      230      235      240
Ser Arg Tyr Lys Asn Trp Ala Ile Glu Phe Gly Ala Arg Ile Pro Phe
      245      250      255
Leu Ile Asn Asp Tyr Phe Lys Thr Pro Leu Tyr Thr Leu His Phe Lys
      260      265      270
Arg Asn Ile Ser Val Tyr Leu Thr Ser Thr Tyr Asp Phe
      275      280      285

```

(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

```

Asn Thr Leu Phe Tyr Phe Phe Leu Leu Gln Ala Val Ile Val Leu Asp
1      5      10      15
Ser Phe Glu Ile Leu Lys Ala Leu Lys Ser Leu Asp Leu Leu Lys Asn
      20      25      30
Ala Pro Ala Trp Trp Trp Pro Asn Ala Leu Lys Phe Glu Ala Leu Leu
      35      40      45
Gly Ala Val Leu Thr Gln Asn Thr Lys Phe Glu Ala Val Leu Lys Ser
      50      55      60
Leu Glu Asn Leu Lys Asn Ala Phe Ile Leu Glu Asn Asp Asp Glu Ile
      65      70      75      80
Asn Leu Lys Lys Ile Ala Tyr Ile Glu Phe Ser Lys Leu Ala Glu Cys
      85      90      95
Val Arg Pro Ser Gly Phe Tyr Asn Gln Lys Ala Lys Arg Leu Ile Asp
      100     105     110
Leu Ser Lys Asn Ile Leu Lys Asp Phe Gln Ser Phe Glu Asn Phe Lys
      115     120     125
Gln Glu Val Thr Lys Glu Trp Leu Leu Asp Gln Lys Gly Ile Gly Lys
      130     135     140
Glu Ser Ala Asp Ala Ile Leu Cys Tyr Val Cys Ala Lys Glu Val Met
      145     150     155     160
Val Val Asp Lys Tyr Ser Tyr Leu Phe Leu Lys Lys Leu Gly Ile Glu
      165     170     175

```

632

```

Ile Glu Asp Tyr Asp Glu Leu Gln His Phe Phe Glu Lys Gly Val Gln
      180                      185                      190
Glu Asn Leu Asn Ser Ala Leu Ala Leu Tyr Glu Asn Thr Ile Ser Leu
      195                      200                      205
Ala Gln Leu Tyr Ala Arg Phe His Gly Lys Ile Val Glu Phe Ser Lys
      210                      215                      220
Gln Lys Leu Glu Leu Lys Leu
225                      230

```

(2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

```

Ile Ser Phe Asn Ala Asp Tyr Phe Arg Ile Trp Ala Arg Asp Phe Ala
1          5          10          15
Thr Gly Gln Tyr Ser Val Tyr Thr Ser Gly Pro Met Lys Gly Asn Val
      20          25          30
Arg Pro Ile Asn Gly Tyr Ser Gln Gly Val Glu Leu Glu Leu Tyr Tyr
      35          40          45
Arg Pro Ile Arg Gly Leu Gln Phe His Ala Ala Phe Asn Tyr Ile Asp
      50          55          60
Thr Arg Val Thr Ser His Gly Pro Leu Thr Asp Leu Asn Gly Asp Val
      65          70          75          80
Leu Lys Gly Thr Ser Tyr Asn Lys His Phe Pro Phe Val Ser Pro Phe
      85          90          95
Gln Phe Ile Phe Asp Ala Arg Tyr Asn Trp Arg Lys Thr Thr Ile Gly
      100         105         110
Ile Ser Ser Tyr Phe Tyr Ser Arg Ala Tyr Ser Gly Ile Ser Asn Ser
      115         120         125
Ala Ala Gly Gly Tyr Tyr Gly Met Gln Tyr Tyr Ser Gly Gly Asn Asn
      130         135         140
Tyr Glu Ser Val Leu Asn Ser Gly Tyr Gln Cys Glu Ala Trp Cys Met
      145         150         155         160
Thr Gln His Glu Gly Leu Leu Pro Trp Tyr Trp Val Trp Asn Ile Gln
      165         170         175
Val Ser Gln Ile Phe Trp Glu Asn Gly Arg His Arg Val Thr Gly Ser
      180         185         190
Leu Gln Ile Asn Asn Ile Phe Asn Met Lys Tyr Tyr Phe Thr Gly Ile
      195         200         205
Gly Ser Ser Pro Ala Gly Leu Gln Pro Ala Pro Gly Arg Ser Val Thr
      210         215         220

```

Ala Tyr Leu Asn Tyr Thr Phe
225 230

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

Ser	Gly	Val	Val	Lys	Met	Lys	Asp	Lys	Lys	Ile	Asp	Glu	Glu	Thr	Asn	1	5	10	15
Ala	Val	Leu	Glu	Gly	Glu	Lys	Tyr	Thr	Val	Cys	Val	Ser	Cys	Gln	Ile	20	25	30	
Gly	Cys	Gln	Val	Gly	Cys	Ser	Phe	Cys	Phe	Thr	Gln	Lys	Gly	Gly	Phe	35	40	45	
Val	Arg	Asp	Leu	Lys	Ala	Ser	Glu	Ile	Ile	Gln	Gln	Ala	Leu	Leu	Ile	50	55	60	
Lys	Glu	Ala	Asn	Asn	Leu	Pro	Ile	Glu	Lys	Ala	Leu	Asn	Ile	Val	Phe	65	70	75	80
Met	Gly	Met	Gly	Glu	Pro	Leu	Asn	Asn	Leu	Asp	Glu	Val	Cys	Lys	Ala	85	90	95	
Val	Glu	Ile	Phe	Asn	Thr	Gly	Met	Gln	Ile	Ser	Pro	Lys	Arg	Val	Thr	100	105	110	
Ile	Ser	Thr	Ser	Gly	Val	Ala	Asp	Lys	Ile	Pro	Ile	Leu	Ala	Gly	Lys	115	120	125	
Asn	Leu	Gly	Val	Gln	Leu	Ala	Ile	Ser	Leu	His	Ala	Val	Asp	Asp	Lys	130	135	140	
Thr	Arg	Ser	Ser	Leu	Met	Pro	Leu	Asn	Lys	Lys	Tyr	Asn	Ile	Glu	Cys	145	150	155	160
Val	Leu	Asn	Glu	Val	Arg	Lys	Trp	Pro	Leu	Glu	Gln	Arg	Lys	Arg	Val	165	170	175	
Met	Phe	Glu	Tyr	Leu	Leu	Ile	Lys	Asp	Leu	Asn	Asp	Ser	Leu	Asp	Cys	180	185	190	
Ala	Lys	Lys	Leu	Leu	Lys	Leu	Leu	Asn	Gly	Ile	Lys	Ser	Lys	Val	Asn	195	200	205	
Leu	Ile	Leu	Phe	Asn	Pro	His	Glu	Gly	Ser	Lys	Phe	Glu	Arg	Pro	Ser	210	215	220	
Leu	Glu	Ser	Ala	Arg	Met	Phe	Ala	Asn	Phe	Leu	Asn	Ala	Lys	Gly	Leu	225	230	235	240
Leu	Cys	Thr	Ile	Arg	Glu	Ser	Lys	Ala	Leu	Asp	Ile	Glu	Ala	Ala	Cys	245	250	255	
Gly	Gln	Leu	Arg	Glu	Lys	Lys	Leu	Gln	Gln	Lys	Ile					260	265		

(2) INFORMATION FOR SEQ ID NO:723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

```

Arg Leu Ser Glu Pro Ile Asp Arg Phe Thr Arg Ile Arg Trp Leu Phe
1           5           10           15
Lys Asn Asp Phe Glu Lys Ile Arg Gln Gln Arg Val Leu Ile Cys Gly
          20           25           30
Val Gly Gly Val Gly Gly Phe Ala Leu Asp Ser Leu Tyr Arg Val Gly
          35           40           45
Ile Gly Gln Ile Thr Ile Ile Asp Lys Asp Met Phe Asp Val Thr Asn
          50           55           60
Gln Asn Arg Gln Ile Gly Ser Glu Arg Ile Gly Glu Ser Lys Val Leu
65           70           75           80
Val Leu Gln Asp Leu Tyr Lys Gly Ile Gln Ala Leu Asn Cys Arg Ile
          85           90           95
Asp Glu Ala Phe Leu Asn Ser Phe Asn Phe Arg Asp Tyr Asp Tyr Ile
          100          105          110
Leu Asp Cys Met Asp Asp Leu Pro Ile Lys Thr Ser Leu Ala Ile Lys
          115          120          125
Cys Gln Asn Phe Ala Tyr Gly Lys Phe Ile Ser Ser Met Gly Ser Ala
          130          135          140
Lys Arg Leu Asn Pro Lys His Ile Gln Val Gly Ser Val Trp Glu Ser
145          150          155          160
Tyr Gly Asp Lys Phe Gly Arg Lys Phe Arg Asp Phe Leu Lys Lys Arg
          165          170          175
Arg Phe Lys Gly Asp Phe Lys Val Val Phe Ser Pro Glu Val Pro His
          180          185          190
Cys Ile Glu Leu Gly Ser Phe Asn Ala Val Thr Ala Ser Phe Gly Leu
          195          200          205
Gln Ile Ala Ser Glu Val Val Gln Asp Ile Ile Lys Asn Glu Arg Gln
          210          215          220
Trp Asn Glu Arg Leu Arg Arg Arg Ile Gly Arg Phe
225          230          235

```

(2) INFORMATION FOR SEQ ID NO:724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid

635

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

```

Ala Lys Ala Arg Val Gln Phe Asn Arg Ala Asn Glu Arg Gln Arg Arg
1      5      10      15
Ala Lys Glu Phe Tyr Tyr Glu Glu Val Gln Lys Ala Ile Lys Glu Ile
20     25     30
Asp Ser Ser Lys Lys His Asn Ile Asn Met Glu Arg Ser Arg Ala Glu
35     40     45
Val Ser Glu Ile Leu Asn Asn Thr Tyr Ser Asn Leu Asp Lys Tyr Glu
50     55     60
Ala Tyr Gln Gly Leu Leu Asn Pro Ala Val Ser Tyr Leu Ser Gly Leu
65     70     75     80
Phe Tyr Ala Leu Asn Gly Asp Lys Asn Lys Gly Leu Gly Tyr Leu Asn
85     90     95
Glu Ala Tyr Gly Ile Ser Gln Ser Pro Phe Val Ala Gln Asp Leu Val
100    105    110
Phe Phe Lys Asn Pro Asn Arg Ser His Phe Thr Trp Ile Ile Ile Glu
115    120    125
Asp Gly Lys Glu Pro Gln Lys Ser Glu Phe Lys Ile Asp Val Pro Ile
130    135    140
Phe Met Ile Asp Ser Val Tyr Asn Val Ser Val Ala Leu Pro Lys Leu
145    150    155    160
Glu Lys Gly Glu Ala Phe Tyr Gln Asn Phe Thr Leu Lys Asp Gly Glu
165    170    175
Lys Val Thr Pro Phe Asp Thr Leu Ala Ser Ile Asp Ala Val Val Ala
180    185    190
Ser Glu Phe Arg Lys Gln Leu Pro Tyr Ile Ile Thr Arg Ala Ile Leu
195    200    205
Ser Ala Thr Phe Lys Val Gly Met Gln Ala Val Ala Asn Tyr Tyr Leu
210    215    220
Gly Phe Val Gly Gly Leu Val Thr Ser Leu Tyr Ser Gly Val Ser Thr
225    230    235    240
Phe Ala Asp Thr Arg Asn Thr Ser Ile Phe Ala His Lys Ile Tyr Leu
245    250    255
Met Arg Ile Lys Asn Lys Ala Phe Glu Ser Tyr Glu Val Arg Ala Asp
260    265    270
Ser Ile Asp Ala Phe Ser Phe Ser Leu Lys Pro Cys Lys Arg Ser Leu
275    280    285
Glu Ser Pro Lys Ile Ile Asp Ala Arg Glu Leu Leu Ser Gly Phe Val
290    295    300
Thr Ala Pro Gln Val Phe Cys Ser Asn Arg His Asn Ile Leu Tyr Val
305    310    315    320
Arg Ser Phe Lys Asn Gly Phe Val Leu Ser His Leu Lys
325    330

```

(2) INFORMATION FOR SEQ ID NO:725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

```

Arg Asn Lys Asp Lys Arg Glu Tyr Phe Glu Asn Ala Thr Ala Gln Ile
1          5          10          15
Gly Ala Lys Leu Leu Val Cys Asp Ile Arg Glu Gln Phe Phe Asn Asp
          20          25          30
Val Leu Phe Lys Pro Lys Tyr Gly Tyr Gly Lys Tyr Phe Asn Pro Cys
          35          40          45
Ile Asp Cys His Ala Asn Met Phe Arg Asn Ala Phe Tyr Lys Met Leu
          50          55          60
Glu Leu Asp Ala Asp Phe Val Leu Ser Gly Glu Val Leu Gly Asn Ala
65          70          75          80
Leu Asn Pro Lys Gly Lys Lys Arg Ser Ile Arg
          85          90

```

(2) INFORMATION FOR SEQ ID NO:726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

```

Gly Glu Val Met Ala Asp Ser Leu Ala Gly Ile Asp Gln Val Thr Ser
1          5          10          15
Leu His Lys Asn Asn Glu Leu Gln Leu Leu Cys Phe Arg Leu Gly Lys

```

637

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

(2) INFORMATION FOR SEQ ID NO:727:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

Ala Val Ala Phe Cys Leu Pro Tyr Ser Ser Pro Lys Thr Ser Leu Ala

638

1		5		10		15									
Thr	Glu	Leu	His	Tyr	Ser	Ala	Asn	Glu	Arg	Ile	Glu	Ala	Phe	Ser	Ser
		20						25					30		
Asn	Asp	Glu	Lys	Thr	Glu	Ser	Phe	Glu	Leu	Asn	Glu	Gln	Ser	Phe	Glu
		35					40					45			
Ala	Ile	Lys	Glu	Asn	Ala	Ala	Lys	Tyr	Ser	Tyr	Leu	Lys	Val	Tyr	Leu
		50				55					60				
Lys	Asn	Val	Ala	Leu	Lys	Asp	Ser	Ala	Pro	Leu	Val	Phe	Val	Asp	Met
65					70					75				80	
Pro	Gly	Phe	Asp	Ser	Pro	Ile	Ser	Ser	His	Thr	His	Ala	Ile	Leu	Glu
			85						90				95		
Tyr	Leu	Glu	Arg	Gly	Val	His	Phe	Val	Ile	Leu	Thr	Ser	Val	Glu	Glu
			100					105					110		
Gly	Asn	Leu	Thr	Lys	Arg	Met	Val	Arg	Glu	Leu	Lys	Thr	Phe		
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

Arg	His	Pro	Ile	Glu	Asn	Ser	Ile	Cys	Asp	Leu	Ser	Glu	Leu	Asn	Asn
1			5					10					15		
Leu	Lys	Pro	Leu	Gly	Ala	Glu	Met	Phe	Val	Gly	Leu	Asp	Gly	Ile	Asp
		20						25				30			
Ala	Met	Ile	Glu	Glu	Cys	Val	Ser	Asn	Leu	Val	Ile	Asn	Ala	Ile	Val
		35					40					45			
Gly	Val	Pro	Gly	Leu	Lys	Ala	Ser	Phe	Lys	Ser	Leu	Gln	Arg	Asn	Lys
		50				55					60				
Lys	Leu	Ala	Leu	Ala	Asn	Lys	Glu	Ser	Leu	Val	Ser	Ala	Gly	His	Leu
65					70					75				80	
Leu	Asp	Ile	Ser	Gln	Ile	Thr	Pro	Val	Asp	Ser	Glu	His	Phe	Gly	Leu
			85						90				95		
Trp	Ala	Leu	Leu	Gln	Asn	Lys	Thr	Leu	Lys	Pro	Lys	Ser	Leu	Ile	Ile
		100						105				110			
Ser	Ala	Ser	Gly	Gly	Ala	Phe	Arg	Asp	Thr	Pro	Leu	Asp	Leu	Ile	Ala
		115					120				125				
Ile	Gln	Asn	Ala	Gln	Asn	Ala	Leu	Lys	His	Pro	Asn	Trp	Ser	Met	Gly
		130				135				140					
Asp	Lys	Ile	Thr	Ile	Asp	Ser	Ala	Ser	Met	Val	Asn	Lys	Leu	Phe	Glu
145					150					155				160	
Ile	Leu	Glu	Thr	Tyr	Trp	Leu	Phe	Gly	Ala	Ser	Leu	Lys	Ile	Asp	Ala

639

[illegible]

(2) INFORMATION FOR SEO ID NO:729:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

Glu	Thr	Leu	Ala	Arg	Val	Leu	Lys	Val	Ser	Cys	Leu	Ala	Met	Gly	Leu
1				5					10					15	
Ala	Gln	Met	Cys	Cys	Leu	Thr	Gln	Leu	Phe	Ser	Ile	Val	Arg	Asn	Leu
		20						25					30		
His	Leu	Gly	Phe	Phe	Leu	Gly	Val	Ala	Ile	Gly	Gly	Thr	Ser	Trp	Gly
		35					40					45			
Pro	Thr	Asn	Tyr	Tyr	Phe	Lys	Asp	Leu	Ala	Glu	Glu	Tyr	Arg	Gly	Ser
		50				55					60				
Phe	His	Pro	Ser	Asn	Phe	Gln	Val	Leu	Val	Asn	Gly	Gly	Ile	Arg	Leu
65					70					75					80
Gly	Thr	Lys	His	Gln	Gly	Phe	Glu	Ile	Gly	Leu	Lys	Ile	Gln	Thr	Ile
				85					90					95	
Arg	Asn	Asn	Tyr	Tyr	Thr	Ala	Ser	Ala	Asp	Asn	Val	Pro	Glu	Gly	Thr
			100					105					110		
Thr	Tyr	Arg	Phe	Thr	Phe	His	Arg	Pro	Tyr	Ala	Phe	Tyr	Trp	Arg	Tyr

115 120 125
 Ile Val Ser Phe
 130

(2) INFORMATION FOR SEQ ID NO:730:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...60
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

Val	Leu	Lys	Asn	Glu	Ile	Ser	Tyr	Asn	Lys	Pro	Ile	Leu	Asn	Thr	Asn
1			5					10					15		
Asp	Tyr	Leu	Asn	Lys	Asp	Asn	Thr	Met	Lys	Asp	Ser	Phe	Leu	Phe	Thr
		20						25				30			
Ser	Glu	Ser	Val	Thr	Glu	Gly	His	Pro	Asp	Lys	Met	Ala	Asp	Gln	Ile
		35				40					45				
Ser	Asp	Ala	Val	Leu	Asp	Tyr	Met	Ile	Glu	Arg	Asp				
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:731:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...111
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

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

641

```

Ala Arg His Met Val Arg Lys Ile Gly Tyr Thr Asn Ala Leu Tyr Cys
  35                      40                      45
Phe Asp Tyr Arg Ser Ala Ala Val Leu Asn Gly Ile Gly Glu Gln Ser
  50                      55                      60
Pro Asp Ile Asn Gln Gly Val Asp Arg Glu Asp Gly Glu Ile Gly Ala
  65                      70                      75                      80
Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Cys Lys Glu Thr Glu Thr
  85                      90                      95
Leu Met Pro Leu Pro Ile His Leu Ala His Gln Leu Ala Phe Ala
  100                     105                     110

```

(2) INFORMATION FOR SEQ ID NO:732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

```

Ser Leu Ser Thr Leu Ala Val Leu Leu Lys Ala Leu Asn Lys Arg Val
  1                      5                      10                      15
Phe Gln Thr Ile Leu Asn Ala Ala Lys Asp Lys Lys Glu Gly Ala Ile
  20                      25                      30
Leu Ile Ala Ser Gly Cys Leu Ser Glu Arg Tyr Lys Asp Glu Ile Lys
  35                      40                      45
Glu Leu Ile Pro Glu Val Asp Ile Phe Thr Gly Val Gly Asp Tyr Asp
  50                      55                      60
Lys Ile Asp Ile Leu Ile Ala Lys Lys Gln Asn Gln Phe Ser Glu Gln
  65                      70                      75                      80
Val Phe Leu Ser Glu His Tyr Asn Ala Arg Ile Ile Thr Gly Ser Ser
  85                      90                      95
Val His Ala Tyr Val Lys Ile Ser Glu Gly Cys Asn Gln Lys Cys Ser
  100                     105                     110
Phe Cys Ala Ile Pro Ser Phe Lys Gly Lys Leu Gln Ser Arg Glu Leu
  115                     120                     125
Asp Ser Ile Leu Lys Glu Val Glu Asp Leu Ala Leu Lys Gly Tyr Lys
  130                     135                     140
Asp Met Thr Phe Ile Ala Gln Asp Ser Ser Ser Phe Leu Ser Asp Arg
  145                     150                     155                     160
Ala Lys Ser Arg Leu Asp Pro Ala His
  165

```

(2) INFORMATION FOR SEQ ID NO:733:

(i) SEQUENCE CHARACTERISTICS:

642

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

```

Asn Leu Arg Thr Ile Met His Tyr Ser Tyr Glu Ala Phe Leu Lys Asp
1           5           10           15
Ser Leu Glu Leu Ala Lys Gln Val Glu Arg Leu Cys Gly Ile Pro Glu
          20           25           30
Ala Leu Val Cys Val Met Arg Gly Gly Met Thr Leu Val His Phe Leu
          35           40           45
Ser Leu His Trp Asn Leu Arg Glu Val Tyr Gly Ile Asn Ala Ile Ser
          50           55           60
Tyr Asp Thr Thr Lys Arg Gln Asn Ala Leu Lys Ile Glu Asn Thr Pro
65           70           75           80
Thr Ile Lys Asp His Leu Lys Thr Ile Leu Val Val Asp Glu Ile Val
          85           90           95
Asp Ser Gly Asn Ser Leu Glu Ala Val Leu Lys Val Leu Gln Asp Lys
          100          105          110
His Pro Asp Lys Lys Phe Tyr Ser Ala Ser Leu Phe Gln Lys Thr Ser
          115          120          125
Ala Lys Tyr Lys Ala Asp Ala Phe Leu Lys Asp Ala Pro Glu Trp Ile
          130          135          140
Asp Phe Phe Trp Glu Val Asp Leu Lys Asn Leu Lys Ser His
145          150          155

```

(2) INFORMATION FOR SEQ ID NO:734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:


```

Ser Ser Ser Leu Glu Arg Leu Pro Ala Ser Leu Lys Asp Ala Arg Ile
1          5          10          15
Leu Tyr Leu Tyr Pro Ser Ser Thr Thr Leu Glu Leu Ile Gly Ala Ile
          20          25          30
Glu Asp Ser Pro Ile Phe Gln Asn Tyr Phe Tyr Met Pro Ile Gln His
          35          40          45
Ile Ser Asp Ser Met Leu Lys Lys Met Arg Arg Asn Ser Ser Gln Ala
          50          55          60
His His Leu Lys Leu Leu Asn Ala Met Lys Gln Val Lys Glu Ser Phe
65          70          75          80
Ile Arg Ser Thr Ile Ile Val Gly His Pro Glu Glu Asn Glu Ser Glu
          85          90          95
Phe Glu Glu Leu Ser Ala Phe Leu Asp Glu Phe Arg Phe Asp Arg Leu
          100          105          110
Asn Ile Phe Ala Phe Ser Ala Glu Glu Asn Thr His Ala Tyr Ser Leu
          115          120          125
Glu Lys Val Pro Lys Lys Ile Ile Asn Ala Arg Ile Lys Ala Leu Asn
          130          135          140
Lys Ile Ala Leu Lys His Gln Asn His Ser Phe Lys Ala Leu Leu Asn
145          150          155          160
Lys Pro Ile Lys Ala Leu Val Glu His Lys Glu Gly Glu Tyr Phe Tyr
          165          170          175
Lys Ala Arg Asp Leu Arg Trp Ala Pro Glu Val Asp Gly Glu Ile Leu
          180          185          190
Ile Asn Asp Ser Glu Leu Thr Thr Pro Leu Lys Pro Gly His Tyr Thr
          195          200          205
Ile Val Pro Ser Ala Phe Lys Asp Asn Ile Leu Leu Ala Lys Val Leu
          210          215          220
Ser Pro Phe
225

```

(2) INFORMATION FOR SEQ ID NO:735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

```

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

```

644

```

      35              40              45
Asp Leu Lys Asp Lys Ile His His Asn Ala Leu Ser Asn Asp Asp Leu
 50      55      60
Glu Arg Met Ile Ala Phe Arg Glu Gln Glu Phe Glu Lys Ser Leu Glu
65      70      75      80
Asp Trp Met Gly Ala Tyr Ser Tyr Asp Ala Thr Leu Arg Cys Phe Ser
      85      90      95
Ser Glu Arg Ile Tyr Leu Asp Arg Leu Gly Trp Glu
      100      105

```

(2) INFORMATION FOR SEQ ID NO:736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

```

Lys Lys Val Val Met Asn Gly Phe Cys Ala Arg Leu Arg Ala Ile Thr
1              5              10              15
Phe Asn Glu Arg Leu Lys Met Lys Ile Ala Val Leu Leu Ser Gly Gly
      20              25              30
Val Asp Ser Ser Tyr Ser Ala Tyr Ser Leu Lys Glu Gln Gly His Glu
      35              40              45
Leu Val Gly Ile Tyr Leu Lys Leu His Ala Ser Glu Lys Lys His Asp
      50              55              60
Leu Tyr Ile Lys Asn Ala Gln Lys Ala Cys Glu Phe Leu Gly Ile Pro
65      70      75      80
Leu Glu Val Leu Asp Phe Gln Lys Asp Phe Lys Ser Ala Val Tyr Asp
      85      90      95
Glu Phe Ile Asn Ala Tyr Glu Glu Gly Gln Thr Pro Asn Pro Cys Ala
      100      105      110
Leu Cys Asn Pro Leu Met Lys Phe Gly Leu Ala Leu Asp His Ala Leu
      115      120      125
Lys Leu Gly Cys Glu Lys Ile Ala Thr Gly His Tyr Ala Arg Val Lys
      130      135      140
Glu Ile Asp Lys Val Ser Tyr Ile Gln Glu Ala Leu Asp Lys Thr Lys
145      150      155      160
Asp Gln Ser Tyr Phe Leu Tyr Ala Leu Glu His Glu Val Ile Ala Lys
      165      170      175
Leu Val Phe Pro Leu Gly Asp Leu Leu Lys Lys Asp Ile Lys Pro Leu
      180      185      190
Ala Leu Asn Ala Met Pro Phe Leu Gly Thr Leu Glu Thr Tyr Lys Glu
      195      200      205
Ser Gln Glu Ile Cys Phe Val Glu Lys Ser Tyr Ile Asp Thr Leu Lys

```

645

```

      210              215              220
Lys His Val Glu Val Glu Lys Glu Gly Val Val Lys Asn Leu Gln Gly
225              230              235              240
Glu Val Ile Gly Thr His Lys Gly Tyr Met Gln Tyr Thr Ile Gly Lys
      245              250              255
Arg Lys Gly Phe Ser Val Lys Gly Ala Leu Glu Pro His Phe Val Val
      260              265              270
Gly Ile Asp Ala Lys Lys Asn Glu Leu Ile Val Gly Lys Lys Glu Asp
      275              280              285
Leu Ala Thr His Ser Leu Lys Ala Lys Asn Lys Ser Leu Thr Lys Asp
      290              295              300
Phe Lys Asp Gly Glu Tyr Phe Ile Lys Ala Arg Tyr Arg Ser Val Pro
305              310              315              320
Thr Lys Ala Phe Val Ser Leu Lys Asp Gly Met Ile Glu Val Glu Phe
      325              330              335
Lys Glu Pro Phe Tyr Gly Val Ala Lys Gly Gln Ala Leu Val Val Tyr
      340              345              350
Lys Asp Asp Ile Leu Leu Gly Gly Gly Val Ile Val
      355              360

```

(2) INFORMATION FOR SEQ ID NO:737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

```

Leu Phe Lys Thr Asn Gly Ile Ser Val Gly Glu Tyr Thr His Phe Ser
1              5              10              15
Glu Asp Ile Gly Ser Gln Ser Arg Ile Asn Thr Val Arg Leu Glu Thr
      20              25              30
Gly Thr Arg Ser Ile Phe Ser Gly Gly Val Lys Phe Lys Ser Gly Glu
      35              40              45
Lys Leu Val Ile Asn Asp Phe Tyr Tyr Ser Pro Trp Asn Tyr Phe Asp
      50              55              60
Ala Arg Asn Val Lys Asn Val Glu Ile Thr Arg Lys Phe Ala Ser Ser
65              70              75              80
Thr Pro Glu Asn Pro Trp Gly Thr Ser Lys Leu Met Phe Asn Asn Leu
      85              90              95
Thr Leu Gly Gln Asn Ala Val Met Asp Tyr Ser Gln Phe Ser Asn Leu
      100             105             110
Thr Ile Gln Gly Ile Leu Ser Thr Ile Lys Arg Tyr His Leu Thr Lys
      115             120             125
Gly Phe Phe Thr Pro

```

130

(2) INFORMATION FOR SEQ ID NO:738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

```

Met Lys Lys Thr Arg Ile Arg Lys Lys Ser Ala Leu Met Asn Gly Cys
1           5           10           15
Trp Ala Glu Phe Asp Ser Val Phe Ser Ala Ile Val Pro Leu Glu Asp
          20           25           30
Leu Asn Lys Thr Ala Cys Ala His His Ala Leu Lys Ala Leu Gln Ala
          35           40           45
Thr Leu Lys Thr Thr Ile Trp Ala Leu Met Arg Gln Ser Trp Asn Arg
          50           55           60
Ser Gln Lys Asp Ser Ser Leu Gly Gly Ile Cys Gly Ile Leu Thr Arg
          65           70           75           80
Met Phe

```

(2) INFORMATION FOR SEQ ID NO:739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

```

Trp Thr Leu Ala Lys Ile Arg Cys Val Lys Asn Phe Lys Glu Ala Ile
1           5           10           15

```

647

```

Glu Gly Phe Thr Glu Lys Ile Lys Glu Ser Pro Asn Asp Ser Asn Ala
      20                      25                      30
Ile Asn Glu Ala Phe Asp Asn Leu Glu Thr Glu Leu Glu Arg Ala Thr
      35                      40                      45
Glu Asn Leu Ser Gln Lys Ile Asp Pro Val Leu Glu Arg Asn Glu Asn
      50                      55                      60
Tyr Thr Gln Lys Ala Leu Glu Tyr Arg Glu Phe Leu Glu Ser Arg Lys
      65                      70                      75                      80
Glu Ser Phe Ile Val Asp Glu Lys Asn Pro Tyr Pro Glu Glu Val Ser
      85                      90                      95
Phe Asn Glu Trp Leu Leu Gly Gly Ile
      100                      105

```

(2) INFORMATION FOR SEQ ID NO:740:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

```

Arg Pro Leu Ala Leu Ile Met Trp Trp Arg Asn Ile Asp Asn Arg Ile
1      5      10      15
Ser Ile Lys Arg Val Val Asn Lys Pro Pro Arg Gly Leu Gly Lys Ile
      20      25      30
Thr Gln Glu Trp Ile Phe Ser Leu Leu Asp Glu Glu Gly Leu Asn Leu
      35      40      45
Glu Glu Ala Leu Lys Ile Gly Ala Phe Lys Asp Lys Leu Asn Pro Lys
      50      55      60
Asn Glu Tyr Ala Leu Lys Lys Phe Thr Ala Met Ile Gly Arg Leu Arg
65      70      75      80
Glu Ala Phe Glu Ile Ser Val Glu Lys Phe Cys Glu Arg Phe Leu Glu
      85      90      95
Glu Thr Asn Leu Leu Lys Ser Tyr Glu Lys Glu Asp Asn Tyr Glu Glu
      100     105     110
Arg Glu Gly Phe Val Lys Glu Leu Ser Leu Val Lys Glu His Phe
      115     120     125
Lys Thr Asn Pro Thr His Ser Leu Leu Asp Phe Leu Asn Glu Ser Ala
      130     135     140
Leu Asp Val His Asn Thr Glu Asn Ala Gln Lys Val Ser Cys Met Ser
145     150     155     160
Val His Met Ser Lys Gly Leu Glu Phe Lys His Val Phe Val Ile Gly
      165     170     175
Leu Glu Glu Gly Phe Phe Pro His Arg Gly Phe Asn Gln Glu Ser Asp
      180     185     190

```

648

```

Leu Glu Glu Glu Arg Arg Leu Ala Tyr Val Ala Ile Thr Arg Ala Lys
    195                200                205
Glu Glu Leu Gln Leu Ser Tyr Val Lys Glu Arg Ser Tyr Phe Gly Arg
    210                215                220
Lys Ile Ser Cys Ser Pro Ser Val Phe Leu Glu Glu Ala Gln Leu Leu
    225                230                235                240
Gln Gln Asp Lys Pro Pro Lys Gln Asn His Gln Lys Asp Thr Pro Ile
    245                250                255
Lys Val Gly Asp Leu Ile Lys His Lys Ile Phe Gly Thr Gly Glu Gly
    260                265                270
Phe Arg Arg Arg Lys Arg Leu Ala Ala Val Cys Ala
    275                280

```

(2) INFORMATION FOR SEQ ID NO:741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

```

Asp Gly Ser Lys Lys Met Lys Ser Asn Lys Lys Ser Asn His Leu Arg
1          5          10          15
Ala Ile Tyr Arg Ala Leu Val Ile Ala Ile Gly Leu Ala Val Ile Ile
    20          25          30
Val Phe Asn Tyr Phe Asn Arg Lys Asn Asn Asn Ala Arg Ser Ser Arg
    35          40          45
Arg Ala Cys Ser Cys Phe Phe Pro Pro Thr Gly Val Asn Leu Glu Lys
    50          55          60
Ile Gly Ser Phe Asp Thr Gly Ala Lys Leu Ile Val Leu Asn His Gln
    65          70          75          80
Ser Leu Leu Asp Ile Ile Tyr Leu Glu Ala Tyr His Pro Ser Asn Ile
    85          90          95
Cys Trp Ile Ala Lys Lys Glu Leu Gly Glu Ile Pro Phe Tyr Gly His
    100         105         110
Ala Leu Thr Asp Thr Gly Met Ile Leu Ile Asp Arg Glu Asp Lys Lys
    115         120         125
Gly Ile Val Ser Leu Leu Lys Ala Cys Lys Glu Lys Leu Asp Gln Asn
    130         135         140
Arg Pro Leu Val Ile Phe Pro Glu Gly Thr Arg Gly Lys Gly Gly Glu
    145         150         155         160
Lys Phe Leu Pro Phe Lys Gln Gly Ala Lys Ile Ile Ala Glu Lys Phe
    165         170         175
Gln Leu Lys Ile Gln Pro Met Val Leu Ile Asn Ser Ile Lys Ile Phe
    180         185         190

```

Asn	Ser	Lys	Pro	Leu	Glu	Ala	Tyr	Lys	Ala	Arg	Thr	Arg	Leu	Val	Met
		195					200					205			
Leu	Glu	Ser	Tyr	Thr	Pro	Asp	Phe	Ser	Ser	Pro	Thr	Trp	Tyr	Glu	Glu
	210					215					220				
Leu	Gln	Glu	Arg	Met	Gln	Lys	Glu	Tyr	Leu	Lys	His	Tyr	His	Glu	Leu
225					230					235					240
Asn	Ala														

(2) INFORMATION FOR SEQ ID NO:742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

Val	Met	Lys	Thr	Ser	Asn	Thr	Lys	Thr	Pro	Lys	Pro	Val	Leu	Ile	Ala
1				5					10					15	
Gly	Pro	Cys	Val	Ile	Glu	Ser	Leu	Glu	Asn	Leu	Arg	Ser	Ile	Ala	Ile
			20					25					30		
Lys	Leu	Gln	Pro	Leu	Ala	Asn	Asn	Glu	Arg	Leu	Asp	Phe	Tyr	Phe	Lys
	35					40					45				
Ala	Asn	Phe	Asp	Asn	Ala	Asn	Arg	Thr	Ser	Leu	Glu	Ser	Tyr	Lys	Glu
	50					55					60				
Pro	Gly	Leu	Glu	Lys	Gly	Leu	Glu	Met	Leu	Gln	Thr	Ile	Lys	Asp	Glu
65				70					75					80	
Phe	Gly	Tyr	Lys	Ile	Leu	Thr	Asp	Val	His	Glu	Ser	Tyr	Gln	Ala	Ser
			85					90						95	
Val	Ala	Ala	Lys	Val	Ala	Asp	Ile	Leu	Gln	Ile	Pro	Ala	Phe	Leu	Cys
			100					105					110		
Arg	Gln	Thr	Asp	Leu	Ile	Val	Glu	Val	Ser	Gln	Thr	Asn	Ala	Ile	Val
	115						120					125			
Asn	Ile	Lys	Lys	Gly	Gln	Phe	Met	Asn	Pro	Lys	Asp	Met	Gln	Tyr	Ser
	130					135					140				
Val	Leu	Lys	Ala	Leu	Lys	Thr	Arg	Asp	Ser	Ser	Ile	Gln	Ser	Pro	Thr
145					150					155				160	
Tyr	Glu	Thr	Ala	Leu	Lys	Asn	Gly	Val	Trp	Leu	Cys	Glu	Arg	Gly	Ser
			165					170						175	
Ser	Phe	Gly	Tyr	Gly	Asn	Leu	Val	Val	Asp	Met	Arg	Ser	Leu	Lys	Ile
			180					185					190		
Met	Arg	Glu	Phe	Ala	Pro	Val	Ile	Phe	Asp	Ala	Thr	His	Ser	Val	Gln
	195						200					205			
Met	Pro	Gly	Gly	Ala	Asn	Gly	Lys	Ser	Ser	Gly	Asp	Ser	Ser	Phe	Pro
	210					215					220				

650

```

Pro Ile Leu Pro Arg Ala Ala Ala Val Gly Ile Asp Gly Leu Phe
225                230                235                240
Ala Glu Thr His Ile Asp Pro Lys Asn Ala Leu Ser Asp Gly Ala Asn
                245                250                255
Met Leu Lys Pro Asp Glu Leu Glu His Leu Val Thr Asn Met Leu Lys
                260                265                270
Ile Gln Asn Leu Phe
                275

```

(2) INFORMATION FOR SEQ ID NO:743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

```

Gln Arg Asp His Gly Val Leu Tyr Leu Leu Asn Asn Thr Ile Ile Lys
1          5          10          15
Phe Leu Ile Arg Arg Tyr Ile Met Leu Glu Asn Val Lys Lys Ser Leu
          20          25          30
Phe Arg Val Leu Cys Leu Gly Ala Leu Cys Leu Gly Gly Leu Ile Ala
          35          40          45
Glu Gln Asp Pro Lys Glu Leu Val Asn Leu Gly Thr Lys Ser Tyr Lys
          50          55          60
Glu Gln Asp Phe Thr Gln Ala Lys Lys Tyr Phe Glu Lys Ala Cys Asp
65          70          75          80
Leu Lys Glu Asn Ser Gly Cys Phe Asn Leu Gly Val Leu Tyr Tyr Gln
          85          90          95
Gly His Gly Val Glu Lys Asn Leu Lys Lys Ala Ala Ser Phe Tyr Ser
          100         105         110
Lys Ala Cys Asp Leu Asn Tyr Ser Asn Gly Cys His Leu Leu Gly Asn
          115         120         125
Leu Tyr Tyr Ser Gly Gln Gly Val Ser Gln Asn Thr Asn Lys Ala Trp
          130         135         140
Gln Tyr Tyr Ser Lys Ala Cys Asp Leu Lys Tyr Ala Glu Gly Cys Ala
145         150         155         160
Ser Leu Gly Gly Ile Tyr His Asp Gly Lys Val Phe Thr Arg Asp Phe
          165         170         175
Lys Lys Ala Val Glu Tyr Phe Thr Lys Ala Cys Asp Leu Asn Asp Gly
          180         185         190
Asp Gly Cys Thr Ile Leu Gly Ser Leu Tyr Asp Ala Gly Arg Gly Thr
          195         200         205
Pro Lys Asp Leu Lys Lys Ala Leu Ala Ser Tyr Asp Lys Ala Cys Asp
210         215         220

```


651

```

Leu Lys Asp Ser Pro Gly Cys Phe Asn Ala Gly Asn Met Tyr His His
225                230                235                240
Gly Glu Gly Ala Ala Lys Asn Phe Lys Glu Ala Leu Ala Arg Tyr Ser
                245                250                255
Lys Ala Cys Glu Leu Glu Asn Gly Gly Gly Cys Phe Asn Leu Gly Ala
                260                265                270
Met Gln Tyr Asn Gly Glu Gly Ala Thr Arg Asn Glu Lys Gln Ala Ile
                275                280                285
Glu Asn Phe Lys Lys Gly Cys Lys Leu Gly Ala Lys Gly Ala Cys Asp
                290                295                300
Ile Leu Lys Gln Leu Lys Ile Lys Val
305                310

```

(2) INFORMATION FOR SEQ ID NO:744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

```

Met Ser Ser Gly Leu Ile Tyr Ile Ser Leu Glu Val Leu Val Ala Cys
1          5          10          15
Leu Ile Thr Ala Leu Ile Met Tyr Tyr Val Met Lys Lys Ile Tyr Tyr
          20          25          30
Ala Arg Gly Gln Ala Ile Leu Lys Gly Ala Ser Ala Lys Ala Lys Leu
          35          40          45
Met Glu Phe Gln Ala Lys Ser Phe Val Glu Ala Glu Glu Met Arg Met
50          55          60
Lys Ser Gln Glu Cys Lys Leu Gln Gln Gln Tyr Glu Asn Lys Asn Leu
65          70          75          80
Gln Leu Gln Thr His Phe Asp Lys Lys Glu Ala His Leu Lys His Leu
          85          90          95
Glu Ala Gln His Lys Glu Phe Val Arg Asp Glu Lys Arg Tyr Leu Glu
          100         105         110
Lys Glu Lys Lys Glu Leu Glu Lys Glu Arg Gln Ile Leu Glu Gln Glu
          115         120         125
Arg Glu Asn Phe Lys Lys Gln Arg Ala Ile Cys Lys Glu Ala Gln Ala
          130         135         140
Lys Ala Leu Asp Ala Met Leu Asn Tyr Met Ala Tyr Thr Lys Asp Glu
          145         150         155         160
Ile Lys Ser Met Ile Leu Glu Gln Leu Glu Glu Glu Leu Glu Ala Gln
          165         170         175
Lys Ser Ala Leu Ile Arg Arg Tyr Glu Lys Glu Ala Lys Glu Glu Gly
          180         185         190

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652

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Lys Lys Lys Ser Tyr Ala Ile Leu Ala Glu Ala Thr Ala Arg Phe Ala
    195                200                205
Gly Asp Tyr Ala Thr Glu Asn Leu Thr Ser Arg Ile Ala Leu Pro Cys
    210                215                220
Ser Asp Tyr Val Gly Arg Val Ile Gly Lys Asp Gly Lys Asn Ile Glu
225                230                235                240
Ala Phe Lys Lys Ile Ser Gly Val Asp Ile Glu Phe Ser Glu Asp Ser
    245                250                255
Ser Glu Leu Cys Leu Ser Ser Phe Asn Ile Tyr Arg Arg Glu Val Ala
    260                265                270
Ser Glu Thr Ile Lys Ile Leu Ile Glu Asp Gly Arg Ile Gln Pro Asn
    275                280                285
Arg Ile Glu Glu Val Tyr His Arg Val Ala Arg Asn Met Glu Lys Glu
    290                295                300
Leu Leu Ser Glu Gly Glu Ser Val Val Leu Glu Leu Glu Leu Gly Thr
305                310                315                320
Met Glu Asp Glu Leu Lys Ile Leu Ile Gly Lys Met Arg Tyr Arg Phe
    325                330                335
Ser Phe Gly Gln Asn Ala Leu Gln His Ser Lys Glu Val Ala Leu Leu
    340                345                350
Ala Gly Leu Ile Ala Glu Gln Leu Gly Gly Asp Lys Lys Leu Ala Arg
    355                360                365
Arg Ala Gly Ile Leu His Asp Ile Gly Lys Ala Leu Thr Gln Glu Leu
    370                375                380
Gly Arg Asp His Val Asn Leu Gly Val Glu Val Cys Lys Arg His Lys
385                390                395                400
Glu Asp Pro Val Val Ile Asn Ala Ile Tyr Ala His His Gly His Glu
    405                410                415
Glu Ile Met Ser Val Glu Cys Ala Ser Val Cys Ala Ala Asp Ala Leu
    420                425                430
Ser Ala Gly Arg Pro Gly Ala Arg Arg Lys Ser Asp Glu Glu Tyr Ala
    435                440                445
Lys Arg Met Gln Ala Leu Glu Glu Ile Ala Leu Glu Phe Asp Gly Val
    450                455                460
Glu Lys Ala Tyr Ala Met Glu Ser Gly Arg Glu Leu Arg Val Ile Val
465                470                475                480
Lys Ser Asn Gln Val Arg Asp Asn Gln Val Pro Ile Ile Ala Arg Lys
    485                490                495
Ile Ala Lys Arg Ile Glu Glu Ser Thr Gln Tyr Val Gly Glu Val Gly
    500                505                510
Val Gln Val Val Arg Glu Asn Arg Phe Lys Thr Thr Ala Thr Leu Lys
    515                520                525
Gln

```

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

653

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

```

Met Lys Lys Gly Ser Leu Ala Ile Val Leu Gly Ser Leu Leu Ala Ser
1      5      10      15
Gly Thr Phe Tyr Thr Ala Leu Ala Asp Gly Met Pro Met Lys Gln Gln
      20      25      30
His Asn Asn Met Gly Glu Ser Val Glu Leu His Phe His Tyr Pro Ile
      35      40      45
Lys Gly Lys Gln Glu Pro Lys Asn Asn His Leu Val Val Leu Ile Asp
50      55      60
Pro Lys Ile Glu Ala Asn Lys Val Ile Pro Glu Asn Tyr Gln Lys Glu
65      70      75      80
Phe Glu Lys Ser Leu Phe Leu Gln Leu Ser Asn Phe Leu Glu Arg Lys
      85      90      95
Gly Tyr Ser Val Ser Gln Phe Lys Asp Val Ser Glu Ile Pro Gln Asp
      100      105      110
Ile Lys Glu Lys Ala Leu Leu Val Leu Arg Met Asp Gly Asn Val Ala
      115      120      125
Ile Leu Glu Asp Ile Val Glu Glu Ser Asp Ala Leu Ser Glu Glu Lys
130      135      140
Val Ile Asp Met Ser Ser Gly Tyr Leu Asn Leu Asn Phe Val Glu Pro
145      150      155      160
Lys Ser Glu Asp Ile Ile His Ser Phe Gly Ile Asp Val Ser Lys Ile
      165      170      175
Lys Ala Val Ile Glu Arg Val Glu Leu Arg Arg Thr Asn Ser Gly Gly
      180      185      190
Phe Val Pro Lys Thr Phe Val His Arg Ile Lys Glu Thr Asp His Asp
      195      200      205
Arg Ala Ile Lys Lys Ile Met Asn Gln Ala Tyr His Lys Val Met Ala
210      215      220
His Ile Thr Lys Glu Leu Ser Lys Lys His Met Glu Arg Tyr Glu Lys
225      230      235      240
Val Ser Ser Glu Met Lys Lys Arg Lys
      245

```

(2) INFORMATION FOR SEQ ID NO:746:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

```

Met Gln Asn Thr Phe Asn Tyr Thr Asn Asn Ala Leu Lys Asn Asn Ala
1           5           10           15
Lys Leu Thr Pro Thr Glu Met Gln Ala Glu Gln Tyr Tyr Leu Gln Ser
          20           25           30
Thr Leu Gln Asn Ile Glu Lys Ile Val Met Leu Ser Gly Gly Val Ala
          35           40           45
Ser Asn Pro Lys Leu Val Gln Ala Leu Glu Lys Met Gln Glu Pro Ile
          50           55           60
Thr Asn Pro Leu Glu Leu Val Glu Asn Leu Lys Asn Leu Glu Leu Gln
65           70           75           80
Phe Ser Gln Ser Gln Asn Ser Met Leu Ser Ser Leu Ser Ser Gln Ile
          85           90           95
Ala Gln Ile Ser Asn Ser Leu Asn Ala Leu Asp Pro Ser Ser Tyr Ser
          100          105          110
Lys Asn Val Ser Ser Met Tyr
          115

```

(2) INFORMATION FOR SEQ ID NO:747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

```

Met Asp Leu Asp Lys Leu Lys Asp Tyr Arg Ala Leu Arg Asn Ala Ile
1           5           10           15
Leu Arg Leu Leu Pro Tyr Leu Asp Ser Gly Ile Thr Glu Leu Ile Met
          20           25           30
Asn Lys Glu Lys Glu Ile Trp Leu Tyr Lys Leu Asn Gly Val Arg Glu
          35           40           45
Lys Val Phe Asp Glu Asn Leu Asp Lys Ala Phe Ile Leu Gly Phe Gly
          50           55           60
Glu Gln Leu Ala Ser Phe Arg Asp Leu Phe Phe Asn Ala Asn Tyr Pro
65           70           75           80
Thr Leu Asn Thr Ser Ile Pro Thr Ser Arg Tyr Arg Val Ser Met Asn
          85           90           95
His Phe Ala Ile Ser Ala Asp Asn Glu Leu Ser Leu Asn Ile Arg Val
          100          105          110
Pro Ser Asp Lys Lys Phe Asp Leu Lys Ala Phe Lys Leu Ser Ser Ile
          115          120          125

```

655

```

Cys Gln Tyr Asp Tyr Glu Tyr Leu Lys Asn Leu Met Ile Asp Gly Lys
 130                      135                      140
Asn Leu Leu Ile Ser Gly Gly Thr Gly Ser Gly Lys Thr Ser Phe Leu
145                      150                      155                      160
Asn Ala Leu Ile Glu Phe Ile Pro Lys His Thr Arg Ile Val Ser Val
                      165                      170                      175
Glu Asp Ser Glu Glu Leu Asp Leu Arg Ala Phe Glu Asn His Lys Ser
                      180                      185                      190
Leu Leu Val Asp Lys Thr Glu Ser Ser Lys Phe Thr Tyr Glu Asn Ala
                      195                      200                      205
Leu Asn Met Ala Met Arg Met Ser Pro Asp Arg Leu Met Val Gly Glu
                      210                      215                      220
Ile Asp Thr Arg Asn Ser Met Leu Phe Leu Arg Phe Gly Asn Thr Gly
225                      230                      235                      240
His Lys Gly Met Val Ser Thr Leu His Ala Asp Ser Val His Gly Val
                      245                      250                      255
Ile Glu Ala Ile Ala Leu Asn Leu Gln Met Asn Lys Ser Gly Leu Asp
                      260                      265                      270
Val Asn Val Ala Lys Lys Phe Phe Lys Ser Ser Val Asp Val Val Val
                      275                      280                      285
Gln Ile Val Leu Asp Lys Ala Thr Asn Thr Arg Tyr Ile Gln Glu Ile
                      290                      295                      300
Leu Pro Ala Lys Asp Leu Arg Asp Ser Leu
305                      310

```

(2) INFORMATION FOR SEQ ID NO:748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

```

Met Asn Ile Ser Val Asn Pro Tyr Leu Met Ala Val Val Phe Val Val
 1                      5                      10                      15
Phe Val Leu Leu Leu Trp Ala Met Asn Val Trp Val Tyr Arg Pro Leu
                      20                      25                      30
Leu Ala Phe Met Asp Asn Arg Gln Ala Glu Ile Lys Asp Ser Leu Ala
                      35                      40                      45
Lys Ile Lys Thr Asp Asn Thr Gln Ser Val Glu Ile Gly His Gln Ile
                      50                      55                      60
Glu Thr Leu Leu Lys Glu Ala Ala Glu Lys Arg Arg Glu Met Leu Ala
65                      70                      75                      80
Glu Ala Ile Gln Lys Ala Thr Glu Ser Tyr Asp Ala Val Ile Lys Gln
                      85                      90                      95

```

656

Lys Glu Asn Glu Leu Asn Gln Glu Phe Glu Ala Phe Ala Lys Gln Leu
 100 105 110
 Gln Asn Glu Lys Gln Ile Leu Lys Glu Gln Leu Gln Ala Gln Met Thr
 115 120 125
 Val Phe Glu Asp Glu Leu Asn Lys Arg Val Ala Met Gly Leu Gly Ser
 130 135 140

(2) INFORMATION FOR SEQ ID NO:749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

Met Ala Ser Gly Leu Phe Glu Asn Asp Glu Ile Lys Asn Asn Lys Ala
 1 5 10 15
 Arg Asp Phe Phe Tyr Ser His Ser Ser Leu Ile Val Phe Phe Leu Leu
 20 25 30
 Leu Leu Gly Phe Gly Tyr Tyr Leu Gly Lys Leu Leu Phe Gly Gly Ser
 35 40 45
 Ser Leu Glu Val Tyr Leu Asp Leu Arg Asp Lys His Glu Arg Leu Gln
 50 55 60
 Gln Glu Ile Thr Glu Leu Gln Ser Lys Asn Val Arg Leu Gln Lys Arg
 65 70 75 80
 Leu Phe Glu Leu Arg Glu Leu Arg Pro Arg Asp
 85 90

(2) INFORMATION FOR SEQ ID NO:750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

```

Met Lys Lys Asn Ile Leu Asn Leu Ala Leu Val Gly Ala Leu Ser Ala
1           5           10           15
Ser Phe Leu Met Ala Lys Pro Ala His Asn Ala Asn Asn Ser Thr His
20           25           30
Asn Thr Lys Glu Thr Thr Asp Ala Ser Ala Gly Val Leu Ala Thr Val
35           40           45
Asp Gly Arg Pro Ile Thr Lys Ser Asp Phe Asp Met Ile Lys Gln Arg
50           55           60
Asn Pro Asn Phe Asp Phe Asp Lys Leu Lys Glu Lys Glu Lys Glu Ala
65           70           75           80
Leu Ile Glu Gln Ala Ile Arg Thr Ala Leu Val Glu Asn Glu Ala Lys
85           90           95
Ala Glu Lys Leu Asn Gln Thr Pro Glu Phe Lys Ala Met Met Glu Ala
100          105          110
Val Lys Lys Gln Ala Leu Val Glu Phe Trp Ala Lys Lys Gln Ala Glu
115          120          125
Glu Val Lys Lys Ile Gln Ile Pro Glu Lys Glu Met Gln Asp Phe Tyr
130          135          140
Asn Ala Asn Lys Asp Gln Leu Phe Val Lys Gln Glu Ala His Ala Arg
145          150          155          160
His Ile Leu Val Lys Thr Glu Asp Glu Ala Lys Arg Ile Ile Ser Glu
165          170          175
Ile Asp Lys Gln Pro Lys Ala Lys Lys Glu Ala Lys Phe Ile Glu Leu
180          185          190
Ala Asn Arg Asp Thr Ile Asp Pro Asn Ser Lys Asn Ala Gln Asn Gly
195          200          205
Gly Asp Leu Gly Lys Phe Gln Lys Asn Gln Met Ala Pro Asp Phe Ser
210          215          220
Lys Ala Ala Phe Ala Leu Thr Pro Gly Asp Tyr Thr Lys Thr Pro Val
225          230          235          240
Lys Thr Glu Phe Gly Tyr His Ile Ile Tyr Leu Ile Ser Lys Asp Ser
245          250          255
Pro Val Thr Tyr Thr Tyr Glu Gln Ala Lys Pro Thr Ile Lys Gly Met
260          265          270
Leu Gln Glu Lys Leu Phe Gln Glu Arg Met Asn Gln Arg Ile Glu Glu
275          280          285
Leu Arg Lys His Ala Lys Ile Val Ile Asn Lys
290          295

```

(2) INFORMATION FOR SEQ ID NO:751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

658

(A) NAME/KEY: misc_feature

(B) LOCATION 1...305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

```

Met Ile Lys Ser Trp Thr Lys Lys Trp Phe Leu Ile Leu Phe Leu Met
1           5           10           15
Ala Ser Cys Phe Gly His Leu Val Ala Thr Thr Gly Glu Lys Tyr Phe
20           25           30
Lys Met Ala Asn Gln Ala Leu Lys Arg Gly Asp Tyr His Arg Ala Val
35           40           45
Ala Phe Tyr Lys Arg Ser Cys Asn Leu Arg Met Gly Val Gly Cys Thr
50           55           60
Ser Leu Gly Ser Met Tyr Glu Tyr Gly Asp Gly Val Asp Gln Asn Ile
65           70           75           80
Ser Lys Ala Val Phe Tyr Tyr Arg Arg Gly Cys Asn Leu Arg Asn His
85           90           95
Leu Ala Cys Ala Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val
100          105          110
Gln Lys Asp Phe Pro Lys Ala Ile Tyr Tyr Tyr Arg Arg Gly Cys His
115          120          125
Leu Lys Gly Gly Val Ser Cys Gly Ser Leu Gly Phe Met Tyr Phe Asn
130          135          140
Gly Thr Gly Val Lys Gln Asn Tyr Ala Lys Ala Leu Ser Phe Ser Lys
145          150          155          160
Tyr Ala Cys Ser Leu Asn Tyr Gly Ile Ser Cys Asn Phe Val Gly Tyr
165          170          175
Met Tyr Lys Ser Ala Lys Gly Val Glu Lys Asp Leu Lys Lys Ala Leu
180          185          190
Ala Asn Phe Lys Arg Gly Cys His Leu Lys Asp Gly Ala Ser Cys Val
195          200          205
Ser Leu Gly Tyr Leu Tyr Glu Ala Gly Met Asp Val Lys Gln Asn Glu
210          215          220
Glu Gln Ala Leu Asn Leu Tyr Lys Lys Gly Cys Ser Leu Lys Glu Gly
225          230          235          240
Ser Gly Cys His Asn Val Ala Val Met Tyr Tyr Thr Gly Lys Gly Ala
245          250          255
Pro Lys Asp Leu Glu Lys Ala Thr Ser Tyr Tyr Lys Lys Gly Cys Ala
260          265          270
Leu Gly Phe Ser Gly Ser Cys Lys Val Leu Glu Val Ile Gly Lys Glu
275          280          285
Ser Asp Asn Leu Gln Asp Asp Ala Gln Asn Asp Thr Gln Asp Ser Val
290          295          300
Gln
305

```

(2) INFORMATION FOR SEQ ID NO:752:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

```

Leu Lys Ile Phe Leu Val Ile Leu Ser Val Phe Phe Phe Asn Gly Cys
1      5      10      15
Phe Gly Leu Ala Tyr Lys Thr Pro Ile Ser Asn Pro Pro Ile Ser Tyr
20      25      30
Asp Pro Tyr Thr Thr Thr Ile Gly Ser Leu Tyr Ala Lys Asn Leu Lys
35      40      45
Glu Asn Pro Lys His Ser Ala Ala Ile Leu Leu Glu Asp Gly Phe Asp
50      55      60
Ala Leu Leu His Arg Val Gly Leu Ile Arg Met Ser Gln Lys Ser Ile
65      70      75      80
Asp Met Gln Thr Tyr Ile Tyr Lys Asn Asp Leu Ser Ser Gln Val Ile
85      90      95
Ala Lys Glu Leu Leu Asn Ala Ala Asn Arg Gly Val Lys Val Arg Ile
100     105     110
Leu Leu Asp Asp Asn Gly Leu Asp Ser Asp Phe Ser Asp Ile Met Leu
115     120     125
Leu Asn Phe His Lys Asn Ile Glu Val Lys Ile Phe Asn Pro Tyr Tyr
130     135     140
Ile Arg Asn Lys Gly Leu Arg Tyr Phe Glu Met Leu Ala Asp Tyr Glu
145     150     155     160
Arg Ile Lys Lys Arg Met His Asn Lys Leu Phe Ile Val Asp Asn Phe
165     170     175
Ala Val Ile Ile Gly Gly Arg Asn Ile Gly Asp Asn Tyr Phe Asp Asn
180     185     190
Asp Leu Asp Thr Asn Phe Leu Asp Leu Asp Ala Leu Phe Phe Gly Gly
195     200     205
Val Ala Ser Lys Ala Lys Glu Ser Phe Glu Asn Tyr Trp Arg Phe His
210     215     220
Arg Ser Ile Pro Val Ser Leu Leu Arg Thr His Lys Arg Leu Lys Asn
225     230     235     240
Asn Val Lys Glu Ile Ala Lys Leu His Glu Lys Ile Pro Ile Ser Ala
245     250     255
Glu Asp Ala Asn Glu Phe Glu Lys Lys Val Asn Asp Phe Ile Glu Arg
260     265     270
Phe Gln Lys Tyr Gln Tyr Pro Ile Tyr Tyr Gly Asn Ala Ile Phe Leu
275     280     285
Ala Asp Leu Pro Ala Lys Ile Asp Thr Pro Leu Tyr Ser Pro Ile Lys
290     295     300
Ile Ala Phe Glu Lys Ala Leu Lys Asn Ala Lys Asp Ser Val Phe Ile
305     310     315     320
Ala Ser Ser Tyr Phe Ile Pro Gly Lys Lys Ile Met Lys Ile Phe Lys
325     330     335
Asn Gln Ile Ser Lys Gly Ile Glu Leu Asn Ile Leu Thr Asn Ser Leu
340     345     350
Ser Ser Thr Asp Ala Ile Val Val Tyr Gly Ala Trp Glu Arg Tyr Arg
355     360     365
Asn Lys Leu Val Arg Met Gly Ala Asn Val Tyr Glu Ile Arg Asn Asp
370     375     380

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660

```

Phe Phe Asn Arg Gln Ile Lys Gly Arg Phe Ser Thr Lys His Ser Leu
385          390          395          400
His Gly Lys Thr Ile Val Phe Asp Asp Ala Leu Thr Leu Leu Gly Ser
          405          410          415
Phe Asn Ile Asp Pro Arg Ser Ala Tyr Ile Asn Thr Glu Ser Ala Val
          420          425          430
Leu Phe Asp Asn Pro Ser Phe Ala Lys Arg Val Arg Leu Ser Leu Lys
          435          440          445
Asp His Ala Gln Gln Ser Trp His Leu Val Leu Tyr Arg His Arg Val
          450          455          460
Ile Trp Glu Ala Thr Glu Glu Gly Ile Leu Ile His Glu Lys Asn Ser
465          470          475          480
Pro Asp Thr Ser Phe Phe Leu Arg Leu Ile Lys Glu Trp Ser Lys Val
          485          490          495
Leu Pro Glu Arg Glu Leu
          500

```

(2) INFORMATION FOR SEQ ID NO:753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

```

Leu Lys Asn Leu Ser Thr Leu Leu Val Phe Leu Phe Phe Cys Leu Gly
1          5          10          15
Cys Val Ser Asn Phe Asn Glu Asp Thr Tyr Thr Leu Asp Leu Val Leu
          20          25          30
Glu Lys Lys Ile Gln Ala Ser Arg Lys Gly Glu Ile Thr Gln Asp Asn
          35          40          45
Val Pro Ile Ile Thr Ala Ile Ala Thr His Leu Asn Asp Val Asp Ser
          50          55          60
Gly Thr Tyr Tyr Asp His Glu Tyr Phe Leu Val Glu Ile Phe Thr Gln
65          70          75          80
Asn Asn Asp Trp Ile Asp Asp Gly Tyr Ile Ser Tyr Glu Leu Phe Gly
          85          90          95
Thr Lys Pro Thr Gly Ser Glu Pro Leu Trp Val Arg Glu Ile Thr Arg
          100          105          110
Asp Glu Phe Asp Gly Ile Leu Glu Thr Thr Asn Arg Trp Ser Arg Ala
          115          120          125
Phe Leu Ile Ala Phe Asp Lys Leu Asp Tyr Leu Ala Val Gln Glu Ala
          130          135          140
Lys Leu Glu Leu Asp Ala Tyr Ser Leu Gly Lys Ile Val Phe Asn Phe
145          150          155          160

```

.661

Ala Tyr Gln Val Pro Leu Pro Gln Phe
165

(2) INFORMATION FOR SEQ ID NO:754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

Met	Lys	Lys	Leu	Leu	Tyr	Thr	Met	Leu	Ala	Leu	Leu	Leu	Ile	Gly	Leu	1	5	10	15
Leu	Thr	Ala	Tyr	Leu	Ile	Leu	Phe	Thr	Glu	Trp	Gly	Asn	Lys	Ile	Ile	20	25	30	
Ala	Ser	Tyr	Ile	Glu	Lys	Lys	Ile	Asn	Pro	Asn	Glu	Arg	Tyr	Leu	Ser	35	40	45	
Val	Lys	Thr	Phe	Lys	Leu	Arg	Phe	Asn	Ser	Leu	Asp	Phe	Lys	Ala	Gln	50	55	60	
Ala	Asn	Asp	Asp	Ser	Thr	Leu	Ile	Leu	Lys	Gly	Asp	Phe	Ser	Leu	Leu	65	70	75	80
Thr	Gln	Ser	Val	Asn	Leu	Asp	Tyr	His	Ile	Asp	Ile	Lys	Asn	Leu	Arg	85	90	95	
Ser	Phe	Lys	Asp	Leu	Ile	Pro	Tyr	Pro	Leu	Arg	Gly	Ala	Ile	Val	Thr	100	105	110	
Ser	Gly	Asn	Ile	Lys	Gly	His	Arg	Lys	Ala	Leu	Val	Val	Gln	Gly	Val	115	120	125	
Ser	Asn	Val	Ala	Gln	Ser	His	Thr	Ala	Tyr	Asn	Ala	Leu	Leu	Asp	Asp	130	135	140	
Phe	Lys	Leu	Ser	His	Leu	Ser	Leu	Asn	Ala	Lys	Asp	Ala	Asn	Leu	Glu	145	150	155	160
Asp	Leu	Leu	Tyr	Leu	Ile	Asn	Arg	Pro	Ala	Tyr	Ala	Asn	Ala	Lys	Val	165	170	175	
Ser	Leu	Gln	Ala	Asp	Phe	Asn	Ser	Leu	Lys	Pro	Leu	Glu	Gly	His	Leu	180	185	190	
Ile	Leu	Thr	Ala	Asn	Asn	Ala	Leu	Ile	Asn	Asn	Ala	Leu	Ile	Asn	Gln	195	200	205	
Ile	Phe	His	Leu	Asn	Leu	Lys	Asp	Thr	Leu	Val	Phe	Asn	Leu	Ser	His	210	215	220	
Ser	Ser	Asp	Phe	Lys	Gly	Asn	Lys	Ala	Ile	Ser	Asp	Thr	Thr	Leu	Thr	225	230	235	240
Ser	Pro	Leu	Val	Asn	Phe	Thr	Ala	Leu	Lys	Ser	Glu	Tyr	Ser	Phe	Pro	245	250	255	
Ala	Leu	Lys	Leu	Asn	Ala	Pro	Tyr	Thr	Leu	Glu	Ile	Pro	His	Leu	Ala	260	265	270	

662

```

Lys Leu Gln Asn Ile Thr Asn His Pro Leu Lys Gly Ser Leu Thr Leu
  275                      280                      285
Lys Gly Asp Ile Glu Gln Ser Pro Lys Leu Leu Lys Val Ser Gly His
  290                      295                      300
Ser Asn Leu Leu Asp Gly Ala Leu Asp Phe Thr Leu Leu Asn Lys Asp
  305                      310                      315                      320
Leu Lys Ala Arg Phe Ser Asn Ile Ser Thr Ser Lys Ala Leu Asp Leu
                      325                      330                      335
Phe His Tyr Pro Lys Phe Phe Gln Ser Ile Ala Asp Ala Asn Leu Asp
                      340                      345                      350
Tyr Asp Leu Ile Ser Lys Gln Gly Val Leu Lys Ala Asn Leu Lys Asn
                      355                      360                      365
Ala Arg Phe Leu Lys Asn Ala Phe Ser Asp Phe Leu Tyr Ser Ile Ser
                      370                      375                      380
Arg Phe Asp Ile Thr Lys Glu Ile Tyr His Asp Ala Asn Leu Val Ser
  385                      390                      395                      400
Gln Ile Asn Gln Gln Arg Leu Leu Ser Asp Leu Ser Leu Lys Ser Pro
                      405                      410                      415
Lys Thr Gln Leu Lys Ile His Asn Gly Leu Leu Asp Leu Asn Thr Lys
                      420                      425                      430
Gln Met Asp Ile Leu Met Asp Ala Glu Ile Leu Lys Phe Ile Phe Lys
                      435                      440                      445
Met Lys Leu Gln Gly Ser Met His Gln Pro Lys Phe Ser Leu Ile Leu
                      450                      455                      460
Asn Glu Lys Ala Ile Gln Gln Asn Leu Gln Gln Gly Leu Lys Glu Ile
  465                      470                      475                      480
Leu Lys Asn Asp Thr Leu Lys Lys Gly Leu Asp His Leu Leu Lys Asp
                      485                      490                      495
Asp Lys Leu Lys Glu Lys Leu Glu Lys Gly Leu Lys Gly Leu Phe
                      500                      505                      510

```

(2) INFORMATION FOR SEQ ID NO:755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

```

Met Phe Gly Met Gly Phe Phe Glu Ile Leu Val Val Leu Ile Val Ala
  1                      5                      10                      15
Ile Ile Phe Leu Gly Pro Glu Lys Phe Pro Gln Ala Val Val Asp Ile
                      20                      25                      30
Val Lys Phe Phe Arg Ala Val Lys Lys Thr Leu Asn Asp Ala Lys Asp
                      35                      40                      45

```

663

```

Thr Leu Asp Lys Glu Ile Asn Ile Glu Glu Ile Lys Lys Glu Thr Leu
 50          55          60
Glu Tyr Gln Lys Leu Phe Glu Asn Lys Val Glu Ser Leu Lys Gly Val
65          70          75          80
Lys Ile Glu Glu Leu Glu Asp Ala Lys Val Thr Ala Glu Asn Glu Ile
          85          90          95
Lys Ser Ile Gln Asp Leu Met Gln Asp Tyr Lys Arg Ser Leu Glu Thr
          100          105          110
Asn Thr Ile Pro Asn His Leu Asn Glu Glu Val Ser Asn Glu Glu Ala
          115          120          125
Leu Asn Lys Glu Val Ser Ser Asp Glu Ser Pro Lys Glu Val Gln Leu
          130          135          140
Thr Thr Asp Asn Asn Ala Lys Glu His Asp Lys Glu Lys Glu His Val
145          150          155          160

```

(2) INFORMATION FOR SEQ ID NO:756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

```

Met Leu Arg Ile Leu Ile Pro Leu Leu Ile Ile Val Trp Val Leu Trp
 1          5          10          15
Arg Leu Phe Leu Arg Gln Lys Pro His Lys Asp Asp His Arg Asp Asn
          20          25          30
His Ser Tyr Thr Gln Gln Thr Pro Lys Glu Leu Glu Asp His Met Ile
          35          40          45
Val Cys Ser Lys Cys Gln Thr Tyr Val Ser Ser Lys Asp Ala Ile Tyr
          50          55          60
Ser Gly Ala Val Ala Tyr Cys Ser Glu Thr Cys Leu Lys Asp Lys Gly
65          70          75          80

```

(2) INFORMATION FOR SEQ ID NO:757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

```

Leu Asp Gly Leu Lys Lys Glu Arg Gln Gly Phe Tyr Lys Gln Val His
1           5           10           15
Tyr Leu Arg Ile Leu Ile Leu Ser Met Ser Phe Leu Asn Ile Leu Asn
20           25           30
Ala Glu Asn Leu Ser Tyr Met Ser Ser Ser Tyr Gln Ile Gly Thr Val
35           40           45
Phe Met Arg Pro Leu Asn Thr Asn Lys Leu Leu Gln Gly Ala Ser Ile
50           55           60
Leu Gln Gly Tyr Glu Val Asn Pro Lys Asn Asp Trp Ala Tyr Ser Arg
65           70           75           80
Tyr Tyr Phe Phe Ile Asp Tyr Gly Asn Val Leu Phe Asn Asn Asp Ser
85           90           95
Thr Leu Gln Ala Asn Met Phe Thr Tyr Gly Val Gly Gly Asp Phe Met
100          105          110
Val Ala Tyr Ala Lys Asn Pro Ile Asn Arg Trp Ala Phe Phe Phe Gly
115          120          125
Leu Gln Leu Ala Ala Asn Thr Trp Ile Leu Asn Asn Lys Val Lys Asp
130          135          140
Leu Val Val Asn Thr Trp Asp Ser Leu Lys Asp Phe Asn Phe His Asn
145          150          155          160
Thr Tyr Phe Arg Ala Ile Gly Lys Phe Gly Val Gln Phe Arg Thr Ile
165          170          175
Val Leu Tyr His Lys Val Asp Val Glu Ile Gly Met Lys Ile Phe Leu
180          185          190
Thr Pro Glu Arg Arg Ser Leu Phe Glu Arg Ser Phe Leu Phe Phe Val
195          200          205
Ser His Ser Trp His Phe
210

```

(2) INFORMATION FOR SEQ ID NO:758:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

665

```

Met Lys Pro Thr Asn Glu Pro Lys Lys Pro Phe Phe Gln Ser Pro Ile
1           5           10           15
Val Leu Ala Val Leu Gly Gly Ile Leu Leu Ile Phe Phe Leu Arg Ser
          20           25           30
Phe Asn Ser Asp Gly Ser Phe Ser Asp Asn Phe Leu Ala Ser Ser Thr
          35           40           45
Lys Asn Val Ser Tyr His Glu Ile Ile Gln Leu Ile Ser Asn His Glu
          50           55           60
Val Gly Asn Val Ser Ile Gly Gln Thr Leu Ile Lys Ala Ser His Lys
65           70           75           80
Glu Gly Asn Asn Arg Val Ile Tyr Ile Ala Lys Arg Val Leu Ile Tyr
          85           90           95
Leu Ser Ala Phe Val Arg Arg Glu Lys Asn Gln Leu Phe Trp Phe
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO:759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

```

Met Leu Arg Val Leu Ser Val Gly Val Val Phe Ile Leu Leu Gly Cys
1           5           10           15
Gln Phe Phe Asn Lys Thr Thr Leu His Leu Lys Tyr Lys Asp Tyr Pro
          20           25           30
Lys Asn Ser Pro Leu Lys Thr Ala Ser Thr Leu Thr Pro Pro Lys Ile
          35           40           45
Phe Phe Asn Ala His Phe Val Pro Pro Phe Tyr Gln Lys Glu Phe Lys
          50           55           60
Lys Ala Leu Ala Gln Gln Ile Ala Tyr Phe Leu Lys Asp Lys Ser Ala
65           70           75           80
Leu Thr Phe Asn Ile Ser Gly Asn Val Phe Phe Ser Phe Glu Glu Ser
          85           90           95
Pro Lys Asp Leu Lys Ala Ile Lys Glu Arg Leu Lys Lys Thr Ile Glu
          100          105          110
Pro Asn Thr Asp Pro Lys Ala Val Met Arg Phe Leu Asn Leu Gln Ala
          115          120          125
Ser Leu Ile Leu Glu Cys Val Pro Gln Thr Ala Cys Pro Phe Asp Thr
          130          135          140
Leu Leu Ile Pro Thr Ala Leu Ser Val Pro Ile Asp Tyr Ala Asn Arg
145          150          155          160
Leu Gly Asp Asn Pro Ser Leu Phe Pro Gln Glu Asp Lys Ser Tyr His

```

666

				165						170						175
Asn	Ala	Leu	Ile	Lys	Ala	Leu	Asn	Lys	Ala	Tyr	Tyr	Ser	Leu	Met	Glu	
				180						185					190	
Gly	Leu	Glu	Lys	Arg	Leu	Asn	Ala	Ile	Glu	Asn	Ala	Ala	Trp	Leu		
			195					200					205			

(2) INFORMATION FOR SEQ ID NO:760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

Met	Lys	Asn	Gln	Val	Lys	Lys	Ile	Leu	Gly	Met	Ser	Val	Val	Ala	Ala	
1				5					10					15		
Met	Val	Ile	Val	Gly	Cys	Ser	His	Ala	Pro	Lys	Ser	Gly	Ile	Ser	Lys	
			20					25					30			
Ser	Asn	Lys	Ala	Tyr	Lys	Glu	Ala	Thr	Lys	Gly	Ala	Pro	Asp	Trp	Val	
		35				40					45					
Val	Gly	Asp	Leu	Glu	Lys	Val	Ala	Lys	Tyr	Glu	Lys	Tyr	Ser	Gly	Val	
	50				55				60							
Phe	Leu	Gly	Arg	Ala	Glu	Asp	Leu	Ile	Thr	Asn	Asn	Asp	Val	Asp	Tyr	
65				70					75				80			
Ser	Thr	Asn	Gln	Ala	Thr	Ala	Lys	Ala	Arg	Ala	Asn	Leu	Ala	Ala	Asn	
			85					90					95			
Leu	Lys	Ser	Thr	Leu	Gln	Lys	Asp	Leu	Glu	Asn	Glu	Lys	Thr	Arg	Thr	
		100						105					110			
Val	Asp	Ala	Ser	Gly	Lys	Arg	Ser	Ile	Ser	Gly	Thr	Asp	Thr	Glu	Lys	
		115				120						125				
Ile	Ser	Gln	Leu	Val	Asp	Lys	Glu	Leu	Ile	Ala	Ser	Lys	Met	Leu	Ala	
		130				135					140					
Arg	Tyr	Val	Gly	Lys	Asp	Arg	Val	Phe	Val	Leu	Val	Gly	Leu	Asp	Lys	
145				150					155					160		
Gln	Ile	Val	Asp	Lys	Val	Arg	Glu	Glu	Leu	Gly	Met	Val	Lys	Lys		
				165					170					175		

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

```

Met Lys Lys Ile Val Val Ser Leu Cys Val Ala Leu Gly Phe Leu Ser
1           5           10           15
Ala Asp Pro Ala Gln Ala Asn Lys Ala Ile Ser Asp Ala Asp Leu Ile
20           25           30
Glu Glu Ile Arg Asp Leu Lys Lys Ile Ile Ser Ala Gln Asn Thr Glu
35           40           45
Ile Asn Gln Leu Arg Lys Val Gln Glu Val Leu Ser Gly Gln Leu Gly
50           55           60
Asp Met Arg Lys Asp Ile Leu Ser Thr Arg Asp Tyr Cys Ile Ser Leu
65           70           75           80
Arg Pro Tyr Ile Tyr Asn Trp Arg
85

```

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

```

Leu Asn Ser Gly Ser Asn Ala Ser Leu Tyr Gly Thr Ser Ala Gly Val
1           5           10           15
Asp Ala Phe Leu Asn Gly Asn Val Glu Ala Ile Val Gly Gly Phe Gly
20           25           30
Ser Tyr Gly Tyr Ser Ser Phe Ser Asn Gln Ala Asn Ser Leu Asn Ser
35           40           45
Gly Ala Asn Asn Ala Asn Phe Gly Val Tyr Ser Arg Phe Phe Ala Asn
50           55           60
Gln His Glu Phe Asp Phe Glu Ala Gln Gly Ala Leu Gly Ser Asp Gln
65           70           75           80
Ser Ser Leu Asn Phe Lys Ser Thr Leu Leu Gln Asp Leu Asn Gln Ser
85           90           95

```

668

```

Tyr Asn Tyr Leu Ala Tyr Ser Ala Thr Ala Arg Ala Ser Tyr Gly Tyr
      100                      105                      110
Asp Phe Ala Phe Phe Arg Asn Ala Leu Val Leu Lys Pro Ser Val Gly
      115                      120                      125
Val Ser Tyr Asn His Leu Gly Ser Thr Asn Phe Lys Ser Asn Ser Gln
      130                      135                      140
Ser Gln Val Ala Leu Lys Asn Gly Ala Ser Ser Gln His Leu Phe Asn
      145                      150                      155                      160
Ala Asn Ala Asn Val Glu Ala Arg Tyr Tyr Tyr Gly Asp Thr Ser Tyr
      165                      170                      175
Phe Tyr Leu His Ala Gly Val Leu Gln Glu Phe Ala His Phe Gly Ser
      180                      185                      190
Asn Asp Val Ala Ser Leu Asn Thr Phe Lys Ile Asn Ala Ala Arg Ser
      195                      200                      205
Pro Leu Ser Thr Tyr Ala Arg Ala Met Met Gly Gly Glu Leu Gln Leu
      210                      215                      220
Ala Lys Glu Val Phe Leu Asn Leu Gly Val Val Tyr Leu His Asn Leu
      225                      230                      235                      240
Ile Ser Asn Ala Ser His Phe Ala Ser Asn Leu Gly Met Arg Tyr Ser
      245                      250                      255
Phe

```

(2) INFORMATION FOR SEQ ID NO:763:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

```

Met Phe Glu Asp Phe Tyr Arg Thr Thr Leu Ser Phe Leu Arg Ser Leu
1      5      10      15
Leu Leu Leu Leu Gly Leu Leu Leu Pro Phe Ser Leu Cys Ile Ala Asp
      20      25      30
Glu Tyr Ile Ser Ile Ser Asp Asp Trp Asp Glu Arg Ala Arg Asn Gln
      35      40      45
Trp Asp Glu Thr Ala Arg Asn His Lys Thr Tyr Tyr Phe Glu Asn Gly
      50      55      60
Leu Asp His Phe Asn Gln Gly Gln Tyr Lys Gln Ala Phe Lys Asp Phe
      65      70      75      80
Lys Leu Ala Gln Glu Tyr Ser Ile Gly Leu Gly Asn Val Tyr Leu Ala
      85      90      95
Lys Met Tyr Leu Glu Gly Lys Gly Val Lys Val Asp Tyr Lys Lys Ala
      100      105      110

```

669

Gln Phe Tyr Ala Gln Asn Ala Ile Lys Gly Tyr Gly Ser Gly Leu Leu
 115 120 125
 Gly Gly Ala Leu Ile Leu Gly Arg Met Gln Ala Glu Gly Leu Gly Met
 130 135 140
 Lys Lys Asp Leu Lys Gln Ala Leu Lys Thr Tyr Arg His Val Val Arg
 145 150 155 160
 Met Phe Ser Asn Lys Ser Ala Asn Phe Ala Asn Lys Phe Gly Ser Asn
 165 170 175
 Leu Ala Glu Phe Thr Ser Met Leu Ile Gly Ser Arg Phe Ile Asp Leu
 180 185 190
 Ser Gly Leu Ser Ala Asn Pro Ile Lys Phe Gly Asn Lys Phe Gly Ile
 195 200 205
 Leu Val Lys Lys Ala Leu Gln Ile Lys Asp Asn Thr Leu Ser Trp Glu
 210 215 220
 Asp Ile Ala Glu Ile Ser Ser Asn Ile Ile Leu Leu Lys Gln Gln Met
 225 230 235 240
 Gly Glu Ile Leu Tyr Arg Ile Gly Ile Ala Tyr Lys Glu Gly Leu Gly
 245 250 255
 Thr Arg Lys Lys Lys Asp Arg Ala Lys Lys Phe Leu Gln Lys Ser Ala
 260 265 270
 Glu Phe Gly Tyr Glu Lys Ala Met Glu Ala Leu
 275 280

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

Leu Cys Lys Ile Pro Leu Ser Leu Thr Leu Met Glu Ala Arg Ser Val
 1 5 10 15
 Leu Thr Gln Glu Ile Arg Ser Phe Leu Pro Glu Thr Thr Thr Ser Leu
 20 25 30
 Ser Leu Thr Ile Leu Glu Arg Ser Ile Cys Cys Leu Ile Lys Phe Leu
 35 40 45
 Thr Leu Thr Ser Pro Cys Leu Thr Gln Gln Arg Pro Lys Ile Asn Ala
 50 55 60
 Thr Asn Asn Asn Val Ser Val Ser Gln Gly Asn Leu Phe Ile Asn Ala
 65 70 75 80
 Ser Cys Val Gln Gln Ser Asp Pro Thr Thr Ala Ser Ala Thr Asn Pro
 85 90 95
 Cys Thr Thr Ala Gln Asn Asn Ala Ser Ser Ser Asn Ala Ser Asn Asn
 100 105 110

670

Ala Pro Ile Ala Leu Asn Asn Asn Asp Glu Ser Leu Val Val Thr Ala
 115 120 125
 Asn Gly Phe Asn Phe Ser Gly Asn Ile Tyr Ala Asn Gly Val Val Asp
 130 135 140
 Phe Ser Lys Ile Lys Gly Ser Ala Asn Val Lys Asn Leu Tyr Leu Tyr
 145 150 155 160
 Asn Asn Ala Gln Phe Gln Ala Asn Asn Leu Thr Ile Ser Asn Gln Ala
 165 170 175
 Val Leu Glu Lys Asn Ala Ser Phe Val Thr Asn Asn Leu Asn Ile Gln
 180 185 190
 Gly Ala Phe Asn Asn Asn Ala Thr Gln Lys Ile Glu Val Leu Gln Asn
 195 200 205
 Leu Val Ile Ala Ser Asn Ala Ser Leu Ser Thr Gly Ile Tyr Gly Leu
 210 215 220
 Glu Val Gly Gly Ala Leu Asn Asn Leu Gly Ala Ile His Phe Asn Leu
 225 230 235 240
 Glu Asn Ser Gln Thr Pro Val Asn Pro Leu Ile Gln Val Gly Gly Ile
 245 250 255
 Ile Asn Leu Asn Thr Thr Gln Thr Pro Phe Met Asn Val Ser Val Ala
 260 265 270
 Asn Gly Gly Thr Tyr Thr Leu Leu Lys Ser Ser Arg Tyr Ile Asp Tyr
 275 280 285
 Asn Ile Asn Pro Asn Ser Leu Gln Ser Tyr Leu Lys Leu Tyr Thr Leu
 290 295 300
 Ile Asn Ile Asn Gly Asn His Ile Glu Glu Lys Asn Gly Val Leu Thr
 305 310 315 320
 Tyr Leu Gly Gln Arg Val Leu Leu Gln Asp Lys Gly Leu Leu Leu Ser
 325 330 335
 Val Ala Leu Pro Asn Ser Asn Asn Ala Ser Gln Asn Asn Ile Leu Ser
 340 345 350
 Leu Ser Val Leu His Asn Gln Ile Lys Met Ser Tyr Gly Asn Lys Val
 355 360 365
 Met Asp Phe Thr Pro Pro Thr Leu Gln Asp Tyr Ile Val Gly Ile Gln
 370 375 380
 Gly Gln Ser Ala Leu Asn Gln Ile Glu Ala Val Gly Gly Asn Asn Ala
 385 390 395 400
 Ile Lys Trp Leu Ser Thr Leu Met Met Glu Thr Lys Glu Asn Pro Leu
 405 410 415
 Phe Ala Pro Ile Tyr Leu Glu Asn His Ser Leu Asn Glu Ile Leu Gly
 420 425 430
 Val Thr Lys Asp Leu Gln Asn Thr Ala Ser Leu Ile Ser Asn Pro Asn
 435 440 445
 Phe Arg Asn Asn Ala Thr Ser Leu Leu Glu Met Ala Ser Tyr Thr Gln
 450 455 460
 Gln Thr Ser Arg Leu Thr Lys Leu Ser Asp Phe Arg Ala Arg Glu Gly
 465 470 475 480
 Glu Ser Asn Phe Ser Glu Arg Leu Leu Glu Leu Lys Asn Lys Arg Phe
 485 490 495
 Ser Asp Pro Asn Pro Ser Glu Val Phe Val Lys Tyr Ser Gln Leu Ser
 500 505 510
 Lys His Pro Asn Asn Leu Trp Ile Gln Gly Val Gly Gly Ala Ser Phe
 515 520 525
 Ile Ser Gly Gly Asn Gly Thr Leu Tyr Gly Leu Asn Val Gly Tyr Asp
 530 535 540
 Arg Leu Val Lys Ser Val Ile Leu Gly Gly Tyr Val Ala Tyr Gly Tyr
 545 550 555 560
 Ser Gly Phe Asn Gly Asn Ile Met His Ser Leu Ala Asn Asn Val Asp

671

				565					570					575			
Val	Gly	Met	Tyr	Ala	Arg	Ala	Phe	Leu	Lys	Arg	Asn	Glu	Phe	Thr	Leu		
				580					585					590			
Ser	Ala	Asn	Glu	Thr	Tyr	Gly	Gly	Asn	Ala	Ser	His	Ile	Asn	Ser	Ser		
		595						600				605					
Asn	Ser	Leu	Leu	Ser	Val	Leu	Asn	Gln	Arg	Tyr	Asn	Tyr	Asn	Thr	Trp		
	610					615					620						
Thr	Thr	Ser	Val	Asn	Gly	Asn	Tyr	Gly	Tyr	Asp	Phe	Met	Phe	Lys	Gln		
625					630					635					640		
Lys	Ser	Val	Val	Leu	Lys	Pro	Gln	Val	Gly	Leu	Ser	Tyr	His	Phe	Ile		
				645					650					655			
Gly	Leu	Ser	Gly	Met	Lys	Gly	Lys	Met	Gln	Asn	Pro	Ala	Tyr	Gln	Gln		
		660						665					670				
Phe	Val	Met	His	Ser	Asn	Pro	Ser	Asn	Glu	Ser	Val	Leu	Thr	Leu	Asn		
		675					680					685					
Met	Gly	Leu	Glu	Ser	Arg	Lys	Tyr	Phe	Gly	Lys	Asn	Ser	Tyr	Tyr	Phe		
	690					695					700						
Val	Thr	Ala	Arg	Leu	Gly	Arg	Asp	Leu	Leu	Ile	Lys	Ala	Lys	Gly	Asp		
705					710					715					720		
Asn	Val	Val	Arg	Phe	Val	Gly	Glu	Asn	Thr	Leu	Leu	Tyr	Arg	Lys	Gly		
				725					730					735			
Glu	Ile	Phe	Asn	Thr	Phe	Ala	Ser	Val	Ile	Thr	Gly	Gly	Glu	Met	His		
			740					745					750				
Leu	Trp	Arg	Leu	Met	Tyr	Val	Asn	Ala	Gly	Val	Gly	Leu	Lys	Met	Gly		
		755					760					765					
Leu	Gln	Tyr	Gln	Asp	Leu	Asn	Ile	Thr	Gly	Asn	Val	Gly	Met	Arg	Val		
	770					775					780						
Ala	Phe																
785																	

(2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

Met	Phe	Arg	Lys	Leu	Ala	Thr	Ser	Val	Ser	Leu	Ile	Ser	Leu	Leu	Ile
1				5					10					15	
Ser	Asn	Ala	Leu	Tyr	Ala	Lys	Glu	Ile	Ser	Glu	Ala	Asp	Lys	Val	Ile
		20						25					30		
Lys	Ala	Thr	Lys	Glu	Thr	Lys	Glu	Thr	Lys	Lys	Glu	Ala	Lys	Arg	Leu
		35					40					45			
Lys	Lys	Glu	Ala	Lys	Gln	Arg	Gln	Gln	Ile	Pro	Asp	Asn	Lys	Lys	Pro

50		55		60	
Gln Tyr Val Ser Val Asp Asp Thr Lys Thr Gln Ala Leu Phe Asp Ile					
65		70		75	80
Tyr Asp Thr Leu Asn Val Asn Asp Lys Ser Phe Gly Asp Trp Phe Gly					
	85		90		95
Asn Ser Ala Leu Lys Asn Lys Thr Tyr Leu Tyr Ala Met Asp Leu Leu					
	100		105		110
Asp Tyr Asn Asn Tyr Leu Ser Ile Glu Asn Pro Ile Ile Lys Thr Arg					
	115		120		125
Ala Met Gly Thr Tyr Ala Asp Leu Ile Ile Ile Thr Gly Ser Leu Glu					
	130		135		140
Gln Val Asn Gly Tyr Tyr Asn Ile Leu Lys Ala Leu Asn Lys Arg Asn					
145		150		155	160
Ala Lys Phe Val Leu Lys Ile Asn Asp Lys Ile Pro Tyr Ala Gln Ala					
	165		170		175
Thr Phe Leu Arg Val Pro Lys Arg Ser Asp Pro Asn Ala His Thr Leu					
	180		185		190
Asp Lys Gly Ala Ser Ile Asp Glu Ser Lys Leu Phe Glu Gln Gln Lys					
	195		200		205
Lys Met Tyr Phe Asn Tyr Ala Asn Asp Val Ile Cys Arg Pro Asn Asp					
	210		215		220
Glu Val Cys Ser Pro Leu Arg Asp Glu Met Val Ala Met Pro Thr Asn					
225		230		235	240
Asp Ser Val Thr Gln Lys Pro Asn Ile Ile Ala Pro Tyr Ser Leu Tyr					
	245		250		255
Arg Leu Lys Glu Thr Asn Asn Ala Asn Glu Ala Gln Pro Ser Pro Tyr					
	260		265		270
Ala Thr Gln Thr Ala Pro Glu Asn Ser Lys Glu Lys Leu Ile Glu Glu					
	275		280		285
Leu Ile Ala Asn Ser Gln Leu Ile Ala Asn Glu Glu Arg Glu Lys					
	290		295		300
Lys Leu Leu Ala Glu Lys Glu Lys Gln Glu Thr Glu Leu Ala Lys Tyr					
305		310		315	320
Lys Leu Lys Asp Leu Glu Asn Gln Lys Lys Leu Lys Ala Leu Glu Ala					
	325		330		335
Glu Leu Lys Lys Lys Asn Thr Lys Lys Pro Arg Val Val Glu Val Pro					
	340		345		350
Ile Pro Pro Lys Thr Ser Asp Ser Asp Glu Thr Met Arg Val Ile Lys					
	355		360		365
Glu Lys Glu Asn Tyr Asn Gly Leu Leu Val Asp Lys Glu Thr Thr Ile					
	370		375		380
Lys Arg Ser Tyr Lys Gly Thr Leu Ile Ser Glu Asn Ser Tyr Ser Lys					
385		390		395	400
Lys Thr Pro Ile Asn Leu Glu Asp Leu Arg Ser Leu Glu Glu Glu Ile					
	405		410		415
Lys Ser Tyr Tyr Val Lys Ser Asn Gly Leu Cys Tyr Ala Asn Gly Ile					
	420		425		430
Asn Leu Tyr Val Lys Ile Lys Asn Asp Pro Tyr Lys Glu Gly Met Leu					
	435		440		445
Cys Gly Tyr Glu Ser Val Gln Lys Leu Leu Ser Pro Leu Arg Asp Lys					
	450		455		460
Leu Lys Tyr Asp Lys Gln Lys Leu Gln Lys Ala Leu Leu Lys Asp Leu					
465		470		475	480
Lys					

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...59

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

```

Leu Leu Ser Arg Ser Met Pro Lys Ile His Ala Val Phe Lys Ala Phe
1           5           10           15
Ile Pro Ile Pro Phe Ala Leu Phe Ala Ile His Phe Val Val Leu Gly
20           25           30
Ile Gly Ser Val Phe Asn Leu Asn Arg Ile Lys Asp Lys Lys Phe Ile
35           40           45
Leu Arg Ala Lys Ile Ser His Ile Ala Gln Ala
50           55

```

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

```

Met Arg Lys Thr Ile Ser Ala Leu Phe Leu Ser Ala Cys Ile Gly Leu
1           5           10           15
Ser Ser Val His Ala Ser Asn Ala Leu Ile Leu Gln Thr Asp Phe Ser
20           25           30
Leu Lys Asp Gly Ala Val Ser Ala Met Lys Gly Val Ala Phe Ser Val
35           40           45
Asp Ser Asn Leu Lys Ile Phe Asp Leu Thr His Glu Ile Pro Pro Tyr
50           55           60
Asn Ile Trp Glu Gly Ala Tyr Arg Leu Tyr Gln Thr Ala Ser Tyr Trp

```

674

```

65          70          75          80
Pro Lys Gly Ser Val Phe Val Ser Val Val Asp Pro Gly Val Gly Thr
                        85          90          95
Asn Arg Lys Ser Val Val Leu Lys Thr Lys Asn Gly Gln Tyr Phe Val
                        100          105          110
Ser Pro Asp Asn Gly Thr Leu Thr Leu Val Ala Gln Thr Leu Gly Ile
                        115          120          125
Asp Ser Val Arg Glu Ile Asp Glu Lys Ala Asn Arg Leu Lys Gly Ser
                        130          135          140
Glu Lys Ser Tyr Thr Phe His Gly Arg Asp Val Tyr Ala Tyr Thr Gly
145          150          155          160
Ala Arg Leu Ala Ser Gly Ala Ile Thr Phe Glu Gln Val Gly Pro Glu
                        165          170          175
Leu Pro Ile Lys Val Val Glu Ile Pro Tyr Gln Lys Ala Lys Ala Thr
                        180          185          190
Lys Gly Gly Val Lys Gly Asn Ile Pro Ile Leu Asp Ile Gln Tyr Gly
                        195          200          205
Asn Val Trp Ser Asn Ile Ser Asp Lys Leu Leu Asn Gln Ala Gly Ile
                        210          215          220
Lys Arg Asn Asp Thr Val Cys Val Thr Ile Leu Lys Ile Pro Arg Asn
225          230          235          240
Asn Thr Lys Gly Lys Cys Arg Met Ser Arg Ala Leu Ala Met Cys Gln
                        245          250          255
Lys Ala Ser Arg Trp Ser Ile
                        260

```

(2) INFORMATION FOR SEQ ID NO:768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

```

Met Asn Ile Lys Thr His Ser Ser Asn Glu Lys Glu Arg Phe Val Arg
1          5          10          15
Ile Glu Glu Asp Glu Lys Lys Glu Leu Phe Ala Glu Ala Thr Asn Glu
20          25          30
Asn Pro His Gly Leu Ser Leu Met Ala Leu Ile Gly Val Leu Val Phe
35          40          45
Gly Gly Ala Phe Leu Ala Leu Leu Val Pro Lys Ile Tyr Leu Ser Asn
50          55          60
Asn Ile Tyr Tyr Ile Ser Arg Lys Ile Asn Thr Leu Glu Asp Gln Lys
65          70          75          80
Arg Leu Leu Leu Glu Glu Gln Gln Ile Leu Lys Asn Glu Leu Glu Lys

```


675

	85		90		95
Glu Arg Phe Lys Tyr Tyr Ile Glu Asn Ser Glu Asn Ile Gly Asp Ile					
	100		105		110
Ala Phe					

(2) INFORMATION FOR SEQ ID NO:769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 941 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

Leu	Gln	His	Lys	Thr	Ile	Met	Asp	Lys	Ile	Ile	Ile	Gln	Gly	Ala	Arg
1				5					10					15	
Glu	Asn	Asn	Leu	Lys	Asn	Ile	Phe	Leu	Glu	Ile	Pro	Lys	Asn	Gln	Phe
			20					25					30		
Val	Val	Phe	Thr	Gly	Leu	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Ala	Phe
			35				40					45			
Asp	Thr	Leu	Tyr	Ala	Glu	Gly	Gln	Arg	Arg	Tyr	Leu	Glu	Ser	Leu	Ser
			50			55				60					
Ser	Tyr	Ala	Arg	Gln	Phe	Leu	Asp	Lys	Val	Gly	Lys	Pro	Asn	Val	Asp
65				70					75					80	
Lys	Ile	Glu	Gly	Leu	Thr	Pro	Ala	Ile	Ala	Ile	Asp	Gln	Lys	Thr	Thr
			85					90					95		
Ser	Lys	Asn	Pro	Arg	Ser	Thr	Val	Gly	Thr	Ile	Thr	Glu	Ile	Tyr	Asp
			100					105					110		
Tyr	Leu	Arg	Leu	Leu	Phe	Ala	Arg	Val	Gly	Glu	Gln	Phe	Cys	Pro	Thr
			115				120					125			
Cys	Leu	Glu	Pro	Ile	Ser	Ser	Met	Ser	Ala	Ser	Asp	Ile	Ile	Ser	Gln
			130				135				140				
Ile	Cys	His	Leu	Glu	Glu	Asn	Ser	Lys	Ile	Ile	Ile	Leu	Ala	Pro	Ile
145				150					155					160	
Ile	Lys	Asp	Lys	Lys	Gly	Ser	Phe	Asn	Asp	Lys	Leu	Glu	Ser	Leu	Arg
			165					170					175		
Leu	Lys	Gly	Tyr	Val	Arg	Ala	Phe	Val	Asp	Gly	Val	Met	Val	Arg	Leu
			180					185					190		
Asp	Glu	Glu	Ile	His	Leu	His	Lys	Thr	Lys	Lys	His	Thr	Ile	Glu	Ala
			195				200					205			
Val	Val	Asp	Arg	Val	Val	Ile	Asn	Ser	Glu	Asn	Ala	Ser	Arg	Ile	Ala
			210			215					220				
Ser	Ala	Val	Glu	Lys	Ala	Leu	Lys	Glu	Ser	Tyr	Gly	Glu	Leu	Glu	Val
225				230					235				240		
Glu	Ile	Leu	Gln	Asp	Asn	Ala	Pro	Ser	Ile	Arg	Lys	His	Tyr	Ser	Glu

677

```

Met Asp Glu Ile Arg Ile Leu Phe Ala Glu Gln Lys Glu Ala Lys Ile
705              710              715              720
Leu Gly Tyr Ser Thr Ser Arg Phe Ser Phe Asn Val Lys Gly Gly Arg
              725              730              735
Cys Glu Lys Cys Gln Gly Asp Gly Asp Ile Lys Ile Glu Met His Phe
              740              745              750
Leu Pro Asp Val Leu Val Gln Cys Asp Ser Cys Lys Gly Ala Lys Tyr
              755              760              765
Asn Pro Gln Thr Leu Glu Ile Lys Val Lys Gly Lys Ser Ile Ala Asp
              770              775              780
Val Leu Asn Met Ser Val Glu Glu Ala Tyr Glu Phe Phe Ala Lys Phe
785              790              795              800
Pro Lys Ile Ala Val Lys Leu Lys Thr Leu Ile Asp Val Gly Leu Gly
              805              810              815
Tyr Ile Thr Leu Gly Gln Asn Ala Thr Thr Leu Ser Gly Gly Glu Ala
              820              825              830
Gln Arg Ile Lys Leu Ala Lys Glu Leu Ser Lys Lys Asp Thr Gly Lys
              835              840              845
Thr Leu Tyr Ile Leu Asp Glu Pro Thr Thr Gly Leu His Phe Glu Asp
              850              855              860
Val Asn His Leu Leu Gln Val Leu His Ser Leu Val Ala Leu Gly Asn
865              870              875              880
Ser Met Leu Val Ile Glu His Asn Leu Asp Ile Ile Lys Asn Ala Asp
              885              890              895
Tyr Ile Ile Asp Met Gly Pro Asp Gly Gly Asp Lys Gly Gly Lys Val
              900              905              910
Ile Ala Ser Gly Thr Pro Leu Glu Val Ala Gln Asn Cys Glu Lys Thr
              915              920              925
Gln Ser Tyr Thr Gly Lys Phe Leu Ala Leu Glu Leu Lys
              930              935              940

```

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

```

Met Asn Tyr Asp Val Leu Met Gly Phe Leu Ala Leu Ile Leu Leu Ile
1              5              10              15
Leu Trp Tyr Ala Tyr Gly Leu Arg Gln Tyr Leu Lys Leu Lys Asp Lys
              20              25              30
Asn Lys Arg Leu Lys Glu Lys Leu Gln Arg Cys Asn Cys Asn Ile Lys
              35              40              45

```

678

```

Ile Pro Ser Ile Leu Glu Met Ala His Lys Pro Ile Ile Met Asp Ile
 50                      55                      60
Lys Gly Glu Leu Leu Pro His Leu Thr Glu Ser Tyr Arg Lys Ser Lys
65                      70                      75                      80
Phe Lys Glu

```

(2) INFORMATION FOR SEQ ID NO:771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

```

Met Arg Val Ile Ile Lys Phe Met Leu Ile Ser Leu Lys Thr Phe Leu
1                      5                      10                      15
Lys Ile Leu Leu Lys Ile Phe Leu Lys Thr Phe Gln Lys Ile Trp Ile
                20                      25                      30
Val Cys Val Val Ile Trp Gly Leu Gly Cys Ser Phe Leu Asn Ala Asn
                35                      40                      45
Ser Val Gln Leu Glu Glu Thr Leu Arg Arg Asn Pro Lys Asn Leu Ile
                50                      55                      60
Trp Gln His Phe Lys Lys Lys Phe Lys Lys Ser Asn Thr Ile Pro Tyr
65                      70                      75                      80
Ala Pro Asn Ser Arg Trp Lys Tyr Leu Gly Thr Ser Ile Gly Ile Leu
                85                      90                      95
Gly Val Ser Leu Val Ile Gly Ile Val Gly Leu Tyr Leu Met Pro Glu
                100                      105                      110
Ser Val Thr Asn Trp Asp Lys Glu Lys Phe Gly Val Lys Ser Trp Phe
                115                      120                      125
Glu Asn Val Arg Met Gly Pro Lys Leu Asp Asn Asp Ser Phe Ile Phe
130                      135                      140
Asn Glu Ile Leu His Pro Tyr Phe Gly Ala Met Tyr Tyr Met Gln Pro
145                      150                      155                      160
Arg Met Ala Gly Phe Ser Trp Met Thr Ser Ala Phe Phe Ser Phe Ile
                165                      170                      175
Thr Ser Thr Leu Phe Trp Glu Tyr Gly Leu Glu Ala Phe Val Glu Val
                180                      185                      190
Pro Ser Trp Gln Asp Leu Val Ile Thr Pro Leu Leu Gly Ser Ile Leu
                195                      200                      205
Gly Glu Gly Phe Tyr Gln Leu Thr Arg Tyr Ile Gln Arg Asn Glu Gly
                210                      215                      220
Lys Leu Phe Gly Ser Leu Phe Leu Gly Arg Leu Ala Ile Ala Leu Met
225                      230                      235                      240

```

679

Asp Pro Ile Gly Phe Ile Ile Arg Asp Leu Gly Leu Gly Glu Ala Leu
 245 250 255
 Gly Ile Tyr Asn Lys His Glu Ile Arg Ser Asn Leu Ser Pro Asn Gly
 260 265 270
 Leu Asn Leu Thr Tyr Lys Phe
 275

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

Met Lys Leu Phe Asn Pro Arg Leu Ile Val Phe Ile Phe Ala Leu Leu
 1 5 10 15
 Leu Gly Val Gly Phe Ser Val Pro Ser Leu Leu Glu Thr Lys Gly Pro
 20 25 30
 Lys Ile Thr Leu Gly Leu Asp Leu Arg Gly Gly Leu Asn Met Leu Leu
 35 40 45
 Gly Val Gln Thr Asp Glu Ala Leu Lys Asn Lys Tyr Leu Ser Leu Ala
 50 55 60
 Ser Ala Leu Glu Tyr Asn Ala Lys Lys Gln Asn Ile Leu Leu Lys Asp
 65 70 75 80
 Ile Lys Ser Ser Leu Glu Gly Ile Ser Phe Glu Leu Leu Asp Glu Asp
 85 90 95
 Glu Ala Lys Lys Leu Asp Ala Leu Leu Glu Leu Gln Gly His Ser
 100 105 110
 Gln Phe Glu Ile Lys Lys Glu Ala Glu Phe Tyr Ser Val Lys Leu Thr
 115 120 125
 Pro Leu Glu Gln Glu Glu Leu Arg Lys Asn Thr Ile Leu Gln Val Ile
 130 135 140
 Gly Ile Ile Arg Asn Arg Leu Asp Arg Phe Gly Leu Ala Glu Pro Val
 145 150 155 160
 Val Ile Gln Gln Gly Arg Val Glu Phe Arg Cys Asn Cys Pro Ala Leu
 165 170 175
 Arg

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 436 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

```

Met Met Lys Phe Phe Leu Leu Lys Lys Phe Ser Glu Phe Leu Asn Thr
1      5      10      15
Gln Thr His Phe Asn Leu Lys Arg Leu Asn Ala Ser Ser Phe Leu Leu
      20      25      30
Glu Thr Phe Ser Lys Glu Lys His Ala Phe Val Val Asp Leu Ser Ala
      35      40      45
Pro Tyr Ile Gly Leu Ser Lys Lys Pro Pro Glu Ser Val Leu Lys Asn
      50      55      60
Thr Leu Ala Leu Asp Phe Cys Leu Asn Lys Phe Thr Lys Asn Ala Lys
      65      70      75      80
Ile Leu Gln Ala Asn Val Ile Asp Asn Asp Arg Ile Leu Glu Ile Lys
      85      90      95
Gly Ala Lys Asp Leu Ala Tyr Lys Ser Glu Thr Phe Ile Leu Arg Leu
      100     105     110
Glu Met Ile Pro Lys Lys Ala Asn Leu Met Ile Leu Asp Gln Glu Lys
      115     120     125
Cys Val Ile Glu Ala Phe Arg Phe Asn Asp Arg Val Ala Lys Asn Asp
      130     135     140
Ile Leu Gly Ala Leu Pro Pro Asn Ile Tyr Glu His Gln Glu Glu Asp
      145     150     155     160
Leu Asp Phe Lys Gly Leu Leu Asp Ile Leu Glu Lys Asp Phe Leu Ser
      165     170     175
Tyr Gln His Lys Glu Leu Glu His Lys Lys Asn Gln Ile Ile Lys Arg
      180     185     190
Leu Asn Ala Gln Lys Glu Arg Leu Lys Glu Lys Leu Glu Lys Leu Glu
      195     200     205
Asp Pro Lys Thr Leu Gln Leu Glu Ala Lys Glu Leu Gln Thr Gln Ala
      210     215     220
Ser Leu Leu Leu Thr Tyr Gln His Leu Ile Asn Arg Arg Glu Asn Arg
      225     230     235     240
Val Ile Leu Lys Asp Phe Glu Asp Lys Glu Cys Met Ile Glu Ile Asp
      245     250     255
Lys Ser Met Pro Leu Asn Ala Phe Ile Asn Lys Lys Phe Thr Leu Ser
      260     265     270
Lys Lys Lys Lys Gln Lys Ser Gln Phe Leu Tyr Leu Glu Glu Glu Asn
      275     280     285
Leu Lys Glu Lys Ile Ala Phe Lys Glu Asn Gln Ile Asn Tyr Val Arg
      290     295     300
Asp Ala Ala Glu Glu Ser Val Leu Glu Met Phe Met Pro Val Lys Asn
      305     310     315     320
Ser Lys Ile Lys Arg Pro Met Asn Gly Tyr Glu Val Leu Tyr Tyr Lys
      325     330     335

```

681

```

Asp Phe Lys Ile Gly Leu Gly Lys Asn Gln Lys Glu Asn Ile Lys Leu
      340                      345                      350
Leu Gln Asp Ala Arg Ala Asn Asp Leu Trp Met His Val Arg Asp Ile
      355                      360                      365
Pro Gly Ser His Leu Ile Val Phe Cys Gln Lys Asn Thr Pro Lys Asp
      370                      375                      380
Glu Val Ile Met Glu Leu Ala Lys Met Leu Ile Lys Met Gln Lys Asp
      385                      390                      395                      400
Ala Phe Asn Gly Tyr Glu Ile Asp Tyr Thr Gln Arg Lys Phe Val Lys
      405                      410                      415
Ile Ile Lys Gly Ala His Val Ile Tyr Ser Lys Tyr Arg Thr Ile Ser
      420                      425                      430
Leu Lys Asp Thr
      435

```

(2) INFORMATION FOR SEQ ID NO:774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

```

Met Gly Gln Thr Lys Glu Ile Ile Thr Thr Leu Leu Pro Leu Leu Val
1           5           10           15
Leu Phe Leu Ile Phe Tyr Phe Leu Ile Val Arg Pro Gln Arg Gln Gln
      20           25           30
Gln Lys Lys His Lys Glu Met Ile Glu Gly Leu Thr Lys Gly Asp Lys
      35           40           45
Ile Val Thr Gln Gly Gly Leu Ile Val Glu Val Leu Lys Ala Glu Ala
      50           55           60
Asn Phe Phe Ser Val Lys Leu Asn Asp Asp Thr Thr Ala Lys Leu Ser
      65           70           75           80
Lys Asn Tyr Val Ala Phe Lys Leu Asp Glu Glu Thr Thr Pro Asn Asn
      85           90           95
Asn

```

(2) INFORMATION FOR SEQ ID NO:775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

682

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

```

Leu Lys Phe Gln Ile Val Ser Leu Leu Leu Ala Phe Leu Leu Ala Ser
1           5           10           15
Cys Leu Pro Pro Lys Gly His His Ser Gly Leu Val Asn Met Tyr Ile
          20           25           30
Ala His Gln Gly Gln Ser Val Arg Thr Tyr Trp Arg Lys Val Asp Arg
          35           40           45
Gly Val Val Ala Lys His Asn Glu Thr Leu Lys Glu Asn Pro Lys Ile
          50           55           60
Lys Leu Lys Asp Pro Lys Gly Pro Leu Phe Met Leu Gly Ser Asn Arg
65           70           75           80
Phe Met Leu Leu Trp Lys Asn Arg Tyr Thr Leu Ala Lys Val Gln Ser
          85           90           95
Phe Lys Leu Glu Pro Gly Phe Tyr Tyr Leu Asp Ser Phe Ser Val Glu
          100          105          110
Thr Gln Lys Gly Ile Leu Gln Ser Ala Pro Gly Tyr Ser Tyr Thr Lys
          115          120          125
Asn Gly Tyr Asp Phe Lys Asn Asn Arg Pro Phe Phe Leu Ala Phe Glu
          130          135          140
Val Lys Pro Asp Ser Lys Ile Val Leu Pro Ser Val Glu Leu Ser Leu
145          150          155          160
Ile Lys Thr Pro Arg Gly Phe Leu Gly Val Phe Leu Phe Asp Asn Asn
          165          170          175
Glu Lys Gly Ala Asn Thr Pro Trp Ile Glu Gly Ser Leu Asn Leu Lys
          180          185          190
Leu Lys Asn Ala Ser Phe Lys Asp Ala Trp Glu Leu Glu Arg
          195          200          205

```

(2) INFORMATION FOR SEQ ID NO:776:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 533 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

Met	Arg	Lys	Val	Ile	Ile	Met	Asn	Gly	Tyr	Leu	Arg	Val	Lys	Thr	Pro	1	5	10	15
Tyr	Phe	Leu	Ala	Ser	Val	Val	Leu	Thr	Phe	Trp	Thr	Phe	Asn	Ser	Phe	20	25	30	
Met	Ser	Ala	Lys	Asp	Lys	His	His	Phe	Leu	Lys	Lys	Val	Thr	Thr	Thr	35	40	45	
Glu	Gln	Lys	Phe	Ser	Ser	Ser	Ala	Pro	Ile	Ser	Trp	Gln	Ser	Glu	Glu	50	55	60	
Val	Arg	Asn	Ser	Thr	Ser	Ser	Arg	Thr	Val	Ile	Ser	Asn	Lys	Glu	Leu	65	70	75	80
Lys	Lys	Thr	Gly	Asn	Leu	Asn	Ile	Glu	Asn	Ala	Leu	Gln	Asn	Val	Pro	85	90	95	
Gly	Ile	Gln	Ile	Arg	Asp	Ala	Thr	Gly	Thr	Gly	Val	Leu	Pro	Lys	Ile	100	105	110	
Ser	Val	Arg	Gly	Phe	Gly	Gly	Gly	Gly	Asn	Gly	His	Ser	Asn	Thr	Asn	115	120	125	
Met	Ile	Leu	Val	Asn	Gly	Ile	Pro	Ile	Tyr	Gly	Ala	Pro	Tyr	Ser	Asn	130	135	140	
Ile	Glu	Leu	Ala	Ile	Phe	Pro	Val	Thr	Phe	Gln	Ser	Val	Asp	Arg	Ile	145	150	155	160
Asp	Val	Ile	Lys	Gly	Gly	Thr	Ser	Val	Gln	Tyr	Gly	Pro	Asn	Thr	Phe	165	170	175	
Gly	Gly	Val	Val	Asn	Val	Ile	Thr	Lys	Glu	Ile	Pro	Lys	Glu	Trp	Glu	180	185	190	
Asn	Gln	Ala	Ala	Glu	Arg	Ile	Thr	Phe	Trp	Gly	Arg	Ser	Ser	Asn	Gly	195	200	205	
Asn	Phe	Val	Asp	Pro	Lys	Glu	Lys	Gly	Lys	Pro	Leu	Ala	Gln	Thr	Leu	210	215	220	
Gly	Asn	Gln	Met	Leu	Phe	Asn	Thr	Tyr	Gly	Arg	Thr	Ala	Gly	Met	Leu	225	230	235	240
Gly	Lys	Tyr	Ile	Gly	Ile	Ser	Ala	Gln	Gly	Asn	Trp	Ile	Asn	Gly	Gln	245	250	255	
Gly	Phe	Arg	Gln	Asn	Ser	Pro	Thr	Lys	Val	Gln	Asn	Tyr	Leu	Leu	Asp	260	265	270	
Ala	Ile	Tyr	Lys	Ile	Asn	Ala	Thr	Asn	Thr	Phe	Lys	Ala	Tyr	Tyr	Gln	275	280	285	
Tyr	Tyr	Gln	Tyr	Asn	Ser	Tyr	His	Pro	Gly	Thr	Leu	Ser	Ala	Gln	Asp	290	295	300	
Tyr	Ala	Tyr	Asn	Arg	Phe	Ile	Asn	Glu	Arg	Pro	Asp	Asn	Gln	Asp	Gly	305	310	315	320
Gly	Arg	Ala	Lys	Arg	Phe	Gly	Ile	Val	Tyr	Gln	Asn	Tyr	Phe	Gly	Asp	325	330	335	
Pro	Asp	Arg	Lys	Val	Gly	Gly	Asp	Phe	Lys	Phe	Thr	Tyr	Phe	Thr	His	340	345	350	
Asp	Met	Ser	Arg	Asp	Phe	Gly	Phe	Ser	Asn	Gln	Tyr	Gln	Ser	Val	Tyr	355	360	365	
Met	Ser	Gly	Gln	Asn	Lys	Ile	Leu	Pro	Phe	Lys	Gly	Lys	Gly	Glu	Ile	370	375	380	
Ser	Ala	Lys	Asn	Pro	Asn	Cys	Gly	Leu	Tyr	Ser	Tyr	Ser	Asp	Thr	Asn	385	390	395	400
Ser	Pro	Cys	Trp	Gln	Phe	Phe	Asp	Asn	Ile	Arg	Arg	Ser	Val	Val	Asn	405	410	415	
Ala	Phe	Glu	Pro	Lys	Leu	Asn	Leu	Ile	Val	Asn	Thr	Gly	Lys	Val	Lys	420	425	430	

684

Gln Thr Phe Asn Met Gly Met Arg Phe Leu Thr Glu Asp Leu Tyr Arg
 435 440 445
 Arg Ser Thr Thr Arg Lys Asn Pro Ser Met Pro Asn Asn Gly Ser Gly
 450 455 460
 Phe Asp Ala Gly Thr Ser Leu Asn Asn Phe Asn Asn Tyr Thr Ala Val
 465 470 475 480
 Tyr Ala Ser Asp Glu Ile Asn Phe Asn Asn Gly Met Leu Thr Ile Thr
 485 490 495
 Pro Gly Leu Arg Tyr Thr Phe Leu Asn Tyr Glu Lys Lys Asp Ala Pro
 500 505 510
 Pro Phe Lys Val Gly Gln Thr Pro Lys Thr Thr Lys Glu Arg Tyr Asn
 515 520 525
 Gln Trp Asn Pro Ala
 530

(2) INFORMATION FOR SEQ ID NO:777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

Met Lys Lys Ile Phe Leu Gly Met Ala Leu Ala Phe Ser Val Ser Met
 1 5 10 15
 Ala Glu Lys Ser Gly Ala Phe Leu Gly Gly Gly Phe Gln Tyr Ser Asn
 20 25 30
 Leu Glu Asn Gln Asn Thr Thr Arg Thr Pro Ser Ala Asn Asn Asn Thr
 35 40 45
 Pro Ile Asn Thr Ser Met Phe Gly Asn Asn Gln Ala Ala Pro Ala Gln
 50 55 60
 Glu Thr Pro Ser Val Ile Asn Thr Asn Asn Tyr Gly Gln Met Tyr Gly
 65 70 75 80
 Val Asp Ala Met Ala Gly Tyr Lys Trp Phe Phe Gly Lys Thr Lys Arg
 85 90 95
 Phe Gly Phe Arg Thr Tyr Gly Tyr Tyr Ser Tyr Asn His Ala Asn Leu
 100 105 110
 Ser Phe Val Gly Ser Lys Leu Gly Ile Met Asp Gly Ala Ser Gln Val
 115 120 125
 Asn Asn Phe Thr Tyr Gly Val Gly Phe Asp Ala Leu Tyr Asn Phe Tyr
 130 135 140
 Glu Ser Lys Glu Gly Tyr Asn Thr Ala Gly Leu Phe Val Gly Phe Gly
 145 150 155 160
 Leu Gly Gly Asp Ser Phe Ile Val Gln Gly Glu Ser Tyr Leu Lys Ser
 165 170 175

685

```

Gln Met Gln Ile Cys Asn Asn Thr Ala Gly Cys Ser Ala Ser Met Asn
      180                      185                      190
Thr Ser Tyr Phe Gln Met Pro Val Glu Phe Gly Phe Arg Ser Asn Phe
      195                      200                      205
Ser Lys His Ser Gly Ile Glu Val Gly Phe Lys Leu Pro Leu Phe Thr
      210                      215                      220
Asn Gln Phe Tyr Lys Glu Arg Gly Val Asp Gly Ser Val Asp Val Phe
      225                      230                      235                      240
Tyr Lys Arg Asn Phe Ser Ile Tyr Phe Asn Tyr Met Ile Asn Leu
      245                      250                      255

```

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

```

Met Leu Ile Ala Arg Phe Lys Lys Ala Leu Ile Ser Tyr Ser Leu Gly
1           5           10           15
Val Leu Leu Val Ser Ser Leu Leu Gly Val Ala Asn Ala Ser Asn Gln
      20           25           30
Glu Ile Gln Val Lys Asp Tyr Phe Gly Glu Gln Thr Ile Lys Leu Pro
      35           40           45
Val Ser Lys Ile Ile Tyr Leu Gly Ser Phe Ala Glu Val Pro Ala Met
      50           55           60
Phe Asn Thr Trp Asp Arg Val Val Gly Ile Ser Asp Tyr Ala Phe Lys
      65           70           75           80
Ser Asp Ile Val Lys Ala Thr Leu Lys Asp Pro Glu Arg Ile Lys Pro
      85           90           95
Met Ser Ser Asp His Val Ala Ala Leu Asn Val Glu Leu Leu Lys Lys
      100          105          110
Leu Ser Pro Asp Leu Val Val Thr Phe Val Gly Asn Pro Lys Ala Val
      115          120          125
Glu His Ala Lys Lys Phe Gly Ile Ser Phe Leu Ser Phe Gln Glu Lys
      130          135          140
Thr Ile Val Glu Val Met Glu Asp Ile Asp Ala Gln Ala Lys Ala Leu
      145          150          155          160
Glu Val Asp Ala Ser Lys Lys Leu Ala Lys Met Gln Glu Thr Leu Asp
      165          170          175
Phe Ile Lys Glu Arg Leu Lys Asn Val Lys Lys Lys Lys Gly Val Glu
      180          185          190
Leu Phe His Lys Ala Asn Lys Ile Ser Gly His Gln Ala Leu Asp Ser
      195          200          205

```

686

```

Asp Ile Leu Glu Lys Gly Gly Ile Asp Asn Phe Gly Leu Lys Tyr Val
 210                      215                      220
Lys Phe Gly Arg Ala Asp Ile Ser Val Glu Lys Ile Val Lys Glu Asn
225                      230                      235                      240
Pro Glu Ile Ile Phe Ile Trp Trp Ile Ser Pro Leu Ser Pro Glu Asp
                      245                      250                      255
Val Leu Asn Asn Pro Lys Phe Ser Thr Ile Lys Ala Ile Lys Asn Lys
                      260                      265                      270
Gln Val Tyr Lys Leu Pro Thr Met Asp Ile Gly Gly Pro Arg Ala Pro
 275                      280                      285
Leu Ile Ser Leu Phe Ile Ala Leu Lys Ala His Pro Glu Ala Phe Lys
 290                      295                      300
Gly Val Asp Ile Asn Ala Ile Ile Lys Asp Tyr Tyr Lys Val Val Phe
305                      310                      315                      320
Asp Leu Asn Asp Ala Glu Val Glu Pro Phe Leu Trp His
                      325                      330

```

(2) INFORMATION FOR SEQ ID NO:779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

```

Met Lys Lys Gln Ile Leu Thr Gly Val Leu Leu Ser Val Leu Ala Val
 1                      5                      10                      15
Ser Ser Ala Tyr Ala His Lys Asp Lys Lys Asp Ala Lys Lys Pro Glu
                      20                      25                      30
Leu Ser Ser Gln Leu Val Ala His Lys Asp Lys Lys Asp Ala Lys Lys
 35                      40                      45
Pro Lys Asn Ser Val Ala
 50

```

(2) INFORMATION FOR SEQ ID NO:780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

```

Met Tyr Lys Leu Gly Ile Phe Leu Leu Ala Thr Leu Leu Ser Ala Asn
1           5           10           15
Thr Gln Lys Val Ser Asp Ile Ala Lys Asp Ile Gln His Lys Glu Thr
          20           25           30
Leu Leu Lys Lys Thr His Glu Glu Lys Asn Gln Leu Asn Ser Arg Leu
          35           40           45
Ser Ser Leu Gly Glu Ala Ile Arg Ser Lys Glu Leu Gln Lys Val Glu
          50           55           60
Ile Glu Arg Gln Met Val Ala Leu Lys Lys Ser Leu Glu Lys Asn Arg
65           70           75           80
Asn Glu Ser Leu Val Gln Glu Lys Val Leu Thr Asn Tyr Arg Lys Ser
          85           90           95
Leu Asp His Leu Gln Lys Gln Arg Ser Phe Leu Gln Lys Arg Val Phe
          100          105          110
Asp Thr Leu Leu Glu Asp Phe Leu Phe Ser Gln Ala Leu Lys Gly Gln
          115          120          125
Asn Leu Ala Ser Ser Asn Asp Val Ile Leu Leu Ser Gly Val
130          135          140

```

(2) INFORMATION FOR SEQ ID NO:781:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

```

Met Asp Lys Asn Asn Asn Asn Leu Arg Leu Ile Leu Ala Ile Ala
1           5           10           15
Leu Ser Phe Leu Phe Ile Ala Leu Tyr Ser Tyr Phe Phe Gln Glu Pro
          20           25           30
Asn Lys Thr Thr Thr Glu Thr Thr Lys Gln Glu Thr Thr Asn Asn His
          35           40           45
Thr Ala Thr Ser Pro Thr Ala Ser Asn Thr Ile Thr Gln Asp Phe Ser
          50           55           60
Val Thr Gln Thr Ile Pro Gln Glu Ser Leu Leu Ser Thr Ile Ser Phe

```

688

```

65          70          75          80
Glu His Ala Lys Ile Glu Ile Asp Ser Leu Gly Arg Ile Lys Gln Val
          85          90          95
Tyr Leu Lys Asp Lys Lys Tyr Leu Thr Pro Lys Glu Lys Gly Phe Leu
          100         105         110
Glu His Val Ser His Leu Phe Ser Ser Lys Glu Asn Ser Gln Pro Ser
          115         120         125
Leu Lys Glu Leu Pro Leu Leu Ala Ala Asp Lys Leu Lys Pro Leu Glu
          130         135         140
Val Arg Phe Leu Asp Pro Thr Leu Asn Asn Lys Ala Phe Asn Thr Pro
145         150         155         160
Tyr Ser Ala Ser Lys Thr Thr Leu Gly Pro Asn Glu Gln Leu Val Leu
          165         170         175
Thr Gln Asp Leu Gly Thr Leu Ser Ile Ile Lys Thr Leu Thr Phe Tyr
          180         185         190
Asp Asp Leu His Tyr
          195

```

(2) INFORMATION FOR SEQ ID NO:782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

```

Met Ala Cys Trp His Lys Arg Leu Ala Val Gly Cys Cys Ile Val Leu
1          5          10          15
Leu Ser Cys Val Met Ser Ala Asn Asn Val Ser Ile Val Arg Asp Asp
          20         25         30
Pro Pro Leu Asp Pro Thr Leu Pro Ala Trp Ile Tyr Ser Val Ala Leu
          35         40         45
Leu Lys Val Tyr Phe Ser Asp Gly Thr Tyr Lys Glu Gly Tyr Ala Thr
          50         55         60
Leu Leu Glu Asn Gly Arg Tyr Ile Ala Ser Ser Glu Thr Leu Tyr Ser
65         70         75         80
Asn Gly Leu Tyr Pro Lys Met Ile Leu Ala Lys Met Gln Asp Ser Ser
          85         90         95
Ala Lys Glu Leu Ile Cys Ile Ala Ser Leu His Leu Glu Ala Met Asp
          100        105        110
Arg Asp Gln Gly Leu Ser Leu Leu Lys Thr Ala Asp Phe Arg Asp Asp
          115        120        125
Tyr Cys His Lys Arg Glu Glu Ser Tyr Tyr His Ala Arg Ile Tyr Ala
          130        135        140
Lys Tyr Ala Gln Thr Phe His Ser Asn Pro Tyr Thr Asn Gln Lys Thr

```

689

```

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

```

(2) INFORMATION FOR SEQ ID NO:783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

```

Met Lys Asn Gln His Lys Asn Pro Leu Thr Lys Ala Leu Met Lys Thr
1          5          10          15
Tyr Pro Tyr Asn His Phe Leu Phe Phe Cys Phe Ile Leu Gly Ala Phe
          20          25          30
Leu Leu Gly Leu Leu Ser Pro Ala Tyr Ala Leu Ser Ile Ile Thr Thr
          35          40          45
Lys Glu Ile Asp Ala Asn Leu Asn Gly Ala Ile Glu Ser Arg Val
          50          55          60
Val Leu Gly Lys Arg Val Phe Lys Val Glu Ala His Gly Phe Tyr Phe
65          70          75          80
Arg Asn Asn Ala Thr Asn Ser Ile Asp Ile Glu Ile Thr Ser Leu Leu
          85          90          95
Arg Asp Asn Gln Ser Phe Pro Leu Thr Ser Ser Ala Lys Thr Ser Leu
          100          105          110
Lys Ile Pro Pro Asn Ala Lys Ile Lys Lys Ser Thr Ile Leu Val Leu
          115          120          125
Lys Gly Glu Asn Ala Glu Glu Val Ala Lys Ile Leu Gly Val Ser Lys
          130          135          140
Glu Glu Tyr Gln Lys Leu Glu Asn Ile Ala Gln Thr Lys Ala Ala Asn
145          150          155          160
Asp Pro Met Tyr Ala Asn Thr Pro Phe Ser Asn Gly Ser Asp Ser Ser

```

				165					170					175			
Phe	Tyr	Asp	Asn	Asn	Pro	Asn	Ser	Pro	Ser	Asn	Asn	Ala	Ile	Asn	Gly		
			180					185					190				
Lys	Asp	Gly	Ala	Asn	Gly	Ser	Asn	Gly	Tyr	Gly	Ala	Asn	Gly	Asn	Asp		
		195					200					205					
Gly	Val	Asn	Gly	Ile	Ser	Gly	Ser	Asn	Gly	Ala	Asn	Gly	Ser	His	Ser		
	210					215					220						
Asn	Asn	Asn	Ala	Ile	Gly	Ser	Gly	Ile	Asp	Thr	Asp	Gly	Val	Leu	Gly		
225					230					235					240		
Val	Asp	Gly	Val	Asn	Gly	Ser	Ser	Ser	Ser	Ser	Gly	Gly	Ser	Val	Gly		
				245						250					255		
Gly	Tyr	Glu	Asn	Asn	Phe	Thr	Asn	His	Gly	Ser	Thr	Asn	Asn	Asn	Thr		
			260					265					270				
Gly	Gly	Tyr	Asp	Asn	Phe	Asn	Asn	Gly	Ser	Ser	Ser	Gly	Gly	Ser	Leu		
		275					280					285					
Gly	Asn	Gly	Gly	Leu	Phe	Pro	Ile	Pro	Phe	Gly	Asn	Gly	Asp	Thr	Asn		
	290					295					300						
Asn	Ser	Asn	Asn	Ser	Thr	Asn	Thr	Thr	Ser	Pro	Thr	Asn	Gly	Ser	Ser		
305					310					315					320		
Ser	Asn	Asn	Ala	Thr	Asn	Pro	Ser	Ser	Gln	Glu	Asn	Asn	Tyr	Ser	Ser		
				325					330					335			
Gln	Tyr	Cys	Lys	Val	Pro	Glu	Leu	Ser	Pro	Asn	Asn	Thr	Met	Lys	Leu		
			340					345					350				
Asp	Val	Ile	Ala	Lys	Asp	Gly	Ser	Cys	Ile	Ser	Met	Asn	Ala	Leu	Arg		
		355					360					365					
Asp	Asp	Thr	Lys	Cys	Ala	Tyr	Arg	Tyr	Asp	Phe	Glu	Ala	Gly	Lys	Ala		
	370					375					380						
Ile	Lys	Gln	Thr	Gln	Tyr	Tyr	Tyr	Val	Asp	Arg	Glu	Asn	Lys	Thr	Gln		
385					390					395					400		
Asn	Ile	Gly	Gly	Cys	Val	Asp	Leu	Gln	Gly	Ala	Gln	Tyr	Ala	Met	Gln		
				405					410					415			
Leu	Tyr	Lys	Asp	Asp	Ser	Lys	Cys	Ala	Leu	Gln	Thr	Thr	Ser	Asp	Lys		
			420					425					430				
Gly	Tyr	Gly	Met	Gly	Lys	Thr	Gln	Thr	Phe	Gln	Thr	Glu	Ile	Val	Phe		
		435					440					445					
Arg	Gly	Met	Asp	Asn	Leu	Ile	His	Val	Ala	Val	Pro	Cys	Ser	Asp	Tyr		
	450					455					460						
Ala	Arg	Val	Gln	Asp	Arg	Ile	Val	Arg	Tyr	Glu	Lys	Asn	Asp	Lys	Thr		
465					470					475					480		
Gln	Thr																

.691

Ala Pro Leu Thr Lys Pro Leu Pro Pro Lys Pro Leu Asn Leu Ile Tyr
 625 630 635 640
 Ala Gln Pro Lys Ile Met Lys Asn Thr Pro Gln Pro Ile Ile Leu Ser
 645 650 655
 Pro Leu Lys Pro Pro Ser Thr Gly Leu Lys Ala Phe
 660 665

(2) INFORMATION FOR SEQ ID NO:784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

Met Thr Tyr Lys Glu Arg Leu Ile His Glu Lys Ile Leu Asn Gln Asn
 1 5 10 15
 Asp Lys Gly Phe Lys Thr Glu Leu Arg Ile Leu Ser Val Phe Ile Val
 20 25 30
 Glu Phe Leu Val Asn Ile Leu Gly Phe Met Leu Ala Lys Met Pro His
 35 40 45
 Phe Trp Phe Leu Arg Cys Val Lys Ala Leu Ala Trp Leu Met Lys Thr
 50 55 60
 Phe Asp Arg Arg Arg Tyr Phe Asp Ala Lys Ala Asn Leu Asp Phe Val
 65 70 75 80
 Phe Gly Asp Ser Lys Ser Glu Glu Glu Lys Lys Arg Ile Ile Lys Lys
 85 90 95
 Gly Tyr Glu Asn Phe Ala Phe Ile Ile Leu Glu Thr Ile Arg Val Ile
 100 105 110
 Phe Ile Pro Lys Asp Glu Tyr Asp Ala Arg Phe Thr Leu Ile Asn Glu
 115 120 125
 Glu Asn Val Trp Lys Ser Leu Asn Lys Glu Gly Gln Ala Ile Thr Leu
 130 135 140
 Cys Met His Phe Gly Tyr Trp Glu Ala Val Gly Thr Thr Leu Ala Gln
 145 150 155 160
 Tyr Tyr Glu Asn Tyr Gly Arg Gly Cys Leu Gly Arg Leu Thr Lys Phe
 165 170 175
 Ala Pro Ile Asn His Met Ile Met Ser Arg Arg Glu Ala Phe Gly Val
 180 185 190
 Arg Phe Val Asn Lys Ile Gly Ala Met Lys Glu Leu Ile Lys Met Tyr
 195 200 205
 Asn Gln Gly Asn Gly Leu Val Gly Ile Leu Val Asp Gln Asn Val Val
 210 215 220
 Pro Lys Asp Gly Val Val Lys Phe Phe Asn Lys Asp Ala Thr Thr
 225 230 235 240

692

```

Thr Thr Ile Ala Ser Ile Leu Ser Arg Arg Tyr Asn Ile Asp Ile Gln
      245                      250                      255
Pro Val Phe Ile Asp Phe Asn Asp Asp Tyr Ser His Tyr Thr Ala Thr
      260                      265                      270
Tyr Tyr Pro Ser Ile Arg Ser Gln Ile Thr Asp Asn Ala Gln Asn Asp
      275                      280                      285
Ile Leu Glu Cys Thr Gln Ala Gln Ala Ser Leu Cys Glu Glu Val Ile
      290                      295                      300
Arg Asn His Pro Glu Ser Tyr Phe Trp Phe His Arg Arg Phe Lys Ser
305                      310                      315                      320
Thr His Pro Glu Ile Tyr Gln Arg
      325

```

(2) INFORMATION FOR SEQ ID NO:785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

```

Met Leu Tyr Leu Arg Lys Glu Asn Gly Val Arg Thr Leu Ile Ser Leu
1      5      10      15
Gly Ile Leu Leu Ser Val Leu Asn Gly Asp Asp Leu Arg Leu Tyr Ser
      20      25      30
Lys Pro Leu Val Tyr Ser Ala Gly Ser Gly Ile Ile Gly Ile Asp Ile
      35      40      45
Asp Lys Arg Thr Phe Tyr Lys Arg Ala Phe Ala Phe Thr Met Lys Ser
50      55      60
Leu Phe Gly Glu Asn Leu Leu Leu Phe Val Lys Leu Lys His Ser Ala
65      70      75      80
Leu Met Ser Lys His Met Lys Gly Pro Leu Glu Asn Arg His His His
      85      90      95
Ser Phe Ala Lys Asn Tyr Glu Lys Ala Val Asn Gly Cys Gln Lys Tyr
      100     105     110
Val His Ile Lys Leu Pro Glu Gly Ala Pro Ser Asn Phe Gln Ser Gly
      115     120     125
Ser Tyr Met Ala Thr Met Val Met Arg Phe
130      135

```

(2) INFORMATION FOR SEQ ID NO:786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

```

Met Arg Lys Val Leu Tyr Ala Leu Met Gly Phe Leu Leu Val Phe Ser
1      5      10      15
Ala Leu Lys Ala Asp Asp Phe Leu Glu Glu Ala Asn Glu Thr Ala Pro
20      25      30
Ala Asn Leu Asn His Pro Met Gln Asp Leu Asn Ala Ile Gln Gly Ser
35      40      45
Phe Phe Asp Lys Asn Arg Ser Lys Met Ser Asn Thr Leu Asn Ile Asp
50      55      60
Tyr Phe Gln Gly Gln Thr Tyr Lys Ile Arg Leu Arg Tyr Ala Met Ala
65      70      75      80
Thr Leu Leu Phe Phe Ser Lys Pro Ile Ser Asp Phe Val Leu Gly Asp
85      90      95
Lys Val Gly Phe Asp Ala Lys Ile Leu Glu Ser Asn Asp Arg Ile Leu
100     105     110
Leu Ile Lys Pro Leu Gln Ile Gly Val Asp Ser Asn Ile Ser Val Ile
115     120     125
Asp Ser Glu Gly Lys Ile Phe Ser Phe Tyr Val Phe Ser Thr Thr Phe
130     135     140
Thr Ser Ser Lys His Pro Asn Leu Gln Val Phe Ile Glu Asp Lys Asn
145     150     155     160
Tyr Tyr Thr Asn Ala Phe Ile Lys Pro Gln Lys Glu Asn Gln Glu Asn
165     170     175
Met Ser Glu Asn Ala Pro Lys Asp Ala Gln Lys Asn Asn Lys Pro Leu
180     185     190
Lys Glu Glu Lys Glu Glu Thr Lys Glu Lys Glu Glu Glu Thr Ile Ile
195     200     205
Ile Gly Asp Asn Thr Asn Ala Met Lys Ile Ile Lys Lys Asp Ile Gln
210     215     220
Lys Gly Tyr Lys Ala Leu Lys Ser Ser Gln Arg Lys Trp Tyr Cys Leu
225     230     235     240
Trp Ala Cys Ser Lys Lys Ser Lys Leu Ser Leu Met Pro Lys Glu Ile
245     250     255
Phe Asn Asp Lys Gln Phe Thr Tyr Phe Lys Phe Asp Lys Arg Leu Ala
260     265     270
Leu Ser Lys Phe Pro Val Ile Tyr Lys Val Val Asp Gly Tyr Asp Asn
275     280     285
Pro Val Asn Thr Arg Ile Val Gly Asp Tyr Ile Ile Ala Glu Asp Val
290     295     300
Ser Thr Lys Trp Thr Leu Arg Leu Gly Lys Asp Tyr Leu Cys Ile Arg
305     310     315     320
Phe Val Lys Arg Arg Lys Gly Glu
325

```

(2) INFORMATION FOR SEQ ID NO:787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

```

Val Met Phe His Lys Ala Leu Ile Thr Phe Ile Val Leu Trp Phe Phe
1           5           10           15
Leu Asn Gly Leu Gly Ala Tyr Asp Phe Lys His Cys Gln Ala Phe Phe
          20           25           30
Lys Lys Ala Ser Leu Gln Lys Gly Gly Val Ala Leu Lys Glu Leu Pro
          35           40           45
Lys Gly Val Tyr Leu Tyr Tyr Ser Lys Thr Tyr Pro Lys His Ala Lys
          50           55           60
Val Ile Lys Ser Asp Pro Phe Ile Gly Leu Tyr Leu Leu Gln Ser Ala
65           70           75           80
Pro Ser Glu Tyr Val Tyr Thr Leu Arg Asp Leu Asp Lys Asp Ala Leu
          85           90           95
Ile Arg Pro Met Ala Ser Ile Gly Ala Asn Gln Ala Thr Glu Ala Arg
          100          105          110
Leu Leu Val Gly Gln Lys Gly Tyr Asp Arg Tyr Ala Gln Ile Ser Gln
          115          120          125
Lys Thr Gln Lys Asn Gly Val Ile Ser Asn Ile Cys Tyr Gln Met Leu
          130          135          140
Gly Leu Gly Val Gly Gly Asn Gly Phe Ile Glu Thr Lys Phe Ile Lys
145          150          155          160
Arg Phe Leu Asn Gln Gln Pro Tyr Tyr Gly Asp Ile Gly Val Arg
          165          170          175
Leu Glu Glu Arg His Lys Arg Leu Val Val Ala Gln Phe Asp Pro Phe
          180          185          190
Phe Pro Lys Asn Pro Phe Leu Lys Asn Asp Glu Ile Leu Ala Ile Asn
          195          200          205
Asp Tyr Lys Ile His Ser Leu Ala Glu Phe Glu Trp Val Val Ser Asn
          210          215          220
Leu Ser Tyr Gln Ser Leu Ala Lys Val Lys Ile Lys Arg Asn His Gln
225          230          235          240
Ile Lys Glu Val Thr Leu Lys Val Asn Lys Arg Tyr Gly Gly Phe Leu
          245          250          255
Leu Lys Asp Thr Phe Leu Glu Arg Tyr Gly Ile Ala Leu Asp Glu Arg
          260          265          270
Phe Ile Ile Thr Lys Ile Gly Ala His Leu Pro Lys Gly Leu Asp Phe
          275          280          285

```

695

```

Leu Lys Leu Gly Asp Arg Ile Leu Trp Val Asn His Arg Ser Val Ser
 290                295                300
Phe Asn Pro Lys Ala Leu Arg Glu Ala Leu Ser Thr Pro Lys Ile Glu
305                310                315                320
Leu Leu Val Trp Arg Gln Gly Phe Glu Phe Tyr Ile Lys Val Arg
                325                330                335

```

(2) INFORMATION FOR SEQ ID NO:788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

```

Met Leu Gly Ser Val Lys Lys Thr Leu Phe Gly Val Leu Cys Leu Gly
 1                5                10                15
Ala Leu Cys Leu Arg Gly Leu Met Ala Glu Pro Asp Ala Lys Glu Leu
                20                25                30
Val Ser Leu Gly Ile Glu Ser Val Lys Lys Gln Asp Phe Ala Gln Ala
                35                40                45
Lys Ala His Phe Glu Lys Ala Cys Glu Leu Lys Glu Gly Phe Gly Cys
 50                55                60
Val Phe Leu Gly Ala Phe Tyr Glu Glu Gly Lys Gly Val Gly Lys Asp
65                70                75                80
Leu Lys Lys Ala Ile Gln Phe Tyr Thr Lys Gly Cys Glu Leu Asn Asp
                85                90                95
Gly Tyr Gly Cys Arg Leu Leu Gly Asn Leu Tyr Tyr Asn Gly Gln Gly
                100                105                110
Val Ser Lys Asp Ala Lys Lys Ala Ser Gln Tyr Tyr Ser Lys Ser Cys
                115                120                125
Glu Leu Asn His Ala Glu Gly Cys Thr Val Leu Gly Ser Leu His His
                130                135                140
Tyr Gly Val Gly Thr Pro Lys Asp Leu Arg Lys Ala Leu Asp Leu Tyr
145                150                155                160
Glu Lys Ala Cys Asp Leu Lys Asp Ser Pro Gly Cys Ile Asn Ala Gly
                165                170                175
Tyr Met Tyr Gly Val Ala Lys Asn Phe Lys Glu Ala Ile Val Arg Tyr
                180                185                190
Ser Lys Ala Cys Glu Leu Lys Asp Gly Arg Gly Cys Tyr Asn Leu Gly
                195                200                205
Val Met Gln Tyr Asn Ala Gln Gly Thr Ala Lys Asp Glu Lys Gln Ala
                210                215                220
Val Glu Asn Phe Lys Lys Gly Cys Lys Ser Ser Val Lys Glu Ala Cys
225                230                235                240

```

696

Asp Ala Leu Lys Glu Leu Lys Ile Glu Leu
 245 250

(2) INFORMATION FOR SEQ ID NO:789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

Met	Arg	Leu	Leu	Ile	Ala	Leu	Val	Leu	Phe	Leu	Trp	Trp	Leu	Asn	Leu
1			5					10					15		
Gly	Ala	Lys	Glu	Ala	Asp	Phe	Ile	Ser	Asp	Trp	Glu	Tyr	Gly	Leu	Ala
		20					25						30		
Leu	Tyr	Lys	Asn	Pro	Arg	Gly	Val	Ala	Cys	Ala	Lys	Cys	His	Gly	Ile
	35					40						45			
Lys	Gly	Glu	Gln	Gln	Glu	Ile	Thr	Phe	Tyr	Tyr	Glu	Lys	Gly	Glu	Lys
	50				55						60				
Lys	Ile	Leu	Tyr	Ala	Pro	Lys	Ile	Asn	His	Leu	Asp	Phe	Lys	Thr	Phe
65				70					75					80	
Lys	Asp	Ala	Leu	Ser	Leu	Gly	Lys	Gly	Met	Met	Pro	Lys	Tyr	Asn	Leu
		85					90							95	
Asn	Leu	Glu	Glu	Ile	Gln	Ala	Ile	Tyr	Leu	Tyr	Ile	Thr	Ser	Leu	Gly
		100					105					110			
His	Lys	Asp	Glu	Arg	Lys	Asp	Pro	Ser	Lys	Pro					
		115					120								

(2) INFORMATION FOR SEQ ID NO:790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

```

Met Leu Asn Lys Phe Lys Lys Ile Val Gly Val Gly Val Leu Val Gly
1          5          10          15
Cys Leu Gly Val Leu Gln Ala Lys Asn Ser Leu Phe Val Leu Pro Tyr
          20          25          30
Glu Gln Arg Asp Ala Leu Asn Ser Leu Ile Ser Gly Ile Ser Ser Ala
          35          40          45
Arg Glu Asn Val Lys Ile Ala Ile Tyr Ser Phe Thr His Arg Asp Ile
          50          55          60
Ala Arg Ala Ile Lys Ser Val Ala Ser Arg Gly Ile Lys Val Gln Ile
65          70          75          80
Ile Tyr Asp Tyr Glu Ser Asn His Asn Asn Lys Gln Ser Thr Ile Gly
          85          90          95
Tyr Leu Asp Lys Tyr Pro Asn Thr Lys Val Cys Leu Leu Lys Gly Leu
          100          105          110
Lys Ala Lys Asn Gly Asn Tyr Tyr Gly Ile Met His Gln Lys Val Ala
          115          120          125
Ile Ile Asp Asp Lys Ile Val Phe Leu Gly Ser Ala Asn Trp Ser Lys
          130          135          140
Asn Ala Phe Glu Asn Asn Tyr Glu Val Leu Leu Lys Thr Asp Asp Thr
145          150          155          160
Glu Thr Ile Leu Lys Ala Lys Ser Tyr Tyr Gln Lys Met Leu Glu Gly
          165          170          175
Cys Val Gly Phe
          180

```

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

```

Met Arg Arg Ser Leu Ala Phe Cys Leu Leu Ala Leu Leu Gly Leu Gln
1          5          10          15
Val Leu Gly Ala Arg Asp Phe Ser Gln Leu Lys Asn Glu Glu Leu Leu
          20          25          30
Lys Leu Ala Gly Thr Leu Pro Ser Asn Glu Ala Ile Asp Tyr Arg Met
          35          40          45
Glu Val Ser Lys Arg Leu Lys Ala Leu Ser Ala Glu Asp Ala Lys Lys
          50          55          60
Phe Arg Ala Asn Phe Ser Arg Ile Ala Arg Lys Asn Leu Ser Lys Met

```

698

65		70		75		80									
Ser	Glu	Glu	Asp	Phe	Lys	Lys	Met	Arg	Glu	Glu	Val	Arg	Lys	Glu	Leu
				85					90					95	
Glu	Glu	Lys	Thr	Lys	Gly	Leu	Ser	Ala	Glu	Glu	Ile	Lys	Ala	Lys	Gly
			100					105					110		
Leu	Asn	Val	Ser	Val	Cys	Ser	Gly	Asp	Thr	Arg	Lys	Val	Trp	Cys	Arg
		115					120					125			
Ala	Val	Lys	Lys	Lys	Asp	Glu	His	Cys	Ser	Pro	Lys				
	130						135				140				

(2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

Met	Lys	Lys	Ala	Leu	Lys	Ile	Leu	Ser	Val	Gly	Ala	Leu	Leu	Phe	Val
1			5					10						15	
Ala	Leu	Asn	Ala	Lys	Asp	Phe	Ser	Lys	Thr	Ser	Asp	Glu	Asp	Leu	Ala
		20						25				30			
Lys	Met	Ala	Gly	Val	Val	Ala	Pro	Gln	Asp	Ile	Val	Asp	Tyr	Thr	Lys
	35					40					45				
Glu	Leu	Lys	Lys	Arg	Met	Glu	Lys	Met	Pro	Glu	Asp	Lys	Arg	Lys	Ala
	50				55					60					
Phe	His	Lys	Gln	Leu	His	Glu	Tyr	Ala	Thr	Lys	Asn	Thr	Asp	Lys	Met
65			70					75						80	
Thr	Val	Ala	Asp	Phe	Glu	Ala	Arg	Gln	Lys	Ala	Ile	Lys	Glu	Ala	Leu
		85						90					95		
Lys	Lys	Gly	Asn	Met	Glu	Asp	Met	Asp	Asp	Asp	Phe	Gly	Leu	Arg	Ser
		100					105					110			
Cys	Lys	His	Gly	Lys	Lys	His	Lys	His	Asp	Lys	His	Gly	Lys	Lys	His
	115					120					125				
Gly	Lys	Lys	His	Asp	Lys	Asp	His	Asp	Asp	Lys	Asp	His	Asp	His	His
	130					135					140				
Asp	Glu	Asp	His	Ser	Asp	Lys	His								
145						150									

(2) INFORMATION FOR SEQ ID NO:793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

```

Met Leu Lys Lys Leu Leu Leu Ile Ser Leu Phe Leu Gly Phe Leu Arg
1           5           10           15
Ala Glu Gly Glu His Tyr Glu Ile Ile Ala Glu Leu Ser Lys Ala Phe
          20           25           30
Leu Lys Ala Lys Glu Val Leu Thr Ala Ile Asn Lys Thr Cys Ile Glu
          35           40           45
Thr Gly His Asp Arg Thr Gln Ile Arg Leu Gln Asn Asp Phe Leu Glu
          50           55           60
Asn Leu Ser Gln Thr Glu Gln Gln Phe Asp Asp Tyr Phe Glu Lys Asp
65           70           75           80
Phe Lys Ser Val Gly Val Leu Lys Thr Leu Leu Lys Asp Ile Gln Ser
          85           90           95
Leu Glu Lys Thr Ser Asn Lys Leu Val Cys Val Ala Pro Lys Asn Ala
          100          105          110
Lys Asn Phe Glu Ile Leu Glu Gly Ala Ile Thr Gln Ile Ile Gly Leu
          115          120          125
Glu Glu Gln Met Asn Gln Phe Ile Asn Gly Ala Lys
          130          135          140

```

(2) INFORMATION FOR SEQ ID NO:794:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

```

Leu Ser Gly Glu Leu Arg Leu Ser Trp Trp Leu Val Ala Arg Cys Lys
1           5           10           15
Thr Leu Phe Val Leu Phe Cys Glu Gly Ser Ala Phe Ser Ser Leu Leu
          20           25           30

```

700

Ile Ser Ser Ile Leu Phe Ser Leu Leu Ile Arg Ser Phe Thr Ser Leu
 35 40 45
 Val Thr Phe Ser Ser Ser Ser Ser Cys Ser Ile Phe Phe Ile Ser Leu
 50 55 60
 Leu Gly
 65

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: Xaa = Unknown
- (B) LOCATION 1...89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

Leu Val Val Ser Gly Ser Leu Gln Asn Ile Val Arg Ser Phe Leu Arg
 1 5 10 15
 Arg Ile Ser Val Phe Phe Ile Ile Asp Phe Ile Asn Phe Ile Phe Val
 20 25 30
 Ile Asp Gln Ile Ile His Phe Phe Gly Asp Phe Phe Ile Phe Phe Phe
 35 40 45
 Met Leu Asn Leu Phe Tyr Ile Leu Ile Arg Leu Ile Asp Leu Ile Val
 50 55 60
 Leu Ser Gly Phe Ser Val Val Leu Val Arg Leu Gly Xaa Phe Phe Arg
 65 70 75 80
 Leu Ile Phe Ala Cys Ala Gln His Ala
 85

(2) INFORMATION FOR SEQ ID NO:796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

```

Met Lys Lys Ser Leu Cys Leu Ser Phe Phe Leu Thr Phe Ser Asn Pro
1           5           10           15
Leu Gln Ala Leu Val Ile Glu Leu Leu Glu Glu Ile Lys Thr Ser Pro
          20           25           30
His Lys Gly Thr Phe Lys Ala Lys Val Leu Asp Ser Lys Glu Pro Arg
          35           40           45
Gln Val Leu Gly Val Tyr Asn Ile Ser Pro His Lys Lys Leu Thr Leu
          50           55           60
Thr Ile Thr His Ile Ser Thr Ala Ile Val Tyr Gln Pro Leu Asp Glu
          65           70           75           80
Lys Leu Ser Leu Glu Thr Thr Leu Ser Pro Asn Arg Pro Thr Ile Pro
          85           90           95
Arg Asn Thr Gln Ile Val Phe Ser Ser Lys Glu Leu Lys Glu Pro His
          100          105          110
Ser Asn Pro Ile Pro Ser
          115

```

(2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

```

Leu Lys Ala Phe Gln Thr Phe Gly Val Phe Gly Thr Ser Val Ile Thr
1           5           10           15
Cys Ile Thr Ala Gln Asn Thr Gln Gly Val His Gly Val Tyr Pro Leu
          20           25           30
Ser Val Glu Ser Val Lys Ala Gln Ile Leu Ala Ile Arg Asp Asp Phe
          35           40           45
Ser Ile Lys Ala Phe Lys Met Gly Ala Leu Cys Asn Ala Gln Ile Ile
          50           55           60
Glu Cys Val Ala Asn Ala Leu Glu Thr Cys Asp Phe Gly Leu Cys Val
          65           70           75           80
Leu Asp Pro Val Met Val Ala Lys Asn Gly Ala Leu Leu Leu Glu Glu
          85           90           95
Glu Ala Ile Leu Ser Leu Lys Lys Arg Leu Leu Pro Lys Thr Asn Leu
          100          105          110
Leu Thr Pro Asn Leu Pro Glu Val Tyr Ala Leu Thr Gly Val Gln Ala
          115          120          125
Arg Asp Asp Lys Ser Ala Ser Lys Ala Met Gly Val Leu Arg Asp Leu

```

702

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

(2) INFORMATION FOR SEQ ID NO:798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

Val	Leu	Glu	Lys	Gln	Asp	Lys	Asp	Leu	Phe	Leu	Leu	Gln	Val	Gly	Asn
1			5					10						15	
Arg	Ile	Ile	Pro	Thr	Lys	Ser	Glu	Gln	Glu	Leu	Lys	Ile	Asn	Gln	Pro
			20					25					30		
Tyr	Phe	Ala	Thr	Met	Gln	Arg	Asn	Gln	Leu	Gly	Asp	Ile	Val	Leu	Lys
		35					40					45			
Asn	Leu	Val	Pro	Ala	Pro	Lys	Ile	Leu	Asp	Ala	Leu	Asp	Asp	Leu	Pro
		50				55					60				
Val	Ile	Glu	Met	Lys	Lys	Leu	Lys	Glu	Ile	Leu	Ser	Ala	Lys	Asp	Asn
65					70				75					80	
Thr	Pro	Leu	Lys	Glu	Tyr	Lys	Glu	Leu	Leu	Ser	Glu	Lys	Leu	Ile	His
				85				90					95		
Ala	Lys	Ser	Ser	Gln	Glu	Phe	Leu	Asn	Thr	Ala	Asn	Met	Leu	Leu	Ser
			100					105					110		
Leu	Gln	Ser	Gln	Val	Leu	Ser	Phe	Val	Val	Glu	Asn	Glu	Arg	Lys	Lys
		115					120					125			
Ala	Phe	Leu	Gln	Met	Lys	Ala	Lys	Lys	Gln	Ser	Val	Asp	Phe	Tyr	Ala
		130				135				140					
Leu	Tyr	Pro	Asn	Leu	Gly	Glu	Ile	Gly	Gly	Val	Ile	Tyr	Leu	Lys	Glu
145				150						155				160	
Lys	Glu	Lys	Gln	Leu	Phe	Leu	Lys	Thr	Thr	Leu	Gln	Arg	Thr	Lys	Glu

703

```

                165                170                175
Val Leu Lys Glu Ala Gln Asn Thr Leu Leu Gly Phe Ser Phe Val Glu
                180                185                190
Ile Val Cys Glu Lys Thr Pro Met Leu Phe Ala Phe Glu Asp Arg Leu
                195                200                205
Leu Asp Thr Leu Gly
                210

```

(2) INFORMATION FOR SEQ ID NO:799:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

```

Met Ser Asp Glu Ile Thr Gln Glu Asn Glu Leu Glu Ile Asn Ser Asn
1          5          10          15
Asn Gln Asn Gln Glu Pro Lys Glu Val Glu Lys Met Pro Leu Asn Asn
20          25          30
Ile Gln Lys Ala Lys Lys Leu Lys Asn His Ala Asn Leu Ile Val Arg
35          40          45
Arg Thr Asp Glu Leu Asp Lys Val Ile Asn Lys Arg Glu Ser Leu Gln
50          55          60
Arg Glu Phe Lys Arg Arg Ile Lys His Leu Asp Asn Lys Ile Glu Thr
65          70          75          80
Leu Ser Asn Asn Ile Glu Glu Leu Lys Arg Lys
85          90

```

(2) INFORMATION FOR SEQ ID NO:800:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

```

Met Lys Lys Tyr Gln Asn Lys Arg Lys Leu Gly Lys Arg Ile Asn Cys
1           5           10           15
Phe Ile Ser Asn Glu Cys Lys Asp Ile Leu Glu Asn Tyr Leu Lys Val
          20           25           30
Lys Lys Ile Ser Val Thr Glu Cys Ile Glu Ser Leu Leu Leu Ala Leu
          35           40           45
Asp Pro Ser Lys Glu Thr Leu Arg Ala Arg Asp Phe Tyr Glu Ser Leu
          50           55           60
Phe Lys Val Ile Ser Leu Asn Gln His Val Tyr Lys Glu Leu Met Ala
65           70           75           80
Asn Gly Asn Asn Ile Asn Gln Ile Ala Lys Asn Thr Asn Ile Ala Ile
          85           90           95
Lys Tyr Asn Lys Pro Phe Tyr Leu Gln Asn Leu Ala Phe Leu Glu Glu
          100          105          110
Ile Phe Lys Val Met Asp Thr Leu Asn Lys Asn Val Glu Glu Cys Lys
          115          120          125
Lys Ile Ser Leu Glu Leu Leu Leu Gln Ile Tyr Lys Glu Gln Lys Ser
          130          135          140
Gln Thr Glu Phe Asn Ala Ile Ser Lys Ile Leu Asn Ala Leu Asn Glu
145          150          155          160
Lys Gln Ser Thr Thr Glu Pro Lys Lys Asp Asn Ala
          165          170

```

(2) INFORMATION FOR SEQ ID NO:801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

```

Met Asn Thr Asn Leu Lys Lys Ala Leu Phe Leu Thr Thr Leu Gly Tyr
1           5           10           15
Leu Gln Ala Asn Glu Gly Phe Leu Ala Ile Met Pro Asp Glu Asn Lys
          20           25           30
Gln Glu Asp Ile Ser Gln Glu Gln Lys Leu Glu His Lys Met Glu Gln
          35           40           45
Lys Ile Ala Pro Gln Asn Thr Leu Lys Lys Gln Gln Ser Ala Pro Leu
          50           55           60
Gln Ser Ala Glu Leu Leu Gln Ser Gln Val Lys Arg Glu Val Lys Glu
65           70           75           80

```

```

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

```

(2) INFORMATION FOR SEQ ID NO:802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

```

Leu Ala Ile Lys Arg Glu Lys Met Lys Asn Ser Ala Pro Leu Lys Asn
1          5          10          15
Lys Val Phe Cys Gly Leu Tyr Val Leu Ser Leu Ser Ala Ser Val Gln
      20          25          30
Ala Phe Asp Tyr Lys Ile Glu Val Leu Ala Glu Ser Phe Ser Lys Val
      35          40          45

```

Gly Phe Asn Lys Lys Lys Ile Asp Ile Ala Arg Gly Ile Tyr Pro Thr
 50 55 60
 Glu Thr Phe Val Thr Ala Val Gly Gln Gly Asn Ile Tyr Ala Asp Phe
 65 70 75 80
 Leu Ser Lys Ser Leu Lys Asp Gln Gly His Val Leu Glu Gly Lys Val
 85 90 95
 Gly Gly Thr Ile Gly Gly Ile Ala Tyr Asp Ser Thr Lys Phe Asn Gln
 100 105 110
 Gly Gly Ser Val Ile Tyr Asn Tyr Ile Gly Tyr Trp Asp Gly Tyr Leu
 115 120 125
 Gly Gly Lys Arg Ala Leu Leu Asp Gly Thr Ser Ile His Glu Cys Ala
 130 135 140
 Leu Gly Ser Asp Gly Lys Val Ile Asp Ser Ile Ala Cys Gly Asn Ala
 145 150 155 160
 Arg Ala Asn Lys Ile Arg Arg Asn Tyr Leu Met Asn Asn Ala Phe Leu
 165 170 175
 Glu Tyr Arg Tyr Lys Asp Ile Phe Ala Ala Lys Gly Gly Arg Tyr Gln
 180 185 190
 Ser Asn Ala Pro Tyr Met Ser Ser Tyr Thr Gln Gly Phe Glu Ile Ser
 195 200 205
 Ala Lys Ile Lys Asp Lys Asn Glu Gly Ser His Lys Leu Trp Trp Phe
 210 215 220
 Ser Ser Trp Gly Arg Ala Phe Ala Tyr Gly Glu Trp Ile Tyr Asp Phe
 225 230 235 240
 Tyr Ser Pro Arg Thr Val Ile Lys Asn Gly Arg Thr Leu Asn Tyr Gly
 245 250 255
 Ile His Leu Val Asp Tyr Thr Tyr Glu Arg Lys Gly Val Ser Val Ser
 260 265 270
 Pro Phe Phe Gln Phe Ser Pro Gly Thr Tyr Tyr Ser Pro Gly Val Ala
 275 280 285
 Val Gly Tyr Asp Ser Asn Pro Asn Phe Asn Gly Val Gly Phe Arg Ser
 290 295 300
 Glu Thr Lys Ala Tyr Ile Leu Leu Pro Val His Ala Pro Leu Lys Arg
 305 310 315 320
 Asp Thr Tyr Arg Tyr Ala Val Lys Ala Gly Thr Ala Gly Gln Ser Leu
 325 330 335
 Leu Ile Arg Gln Arg Phe Asp Tyr Asn Glu Phe Asn Phe Gly Gly Ala
 340 345 350
 Phe Tyr Lys Val Trp Lys Asn Ala Asn Ala Tyr Ile Gly Thr Thr Gly
 355 360 365
 Asn Pro Leu Gly Ile Asp Phe Trp Thr Asn Ser Val Tyr Asp Ile Gly
 370 375 380
 Gln Ala Leu Ser His Val Val Thr Ala Asp Ala Val Ser Gly Trp Val
 385 390 395 400
 Phe Gly Gly Gly Val His Lys Lys Trp Leu Trp Gly Thr Leu Trp Arg
 405 410 415
 Trp Thr Ser Gly Ala Leu Ala Asn Glu Ala Ser Ala Ala Val Asn Val
 420 425 430
 Gly Tyr Lys Ile Ser Lys Ser Leu Thr Ala Ser Val Lys Leu Glu Tyr
 435 440 445
 Leu Gly Val Met Thr His Ser Gly Phe Thr Val Gly Ser Tyr Arg Pro
 450 455 460
 Thr Pro Gly Ser Lys Ala Leu Tyr Ser Asp Arg Ser His Leu Met Thr
 465 470 475 480
 Thr Leu Ser Ala Lys Phe
 485

(2) INFORMATION FOR SEQ ID NO:803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

```

Val Cys Ile Ile Phe Asp Ala Asp Ile Lys Lys Glu Asn Gln Glu Ser
1           5           10           15
Asp Ala Gly Phe Asp Asn Lys Leu Lys His Ile Arg Glu Lys Phe Lys
20           25           30
Glu Lys Gly Thr Asp Phe Pro Lys Glu Gln Ile Phe Leu Phe Pro Asn
35           40           45
Asn Gln Asp Asp Gly Asp Leu Glu Thr Leu Leu Leu Glu Ile Ala Lys
50           55           60
His Asp Glu Phe Leu Lys Cys Phe Glu Gly Tyr Leu Glu Cys Ile Lys
65           70           75           80
Ser Lys Glu His Tyr Lys Pro Ile Lys Asn Ile Arg Lys Asn Met Leu
85           90           95
Tyr Ala Tyr Leu Glu Ala Leu Gly Leu Glu Asn Leu Thr Lys Thr Asn
100          105          110
Ile Asp Val Phe Asp Ser Lys Gly Lys Ile Lys Ser Arg Tyr Glu Glu
115          120          125
Asn Tyr Lys Lys Leu Thr Glu Glu Val Ile Asp Phe Ser Ser Asn Ser
130          135          140
Leu Ile Pro Leu Lys Asn Phe Leu Gly Gln Phe Ala Glu Asn Lys Gln
145          150          155          160
Lys Thr Asn Pro Lys Ile Phe
165

```

(2) INFORMATION FOR SEQ ID NO:804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

```

Met Val Leu Lys Thr Lys Leu Lys Ile Ile Ser Ser Val Ile Leu Ser
1           5           10           15
Thr Leu Leu Trp Val Gly Cys Ser Ser Glu Met Ala Thr Tyr Gln Asn
20           25           30
Val Asn Asp Ala Thr Lys Asn Thr Thr Ala Ser Ile Asn Ser Thr Asp
35           40           45
Leu Leu Leu Thr Ala Asn Ala Met Leu Asp Ser Met Phe Ser Asp Pro
50           55           60
Asn Phe Glu Gln Leu Lys Gly Lys His Leu Ile Glu Val Ser Asp Val
65           70           75           80
Ile Asn Asp Thr Thr Gln Pro Asn Leu Asp Met Asn Leu Leu Thr Thr
85           90           95
Glu Ile Ala Arg Gln Leu Arg Leu Arg Ser Asn Gly Arg Phe Asn Ile
100          105          110
Thr Arg Ala Ser Gly Gly Ser Gly Ile Glu Ala Asp Ser Arg Met Val
115          120          125
Lys Gln Arg Glu Lys Glu Arg Glu Ser Glu Glu Tyr Asn Gln Asp Thr
130          135          140
Thr Val Glu Lys Gly Thr Leu Lys Ala Ala Asp Leu Ser Leu Ser Gly
145          150          155          160
Lys Val Ser Ser Ile Ala Ala Ser Ile Ser Ser Ser Arg Gln Arg Leu
165          170          175
Asp Tyr Asp Phe Thr Leu Ser Leu Thr Asn Arg Lys Thr Gly Glu Glu
180          185          190
Val Trp Ser Asp Val Lys Pro Ile Val Lys Asn Ala Ser Asn Lys Arg
195          200          205
Met Phe
210

```

(2) INFORMATION FOR SEQ ID NO:805:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

```

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

```

Ala His Ala Lys Asn Pro Leu Thr Leu Ser Lys Glu Glu Glu Val Leu
 20 25 30
 Gln Asn Leu Gln Ser Phe Ser Ala His Phe Lys Gln Val Leu Lys Asn
 35 40 45
 Glu Lys Pro Leu Val Tyr Tyr Gly Val Leu Lys Ala Lys Ala Pro Asn
 50 55 60
 Trp Ala Leu Trp Val Tyr Glu Lys Pro Leu Lys Lys Glu Ile Tyr Met
 65 70 75 80
 Asn Asp Lys Glu Val Val Val Tyr Glu Pro Asn Leu Phe Gln Ala Thr
 85 90 95
 Ile Thr Pro Leu Lys Asp Lys Thr Asp Phe Phe Thr Ile Leu Lys Gln
 100 105 110
 Leu Lys Lys Gln Thr Asp Gly Ser Phe Lys Thr Thr Ile Asn Lys Thr
 115 120 125
 Thr Tyr Arg Leu Val Phe Lys Asp Gly Lys Pro Phe Ser Leu Glu Phe
 130 135 140
 Lys Asp Asp Met Asn Asn Leu Val Thr Ile Thr Phe Ser Gln Ala Glu
 145 150 155 160
 Ile Asn Pro Lys Ile Pro Asn Glu Ile Phe Val Phe Asn Pro Lys Asp
 165 170 175
 Glu Asn Ile Asp Ile Val Arg Gln
 180

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

Met Arg Ile Lys Ala Tyr Phe Leu Arg Phe Ile Ala Leu Val Phe Ile
 1 5 10 15
 Val Leu Leu Gly Phe Ser Ala Cys Lys Asn Ser Gln Lys Ser Gln Asp
 20 25 30
 Ser Gln Asn Asn Thr Thr Gln Gln Asp Ser Pro Lys Thr Tyr Thr Ala
 35 40 45
 Met Asp Leu Asn Asn Gln Glu Tyr Thr Ile Met Gly Asp Leu Asp Ser
 50 55 60
 Leu Asn Ile Ser Pro Asp Pro Asn Thr Pro Thr Leu Leu Ile Leu Ser
 65 70 75 80
 Ala Leu Asp Asn Ser Leu Lys Asp Tyr Ala Pro Thr Phe Asn Val Leu
 85 90 95
 Lys Lys Thr Phe Lys Asp Arg Leu Arg Val Leu Ile Leu Leu Asn Gln
 100 105 110

710

```

Pro Tyr Ser Ser Asp Ala Ile Lys Gly Phe Ile Ala Pro Ser Gln Thr
    115                      120                      125
Asp Leu Met Ile Leu Asn Pro Lys Asp Thr Ala Leu Phe Asp His Leu
    130                      135                      140
Asn His Asp Ala Leu Asn His Ser Phe Asn Met Leu Leu Tyr Asp Lys
    145                      150                      155                      160
His Gln Leu Ile Lys Met Tyr Gln Gly Ile Val Pro Ala Glu Met Leu
                      165                      170                      175
Gln Phe Asp Ile Ser Asn Leu Lys Asp
    180                      185

```

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

```

Met Val Ser Thr Leu Lys Pro Leu Lys Ile Gly Lys His Thr Ile Lys
1                      5                      10                      15
Phe Pro Ile Phe Gln Gly Gly Met Gly Val Gly Ile Ser Trp Asp Glu
    20                      25                      30
Leu Ala Gly Asn Val Ala Lys Glu Gly Ala Leu Gly Val Ile Ser Ala
    35                      40                      45
Val Gly Thr Gly Tyr Tyr Lys Asn Met Arg Phe Val Glu Arg Ile Val
    50                      55                      60
Ala Lys Lys Pro Phe Glu Ala Leu Asn Phe Tyr Ser Lys Lys Ala Leu
    65                      70                      75                      80
Asn Glu Ile Phe Ala Asn Ala Arg Lys Ile Cys Gly Asn Lys Pro Leu
    85                      90                      95
Gly Ala Asn Ile Leu Tyr Ala Ile Asn Asp Tyr Gly Arg Val Leu Arg
    100                      105                      110
Asp Ser Cys Glu Ala Gly Ala Asn Ile Ile Ile Thr Gly Ala Gly Leu
    115                      120                      125
Pro Thr Asn Met Pro Glu Phe Ala Lys Asp Phe Ser Asp Val Ala Leu
    130                      135                      140
Ile Pro Ile Ile Ser Ser Ala Lys Ala Leu Lys Ile Leu Cys Lys Arg
    145                      150                      155                      160
Trp Ser Asp Arg Tyr Lys Arg Ile Pro Asp Ala Phe Ile Val Glu Gly
    165                      170                      175
Pro Leu Ser Gly Gly His Gln Gly Phe Lys Tyr Glu Asp Cys Phe Lys
    180                      185                      190
Glu Glu Phe Gln Leu Glu Asn Leu Val Pro Lys Val Val Glu Ala Ser
    195                      200                      205

```

711

```

Lys Glu Trp Gly Asn Ile Pro Ile Ile Ala Ala Gly Gly Ile Trp Asp
 210                215                220
Lys Lys Asp Ile Asp Thr Met Leu Ser Leu Gly Ala Ser Gly Val Gln
 225                230                235                240
Met Ala Thr Arg Phe Leu Gly Thr Lys Glu Cys Asp Ala Lys Ala Tyr
                245                250                255
Ala Asp Leu Leu Pro Thr Leu Lys Lys Glu Asp Ile Leu Leu Ile Lys
                260                265                270
Ser Pro Val Gly Tyr Pro Ala Arg Ala Ile Asn Thr Gly Val Ile Lys
                275                280                285
Arg Ile Glu Glu Gly Asn Ala Pro Lys Ile Ala Cys Val Ser Asn Cys
                290                295                300
Val Ala Pro Cys Asn Arg Gly Glu Glu Ala Lys Lys Val Gly Tyr Cys
 305                310                315                320
Ile Ala Asp Gly Leu Gly Arg Ser Tyr Leu Gly Asn Arg Glu Glu Gly
                325                330                335
Leu Tyr Phe Thr Gly Ala Asn Gly Tyr Arg Val Asp Lys Ile Ile Ser
                340                345                350
Val His Glu Leu Ile Lys Glu Leu Thr Glu Gly
                355                360

```

(2) INFORMATION FOR SEQ ID NO:808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

```

Met Val Ser Thr Leu Lys Pro Leu Lys Ile Gly Lys His Thr Ile Lys
 1                5                10                15
Phe Pro Ile Phe Gln Gly Gly Met Gly Val Gly Ile Ser Trp Asp Glu
                20                25                30
Leu Ala Gly Asn Val Ala Lys Glu Gly Ala Leu Gly Val Ile Ser Ala
                35                40                45
Val Gly Thr Gly Tyr Tyr Lys Asn Met Arg Phe Val Glu Arg Ile Val
                50                55                60
Ala Lys Lys Pro Phe Glu Ala Leu Asn Phe Tyr Ser Lys Lys Ala Leu
 65                70                75                80
Asn Glu Ile Phe Ala Asn Ala Arg Lys Ile Cys Gly Asn Lys Pro Leu
                85                90                95
Gly Ala Asn Ile Leu Tyr Ala Ile Asn Asp Tyr Gly Arg Val Leu Arg
                100                105                110
Asp Ser Cys Glu Ala Gly Ala Asn Ile Ile Ile Thr Gly Ala Gly Leu
                115                120                125

```

```

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

```

(2) INFORMATION FOR SEQ ID NO:809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

```

Leu Leu Gly Arg Asn Gly Val Thr Leu Asn Ile Arg Gln Val Phe Trp
1                      5                      10                      15
Trp Asp Asn Phe Asn Trp Ser Ile Gly Phe Tyr Asn Thr Phe Gly Asn
                      20                      25                      30
Ser Asp Ala Phe Leu Gly Ser His Thr Met Pro Arg Gly Asn Asn Thr
                      35                      40                      45

```

713

```

Ser Tyr Ile Ser Asn Glu Ile Ser Val Thr Thr Arg His Ala Gly Met
 50          55          60
Ile Gly Tyr Asp Phe Trp Asp Asn Thr Ala Tyr Asp Gly Leu Ala Asp
65          70          75          80
Ala Ile Thr Asn Ala Asn Thr Phe Thr Phe Tyr Thr Ser Val Gly Gly
          85          90          95
Ile His Lys Arg Phe Ala Trp His Val Phe Gly Arg Val Ser His Ala
          100          105          110
Asn Lys Asn Ala Leu Gly Gln Val Gly Arg Ala Asn Glu Tyr Ser Leu
          115          120          125
Gln Phe Asn Ala Ser Tyr Ala Phe Thr Glu Ser Val Leu Leu Asn Phe
          130          135          140
Arg Ile Thr Tyr Tyr Gly Ala Arg Ile Asn Lys Gly Tyr Gln Ala Gly
145          150          155          160
Tyr Phe Gly Ala Pro Lys Phe Asn Asn Pro Asp Gly Asp Phe Ser Ala
          165          170          175
Asn Tyr Gln Asp Arg Ser Tyr Met Met Thr Asn Leu Thr Leu Lys Phe
          180          185          190

```

(2) INFORMATION FOR SEQ ID NO:810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

```

Met Gln Gln Gln Leu Thr Tyr Leu Asn Ala Gly Asn Val Phe Phe Asn
1          5          10          15
Ala Met Asn Lys Ala Leu Glu Lys Asn Gly Thr Ala Thr Ala Asn Ser
          20          25          30
Thr Ser Ser Thr Ser Gly Ala Thr Gly Ser Asp Gly Gln Thr Tyr Ser
          35          40          45
Gln Gln Ala Ile Gln Tyr Leu Gln Gly Gln Gln Asn Ile Leu Asn Asn
50          55          60
Ala Ala Asn Leu Leu Lys Gln Asp Glu Leu Leu Glu Ala Phe Asn
65          70          75          80
Ser Ala Val Ala Ala Asn Ile Gly Asn Lys Glu Phe Asn Ser Ala Ala
          85          90          95
Phe Thr Gly Leu Val Gln Gly Ile Ile Asp Gln Ser Gln Leu Val Tyr
          100          105          110
Asn Glu Leu Thr Lys Asn Thr Ile Ser Gly Ser Ala Val Asn Asn Ala
          115          120          125
Gly Ile Asn Ser Asn Gln Ala Asn Ala Val Gln Gly Arg Ala Ser Gln
130          135          140

```

714

```

Leu Pro Asn Ala Leu Tyr Asn Val Gln Val Thr Leu Asp Lys Ile Asn
145              150              155              160
Ala Leu Asn Asn Gln Val Arg Ser Met Pro Tyr Leu Pro Gln Phe Arg
              165              170              175
Ala Gly Asn Ser Arg Ala Thr Asn Ile Leu Asn Gly Phe Tyr Thr Lys
              180              185              190
Val Gly Tyr Lys Gln Phe Phe Gly Lys Lys Arg Asn Ile Gly Leu Arg
              195              200              205
Tyr Tyr Gly Phe Phe Ser Tyr Asn Gly Ala Ser Val Gly Phe Arg Ser
              210              215              220
Thr Gln Asn Asn Val Gly Leu Tyr Thr Tyr Gly Val Gly Thr Asp Val
225              230              235              240
Leu Tyr Asn Ile Phe Ser Arg Ser Tyr Gln Asn Arg Ser Val Asp Met
              245              250              255
Gly Phe Phe Ser Gly Ile Gln Leu Ala Gly Glu Thr Phe Gln Ser Thr
              260              265              270
Leu Arg Asp Asp Pro Asn Val Lys Leu His Gly Lys Ile Asn Asn Thr
              275              280              285
His Phe Gln Phe Leu Phe Asp Phe Gly Met Arg Met Asn Phe Gly Lys
              290              295              300
Leu Asp Gly Lys Ser Asn Arg His Asn Gln His Thr Val Glu Phe Gly
305              310              315              320
Val Val Val Pro Thr Ile Tyr Asn Thr Tyr Tyr Lys Ser Ala Gly Thr
              325              330              335
Thr Val Lys Tyr Phe Arg Pro Tyr Ser Val Tyr Trp Ser Tyr Gly Tyr
              340              345              350
Ser Phe

```

(2) INFORMATION FOR SEQ ID NO:811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

```

Met Glu Asp Phe Leu Tyr Asn Thr Leu Tyr Phe Ile Glu Asp Tyr Lys
1              5              10              15
Leu Val Val Ile Phe Ser Phe Ile Gly Leu Ile Ala Leu Phe Phe Leu
              20              25              30
Tyr Lys Phe Ile Lys Thr Gln Lys Lys Val Phe Lys Asp Lys Ala Asn
              35              40              45
Gln Pro Gln Lys Lys Lys Ser Phe Lys Glu Ile Ile Ile Asp Gly Leu
50              55              60

```


Lys Glu Arg Val Lys Thr Phe Gly Phe Trp Leu Gln Ala Ile Leu Leu
 65 70 75 80
 Leu Ser Tyr Ser Phe Ile Thr Ser Gly Leu Phe Phe Leu Ile Leu Leu
 85 90 95
 Gly Asn Phe Tyr Asp Asp Asn Arg Leu Pro Glu Ser Asp Asp Asp Leu
 100 105 110
 Phe Asp Ile Trp Val Tyr Ala Ile Gln Asp Phe Pro Ala Tyr Tyr Phe
 115 120 125
 Lys Ala Leu Thr Phe Ser Ser Leu Lys Ile Tyr Gly Phe Asn Ile Ser
 130 135 140
 Leu Val Val Tyr Ser Ser Ile Leu Cys Ser Tyr Ile Phe Ile Thr Phe
 145 150 155 160
 Phe Val Trp Phe Leu Lys Tyr Leu Thr Arg Thr Arg Asp Ile Gly Ala
 165 170 175
 Asn Lys Lys Val Asp Asp Leu Phe Gly Ser Ala Ser Trp Glu Thr Glu
 180 185 190
 Glu Lys Met Ile Lys Ala Lys Leu Ile Thr Pro Asn Asn Lys Lys Arg
 195 200 205
 Ala Phe Asp Lys Arg Glu Val Ile Val Gly Arg Arg Gly Leu Gly Asp
 210 215 220
 Phe Ile Ala Tyr Ala Gly Gln Ala Phe Ile Gly Leu Ile Ala Pro Thr
 225 230 235 240
 Arg Ser Gly Lys Gly Val Gly Phe Ile Met Pro Asn Met Ile Asn Tyr
 245 250 255
 Pro Gln Asn Ile Val Val Phe Asp Pro Lys Ala Asp Thr Met Glu Thr
 260 265 270
 Cys Gly Lys Ile Arg Glu Lys Arg Phe Asn Gln Lys Val Phe Ile Tyr
 275 280 285
 Glu Pro Phe Ser Leu Lys Thr His Arg Phe Asn Pro Phe Ala Tyr Val
 290 295 300
 Asp Phe Gly Asn Asp Val Val Leu Thr Glu Asp Ile Leu Ser Gln Ile
 305 310 315 320
 Asp Thr Arg Leu Lys Gly His Gly Met Val Ala Ser Gly Gly Asp Phe
 325 330 335
 Ser Thr Gln Ile Phe Gly Leu Ala Lys Leu Val Phe Pro Glu Arg Pro
 340 345 350
 Asn Glu Lys Asp Pro Phe Phe Ser Asn Gln Ala Arg Asn Leu Phe Val
 355 360 365
 Ile Asn Cys Asn Ile Tyr Arg Asp Leu Met Trp Thr Lys Lys Gly Leu
 370 375 380
 Glu Phe Val Lys Arg Lys Lys Ile Ile Met Pro Glu Thr Pro Thr Met
 385 390 395 400
 Phe Phe Ile Gly Ser Met Ala Ser Gly Ile Asn Leu Ile Asp Glu Asp
 405 410 415
 Thr Asn Met Glu Lys Val Val Ser Leu Met Glu Phe Phe Gly Gly Glu
 420 425 430
 Glu Asp Lys Ser Gly Asp Asn Leu Arg Ala Leu Ser Pro Ala Thr Arg
 435 440 445
 Asn Met Trp Asn Asn Phe Lys Thr Met Gly Gly Ala Lys Glu Thr Tyr
 450 455 460
 Ser Ser Val Gln Gly Val Tyr Thr Ser Ala Phe Ala Pro Tyr Asn Asn
 465 470 475 480
 Ala Met Ile Arg Asn Phe Thr Ser Ala Asn Asp Phe Asp Phe Arg Arg
 485 490 495
 Leu Arg Ile Asp Ala Val Ser Ile Gly Val Ile Ala Asn Pro Lys Glu
 500 505 510
 Ser Thr Ile Val Gly Pro Ile Leu Glu Leu Phe Phe Asn Val Met Ile

716

```

      515              520              525
Tyr Ser Asn Leu Ile Leu Pro Ile His Asp Pro Gln Cys Lys Arg Ser
530              535              540
Cys Leu Met Leu Met Asp Glu Phe Thr Leu Cys Gly Tyr Leu Glu Thr
545              550              555              560
Phe Val Lys Ala Val Gly Ile Met Ala Glu Tyr Asn Met Arg Pro Ala
565              570              575
Phe Val Phe Gln Ser Lys Ala Gln Leu Glu Asn Asp Pro Pro Leu Gly
580              585              590
Tyr Gly Arg Asn Gly Ala Lys Thr Ile Leu Asp Asn Leu Ser Leu Asn
595              600              605
Met Tyr Tyr Gly Ile Asn Asn Asp Asn Tyr Tyr Glu His Phe Glu Lys
610              615              620
Leu Ser Lys Val Leu Gly Lys Tyr Thr Arg Gln Asp Val Ser Arg Ser
625              630              635              640
Ile Asp Asp Asn Thr Gly Lys Thr Asn Thr Ser Ile Ser Asn Lys Glu
645              650              655
Arg Phe Leu Met Thr Pro Asp Glu Leu Met Thr Met Gly Asp Glu Leu
660              665              670
Ile Ile Leu Glu Asn Thr Leu Lys Pro Ile Lys Cys His Lys Ala Leu
675              680              685
Tyr Tyr Asp Asp Pro Phe Phe Thr Asp Glu Leu Ile Lys Val Ser Pro
690              695              700
Ser Leu Ser Lys Lys Tyr Lys Leu Gly Lys Val Pro Asn Gln Ala Thr
705              710              715              720
Phe Tyr Asp Asp Leu Gln Ala Ala Lys Thr Arg Gly Glu Leu Ser Tyr
725              730              735
Asp Lys Ser Leu Val Pro Val Gly Ser Ser Glu Leu
740              745

```

(2) INFORMATION FOR SEQ ID NO:812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...34

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

```

Leu Ser His Leu Phe Leu Val Lys Arg Pro Tyr Ser Arg Leu Tyr Leu
1              5              10              15
His Asn Gln Ser Asn His Lys Met Arg His His Ser Ile Leu Phe Val
20              25              30
Ser Phe

```

717

(2) INFORMATION FOR SEQ ID NO:813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

```

Met Glu His His Lys Ala His Thr Thr Ile Gln Ala Leu Gln Ala Lys
1           5           10           15
Arg Lys Arg Leu Leu Thr Glu Leu Ala Glu Leu Glu Ala Glu Ile Lys
20           25           30
Val Ser Ser Glu Arg Arg Ser Ser Phe Asn Val Ser Leu Ser Pro Ser
35           40           45
Leu Leu Ala Glu Ile Glu Glu Ile Glu Tyr Glu Glu Lys Met Ser Lys
50           55           60
Glu Arg Arg Ile His His Asn Leu Leu Leu Ser Pro Ser Phe Met Ala
65           70           75           80
Lys Val Asp Glu Tyr Met Lys Glu Lys Gly Phe Pro Asn Arg Ser Leu
85           90           95
Leu Phe Glu Lys Ala Leu Glu Phe Tyr Met Leu Lys His Pro
100          105          110

```

(2) INFORMATION FOR SEQ ID NO:814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

```

Val Met Arg Phe Phe Ser Phe Cys Tyr Phe Leu Phe Tyr Phe Leu Gly
1           5           10           15

```

718

```

Val Ser Leu His Ala Leu Ser Pro Leu Glu Glu Gln Glu Phe Leu Ile
      20                      25                      30
Ser Tyr Arg Leu Lys Ile Val Asp Ser Arg Val Met Gly Glu Glu Tyr
      35                      40                      45
Ser Val Ser Lys Pro Ile Val Ser Arg Ile Lys Thr Ala Pro Tyr Val
      50                      55                      60
Leu Asp Tyr His Cys Ser Ile Ile Thr Arg Asn Leu Pro Asp Leu Lys
      65                      70                      75                      80
Asn Pro Leu Leu Gln Ile Lys Leu Glu Arg Phe Leu Leu Glu Ile Ala
      85                      90                      95
Leu Lys Lys Glu Lys Glu Arg Val Ile Asp Cys Leu Leu Lys Ser Gln
      100                     105                     110
Val Ala Ile Thr His Tyr Asp His Ser Tyr Lys Asn Gly Thr Thr Thr
      115                     120                     125
Thr Ser Ile Leu Asn Leu Lys Ala Leu Ser Val Lys Ala Ser Leu Glu
      130                     135                     140
Gly Asp Met Leu Ser Leu Asp Ile Phe Arg Lys Glu Glu Glu
      145                     150                     155

```

(2) INFORMATION FOR SEQ ID NO:815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

```

Met Glu Leu Ile Lys Lys Leu Glu Lys Glu Ser Glu Val Leu Lys Lys
1      5      10      15
Asp Leu Gln Gln His Ser Asn Glu Leu Phe Lys Met Leu Ile Ile Asp
      20      25      30
Asn Glu Asp Leu Phe Lys Glu Gln Phe Glu Ile Met Phe Lys Ala Trp
      35      40      45
Val Glu Ile Val Lys Met Met Phe Glu Leu Thr Lys Lys Thr Lys Phe
      50      55      60
Asp Gly Glu Met Ile Gly Tyr Thr Glu Glu Leu Leu Thr Phe Leu Val
      65      70      75      80
Arg Asp Phe Phe Asn Gly Ile Phe Lys Ser Lys Val Ile Pro Lys Met
      85      90      95
Pro Ile Phe Cys Gly Asp Val Lys Cys Glu Asp Phe Asn Ala Leu Arg
      100     105     110
Ser Leu Val Tyr Leu
      115

```

(2) INFORMATION FOR SEQ ID NO:816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

```

Leu Lys Arg Ala Leu Trp Leu Ile Leu Gly Leu Phe Tyr Ala Leu Asn
1           5           10           15
Ala Glu Ser Phe Lys Asp Val Leu Thr Lys Gly Asp Tyr Thr Phe Phe
20           25           30
Asn Lys Lys Val Val Ser Pro Ile Lys Arg Tyr Ala Asp Arg Ser Ala
35           40           45
Phe Tyr Leu Gly Leu Gly Tyr Gln Leu Gly Ser Ile Gln His Asn Ser
50           55           60
Ser Asn Leu Asn Leu Ser Gln Arg Phe Asn Lys Ser Gln Ile Ile Phe
65           70           75           80
Ser Asp Ser Leu Ser Pro Val Phe Lys Asn Ser Tyr Val Ser Asn Gly
85           90           95
Leu Gly Val Gln Val Gly Tyr Lys Trp Val Gly Lys His Glu Glu Thr
100          105          110
Lys Trp Phe Gly Phe Arg Trp Gly Leu Phe Tyr Asp Leu Ser Ala Ser
115          120          125
Leu Tyr Gly Ser Gln Glu Ser Gln Ser Ile Ile Ile Ser Thr Tyr Gly
130          135          140
Thr Tyr Met Asp Leu Leu Leu Asn Ala Tyr Asn Gly Asp Lys Phe Phe
145          150          155          160
Ala Gly Phe Asn Leu Gly Ile Ala Phe Ala Gly Val Tyr Asp Arg Leu
165          170          175
Ser Asp Ala Leu Leu Tyr Gln Thr Leu Leu Gln Asn Thr Phe Gly Gly
180          185          190
Lys Val Asn Leu Asn Gly Phe Gln Phe Leu Val Asp Leu Gly Val Arg
195          200          205
Leu Gly Asn Glu His Asn Gln Phe Gly Phe Gly Ile Lys Ile Pro Thr
210          215          220
Tyr Tyr Phe Asn His Tyr Tyr Ser Met Asn Asn Ile Ser Asn Asn Ser
225          230          235          240
Glu Asn Val Leu Lys Val Leu Arg Phe Leu Glu Tyr Gly Ile Asn Ser
245          250          255
Leu Leu Tyr Gln Val Asp Phe Arg Arg Asn Tyr Ser Val Tyr Phe Asn
260          265          270
Tyr Thr Tyr Ser Phe
275

```

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

```

Met Pro Ala Leu Asn Ser Ser Lys Asn Met Val Val Asn Ile Asn Gln
1           5           10           15
Thr Phe Thr Lys Asn Pro Thr Thr Glu Tyr Thr Tyr Pro Asp Gly Asn
20           25           30
Gly Asn Tyr Tyr Ser Gly Gly Ser Ser Ile Pro Ile Gln Leu Lys Ile
35           40           45
Ser Ser Val Asn Asp Ala Glu Asn Leu Leu Gln Gln Ala Ala Thr Ile
50           55           60
Ile Asn Val Leu Thr Thr Gln Asn Pro His Val Asn Gly Gly Gly Gly
65           70           75           80
Ala Trp Gly Phe Gly Gly Lys Thr Gly Asn Val Met Asp Ile Phe Gly
85           90           95
Asp Ser Phe Asn Ala Ile Asn Glu Met Ile Lys Asn Ala Gln Ala Val
100          105          110
Leu Glu Lys Thr Gln Gln Leu Asn Ala Asn Glu Asn Thr Gln Ile Thr
115          120          125
Gln Pro Asp Asn Phe Asn Pro Tyr Thr Ser Lys Asp Thr Gln Phe Ala
130          135          140
Gln Glu Met Leu Asn Arg Ala Asn Ala Gln Ala Glu Ile Leu Ser Leu
145          150          155          160
Ala Gln Gln Val Ala Asp Asn Phe His Ser Ile Gln Gly Pro Ile Gln
165          170          175
Gln Asp Leu Glu Glu Cys Thr Ala Gly Ser Ala Gly Val Ile Asn Asp
180          185          190
Asn Thr Tyr Gly Ser Gly Cys Ala Phe Val Lys Glu Thr Leu Asn Ser
195          200          205
Leu Glu Gln His Thr Ala Tyr Tyr Gly Asn Gln Val Asn Gln Asp Arg
210          215          220
Ala Leu Ser Gln Thr Ile Leu Asn Phe Lys Glu Ala Leu Ser Thr Leu
225          230          235          240
Gly Asn Asp Ser Lys Ala Ile Asn Ser Gly Ile Ser Asn Leu Pro Asn
245          250          255
Ala Lys Ser Leu Gln Asn Met Thr His Ala Thr Gln Asn Pro Asn Ser
260          265          270
Pro Glu Gly Leu Leu Thr Tyr Ser Leu Asp Thr Ser Lys Tyr Asn Gln
275          280          285
Leu Gln Thr Val Ala Gln Glu Leu Gly Lys Asn Pro Phe Arg Arg Ile
290          295          300

```

721

Gly Val Ile Asn Tyr Gln Asn Asn Asn Gly Ala Met Asn Gly Ile Gly
 305 310 315 320
 Val Gln Ala Gly Tyr Lys Gln Phe Phe Gly Lys Lys Arg Asn Trp Gly
 325 330 335
 Leu Arg Tyr Tyr Gly Phe Phe Asp Tyr Asn His Ala Tyr Ile Lys Ser
 340 345 350
 Asn Phe Phe Asn Ser Ala Ser Asp Val Trp Thr Tyr Gly Val Gly Met
 355 360 365
 Asp Ala Leu Tyr Asn Phe Ile Asn Asp Lys Asn Thr Asn Phe Leu Gly
 370 375 380
 Lys Asn Asn Lys Leu Ser Val Gly Leu Phe Gly Gly Phe Ala Leu Ala
 385 390 395 400
 Gly Thr Ser Trp Leu Asn Ser Gln Gln Val Asn Leu Thr Met Met Asn
 405 410 415
 Gly Ile Tyr Asn Ala Asn Val Ser Ala Ser Asn Phe Gln Phe Leu Phe
 420 425 430
 Asp Leu Gly Leu Arg Met Asn Leu Ala Arg Pro Lys Lys Lys Asp Ser
 435 440 445
 Asp His Ala Ala Gln His Gly Met Glu Leu Gly Val Lys Ile Pro Thr
 450 455 460
 Ile Asn Thr Asp Tyr Tyr Ser Phe Met Gly Ala Glu Leu Lys Tyr Arg
 465 470 475 480
 Arg Leu Tyr Ser Val Tyr Leu Asn Tyr Val Phe Ala Tyr
 485 490

(2) INFORMATION FOR SEQ ID NO:818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

Val Leu Asn Thr Thr Gln Lys Ser Leu Leu Val Phe Met Gly Val Phe
 1 5 10 15
 Phe Leu Ile Phe Gly Val Asp Gln Ala Ile Lys His Ala Ile Leu Glu
 20 25 30
 Gly Phe His Tyr Glu Ser Leu Val Ile Asp Ile Val Leu Val Phe Asn
 35 40 45
 Lys Gly Val Ala Phe Ser Leu Leu Ser Phe Leu Glu Gly Gly Leu Lys
 50 55 60
 Tyr Leu Gln Ile Leu Leu Ile Leu Gly Leu Phe Ile Phe Leu Met Arg
 65 70 75 80
 Gln Lys Glu Leu Phe Lys Ser His Ala Ile Glu Phe Gly Met Val Phe
 85 90 95

```

Gly Ala Gly Val Ser Asn Val Leu Asn Arg Leu Val Ser Leu Gly Gln
      100                      105                      110
Leu Tyr Ile Leu Tyr Asp Val Leu Ala Ile Arg Arg Glu Lys Met Lys
      115                      120                      125
Asn Ser Ala Pro Leu Lys Asn Lys Val Phe Cys Gly Leu Tyr Val Leu
      130                      135                      140
Ser Leu Ser Ala Ser Val Gln Ala Phe Asp Tyr Lys Ile Glu Val Leu
      145                      150                      155                      160
Ala Glu Ser Phe Ser Lys Val Gly Phe Asn Lys Lys Lys Ile Asp Ile
      165                      170                      175
Ala Arg Gly Ile Tyr Pro Thr Glu Thr Phe Val Thr Ala Val Gly Gln
      180                      185                      190
Gly Asn Ile Tyr Ala Asp Phe Leu Ser Lys Ser Leu Lys Asp Gln Gly
      195                      200                      205
His Val Leu Glu Gly Lys Val Gly Gly Thr Ile Gly Gly Ile Ala Tyr
      210                      215                      220
Asp Ser Thr Lys Phe Asn Gln Gly Gly Ser Val Ile Tyr Asn Tyr Ile
      225                      230                      235                      240
Gly Tyr Trp Asp Gly Tyr Leu Gly Gly Thr Lys Ala Cys Leu Met Ala
      245                      250                      255
Gln Val Ser Met Thr Ala Arg Leu Ala Leu Met Ala Arg
      260                      265

```

(2) INFORMATION FOR SEQ ID NO:819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

```

Met Leu Val Thr Lys Leu Ala Pro Asp Phe Lys Ala Pro Ala Val Leu
1      5      10      15
Gly Asn Asn Glu Val Asp Glu His Phe Glu Leu Ser Lys Asn Leu Gly
      20      25      30
Lys Asn Gly Val Ile Leu Phe Phe Trp Pro Lys Asp Phe Thr Phe Val
      35      40      45
Cys Pro Thr Glu Ile Ile Ala Phe Asp Lys Arg Val Lys Asp Phe His
      50      55      60
Glu Lys Gly Phe Asn Val Ile Gly Val Ser Ile Asp Ser Glu Gln Val
      65      70      75      80
His Phe Ala Trp Lys Asn Thr Pro Val Glu Lys Gly Gly Ile Gly Gln
      85      90      95
Val Ser Phe Pro Met Val Ala Asp Ile Thr Lys Ser Ile Ser Arg Asp
      100      105      110

```


723

```

Tyr Asp Val Leu Phe Glu Glu Ala Ile Ala Leu Arg Gly Ala Phe Leu
  115                      120                      125
Ile Asp Lys Asn Met Lys Val Arg His Ala Val Ile Asn Asp Leu Pro
  130                      135                      140
Leu Gly Arg Asn Ala Asp Glu Met Leu Arg Met Val Asp Ala Leu Leu
  145                      150                      155                      160
His Phe Glu Glu His Gly Glu Val Cys Pro Ala Gly Trp Arg Lys Gly
                165                      170                      175
Asp Lys Gly Met Lys Ala Thr His Gln Gly Val Ala Glu Tyr Leu Lys
                180                      185                      190
Glu Asn Ser Ile Lys Leu
                195

```

(2) INFORMATION FOR SEQ ID NO:820:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

```

Met Leu Lys Leu Ala Ser Lys Thr Ile Cys Leu Ser Leu Ile Ser Ser
  1                      5                      10                      15
Phe Thr Ala Val Glu Ala Phe Gln Lys His Gln Lys Asp Gly Phe Phe
                20                      25                      30
Ile Glu Ala Gly Phe Glu Thr Gly Leu Leu Gln Gly Thr Gln Thr Gln
                35                      40                      45
Glu Gln Thr Ile Ala Thr Thr Gln Glu Lys Pro Lys Pro Lys Pro Lys
                50                      55                      60
Pro Lys Pro Ile Thr Pro Gln Ser Thr Tyr Gly Lys Tyr Tyr Ile Ser
  65                      70                      75                      80
Gln Ser Thr Ile Leu Lys Asn Ala Thr Glu Leu Phe Ala Glu Asp Asn
                85                      90                      95
Ile Thr Asn Leu Thr Phe Tyr Ser Gln Asn Pro Val Tyr Val Thr Ala
                100                      105                      110
Tyr Asn Gln Glu Ser Ala Glu Glu Ala Gly Tyr Gly Asn Asn Ser Leu
                115                      120                      125
Ile Met Ile Gln Asn Phe Leu Pro Tyr Asn Leu Asn Asn Ile Glu Leu
                130                      135                      140
Ser Tyr Thr Asp Asp Gln Gly Asn Val Val Ser Leu Gly Val Ile Glu
  145                      150                      155                      160
Thr Ile Pro Lys Gln Ser Gln Ile Ile Leu Pro Ala Ser Leu Phe Asn
                165                      170                      175
Asp Pro Gln Leu Asn Ala Asp Gly Ser Asn Asn Ser Lys Pro Thr Pro
                180                      185                      190

```

724

His Asp Phe Leu Met Pro Ala Arg Arg Ile Cys Leu Thr Ser Ser Ala
 195 200 205
 Arg Leu Gln Pro Ile Phe Lys
 210 215

(2) INFORMATION FOR SEQ ID NO:821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

Met Leu Ser Ser Asn Asp Leu Phe Met Val Val Leu Gly Ala Ile Leu
 1 5 10 15
 Leu Val Leu Val Cys Leu Val Gly Tyr Leu Tyr Leu Lys Glu Lys Glu
 20 25 30
 Phe Tyr His Lys Met Arg Arg Leu Glu Lys Thr Leu Asp Glu Ser Tyr
 35 40 45
 Gln Glu Asn Tyr Leu Tyr Ser Lys Arg Leu Arg Glu Leu Glu Gly Arg
 50 55 60
 Leu Glu Gly Leu Ser Leu Glu Lys Ser Ala Lys Glu Asp Ser Ser Leu
 65 70 75 80
 Lys Thr Thr Leu Ser His Leu Tyr Asn Gln Leu Gln Glu Ile Gln Lys
 85 90 95
 Ser Met Asp Lys Glu Arg Asp Tyr Leu Glu Glu Lys Ile Ile Thr Leu
 100 105 110
 Glu Asn Lys Phe Lys Asp Met Gly His Tyr Ala Ala Ser Asp Glu Val
 115 120 125
 Asn Glu Lys Gln Val Leu Lys Met Tyr Gln Glu Gly Tyr Ser Val Asp
 130 135 140
 Ser Ile Ser Lys Glu Phe Lys Val Ser Lys Gly Glu Val Glu Phe Ile
 145 150 155 160
 Leu Asn Met Ala Gly Leu Lys Trp
 165

(2) INFORMATION FOR SEQ ID NO:822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

725

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

```

Val Gly Phe Glu Tyr Ser Ile Ser His Ala Val Glu His Asn Asn Pro
1      5      10      15
Phe Leu Asp Gln Glu Arg Ile Gln Ala Ile Ser Asn Ala Arg Gly Glu
20     25     30
Val Cys Gly Leu Asp Arg Val Lys Asn Glu Ile Thr Asp Met Pro Asn
35     40     45
Thr Phe Asn Tyr Ile Asn Asn Ala Leu Lys Asn Asn Ala Lys Leu Thr
50     55     60
Pro Thr Glu Lys Gln Ala Glu Thr Tyr Tyr Leu Gln Ser Thr Leu Gln
65     70     75     80
Asn Ile Glu Lys Ile Val Met Leu Ser Gly Gly Val Ala Ser Asn Pro
85     90     95
Lys Leu Ala Gln Ala Leu Glu Lys Met Gln Glu Pro Ile Thr Asn Pro
100    105    110
Leu Glu Leu Val Glu Asn Leu Lys Asn Leu Glu Leu Gln Phe Ser Gln
115    120    125
Ser Gln Asn Ser Met Leu Ser Ser Leu Ser Ser Gln Ile Ala Gln Ile
130    135    140
Ser Asn Ser Leu Asn Ala Leu Asp Pro Ser Ser Tyr Ser Lys Asn Val
145    150    155    160
Ser Ser Met Tyr Gly Val Gly Leu Ser Val Gly Tyr Lys His Phe Phe
165    170    175
Thr Lys Lys Lys Asn Gln Gly Phe Arg Tyr Tyr Leu Phe Tyr Asp Tyr
180    185    190
Gly Tyr Thr Asn Phe Gly Phe Val Gly Asn Gly Phe Asp Gly Leu Gly
195    200    205
Lys Met Asn Asn His Leu Tyr Gly Leu Gly Ile Asp Tyr Leu Phe Asn
210    215    220
Phe Ile Asp Asn Ala Gln Lys His Ser Ser Val Gly Phe Tyr Val Gly
225    230    235    240
Phe Ala Leu Ala Gly Ser Ser Trp Val Gly Ser Gly Leu Gly Met Trp
245    250    255
Val Ser Gln Met Asp Phe Ile Asn Asn Tyr Leu Thr Asp Tyr Arg Ala
260    265    270
Lys Met His Thr Ser Phe Phe Gln Ile Pro Leu Asn Phe Gly Val Arg
275    280    285
Val Asn Val Asp Arg His Asn Gly Phe Glu Met Gly Leu Lys Ile Pro
290    295    300
Leu Ala Val Asn Ser Phe Tyr Glu Thr His Gly Lys Gly Leu Asn Ala
305    310    315    320
Ser Leu Phe Phe Lys Arg Leu Val Met Phe Asn Val Ser Tyr Val Tyr
325    330    335
Ser Phe

```

(2) INFORMATION FOR SEQ ID NO:823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

```

Met Met Phe Glu Leu Thr Lys Lys Thr Lys Phe Asp Gly Glu Met Ile
1           5           10           15
Gly Tyr Thr Glu Glu Leu Leu Thr Phe Leu Val Arg Asp Phe Phe Asn
          20           25           30
Gly Ile Phe Lys Ser Lys Val Ile Pro Lys Met Pro Ile Phe Cys Gly
          35           40           45
Asp Val Lys Cys Glu Asp Phe Asn Ala Leu Arg Ser Leu Val Tyr Leu
          50           55           60
Ser Val Leu Glu Leu Glu Thr Ile Asn Pro Asn Lys Ile Pro Phe
65           70           75           80

```

(2) INFORMATION FOR SEQ ID NO:824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

```

Val Gln Leu Leu Lys Asp Asn Lys Glu Val Val Val Leu Asp Thr Asp
1           5           10           15
Ser Gln Lys Ser Met Glu Thr Phe Ala Thr Ile Arg Ala Glu Lys Glu
          20           25           30
Arg Pro Thr Phe Ser Leu Phe Asn Arg Ser Ser Gly Phe Ser Asp Thr
          35           40           45
Leu Lys Gln Met Val Ser Lys Tyr Glu Asn Ile Leu Ile Asp Thr Lys

```

727

50		55		60											
Gly	Glu	Tyr	Ser	Lys	Glu	Thr	Gln	Lys	Ala	Met	Leu	Leu	Ser	Asn	Ile
65				70					75					80	
Val	Leu	Val	Pro	Thr	Pro	Ser	Gln	Leu	Asp	Thr	Glu	Val	Leu	Ala	
			85					90					95		
Asn	Met	Leu	Glu	Arg	Ile	Glu	Gln	Leu	Gln	Glu	Leu	Asn	Glu	Asn	Leu
		100					105					110			
Arg	Ala	Leu	Ile	Val	Ile	Asn	Arg	Met	Pro	Thr	Ile	Pro	Thr	Leu	Lys
	115					120					125				
Glu	Arg	Gln	Ala	Leu	Ile	Glu	Phe	Ile	Lys	Glu	Asn	Asn	Pro	Ser	Asp
	130					135					140				
Arg	Ile	Thr	Leu	Leu	Glu	Ser	Ser	Leu	Ser	Glu	Arg	Ile	Val	Tyr	Lys
145				150					155					160	
Arg	Ser	Val	Ser	Glu	Gly	Leu	Gly	Val	Ile	Glu	Tyr	Ser	Asp	Lys	Lys
			165					170					175		
Ala	Ile	Asn	Glu	Trp	Val	Asn	Phe	Tyr	Asn	Glu	Leu	Lys	Ser	His	Leu
		180					185						190		
Glu	Lys	Glu	Lys	Ile	His	Thr	Phe								
	195					200									

(2) INFORMATION FOR SEQ ID NO:825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

Met	Arg	Ser	Asp	Val	Glu	Val	Leu	Ser	Pro	Leu	His	Lys	Ile	Asp	Glu
1				5				10					15		
Lys	Tyr	Leu	Phe	His	Leu	Lys	Ile	Ala	Gly	Glu	Leu	Ala	Ser	Met	Gly
		20					25					30			
Lys	Ile	Leu	Ser	Val	Tyr	Leu	Ala	His	Lys	His	Ser	Ala	Tyr	Phe	Ile
	35					40					45				
Leu	Asn	Ala	Leu	Ser	Tyr	Gly	Phe	Ser	His	Gln	Asp	Arg	Ala	Ile	Ile
	50				55					60					
Cys	Leu	Leu	Gly	Ala	Ile										
65				70											

(2) INFORMATION FOR SEQ ID NO:826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

728

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

```

Met Ser Ala Met Met Pro Ser Leu Leu Thr Leu Gln Trp Leu Ser Phe
1           5           10           15
Ile Leu Ser Leu Ala Glu Asn Leu Cys Leu Thr Asp Ser His His Leu
20           25           30
Lys Tyr Thr Leu Glu Lys Asn Lys Leu Val Ile His Ser Asn Asp Ala
35           40           45
Leu Tyr Leu Ala Lys Glu Met Leu Pro Lys Leu Ile Lys Pro Ile Pro
50           55           60
Leu Thr Ile Glu Phe Ala
65           70

```

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 478 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

```

Leu Lys Lys Ile Ala Leu Ile Leu Asp Gly Ile Val Ala Lys Asn Phe
1           5           10           15
Leu Asp Leu Val Leu Arg His Tyr Ser Asn His Asn Phe Tyr Ile Val
20           25           30
Val Val Lys Asp Glu Ser Leu Ile Pro Lys Asn Tyr Pro Ser Thr Phe
35           40           45
Ala Phe His Cys Phe Asp Ala Thr Ser Ser Phe Arg Leu Leu Gln Val
50           55           60
Leu Asn Asp Glu Val Ser Asp Ala Phe Leu Ile Ile Gln Asp Phe Lys
65           70           75           80
Glu Gln Arg Ile Ile His Lys Ile Ile Gln Thr His Phe Lys Arg Met
85           90           95

```

729

```

Arg Val Val Leu Ser Val Lys Arg Asp Ser Glu Lys Thr Leu Glu Asn
      100      105      110
Asn Glu Glu Asn Lys Asp Glu Lys Leu Ile Leu Ile Asp Glu Phe Glu
      115      120      125
Val Leu Ala Asn Lys Phe Ile Ser Arg Leu Pro Asn Ile Pro Ser Thr
      130      135      140
Pro Arg Glu Phe Gly Leu Gly Lys Gly Glu Ile Met Glu Ile Asp Val
      145      150      155      160
Pro Phe Gly Ser Ile Phe Ala Tyr Arg His Ile Gly Ser Ile Arg Gln
      165      170      175
Lys Glu Tyr Arg Ile Val Gly Leu Tyr Arg Asn Asp Val Leu Leu Leu
      180      185      190
Ser Thr Lys Ser Leu Val Ile Gln Pro Arg Asp Ile Leu Leu Val Ala
      195      200      205
Gly Asn Pro Glu Ile Leu Asn Ala Val Tyr His Gln Val Lys Ser Asn
      210      215      220
Val Gly Gln Phe Pro Ala Pro Phe Gly Lys Ser Ile Tyr Leu Tyr Ile
      225      230      235      240
Asp Met Arg Leu Gln Ser Arg Lys Ala Met Met Arg Asp Val Tyr Gln
      245      250      255
Ala Leu Phe Leu His Lys Arg Leu Lys Ser Tyr Lys Leu Tyr Ile Gln
      260      265      270
Val Leu His Pro Thr Ser Pro Lys Phe Tyr His Lys Phe Leu Ser Leu
      275      280      285
Glu Thr Glu Ser Ile Glu Val Asn Phe Asp Phe Tyr Gly Lys Ser Phe
      290      295      300
Ile Gln Lys Leu His Glu Asp His Gln Lys Lys Met Gly Leu Ile Val
      305      310      315      320
Val Gly Arg Glu Leu Phe Phe Leu Lys Lys His Arg Arg Ala Leu His
      325      330      335
Lys Thr Ala Thr Pro Val Tyr Lys Thr Asn Thr Ser Gly Leu Ser Lys
      340      345      350
Thr Thr Gln Ser Ile Val Val Leu Asn Glu Ser Leu Ser Ile Asn Glu
      355      360      365
Asp Met Ser Ser Val Ile Phe Asp Val Ser Met Gln Met Asp Leu Gly
      370      375      380
Leu Leu Leu Tyr Asp Phe Asp Pro Asn Lys His Tyr Lys Asn Glu Ile
      385      390      395      400
Val Asn His Tyr Glu Asn Leu Ala Asn Thr Phe Asn Arg Lys Ile Glu
      405      410      415
Ile Phe Gln Thr Asp Ile Lys Asn Pro Ile Met Tyr Leu Asn Ser Leu
      420      425      430
Arg Asn Pro Ile Leu His Phe Met Pro Phe Glu Glu Cys Ile Thr Gln
      435      440      445
Thr Arg Tyr Leu Trp Phe Leu Ser Thr Lys Val Glu Lys Leu Ala Phe
      450      455      460
Leu Asn Asp Asp His Pro Gln Ile Phe Ile Pro Val Ala Glu
      465      470      475

```

(2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

```

Met Lys Lys Val Tyr Phe Lys Thr Phe Gly Cys Arg Thr Asn Leu Phe
 1          5          10          15
Asp Thr Gln Val Met Gly Glu Asn Leu Lys Asp Phe Ser Ala Thr Leu
          20          25          30
Glu Glu Gln Glu Ala Asp Ile Ile Ile Ile Asn Ser Cys Thr Val Thr
          35          40          45
Asn Gly Thr Asp Ser Ala Val Arg Ser Tyr Ala Arg Lys Met Ala Arg
 50          55          60
Leu Asp Lys Glu Val Leu Phe Thr Gly Cys Gly Val Lys Thr Gln Gly
65          70          75          80
Lys Glu Leu Phe Glu Lys Gly Leu Leu Lys Gly Val Phe Gly His Asp
          85          90          95
Asn Lys Glu Lys Ile Asn Ala Leu Leu Gln Glu Lys Lys Arg Phe Phe
          100          105          110
Ile Asp Asp Asn Leu Glu Asn Lys His Leu Asp Thr Thr Met Val Ser
          115          120          125
Glu Phe Val Gly Lys Thr Arg Ala Phe Ile Lys Ile Gln Glu Gly Cys
          130          135          140
Asp Phe Asp Cys Asn Tyr Cys Ile Ile Pro Ser Val Arg Gly Arg Ala
145          150          155          160
Arg Ser Phe Glu Glu Arg Lys Ile Leu Glu Gln Val Gly Leu Leu Cys
          165          170          175
Ser Lys Gly Val Gln Glu Val Val Leu Thr Gly Thr Asn Val Gly Ser
          180          185          190
Tyr Gly Lys Asp Arg Gly Ser Asn Ile Ala Arg Leu Ile Lys Lys Leu
          195          200          205
Ser Gln Ile Thr Gly Leu Lys Arg Ile Arg Ile Gly Ser Leu Glu Pro
          210          215          220
Asn Gln Ile Asn Asp Glu Phe Leu Glu Leu Leu Glu Glu Asp Phe Leu
225          230          235          240
Glu Lys His Leu His Ile Ala Leu Gln His Ser His Asp Phe Met Leu
          245          250          255
Glu Arg Met Asn Arg Arg Asn Arg Thr Lys Ser Asp Arg Glu Leu Leu
          260          265          270
Glu Ile Ile Ala Ser Lys Asn Phe Ala Ile Gly Thr Asp Phe Ile Val
          275          280          285
Gly His Pro Gly Glu Ser Glu Ser Val Phe Glu Lys Ala Phe Lys Asn
          290          295          300
Leu Glu Ser Leu Pro Leu Thr His Ile His Pro Phe Ile Tyr Ser Lys
305          310          315          320
Arg Lys Asp Thr Pro Ser Ser Leu Met Arg Asp Ser Val Ser Leu Glu
          325          330          335
Asp Ser Lys Lys Arg Leu Asn Ala Ile Lys Asp Leu Ile Phe His Lys
          340          345          350
Asn Lys Ala Phe Arg Gln Leu Gln Leu Lys Leu Asn Thr Pro Leu Lys

```


731

```

          355              360              365
Ala Leu Val Glu Ala Gln Lys Asp Gly Glu Phe Lys Ala Leu Asp Gln
  370              375              380
Phe Phe Asn Pro Ile Lys Ile Lys Ser Asp Lys Pro Leu Arg Ala Ser
385              390              395              400
Phe Leu Glu Ile Lys Glu Tyr Glu Ile Lys Glu Arg Glu Asn His Ala
          405              410              415
Val Phe

```

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

```

Leu Lys Ile Ala Tyr Arg Leu Leu Gly Leu Met Ser Phe Ile Ala Leu
1              5              10              15
Val Leu Ala Ile Val Leu Ile Ser Ile Leu Pro Leu Gln Lys Thr Glu
  20              25              30
His His Phe Val Asp Phe Leu Asn Gln Asp Lys His Tyr Ala Ile Ile
  35              40              45
Gln Arg Ala Asp Lys Ser Ile Ser Ser Asn Glu Ala Leu Ala Arg Ser
  50              55              60
Leu Ile Gly Ala Tyr Val Leu Asn Arg Glu Ser Ile Asn Arg Ile Asp
65              70              75              80
Asp Lys Ser Arg Tyr Glu Leu Val Arg Leu Gln Ser Ser Ser Lys Val
  85              90              95
Trp Gln Arg Phe Glu Asp Leu Ile Lys Ala Gln Asn Ser Ile Tyr Val
  100             105             110
Gln Ser His Leu Glu Arg Glu Val His Ile Val Asn Ile Ala Ile Tyr
  115             120             125
Gln Gln Asp Asn Asn Pro Ile Ala Ser Val Ser Ile Ala Ala Lys Leu
  130             135             140
Leu Asn Glu Asn Lys Leu Val Tyr Glu Lys Arg Tyr Lys Ile Val Leu
145             150             155             160
Ser Tyr Leu Phe Asp Thr Pro Asp Phe Asp Tyr Ala Ser Met Pro
          165              170              175

```

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids

732

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

```

Leu Leu Leu Val Ser Arg Phe Leu Asn Ala Ile Asp Pro Phe Asn Leu
1           5           10           15
Gly Val Leu Leu Ser Arg Phe Gln Ile Lys Asn Gly Cys Ile Tyr Gly
20           25           30
Val Cys Ser Tyr Lys Val Ser Lys Phe Thr Pro Gly Tyr Glu Glu Ser
35           40           45
Lys Ala Arg Val Leu Asn Ala Leu Asn Ile Leu Ser Lys His Gln Ile
50           55           60
Trp Gln Ser Asn Gln Glu Ser Val Thr Lys Val Lys Gly Thr Phe Val
65           70           75           80
Phe Ile Leu Glu Asn Asp Leu His Leu Asp Glu Asn Ser Phe Tyr Lys
85           90           95
Lys Leu Leu Asn Leu Ile Ile Asp Asn Asp Phe Phe Asn Arg Ser His
100          105          110
Leu Val Thr Pro Ser Asn Gly Thr Asn Ser His Pro Glu Leu His Arg
115          120          125
Ser Ile Thr Pro Arg Glu Ala Ala Arg Ile Gln Ser Phe Ser Asp Asp
130          135          140
Tyr Ile Phe Tyr Gly Asn Lys Thr Ser Val Cys Lys Gln Ile Gly Asn
145          150          155          160
Ala Val Pro Pro Leu Leu Ala Leu Ala Leu Gly Lys Ala Ile Leu Lys
165          170          175
Ser Ala Arg Asn Asp Thr Asn Pro Ser Arg
180          185

```

(2) INFORMATION FOR SEQ ID NO:831:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

```

Met Gly Leu Lys Asn Lys Ile Lys Gly Phe Val Lys Glu Arg Met Pro
1           5           10           15
Phe Val Met Arg Cys Val Arg Gly Leu Lys Gly Ala Lys Asp Thr His
20           25           30
Glu Asn Ala His Asp Arg Asp Ala Tyr Cys Gly Ile Asn Arg Glu Ile
35           40           45
Lys Glu Met Leu Glu Ala Lys Lys Leu His Phe Leu Gln Glu Lys Ala
50           55           60
Leu Phe Asn His Asp His Gln Glu Ser Val Phe Leu Ala Ile Ala Ser
65           70           75           80
Leu Asn Asn Glu Ser Phe Ile Glu Tyr Asn Lys Ser Ile Tyr Lys Asn
85           90           95
Ser Ser Leu Asn Tyr Asn Tyr Gly Gly His Leu Glu Asp Arg Val Ile
100          105          110
His Pro Thr Leu Thr Leu Pro Asn Pro Thr His Ser Gly Tyr Phe Asp
115          120          125
Tyr Asp Lys Lys Ser Gln Asn Pro Lys Ser Pro Leu Asn Pro Trp Ala
130          135          140
Phe Ile Arg Val Lys Asn Glu Ile Val Thr Leu Glu Glu Ser Leu Phe
145          150          155          160
Ser Met Leu Pro Ala Val Gln Arg Gly Gly His Trp Phe
165          170

```

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

```

Leu Trp His Gln Leu Tyr His Tyr Cys Asn Tyr Thr Leu Ser Phe Ile
1           5           10           15
Pro Lys Asn Glu Trp Val Val Lys Ile Asp Cys Asp His Ile Tyr Asp
20           25           30
Ala Lys Lys Leu Tyr Lys Ser Phe Tyr Ile Pro Lys Asn Ile Lys Glu
35           40           45
Val Val Met Tyr Ser Arg Ile Asn Phe Val Val Arg Asp Phe Glu Val
50           55           60
Phe Val Arg Asn Asp Gly Asp Phe Gly Phe Leu Asp Ala Trp Gly Asp
65           70           75           80

```

734

```

His Trp Leu Leu Tyr Asn Asp Cys Glu Pro Phe Glu Ile Trp Arg Tyr
      85                      90                      95
Asn Asp Glu Ser Tyr Glu Val Leu Lys Leu Lys Asp Lys His His Ile
      100                    105                    110
Lys Asp Lys Glu Met Val Gln Trp His Phe Pro Leu Ala Lys Lys Arg
      115                    120                    125
Arg Asn Ala Ile Val Tyr Asp Asp Leu Ile Pro Leu Glu Glu Phe Lys
      130                    135                    140
Lys Arg His Ala Asp Leu Ile Gly Thr Arg Ile Glu Glu Ser Met Leu
145                      150                      155                      160
Asp Glu Lys Arg Ile Leu Glu Val Tyr Gln Lys Phe Arg Leu Pro
      165                      170                      175

```

(2) INFORMATION FOR SEQ ID NO:833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

```

Met Gln Lys Pro Gln Asn Lys Pro Ser Ser Ser Gln Gln Ser Pro Gln
1      5                      10                      15
Asn Phe Ser Tyr Pro Glu Ser Lys Leu Gly Ser Lys Asn Ser Lys Asn
      20                    25                    30
Ser Leu Leu Gln Pro Leu Val Thr Pro Ser Lys Val Ser Pro Thr Asn
      35                    40                    45
Glu Val Lys Thr Pro Thr Asn Asp Ala Asn Pro Pro Leu Lys His Ser
      50                    55                    60
Ser Gln Asp Gln Glu Asn Asn Leu Phe Val Ala Pro Pro Thr Glu Lys
      65                    70                    75                    80
Thr Leu Pro Asn Asn Thr Ser Ser Ala Asp Ala Ser Glu Asn Asn Glu
      85                    90                    95
Ser Asn Glu Asn Arg Asp Asn Val Glu Lys Gln Ala Ile Arg Asp Pro
      100                   105                   110
Asn Ile Lys Glu Phe Ala Cys Gly Lys Trp Val Tyr Asp Asp Glu Asn
      115                   120                   125
Leu Gln Ala Tyr Arg Pro Ser Ile Leu Lys Arg Val Asp Lys Asp Lys
      130                   135                   140
Glu Ile Thr Thr Asp Ile Thr Pro Cys Asp Tyr Ser Thr Ala Glu Asn
      145                   150                   155                   160
Lys Ser Gly Lys Ile Ile Thr Pro Tyr Thr Lys Ile Ser Val His Lys
      165                   170                   175
Thr Glu Pro Leu Glu Asp Pro Gln Thr Phe Glu Ala Lys Asn Asn Phe
      180                   185                   190

```

- 735

```

Ala Ile Leu Gln Ala Arg Ser Ser Thr Glu Lys Cys Lys Arg Ala Arg
    195                200                205
Ala Arg Lys Asp Gly Thr Thr Arg Gln Cys Tyr Leu Ile Glu Glu Pro
    210                215                220
Leu Lys Gln Ala Trp Glu Ser Glu Tyr Glu Ile Thr Thr Gln Leu Val
    225                230                235                240
Lys Ala Ile Tyr Glu Arg Pro Lys Gln Asp Asp Gln Val Glu Pro Thr
                245                250                255
Phe Tyr Glu Thr Ser Glu Leu Ala Tyr Ser Ser Thr Arg Lys Ser Glu
                260                265                270
Ile Thr Arg Asn Glu Leu Asn Leu Asn Glu Lys Phe Met Glu Phe Val
                275                280                285
Glu Val Tyr Glu Gly His Tyr Leu Asn Asp Ile Ile Lys Glu Ser Ser
    290                295                300
Glu Tyr Lys Glu Trp Val Lys Asn His Val Arg Phe Lys Glu Gly Val
    305                310                315                320
Cys Met Ala Leu Glu Ile Glu Glu Gln Pro Arg Ala Lys Ser Thr Pro
                325                330                335
Leu Ser Ile Glu Asn Ser Arg Val Val Cys Val Lys Lys Gly Asn Tyr
                340                345                350
Leu Phe Asn Glu Val
    355

```

(2) INFORMATION FOR SEQ ID NO:834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

```

Ile Gln Tyr Pro Lys Ser Ser Phe Phe Gln Lys Arg Gly Arg Asn Gly
1      5      10      15
Asn His Ser Thr Ile Gln Pro Phe Asn His Ser Thr Ile Gln Pro Phe
    20      25      30
Asn His Ser Ile Ile Gln Ser Phe Asn His Ser Ile Ile Gln Ser Phe
    35      40      45
Asn His Ser Ile Ile Gln Ser Phe Asn His Ser Thr Ile Gln Ala Thr
    50      55      60
Leu Pro Tyr Phe Tyr Asn Tyr Leu Ser Phe Tyr Lys Asn Leu Phe Lys
    65      70      75      80
Asn Pro Leu Phe Phe Ile Ile Pro Pro Phe Ile Asn Pro Phe Ile Asn
    85      90      95
Pro Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn
    100      105      110

```

736

Pro Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn
 115 120 125
 Pro Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile
 130 135 140

(2) INFORMATION FOR SEQ ID NO:835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

Leu Lys Val Asn Phe Phe Ala Thr Cys Leu Gly Ala Ala Ile Tyr Ser
 1 5 10 15
 Asn Ala Ser Leu Asn Ala Ile Lys Leu Arg Lys Glu Asn Leu Glu
 20 25 30
 Val Val Phe Lys Lys Asp Gln Thr Cys Cys Gly Gln Pro Ser Tyr Asn
 35 40 45
 Ser Gly Tyr Tyr Glu Glu Thr Lys Lys Val Val Leu Tyr Asn Ile Lys
 50 55 60
 Leu Tyr Ser Asn Asn Asp Tyr Pro Ile Ile Leu Pro Ser Gly Ser Cys
 65 70 75 80
 Thr Gly Met Met Arg His Asp Tyr Leu Glu Leu Phe Glu Gly His Ala
 85 90 95
 Glu Phe Asn Met Val Lys Asp Phe Cys Ser Arg Val Tyr Glu Leu Ser
 100 105 110
 Glu Phe Leu Asp Lys Lys Leu Gln Val Lys Tyr Glu Asp Lys Gly Glu
 115 120 125
 Pro Leu Lys Ile Thr Trp His Ser Asn Cys His Ala Leu Arg Val Ala
 130 135 140
 Lys Val Ile Asp Ser Ala Lys Asn Leu Ile Arg Gln Leu Lys Asn Val
 145 150 155 160
 Glu Leu Ile Glu Leu Glu Lys Glu Glu Glu Cys Cys Gly Phe Gly Gly
 165 170 175
 Thr Phe Ser Val Lys Glu Pro Glu Ile Ser Ala Val Met Val Lys Glu
 180 185 190
 Lys Ile Lys Asp Ile Glu Ser Arg His Val Asp Val Ile Val Ser Ala
 195 200 205
 Asp Ala Gly Cys Leu Met Asn Ile Ser Thr Ala Met Gln Lys Met Gly
 210 215 220
 Ser Leu Thr Lys Pro Met His Phe Tyr Asp Phe Leu Ala Ser Arg Leu
 225 230 235 240
 Gly Leu

(2) INFORMATION FOR SEQ ID NO:836:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

```

Met Ile Phe Gly Asp Phe Lys Tyr Gln Lys Ser Val Lys Lys Leu Thr
1           5           10           15
Ala Thr Asn Leu Asn Glu Leu Lys Asn Ala Leu Asp Phe Ile Ser Gln
          20           25           30
Asn Arg Gly Lys Gly Tyr Phe Val Gly Tyr Leu Leu Tyr Glu Ala Arg
          35           40           45
Leu Ala Phe Leu Asp Glu Asn Phe Gln Ser Gln Thr Pro Phe Leu Tyr
          50           55           60
Phe Glu Gln Phe Leu Glu Arg Lys Lys Tyr Pro Leu Glu Pro Leu Lys
65           70           75           80
Glu His Ala Phe Tyr Pro Lys Ile His Ser Ser Leu Asp Gln Lys Thr
          85           90           95
Tyr Phe Lys Gln Phe Lys Ala Val Lys Glu His Leu Lys Asn Gly Asp
          100          105          110
Thr Tyr Gln Val Asn Leu Thr Met Asp Leu Leu Leu Asn Thr Lys Ala
          115          120          125
Lys Pro Lys Arg Val Phe Lys Glu Val Ile His Asn Gln Asn Thr Pro
          130          135          140
Phe Lys Ala Phe Ile Glu Asn Glu Phe Gly Ser Val Leu Ser Phe Ser
145           150           155           160
Pro Glu Leu Phe Phe Glu Leu Glu Phe Leu Asp Thr Ala Ile Lys Ile
          165          170          175
Ile Thr Lys Pro Met Lys Gly Thr Ile Ala Arg Ser Asn Asn Pro Leu
          180          185          190
Ile Asp Glu Lys Asn Arg Leu Phe Leu Gln Asn Asp Asp Lys Asn Arg
          195          200          205
Ser Glu Asn Val Met Ile Val Asp Leu Leu Arg Asn Asp Leu Ser Arg
          210          215          220
Leu Ala Leu Lys Asn Ser Val Lys Val Asn Gln Leu Phe Glu Ile Ile
225           230           235           240
Ser Leu Pro Ser Val Tyr Gln Met Ile Ser Glu Ile Glu Ala Gln Leu
          245          250          255
Pro Leu Lys Thr Ser Leu Phe Glu Ile Phe Lys Ala Leu Phe Pro Cys
          260          265          270
Gly Ser Val Thr Gly Cys Pro Lys Ile Lys Thr Met Gln Ile Ile Glu
          275          280          285

```

738

```

Ser Leu Glu Lys Arg Pro Arg Gly Val Tyr Cys Gly Ala Ile Gly Met
 290                               295                 300
Val Gly Gly Lys Lys Ala Leu Phe Ser Val Pro Ile Arg Thr Leu Glu
305                               310                 315                 320
Lys Arg Ala His Glu Asp Phe Leu His Leu Gly Val Gly Ser Gly Val
                               325                 330                 335
Thr Tyr Lys Ser Lys Ala Ser Lys Glu Tyr Glu Glu Ser Phe Leu Lys
                               340                 345                 350
Ser Phe Phe Val Met Pro Lys Ile Glu Phe Glu Ile Val Glu Thr Met
                               355                 360                 365
Arg Val Ile Lys Arg Asp Gln Lys Leu Glu Ile Asn Asn Lys Asn Ala
370                               375                 380
His Lys Glu Arg Leu Met His Ser Ala Gln Tyr Phe Asn Phe Lys Tyr
385                               390                 395                 400
Arg

```

(2) INFORMATION FOR SEQ ID NO:837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

```

Met Lys Ile Ser Val Ser Lys Asn Asp Leu Glu Asn Thr Leu Arg Tyr
 1                               5                 10                 15
Leu Gln Ala Phe Leu Asp Lys Lys Asp Ala Ser Ser Ile Ala Ser His
                               20                 25                 30
Ile His Leu Glu Val Ile Lys Glu Lys Leu Phe Leu Lys Ala Ser Asp
35                               40                 45
Ser Asp Ile Gly Leu Lys Ser Tyr Ile Ser Thr Gln Ser Thr Asp Lys
50                               55                 60
Glu Gly Val Gly Thr Ile Asn Gly Lys Lys Phe Leu Asp Ile Ile Ser
65                               70                 75                 80
Cys Leu Lys Asp Ser Asn Ile Val Leu Glu Thr Lys Asp Asp Ser Leu
                               85                 90                 95
Val Ile Lys Gln Asn Lys Ser Ser Phe Lys Leu Pro Met Phe Asp Ala
100                               105                 110
Asp Glu Phe Pro Glu Phe Pro Val Ile Asp Pro Lys Val Ser Leu Glu
115                               120                 125
Ile Asn Ala Pro Phe Leu Val Asp Ala Phe Lys Lys Ile Ala Pro Val
130                               135                 140
Ile Glu Gln Thr Ser His Lys Arg Glu Leu Ala Gly Val Leu Met Gln
145                               150                 155                 160

```


739

```

Phe Asn Gln Lys His Gln Thr Leu Ser Val Val Gly Thr Asp Thr Lys
      165                      170                      175
Arg Leu Ser Tyr Thr Gln Leu Glu Lys Ile Ser Ile His Ser Thr Glu
      180                      185                      190
Glu Asp Ile Ser Cys Ile Leu Pro Lys Arg Ala Leu Leu Glu Ile Leu
      195                      200                      205
Lys Leu Phe Tyr Glu Asn Phe Ser Phe Lys Ser Asp Gly Met Leu Ala
      210                      215                      220
Val Val Glu Asn Glu Thr His Ala Phe Phe Thr Lys Leu Ile Asp Gly
      225                      230                      235                      240
Asn Tyr Pro Asp Tyr Gln Lys Ile Leu Pro Lys Glu Tyr Thr Ser Ser
      245                      250                      255
Phe Thr Leu Gly Lys Glu Glu Phe
      260

```

(2) INFORMATION FOR SEQ ID NO:838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

```

Leu Asn Asn Leu Glu Pro Leu Gly Ala Glu Val Phe Val Gly Leu Asp
1      5      10      15
Gly Ile Asp Ala Met Ile Glu Glu Cys Val Ser Asn Leu Val Ile Asn
      20      25      30
Ala Ile Val Gly Val Ala Gly Leu Lys Ala Ser Phe Lys Ser Leu Gln
      35      40      45
Arg Asn Lys Lys Leu Ala Leu Ala Asn Lys Glu Ser Leu Val Ser Ala
      50      55      60
Gly His Leu Leu Asp Ile Ser Gln Ile Thr Pro Val Asp Ser Glu His
      65      70      75      80
Phe Gly Leu Trp Ala Leu Leu Gln Asn Lys Thr Leu Lys Pro Lys Ser
      85      90      95
Leu Ile Ile Ser Ala Ser Gly Gly Ala Phe Arg Asp Thr Pro Leu Asp
      100     105     110
Leu Ile Ala Ile Gln Asn Ala Gln Asn Ala Leu Lys His Pro Asn Trp
      115     120     125
Ser Met Gly Asp Lys Ile Thr Ile Asp Ser Ala Ser Met Val Asn Lys
      130     135     140
Leu Phe Glu Ile Leu Glu Thr Tyr Trp Leu Phe Gly Ala Ser Leu Lys
      145     150     155     160
Ile Asp Ala Leu Ile Glu Arg Ser Ser Ile Val His Ala Leu Val Glu
      165     170     175

```

```

Phe Glu Asp Asn Ser Val Ile Ala His Leu Ala Ser Ala Asp Met Gln
      180                      185                      190
Leu Pro Ile Ser Tyr Ala Ile Asn Pro Lys Leu Ala Ser Leu Ser Ala
      195                      200                      205
Ser Ile Lys Pro Leu Asp Leu Tyr Ala Leu Ser Ala Ile Lys Phe Glu
      210                      215                      220
Pro Ile Ser Val Glu Arg Tyr Thr Leu Trp Arg Tyr Lys Asp Leu Leu
      225                      230                      235                      240
Leu Glu Asn Pro Lys Leu Gly Val Val Leu Asn Ala Ser Asn Glu Val
      245                      250                      255
Ala Met Lys Lys Phe Leu Asn Gln Glu Ile Ala Phe Gly Gly Phe Ile
      260                      265                      270
Gln Ile Ile Ser Gln Ala Leu Glu Leu Tyr Ala Lys Lys Ser Phe Lys
      275                      280                      285
Leu Ser Ser Leu Asp Glu Val Leu Ala Leu Asp Lys Glu Val Arg Glu
      290                      295                      300
Arg Phe Gly Ser Val Ala Arg Val
      305                      310

```

(2) INFORMATION FOR SEQ ID NO:839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

```

Met Leu Glu Asn Val Lys Lys Ser Leu Phe Arg Val Leu Cys Leu Gly
1      5      10      15
Ala Leu Cys Leu Gly Gly Leu Met Ala Glu Gln Asp Pro Lys Glu Leu
      20      25      30
Val Gly Leu Gly Ala Lys Ser Tyr Lys Glu Gln Asp Phe Thr Gln Ala
      35      40      45
Lys Lys Tyr Phe Glu Lys Ala Cys Asp Leu Lys Glu Asn Ser Gly Cys
      50      55      60
Phe Asn Leu Gly Val Leu Tyr Tyr Gln Gly His Gly Val Glu Lys Asn
      65      70      75      80
Leu Lys Lys Ala Ala Ser Phe Tyr Ser Lys Ala Cys Asp Leu Asn Tyr
      85      90      95
Ser Asn Gly Cys His Leu Leu Gly Asn Leu Tyr Tyr Ser Gly Gln Gly
      100     105     110
Val Ser Gln Asn Thr Asn Lys Ala Leu Gln Tyr Tyr Ser Lys Ala Cys
      115     120     125
Asp Leu Lys Tyr Ala Glu Gly Cys Ala Ser Leu Gly Gly Ile Tyr His
      130     135     140

```

741

```

Asp Gly Lys Val Val Thr Arg Asp Phe Lys Lys Ala Val Glu Tyr Phe
145                      150                      155                      160
Thr Lys Ala Cys Asp Leu Asn Asp Gly Asp Gly Cys Thr Ile Leu Gly
                      165                      170                      175
Ser Leu Tyr Asp Ala Gly Arg Gly Thr Pro Lys Asp Leu Lys Lys Ala
                      180                      185                      190
Leu Ala Ser Tyr Asp Lys Ala Cys Asp Leu Lys Asp Ser Pro Gly Cys
                      195                      200                      205
Phe Asn Ala Gly Asn Met Tyr His His Gly Glu Gly Ala Ala Lys Asn
210                      215                      220
Phe Lys Glu Ala Leu Ala Arg Tyr Ser Lys Ala Cys Glu Leu Glu Asn
225                      230                      235                      240
Gly Gly Gly Cys Phe Asn Leu Gly Ala Met Gln Tyr Asn Gly Glu Gly
                      245                      250                      255
Ala Thr Arg Asn Glu Lys Gln Ala Ile Glu Asn Phe Lys Lys Gly Cys
                      260                      265                      270
Lys Leu Gly Ala Lys Gly Ala Cys Asp Ile Leu Lys Gln Leu Lys Ile
275                      280                      285
Lys Val
290

```

(2) INFORMATION FOR SEQ ID NO:840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

```

Met Lys Ser Asn Lys Lys Ser Asn His Leu Arg Ala Ile Tyr Arg Ala
1      5      10      15
Leu Val Ile Ala Ile Gly Leu Ala Val Ile Ile Val Phe Asn Tyr Phe
20      25      30
Asn Arg Lys Asn Asn Asn Ala Arg Ser Ser Arg Arg Ala Cys Ser Cys
35      40      45
Phe Phe Ser Leu Thr Gly Val Asn Leu Glu Lys Ile Gly Ser Phe Asp
50      55      60
Thr Gly Ala Lys Leu Ile Val Leu Asn His Gln Ser Leu Leu Asp Ile
65      70      75      80
Ile Tyr Leu Glu Ala Tyr His Pro Ser Asn Ile Cys Trp Ile Ala Lys
85      90      95
Lys Glu Leu Gly Glu Ile Pro Phe Tyr Gly His Ala Leu Thr Asp Thr
100     105     110
Gly Met Ile Leu Ile Asp Arg Glu Asp Lys Lys Gly Ile Val Ser Leu
115     120     125

```

```

Leu Lys Ala Cys Lys Glu Lys Leu Asp Gln Asn Arg Pro Leu Val Ile
130          135          140
Phe Pro Glu Gly Thr Arg Gly Lys Gly Gly Glu Lys Phe Leu Pro Phe
145          150          155          160
Lys Gln Gly Ala Lys Ile Ile Ala Glu Lys Phe Gln Leu Lys Ile Gln
          165          170          175
Pro Met Val Leu Ile Asn Ser Ile Lys Ile Phe Asn Ser Lys Pro Leu
          180          185          190
Glu Ala Tyr Lys Ala Arg Thr Arg Leu Val Met Leu Glu Ser Tyr Thr
          195          200          205
Pro Asp Phe Ser Ser Pro Thr Trp Tyr Glu Glu Leu Gln Glu Arg Met
          210          215          220
Gln Lys Glu Tyr Leu Lys His Tyr His Glu Leu Asn Ala
225          230          235

```

(2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

```

Met Gly Phe Glu Lys Ser Ile Leu Asp Asn Leu Asn Gly Ala Gln Lys
1          5          10          15
Ile Ala Ala Cys His Ile Gln Gly Pro Leu Leu Ile Leu Ala Gly Ala
          20          25          30
Gly Ser Gly Lys Thr Lys Thr Leu Thr Ser Arg Leu Ala Tyr Leu Ile
          35          40          45
Gly Ala Cys Gly Val Pro Ser Glu Asn Thr Leu Thr Leu Thr Phe Thr
          50          55          60
Asn Lys Ala Ser Lys Glu Met Gln Glu Arg Ala Leu Lys Leu Leu Lys
65          70          75          80
Asn Gln Ala Leu Ile Pro Pro Leu Leu Cys Thr Phe His Arg Phe Gly
          85          90          95
Leu Leu Phe Leu Arg Gln His Met Asn Leu Leu Lys Arg Ala Cys Asp
          100          105          110
Phe Ser Val Leu Asp Ser Asp Glu Val Lys Thr Leu Cys Lys Gln Leu
          115          120          125
Lys Ile Ser Asn Phe Arg Ala Ser Ile Ser Gln Ile Lys Asn Gly Met
          130          135          140
Met Asp Leu Ser Val Gln Asp Ser Glu Cys Tyr Lys Ala Tyr Glu Leu
145          150          155          160
Tyr Gln Asn Ala Leu Lys Lys Asp Asn Leu Val Asp Phe Asp Asp Leu
          165          170          175

```

Leu Cys Leu Ser Leu Lys Ile Leu Gln Asp Asn Glu Lys Leu Ala Lys
 180 185 190
 Glu Thr Ser Glu Arg Tyr His Tyr Ile Met Val Asp Glu Tyr Gln Asp
 195 200 205
 Thr Asn Ala Leu Gln Leu Glu Phe Leu Lys Gln Leu Ser Phe Thr His
 210 215 220
 His Asn Leu Cys Val Val Gly Asp Asp Asp Gln Ser Ile Tyr Gly Phe
 225 230 235 240
 Arg Gly Ala Asp Ile Ser Asn Ile Leu Asn Phe Ser Lys His Phe Lys
 245 250 255
 Gly Ala Lys Ile Val Lys Leu Glu Thr Asn Tyr Arg Ser Ser Ala Glu
 260 265 270
 Ile Leu Ala Cys Ala Asn Ser Leu Ile Ser His Asn Gln His Arg His
 275 280 285
 Ile Lys Thr Leu Gln Ser Phe Lys Gly Ser His Lys Ser Val Ile Cys
 290 295 300
 Lys Glu Tyr Pro Thr Gln Lys Glu Glu Ser Leu Asp Val Ala Tyr Gln
 305 310 315 320
 Ile Lys Ala Leu Leu Lys Lys Gly Glu Asn Leu Glu Asn Ile Ala Ile
 325 330 335
 Leu Tyr Arg Leu Asn Gly Leu Ser Arg Ser Ile Glu Glu Ser Leu Asn
 340 345 350
 Ala Leu Asn Ile Pro Tyr Arg Leu Ile Gly Ala Val Ser Phe Tyr Glu
 355 360 365
 Arg Ala Glu Val Lys Asp Ala Leu Ala Leu Met His Val Val Ala Lys
 370 375 380
 Lys Asp Asp Arg Phe Phe Ile Lys Arg Val Leu Asn Lys Pro Pro Arg
 385 390 395 400
 Gly Leu Gly Lys Ile Thr Gln Glu Trp Ile Phe Ser Leu Leu Asp Glu
 405 410 415
 Glu Gly Leu Asn Leu Glu Glu Ala Leu Lys Ile Gly Ala Phe Lys Asp
 420 425 430
 Lys Leu Asn Pro Lys Asn Glu Tyr Ala Leu Lys Lys Phe Thr Ala Met
 435 440 445
 Ile Gly Arg Leu Arg Glu Ala Phe Glu Ile Ser Val Glu Lys Phe Cys
 450 455 460
 Glu Arg Phe Leu Glu Glu Thr Asn Leu Leu Lys Ser Tyr Glu Lys Glu
 465 470 475 480
 Asp Asn Tyr Glu Glu Arg Glu Gly Phe Val Lys Glu Leu Leu Ser Leu
 485 490 495
 Val Lys Glu His Phe Lys Thr Asn Pro Thr His Ser Leu Leu Asp Phe
 500 505 510
 Leu Asn Glu Ser Ala Leu Asp Val His Asn Thr Glu Asn Ala Gln Lys
 515 520 525
 Val Ser Cys Met Ser Val His Met Ser Lys Gly Leu Glu Phe Lys His
 530 535 540
 Val Phe Val Ile Gly Leu Glu Glu Gly Phe Phe Pro His Arg Gly Phe
 545 550 555 560
 Asn Gln Glu Ser Asp Leu Glu Glu Glu Arg Arg Leu Ala Tyr Val Ala
 565 570 575
 Ile Thr Arg Ala Lys Glu Glu Leu Gln Leu Ser Tyr Val Lys Glu Arg
 580 585 590
 Ser Tyr Phe Gly Arg Lys Ile Ser Cys Ser Pro Ser Val Phe Leu Glu
 595 600 605
 Glu Ala Gln Leu Leu Gln Gln Asp Lys Pro Pro Lys Gln Asn His Gln
 610 615 620
 Lys Asp Thr Pro Ile Lys Val Gly Asp Leu Ile Lys His Lys Ile Phe

744

```

625          630          635          640
Gly Thr Gly Arg Val Leu Gly Val Glu Lys Gly Leu Ser Gly Leu Cys
          645          650          655
Leu Lys Ile Asn Cys Gly Gly Asn Val Tyr Asp Lys Ile Ser Glu Lys
          660          665          670
Phe Val Glu Lys Val Asp Asn Glu Phe
          675          680

```

(2) INFORMATION FOR SEQ ID NO:842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

```

Met Lys Thr Ser Asn Thr Lys Thr Pro Lys Pro Val Leu Ile Ala Gly
1          5          10          15
Pro Cys Val Ile Glu Ser Leu Glu Asn Leu Arg Ser Ile Ala Ile Lys
          20          25          30
Leu Gln Pro Leu Ala Asn Asn Glu Arg Leu Asp Phe Tyr Phe Lys Ala
          35          40          45
Ser Phe Asp Lys Ala Asn Arg Thr Ser Leu Glu Ser Tyr Arg Gly Pro
          50          55          60
Gly Leu Glu Lys Gly Leu Glu Met Leu Gln Thr Ile Lys Asp Glu Phe
          65          70          75          80
Gly Tyr Lys Ile Leu Thr Asp Val His Glu Ser Tyr Gln Ala Ser Val
          85          90          95
Ala Ala Lys Val Ala Asp Ile Leu Gln Ile Pro Ala Phe Leu Cys Arg
          100          105          110
Gln Thr Asp Leu Ile Val Glu Val Ser Gln Thr Asn Ala Ile Val Asn
          115          120          125
Ile Lys Lys Gly Gln Phe Met Asn Pro Lys Asp Met Gln Tyr Ser Val
          130          135          140
Leu Lys Ala Leu Lys Thr Arg Asp Ser Ser Ile Gln Ser Pro Thr Tyr
          145          150          155          160
Glu Thr Ala Leu Lys Asn Gly Val Trp Leu Cys Glu Arg Gly Ser Ser
          165          170          175
Phe Gly Tyr Gly Asn Leu Val Val Asp Met Arg Ser Leu Lys Ile Met
          180          185          190
Arg Glu Phe Ala Pro Val Ile Phe Asp Ala Thr His Ser Val Gln Met
          195          200          205
Pro Gly Gly Ala Asn Gly Lys Ser Ser Gly Asp Ser Ser Phe Pro Pro
          210          215          220
Ile Leu Pro Arg Ala Ala Ala Val Gly Ile Asp Gly Leu Phe Ala

```

745

```

225          230          235          240
Glu Thr His Ile Asp Pro Lys Asn Ala Leu Ser Asp Gly Ala Asn Met
          245          250          255
Leu Lys Pro Asp Glu Leu Glu His Leu Val Thr Asp Met Leu Lys Ile
          260          265          270
Gln Asn Leu Phe
          275

```

(2) INFORMATION FOR SEQ ID NO:843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

```

Met Met Lys Phe Phe Leu Leu Lys Lys Phe Ser Glu Phe Leu Asn Thr
1          5          10          15
Gln Thr His Phe Asn Leu Lys Arg Leu Asn Ala Ser Ser Phe Leu Leu
          20          25          30
Glu Thr Phe Ser Lys Glu Lys His Ala Phe Val Val Asp Leu Ser Ala
          35          40          45
Pro Tyr Ile Gly Leu Ser Lys Lys Pro Pro Glu Ser Val Leu Lys Asn
          50          55          60
Thr Leu Ala Leu Asp Phe Cys Leu Asn Lys Phe Thr Lys Asn Ala Lys
          65          70          75          80
Ile Leu Gln Ala Asn Val Ile Asp Asn Asp Arg Ile Leu Glu Ile Lys
          85          90          95
Gly Ala Lys Asp Leu Ala Tyr Lys Ser Glu Thr Phe Ile Leu Arg Leu
          100          105          110
Glu Met Ile Pro Lys Lys Ala Asn Leu Met Ile Leu Asp Gln Glu Lys
          115          120          125
Cys Val Ile Glu Ala Phe Arg Phe Asn Asp Arg Val Ala Lys Asn Asp
          130          135          140
Ile Leu Gly Ala Leu Pro Pro Asn Ile Tyr Glu His Gln Glu Glu Asp
          145          150          155          160
Leu Asp Phe Lys Gly Leu Leu Asp Ile Leu Glu Lys Asp Phe Leu Ser
          165          170          175
Tyr Gln His Lys Glu Leu Glu His Lys Lys Asn Gln Ile Ile Lys Arg
          180          185          190
Leu Asn Ala Gln Lys Glu Arg Leu Lys Glu Lys Leu Glu Lys Leu Glu
          195          200          205
Asp Pro Lys Thr Leu Gln Leu Glu Ala Lys Glu Leu Gln Thr Gln Ala
          210          215          220
Ser Leu Leu Leu Thr Tyr Gln His Leu Ile Asn Arg Arg Glu Asn Arg

```

746

```

225          230          235          240
Val Ile Leu Lys Asp Phe Glu Asp Lys Glu Cys Met Ile Glu Ile Asp
          245          250          255
Lys Ser Met Pro Leu Asn Ala Phe Ile Asn Lys Lys Phe Thr Leu Ser
          260          265          270
Lys Lys Lys Lys Gln Lys Ser Gln Phe Leu Tyr Leu Glu Glu Glu Asn
          275          280          285
Leu Lys Glu Lys Ile Ala Phe Lys Glu Asn Gln Ile Asn Tyr Val Arg
          290          295          300
Asp Ala Ala Glu Glu Ser Val Leu Glu Met Phe Met Pro Val Lys Asn
305          310          315          320
Ser Lys Ile Lys Arg Pro Met Asn Gly Tyr Glu Val Leu Tyr Tyr Lys
          325          330          335
Asp Phe Lys Ile Gly Leu Gly Lys Asn Gln Lys Glu Asn Ile Lys Leu
          340          345          350
Leu Gln Asp Ala Arg Ala Asn Asp Leu Trp Met His Val Arg Asp Ile
          355          360          365
Pro Gly Ser His Leu Ile Val Phe Cys Gln Lys Asn Thr Pro Lys Asp
          370          375          380
Glu Val Ile Met Glu Leu Ala Lys Met Leu Ile Lys Met Gln Lys Asp
385          390          395          400
Ala Phe Asn Gly Tyr Glu Ile Asp Tyr Thr Gln Arg Lys Phe Val Lys
          405          410          415
Ile Ile Lys Gly Ala His Val Ile Tyr Ser Lys Tyr Arg Thr Ile Ser
          420          425          430
Leu Lys Asp Thr
          435

```

(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

```

Met Phe Lys Lys Ile Ile Phe Leu Cys Val Phe Leu Ile Gly Gly Phe
1          5          10          15
Val Ile Pro Pro Leu Glu Ala Met Pro Ile Leu Arg Asn Lys Thr Pro
          20          25          30
Lys Lys Asn Tyr Gln Glu Ala His Glu Lys Leu Tyr Arg Ser Ile Ile
          35          40          45
Asn Arg Gln Lys Leu Thr Arg Lys Lys Ser Gly Trp Tyr Phe Leu Gly
          50          55          60
Gly Val Gly Ala Val Glu Ala Ile Lys Asp Tyr Gln Gly Lys Glu Met

```


747

```

65          70          75          80
Lys Asp Trp Ile Ala Thr Leu Asn Leu Lys Thr Gly Val Gln Ser Phe
      85          90          95
Phe Lys Lys Tyr Ile Gly Ile Arg Gly Val Phe Ala Trp Asp Leu Gly
      100        105        110
Ser Gly Lys Val Asn Tyr Gln Ser Tyr Lys Asp Pro Thr Asn Ser Phe
      115        120        125
Phe Thr Met Leu Ala Val Gly Leu Asp Val Ile Met Glu Phe Pro Leu
      130        135        140
Gly Ser Tyr Lys His Tyr Leu Gly Ala Phe Gly Gly Ala Arg Gly Ala
      145        150        155        160
Leu Val Val Tyr Thr Asp Lys Gln Asn Phe Lys Phe Phe Lys His Ser
      165        170        175
Val Val Ser Gly Gly Leu Ala Ile Ser Gly Gly Val Met Leu Thr Leu
      180        185        190
Phe Leu Arg His Arg Ile Glu Leu Gly Phe Lys Ile Leu Pro Thr Ala
      195        200        205
Arg Leu Leu Ser Ser Ser Ser Arg Phe Glu Thr Ser Pro Leu Phe Tyr
      210        215        220
Ala Ala Tyr Ser Tyr Lys Phe
      225        230

```

(2) INFORMATION FOR SEQ ID NO:845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

```

Met Leu Lys Lys Ile Phe Tyr Gly Phe Ile Val Leu Phe Leu Ile Ile
1          5          10          15
Val Gly Leu Leu Ala Val Leu Val Ala Gln Val Trp Val Thr Thr Asp
      20          25          30
Lys Asp Ile Ala Lys Ile Lys Asp Tyr Arg Pro Ser Val Ala Ser Gln
      35          40          45
Ile Leu Asp Arg Lys Gly Arg Leu Ile Ala Asn Ile Tyr Asp Lys Glu
      50          55          60
Phe Arg Phe Tyr Ala Arg Phe Glu Glu Ile Pro Pro Arg Phe Val Glu
      65          70          75          80
Ser Leu Leu Ala Val Glu Asp Thr Leu Phe Phe Glu His Gly Gly Ile
      85          90          95
Asn Leu Asp Ala Val Met Arg Ala Met Ile Lys Asn Ala Lys Ser Gly
      100        105        110
Arg Tyr Thr Glu Gly Gly Ser Thr Leu Thr Gln Gln Leu Val Lys Asn

```

115	120	125
Met Val Leu Thr Arg Glu Lys Thr Leu Thr Arg Lys Leu Lys Glu Ala		
130	135	140
Ile Ile Ser Ile Arg Ile Glu Lys Val Leu Ser Lys Glu Glu Ile Leu		
145	150	155
Glu Arg Tyr Leu Asn Gln Thr Phe Phe Gly His Gly Tyr Tyr Gly Val		
165	170	175
Lys Thr Ala Ser Leu Gly Tyr Phe Lys Lys Pro Leu Asp Lys Leu Thr		
180	185	190
Leu Lys Glu Ile Thr Met Leu Val Ala Leu Pro Arg Ala Pro Ser Phe		
195	200	205
Tyr Asp Pro Thr Lys Asn Leu Glu Phe Ser Leu Ser Arg Ala Asn Asp		
210	215	220
Ile Leu Arg Arg Leu Tyr Ser Leu Gly Trp Ile Ser Ser Asn Glu Leu		
225	230	235
Lys Ser Ala Leu Asn Glu Val Pro Ile Val Tyr Asn Gln Thr Ser Thr		
245	250	255
Gln Asn Ile Ala Pro Tyr Val Val Asp Glu Val Leu Lys Gln Leu Asp		
260	265	270
Gln Leu Asp Gly Leu Lys Thr Gln Gly Tyr Thr Ile Lys Leu Thr Ile		
275	280	285
Asp Leu Asp Tyr Gln Arg Leu Ala Leu Glu Ser Leu Arg Phe Gly His		
290	295	300
Gln Lys Ile Leu Glu Lys Ile Ala Lys Glu Lys Pro Lys Thr Asn Ala		
305	310	315
Ser Asn Asp Lys Asp Glu Asp Asn Leu Asn Ala Ser Met Ile Val Thr		
325	330	335
Glu Thr Ser Thr Gly Lys Ile Leu Ala Leu Val Gly Gly Ile Asp Tyr		
340	345	350
Lys Lys Ser Ala Phe Asn Arg Ala Thr Gln Ala Lys Arg Gln Phe Gly		
355	360	365
Ser Ala Ile Lys Pro Phe Val Tyr Gln Ile Ala Phe Asp Asn Gly Tyr		
370	375	380
Ser Thr Thr Ser Lys Ile Pro Asp Thr Ala Arg Asn Phe Glu Asn Gly		
385	390	395
Asn Tyr Ser Lys Asn Ser Val Gln Asn His Ala Trp His Pro Ser Asn		
405	410	415
Tyr Thr Arg Lys Phe Leu Gly Leu Val Thr Leu Gln Glu Ala Leu Ser		
420	425	430
His Ser Leu Asn Leu Ala Thr Ile Asn Leu Ser Asp Gln Leu Gly Phe		
435	440	445
Glu Lys Ile Tyr Gln Ser Leu Ser Asp Met Gly Phe Lys Asn Leu Pro		
450	455	460
Lys Asp Leu Ser Ile Val Leu Gly Ser Phe Ala Ile Ser Pro Ile Asp		
465	470	475
Ala Ala Glu Lys Tyr Ser Leu Phe Ser Asn Tyr Gly Thr Met Leu Lys		
485	490	495
Pro Met Leu Ile Glu Ser Ile Thr Asn Gln Gln Asn Glu Val Lys Thr		
500	505	510
Phe Thr Pro Ile Glu Thr Lys Lys Ile Thr Ser Lys Glu Gln Ala Phe		
515	520	525
Leu Thr Leu Ser Ala Leu Met Asp Ala Val Glu Asn Gly Thr Gly Ser		
530	535	540
Leu Ala Arg Ile Lys Gly Leu Glu Ile Ala Gly Lys Thr Gly Thr Ser		
545	550	555
Asn Asn Asn Ile Asp Ala Trp Phe Ile Gly Phe Thr Pro Thr Leu Gln		
565	570	575

749

```

Ser Val Ile Trp Phe Gly Arg Asp Asp Asn Thr Pro Ile Gly Lys Gly
      580      585      590
Ala Thr Gly Gly Val Val Ser Ala Pro Val Tyr Ser Tyr Phe Met Arg
      595      600      605
Asn Ile Leu Ala Ile Glu Pro Ser Leu Lys Arg Lys Phe Asp Val Pro
      610      615      620
Lys Gly Leu Arg Lys Glu Ile Val Asp Lys Ile Pro Tyr Tyr Ser Ser
      625      630      635      640
Pro Asn Ser Ile Thr Pro Thr Pro Lys Lys Thr Asp Asp Ser Glu Glu
      645      650      655
Arg Leu Leu Phe
      660

```

(2) INFORMATION FOR SEQ ID NO:846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

```

Met Lys Tyr Leu Trp Leu Phe Leu Ile Tyr Ala Ile Gly Leu Phe Ala
1      5      10      15
Thr Asp Lys Thr Leu Asp Ile Ile Lys Thr Ile Gln Lys Leu Pro Lys
      20      25      30
Ile Glu Val Arg Tyr Ser Ile Asp Asn Asp Ala Asn Tyr Ala Leu Lys
      35      40      45
Leu His Glu Val Leu Ala Asn Asp Leu Lys Thr Ser Gln His Phe Asp
      50      55      60
Val Ser Gln Asn Lys Glu Gln Gly Ala Ile Asn Tyr Ala Glu Leu Lys
      65      70      75      80
Asp Lys Lys Val His Leu Val Ala Leu Val Ser Val Ala Val Glu Asn
      85      90      95
Gly Asn Lys Ile Ser Arg Leu Lys Leu Tyr Asp Val Asp Thr Gly Thr
      100      105      110
Leu Lys Lys Thr Phe Asp Tyr Pro Ile Val Ser Leu Asp Leu Tyr Pro
      115      120      125
Phe Ala Ala His Asn Met Ala Ile Val Val Asn Asp Tyr Leu Lys Ala
      130      135      140
Pro Ser Ile Ala Trp Met Lys Arg Leu Ile Val Phe Ser Lys Tyr Ile
      145      150      155      160
Gly Pro Gly Ile Thr Asn Ile Ala Leu Ala Asp Tyr Thr Met Arg Tyr
      165      170      175
Gln Lys Glu Ile Ile Lys Asn Asn Arg Leu Asn Ile Phe Pro Lys Trp
      180      185      190

```

750

Ala Asn Ala Glu Gln Thr Glu Phe Tyr Tyr Thr Gln Tyr Gly Glu Lys
 195 200 205
 Thr Pro Met Ile Leu Lys Tyr Asn Ile Gln Lys Ala Thr His Glu Asn
 210 215 220
 Ile Ala Ser Ser Gln Gly Met Ala Val Val Ser Ser Val Ser Ser Asp
 225 230 235 240
 Gly Ser Lys Ile Leu Met Ser Leu Ala Pro Asp Gly Gln Pro Asp Val
 245 250 255
 Tyr Leu Tyr Asp Thr His Lys Lys Thr Lys Thr Lys Ile Thr Arg Tyr
 260 265 270
 Pro Gly Ile Asp Val Ser Gly Val Phe Leu Glu Asp Asp Lys Ser Met
 275 280 285
 Ala Phe Val Ser Asp Arg Ser Gly Tyr Pro Asn Ile Tyr Met Lys Lys
 290 295 300
 Leu Gly Leu Lys Glu Ser Ala Glu Gln Leu Leu Tyr Glu Gly Arg Ser
 305 310 315 320
 Asn Glu Ser Ile

(2) INFORMATION FOR SEQ ID NO:847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1288 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

Met Glu Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser
 1 5 10 15
 Leu Val Leu Ala Gly Ala Leu Ile Ser Ala Ile Pro Gln Glu Ser His
 20 25 30
 Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile
 35 40 45
 Ala Thr Gly Thr Ala Val Gly Thr Val Ser Gly Leu Leu Ser Trp Gly
 50 55 60
 Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys
 65 70 75 80
 Val Trp Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys
 85 90 95
 Glu Tyr Asp Leu Tyr Lys Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly
 100 105 110
 Trp Asp Trp Gly Asn Ala Ala Arg His Tyr Trp Val Lys Gly Gly Gln
 115 120 125
 Trp Asn Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Lys
 130 135 140

Leu	Ser	Gly	Leu	Arg	Asn	Phe	Thr	Gly	Gly	Asp	Leu	Asp	Val	Asn	Met
145					150					155					160
Gln	Lys	Ala	Thr	Leu	Arg	Leu	Gly	Gln	Phe	Asn	Gly	Asn	Ser	Phe	Thr
				165					170						175
Ser	Tyr	Lys	Asp	Ser	Ala	Asp	Arg	Thr	Thr	Arg	Val	Asn	Phe	Asn	Ala
			180					185					190		
Lys	Asn	Ile	Ser	Ile	Asp	Asn	Phe	Val	Glu	Ile	Asn	Asn	Arg	Val	Gly
	195						200					205			
Ser	Gly	Ala	Gly	Arg	Lys	Ala	Ser	Ser	Thr	Val	Leu	Thr	Leu	Gln	Ala
	210					215					220				
Ser	Glu	Gly	Ile	Thr	Ser	Ser	Lys	Asn	Ala	Glu	Ile	Ser	Leu	Tyr	Asp
225					230					235					240
Gly	Ala	Thr	Leu	Asn	Leu	Ala	Ser	Asn	Ser	Val	Lys	Leu	Asn	Gly	Asn
				245					250						255
Val	Trp	Met	Gly	Arg	Leu	Gln	Tyr	Val	Gly	Ala	Tyr	Leu	Ala	Pro	Ser
			260					265						270	
Tyr	Ser	Thr	Ile	Asn	Thr	Ser	Lys	Val	Gln	Gly	Glu	Val	Asp	Phe	Asn
	275						280						285		
His	Leu	Thr	Val	Gly	Asp	Gln	Asn	Ala	Ala	Gln	Ala	Gly	Ile	Ile	Ala
	290					295						300			
Ser	Asn	Lys	Thr	His	Ile	Gly	Thr	Leu	Asp	Leu	Trp	Gln	Ser	Ala	Gly
305					310					315					320
Leu	Asn	Ile	Ile	Ala	Pro	Pro	Glu	Gly	Gly	Tyr	Lys	Asp	Lys	Pro	Asn
				325					330						335
Ser	Thr	Thr	Ser	Gln	Ser	Gly	Thr	Lys	Asn	Asp	Lys	Lys	Glu	Ile	Ser
			340					345						350	
Gln	Asn	Asn	Asn	Ser	Asn	Thr	Glu	Val	Ile	Asn	Pro	Pro	Asn	Asn	Thr
	355						360						365		
Gln	Lys	Thr	Glu	Thr	Glu	Pro	Thr	Gln	Val	Ile	Asp	Gly	Pro	Phe	Ala
	370					375					380				
Gly	Gly	Lys	Asp	Thr	Val	Val	Asn	Ile	Phe	His	Leu	Asn	Thr	Lys	Ala
385					390					395					400
Asp	Gly	Thr	Ile	Lys	Val	Gly	Gly	Phe	Lys	Ala	Ser	Leu	Thr	Thr	Asn
				405					410						415
Ala	Ala	His	Leu	Asn	Ile	Gly	Lys	Gly	Gly	Val	Asn	Leu	Ser	Asn	Gln
			420					425						430	
Ala	Ser	Gly	Arg	Thr	Leu	Leu	Val	Glu	Asn	Leu	Thr	Gly	Asn	Ile	Thr
	435						440						445		
Val	Asp	Gly	Pro	Leu	Arg	Val	Asn	Asn	Gln	Val	Gly	Gly	Tyr	Ala	Leu
	450					455					460				
Ala	Gly	Ser	Ser	Ala	Asn	Phe	Glu	Phe	Lys	Ala	Gly	Val	Asp	Thr	Lys
465					470					475					480
Asn	Gly	Thr	Ala	Thr	Phe	Asn	Asn	Asp	Ile	Ser	Leu	Gly	Arg	Phe	Val
				485					490					495	
Asn	Leu	Lys	Val	Asp	Ala	His	Thr	Ala	Asn	Phe	Lys	Gly	Ile	Asp	Thr
		500						505						510	
Gly	Asn	Gly	Gly	Phe	Asn	Thr	Leu	Asp	Phe	Ser	Gly	Val	Thr	Asp	Lys
	515						520						525		
Val	Asn	Ile	Asn	Lys	Leu	Ile	Thr	Ala	Ser	Thr	Asn	Val	Ala	Val	Lys
	530						535					540			
Asn	Phe	Asn	Ile	Asn	Glu	Leu	Ile	Val	Lys	Thr	Asn	Gly	Ile	Ser	Val
545					550					555					560
Gly	Glu	Tyr	Thr	His	Phe	Ser	Glu	Asp	Ile	Gly	Ser	Gln	Ser	Arg	Ile
				565						570					575
Asn	Thr	Val	Arg	Leu	Glu	Thr	Gly	Thr	Arg	Ser	Ile	Phe	Ser	Gly	Gly
			580						585					590	
Val	Lys	Phe	Lys	Ser	Gly	Glu	Lys	Leu	Val	Ile	Asn	Asp	Phe	Tyr	Tyr

595					600					605					
Ser	Pro	Trp	Asn	Tyr	Phe	Asp	Ala	Arg	Asn	Val	Lys	Asn	Val	Glu	Ile
610					615					620					
Thr	Arg	Lys	Phe	Ala	Ser	Ser	Thr	Pro	Glu	Asn	Pro	Trp	Gly	Thr	Ser
625					630					635					640
Lys	Leu	Met	Phe	Asn	Asn	Leu	Thr	Leu	Gly	Gln	Asn	Ala	Val	Met	Asp
				645					650					655	
Tyr	Ser	Gln	Phe	Ser	Asn	Leu	Thr	Ile	Gln	Gly	Asp	Phe	Ile	Asn	Asn
			660					665					670		
Gln	Gly	Thr	Ile	Asn	Tyr	Leu	Val	Arg	Gly	Gly	Lys	Val	Ala	Thr	Leu
		675					680					685			
Asn	Val	Gly	Asn	Ala	Ala	Ala	Met	Met	Phe	Asn	Asn	Asp	Ile	Asp	Ser
690					695					700					
Ala	Thr	Gly	Phe	Tyr	Lys	Pro	Leu	Ile	Lys	Ile	Asn	Ser	Ala	Gln	Asp
705				710						715					720
Leu	Ile	Lys	Asn	Thr	Glu	His	Val	Leu	Leu	Lys	Ala	Lys	Ile	Ile	Gly
			725						730					735	
Tyr	Gly	Asn	Val	Ser	Thr	Gly	Thr	Asn	Gly	Ile	Ser	Asn	Val	Asn	Leu
			740					745					750		
Glu	Glu	Gln	Phe	Lys	Glu	Arg	Leu	Ala	Leu	Tyr	Asn	Asn	Asn	Asn	Arg
		755					760					765			
Met	Asp	Thr	Cys	Val	Val	Arg	Asn	Thr	Asp	Asp	Ile	Lys	Ala	Cys	Gly
770					775					780					
Met	Ala	Ile	Gly	Asn	Gln	Ser	Met	Val	Asn	Asn	Pro	Asp	Asn	Tyr	Lys
785				790						795					800
Tyr	Leu	Ile	Gly	Lys	Ala	Trp	Arg	Asn	Ile	Gly	Ile	Ser	Lys	Thr	Ala
				805					810					815	
Asn	Gly	Ser	Lys	Ile	Ser	Val	Tyr	Tyr	Leu	Gly	Asn	Ser	Thr	Pro	Thr
			820					825					830		
Glu	Asn	Gly	Gly	Asn	Thr	Thr	Asn	Leu	Pro	Thr	Asn	Thr	Thr	Asn	Asn
		835					840					845			
Ala	His	Ser	Ala	Asn	Tyr	Ala	Leu	Val	Lys	Asn	Ala	Pro	Phe	Ala	His
850				855						860					
Ser	Ala	Thr	Pro	Asn	Leu	Val	Ala	Ile	Asn	Gln	His	Asp	Phe	Gly	Thr
865				870						875					880
Ile	Glu	Ser	Val	Phe	Glu	Leu	Ala	Asn	Arg	Ser	Lys	Asp	Ile	Asp	Thr
				885					890					895	
Leu	Tyr	Thr	His	Ser	Gly	Ala	Gln	Gly	Arg	Asp	Leu	Leu	Gln	Thr	Leu
			900					905					910		
Leu	Ile	Asp	Ser	His	Asp	Ala	Gly	Tyr	Ala	Arg	Gln	Met	Ile	Asp	Asn
		915					920					925			
Thr	Ser	Thr	Gly	Glu	Ile	Thr	Lys	Gln	Leu	Asn	Ala	Ala	Thr	Asp	Ala
930							935					940			
Leu	Asn	Asn	Val	Ala	Ser	Leu	Glu	His	Lys	Gln	Ser	Gly	Leu	Gln	Thr
945				950						955					960
Leu	Ser	Leu	Ser	Asn	Ala	Met	Ile	Leu	Asn	Ser	Arg	Leu	Val	Asn	Leu
				965					970					975	
Ser	Arg	Lys	His	Thr	Asn	His	Ile	Asn	Ser	Phe	Ala	Gln	Arg	Leu	Gln
			980					985					990		
Ala	Leu	Lys	Gly	Gln	Glu	Phe	Ala	Ser	Leu	Glu	Ser	Ala	Ala	Glu	Val
		995					1000					1005			
Leu	Tyr	Gln	Phe	Ala	Pro	Lys	Tyr	Glu	Lys	Pro	Thr	Asn	Val	Trp	Ala
1010							1015					1020			
Asn	Ala	Ile	Gly	Gly	Ala	Ser	Leu	Asn	Ser	Gly	Ser	Asn	Ala	Ser	Leu
1025				1030						1035					1040
Tyr	Gly	Thr	Ser	Ala	Gly	Val	Asp	Ala	Phe	Leu	Asn	Gly	Asn	Val	Glu
				1045					1050					1055	

753

Ala Ile Val Gly Gly Phe Gly Ser Tyr Gly Tyr Ser Ser Phe Ser Asn
 1060 1065 1070
 Gln Ala Asn Ser Leu Asn Ser Gly Ala Asn Asn Ala Asn Phe Gly Val
 1075 1080 1085
 Tyr Ser Arg Phe Phe Ala Asn Gln His Glu Phe Asp Phe Glu Ala Gln
 1090 1095 1100
 Gly Ala Leu Gly Ser Asp Gln Ser Ser Leu Asn Phe Lys Ser Thr Leu
 1105 1110 1115 1120
 Leu Gln Asp Leu Asn Gln Ser Tyr Asn Tyr Leu Ala Tyr Ser Ala Thr
 1125 1130 1135
 Ala Arg Ala Ser Tyr Gly Tyr Asp Phe Ala Phe Phe Arg Asn Ala Leu
 1140 1145 1150
 Val Leu Lys Pro Ser Val Gly Val Ser Tyr Asn His Leu Gly Ser Thr
 1155 1160 1165
 Asn Phe Lys Ser Asn Ser Gln Ser Gln Val Ala Leu Lys Asn Gly Ala
 1170 1175 1180
 Ser Ser Gln His Leu Phe Asn Ala Asn Ala Asn Val Glu Ala Arg Tyr
 1185 1190 1195 1200
 Tyr Tyr Gly Asp Thr Ser Tyr Phe Tyr Leu His Ala Gly Val Leu Gln
 1205 1210 1215
 Glu Phe Ala His Phe Gly Ser Asn Asp Val Ala Ser Leu Asn Thr Phe
 1220 1225 1230
 Lys Ile Asn Ala Ala Arg Ser Pro Leu Ser Thr Tyr Ala Arg Ala Met
 1235 1240 1245
 Met Gly Gly Glu Leu Gln Leu Ala Lys Glu Val Phe Leu Asn Leu Gly
 1250 1255 1260
 Val Val Tyr Leu His Asn Leu Ile Ser Asn Ala Ser His Phe Ala Ser
 1265 1270 1275 1280
 Asn Leu Gly Met Arg Tyr Ser Phe
 1285

(2) INFORMATION FOR SEQ ID NO:848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

Met Lys Asp Ser Phe Leu Phe Thr Ser Glu Ser Val Thr Glu Gly His
 1 5 10 15
 Pro Asp Lys Met Ala Asp Gln Ile Ser Asp Ala Val Leu Asp Tyr Ile
 20 25 30
 Ile Glu Arg Asp Lys Lys Ala Lys Val Ala Cys Glu Thr Leu Val Ser
 35 40 45

754

```

Asn Gly Phe Cys Met Ile Thr Gly Glu Leu Lys Thr Ser Val Tyr Ala
 50          55          60
Pro Met Gln Glu Ile Ala Arg Glu Val Val Lys Lys Ile Gly Tyr Thr
 65          70          75          80
Asp Ala Leu Tyr Gly Phe Asp Tyr Arg Ser Ala Ala Val Leu Asn Gly
          85          90          95
Ile Gly Glu Gln Ser Pro Asp Ile Asn Gln Gly Val Asp Arg Glu Asp
          100          105          110
Gly Glu Ile Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Cys
          115          120          125
Lys Glu Thr Glu Thr Leu Met Pro Leu Pro Ile His Leu Ala His Gln
          130          135          140
Leu Ala Phe Ala Leu Ala Gln Lys Arg Lys Asp Asn Thr Leu Pro Phe
          145          150          155          160
Leu Arg Pro Asp Gly Lys Ser Gln Val Ser Val Arg Tyr Glu Asn Asn
          165          170          175
Lys Pro Val Ser Val Asp Thr Ile Val Ile Ser Thr Gln His Ser Pro
          180          185          190
Glu Val Ser Gln Lys His Leu Lys Glu Ala Val Ile Glu Glu Ile Val
          195          200          205
Tyr Lys Val Leu Pro Lys Glu Tyr Leu His Asp Asn Ile Lys Phe Phe
          210          215          220
Ile Asn Pro Thr Gly Lys Phe Val Ile Gly Gly Pro Gln Gly Asp Ala
          225          230          235          240
Gly Leu Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Phe Cys
          245          250          255
Pro His Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp
          260          265          270
Arg Ser Ala Ala Tyr Ala Ala Arg Tyr Val Ala Lys Asn Leu Val Ala
          275          280          285
Ser Gly Val Cys Asp Lys Ala Thr Val Gln Leu Ala Tyr Ala Ile Gly
          290          295          300
Val Ile Glu Pro Val Ser Ile Tyr Val Asn Thr His Asn Thr Ser Lys
          305          310          315          320
His Ser Ser Ala Glu Leu Glu Lys Cys Val Lys Ser Val Phe Lys Leu
          325          330          335
Thr Pro Lys Gly Ile Ile Glu Ser Leu Asp Leu Leu Arg Pro Ile Tyr
          340          345          350
Ser Leu Thr Ser Ala Tyr Gly His Phe Gly Arg Glu Leu Glu Glu Phe
          355          360          365
Thr Trp Glu Lys Thr Asn Lys Val Glu Glu Ile Lys Ala Phe Phe Lys
          370          375          380
Arg
          385

```

(2) INFORMATION FOR SEQ ID NO:849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

755

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

```

Met Lys Phe Leu Asn Gly Leu Ala Gly Asn Leu Leu Ile Val Val Ile
1           5           10           15
Leu Leu Cys Val Val Val Phe Phe Ala Leu Lys Ala Ile His Ile Gln
20           25           30
Lys Glu Gln Ala Thr Asn Tyr Tyr Arg Tyr Lys Asp Ile Asn Ala Leu
35           40           45
Glu Ala Lys Asn Thr Gln Asn His Ala Asn Tyr Glu Leu Val Asn Gln
50           55           60
Gly Ser Lys Lys
65

```

(2) INFORMATION FOR SEQ ID NO:850:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

```

Leu Lys Ile Phe Leu Val Ile Leu Ser Val Phe Phe Phe Asn Gly Cys
1           5           10           15
Phe Gly Leu Val Tyr Lys Thr Pro Ile Ser Asn Pro Pro Ile Ser Tyr
20           25           30
Asp Pro Tyr Thr Thr Thr Ile Gly Ser Leu Tyr Ala Lys Asn Leu Lys
35           40           45
Glu Asn Pro Lys His Ser Ala Ala Ile Leu Leu Glu Asp Gly Phe Asp
50           55           60
Ala Leu Leu His Arg Val Gly Leu Ile Arg Met Ser Gln Lys Ser Ile
65           70           75           80
Asp Met Gln Thr Tyr Ile Tyr Lys Asn Asp Leu Ser Ser Gln Val Ile
85           90           95
Ala Lys Glu Leu Leu Asn Ala Ala Asn Arg Gly Val Lys Val Arg Ile
100          105          110
Leu Leu Asp Asp Asn Gly Leu Asp Ser Asp Phe Ser Asp Ile Met Leu
115          120          125
Leu Asn Phe His Lys Asn Ile Glu Val Lys Ile Phe Asn Pro Tyr Tyr
130          135          140

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756

```

Ile Arg Asn Lys Gly Leu Arg Tyr Phe Glu Met Leu Ala Asp Tyr Glu
145                      150                      155                      160
Arg Ile Lys Lys Arg Met His Asn Lys Leu Phe Ile Val Asp Asn Phe
                      165                      170                      175
Ala Val Ile Ile Gly Gly Arg Asn Ile Gly Asp Asn Tyr Phe Asp Asn
                      180                      185                      190
Asp Leu Asp Thr Asn Phe Leu Asp Leu Asp Ala Leu Phe Phe Gly Gly
                      195                      200                      205
Val Ala Ser Lys Ala Lys Glu Ser Phe Glu Asn Tyr Trp Arg Phe His
                      210                      215                      220
Arg Ser Ile Pro Val Ser Leu Leu Arg Thr His Lys Arg Leu Lys Asn
225                      230                      235                      240
Asn Val Lys Glu Ile Ala Lys Leu His Glu Lys Ile Pro Ile Ser Ala
                      245                      250                      255
Glu Asp Ala Asn Glu Phe Glu Lys Lys Val Asn Asp Phe Ile Glu Arg
                      260                      265                      270
Phe Gln Lys Tyr Gln Tyr Pro Ile Tyr Tyr Gly Asn Ala Ile Phe Leu
                      275                      280                      285
Ala Asp Leu Pro Ala Lys Ile Asp Thr Pro Leu Tyr Ser Pro Ile Lys
                      290                      295                      300
Ile Ala Phe Glu Lys Ala Leu Lys Asn Ala Lys Asp Ser Val Phe Ile
305                      310                      315                      320
Ala Ser Ser Tyr Phe Ile Pro Gly Lys Lys Ile Met Lys Ile Phe Lys
                      325                      330                      335
Asn Gln Ile Ser Lys Gly Ile Glu Leu Asn Ile Leu Thr Asn Ser Leu
                      340                      345                      350
Ser Ser Thr Asp Ala Ile Val Val Tyr Gly Ala Trp Glu Arg Tyr Arg
                      355                      360                      365
Asn Lys Leu Val Arg Met Gly Ala Asn Val Tyr Glu Ile Arg Asn Asp
                      370                      375                      380
Phe Phe Asn Arg Gln Ile Lys Gly Arg Phe Ser Thr Lys His Ser Leu
385                      390                      395                      400
His Gly Lys Thr Ile Val Phe Asp Asp Ala Leu Thr Leu Leu Gly Ser
                      405                      410                      415
Phe Asn Ile Asp Pro Arg Ser Ala Tyr Ile Asn Thr Glu Ser Ala Val
                      420                      425                      430
Leu Phe Asp Asn Pro Ser Phe Ala Lys Arg Val Arg Leu Ser Leu Lys
                      435                      440                      445
Asp His Ala Gln Gln Ser Trp His Leu Val Leu Tyr Arg His Arg Val
                      450                      455                      460
Ile Trp Glu Ala Thr Glu Glu Gly Ile Leu Ile His Glu Lys Asn Ser
465                      470                      475                      480
Pro Asp Thr Ser Phe Phe Leu Arg Leu Ile Lys Glu Trp Ser Lys Val
                      485                      490                      495
Leu Pro Glu Arg Glu Leu
                      500

```

(2) INFORMATION FOR SEQ ID NO:851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

757

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

```

Met Arg Phe Ser Tyr Ile Glu Pro Arg Ala Lys Tyr Leu Ile Ser Lys
1           5           10           15
Leu Ser Lys Ile Trp Val Phe Tyr Ile Phe Leu Ser Phe Val Leu Ile
          20           25           30
Gly Gly Leu Val Trp Phe Met His Asn Ala Ile Lys Arg Ala Gln Asp
          35           40           45
Asn Ala Ser Ser Leu Thr Ile Gln Glu Arg Leu Tyr Arg His Glu Ile
          50           55           60
Ser Arg Leu Gln Val Lys Thr Asp Glu Thr Leu Lys Leu Ile Lys Glu
65           70           75           80
Ala Lys Lys Arg Leu Asn Tyr Asn Asp Asp Ile Arg Asp Val Leu Gln
          85           90           95
Gly Leu Leu Asn Ile Val Pro Asp Leu Ile Thr Ile Asn Ser Ile Glu
          100          105          110
Ile Asp Gln Gln Ser Val Val Val Ser Gly Lys Thr Pro Ser Lys Glu
          115          120          125
Ala Phe Tyr Phe Leu Phe Gln Asn Lys Leu Asn Pro Met Phe Asp Tyr
          130          135          140
Ser Arg Ala Glu Phe Phe Pro Leu Ser Asp Gly Trp Phe Asn Phe Val
145          150          155          160
Ser Thr Asn Phe Ser Asn Ser Leu Leu Ile Lys Asn Pro Glu Ser Ile
          165          170          175
Lys

```

(2) INFORMATION FOR SEQ ID NO:852:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

```

Met Arg Lys Ile Leu Leu Met Gly Leu Ile Leu Gln Ala Leu Phe Gly
1           5           10           15

```

758

```

Glu Glu Ala Ala Gln Glu Leu Leu Gln Cys Ser Ala Ile Phe Glu Ser
      20      25      30
Lys Lys Ala Glu Leu Lys Glu Asp Leu Arg Gln Leu Ser Glu Lys Glu
      35      40      45
Gln Ser Leu Arg Ile Leu Gln Thr Glu Asn Ala Arg Leu Leu Asp Glu
      50      55      60
Lys Ser Asp Leu Leu Asn Lys Lys Glu Lys Glu Ile Asp Glu Lys Leu
      65      70      75      80
Lys Asn Leu Ala Ala Lys Glu Glu Ala Phe Lys Thr Leu Gln Thr Glu
      85      90      95
Glu Lys Lys Arg Leu Lys Asn Leu Ile Glu Glu Asn Glu Gly Ile Leu
      100      105      110
Arg Glu Ile Lys Gln Ala Lys Asp Ser Lys Ile Gly Glu Thr Tyr Ser
      115      120      125
Lys Met Lys Asp Ser Lys Ser Ala Leu Ile Leu Glu Asn Leu Pro Thr
      130      135      140
Gln Asn Ala Leu Glu Ile Leu Met Ala Leu Lys Pro Gln Glu Leu Gly
      145      150      155      160
Lys Ile Leu Ala Lys Met Asp Pro Lys Lys Ala Ala Ala Leu Thr Glu
      165      170      175
Leu Trp Gln Lys Pro Pro Lys Glu Asn Lys Glu Asn Lys Glu Ser Gln
      180      185      190
Lys Thr Thr Asp Pro Thr Pro Pro Thr Pro Pro Thr Pro Pro Lys Glu
      195      200      205
Pro Thr Leu Lys Asp Pro Asn Val Lys Glu Pro Thr Gly Val
      210      215      220

```

(2) INFORMATION FOR SEQ ID NO:853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein.

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

```

Met Asn Ile Gln Thr Lys Lys Arg Phe Leu Ala Asn Leu Leu Leu Phe
1      5      10      15
Ser Leu Phe Ser Cys Leu Lys Ala Glu Thr Leu Ser Glu Asp His Gln
      20      25      30
Ile Leu Leu Ser Ser Asp Ala Phe His Arg Gly Asp Phe Ala Thr Ala
      35      40      45
Gln Lys Gly Tyr Met Asn Leu Tyr Lys Gln Thr Asn Lys Val Val Tyr
      50      55      60
Ala Lys Glu Ala Ala Ile Ser Ala Ala Ser Leu Gly Asp Ile Lys Thr
      65      70      75      80

```

759

Ala Met His Leu	Ala Met Leu Tyr Gln Lys Ile Thr Asn Asn Arg Asn	85	90	95
Asp Val Ser Ile	Asn Lys Ile Leu Val Asp Gly Tyr Ala Gln Met Gly	100	105	110
Gln Ile Asp Lys	Ala Ile Glu Leu Leu His Lys Ile Arg Lys Glu Glu	115	120	125
Lys Thr Ile Ala	Thr Asp Asn Val Leu Gly Thr Leu Tyr Leu Thr Gln	130	135	140
Lys Arg Leu Asp	Lys Ala Phe Pro Leu Leu Asn Lys Phe Tyr Asn Gln	145	150	155
Val His Asp Glu	Asp Ser Leu Glu Lys Leu Ile Thr Ile Tyr Phe Leu	165	170	175
Gln Asn Arg Lys	Lys Glu Gly Leu Asp Leu Leu Gln Ser His Ile Asp	180	185	190
Arg Tyr Gly Cys	Ser Glu Gln Leu Cys Gln Lys Ala Leu Asn Thr Phe	195	200	205
Thr Gln Phe Asn	Glu Leu Asp Leu Ala Lys Thr Thr Phe Ala Arg Leu	210	215	220
Tyr Glu Lys Asn	Pro Ile Val Gln Asn Ala Gln Phe Tyr Ile Gly Val	225	230	235
Leu Ile Leu Leu	Lys Glu Phe Asp Lys Ala Gln Gln Ile Ala Glu Leu	245	250	255
Phe Pro Phe Asp	Arg Arg Leu Leu Leu Asp Leu Tyr Thr Ala Gln Lys	260	265	270
Lys Phe Asp Gln	Ala Ser Lys Gln Ala Ser Leu Ile Tyr Gln Glu Arg	275	280	285
Lys Asp Pro Lys	Phe Leu Gly Leu Glu Ala Ile Tyr His Tyr Glu Ser	290	295	300
Leu Ser Ala Asn	Lys Lys Lys Leu Thr Lys Glu Glu Met Leu Pro Ile	305	310	315
Ile Gln Lys Leu	Glu Gln Ala Thr Lys Glu Arg Gln Ala Trp Leu Ala	325	330	335
Lys Thr Lys Asp	Lys Glu Asp Ala Gln Asp Ala Phe Phe Tyr Asn Phe	340	345	350
Leu Gly Tyr Ser	Leu Ile Asp Tyr Asp Met Asp Val Lys Arg Gly Met	355	360	365
Asp Leu Val Arg	Lys Ala Leu Ala Leu Asp Ser Asn Ser Val Leu Tyr	370	375	380
Leu Asp Ser Leu	Ala Trp Gly Tyr Tyr Lys Leu Gly Asn Cys Leu Glu	385	390	395
Ala Lys Lys Ile	Phe Ser Ser Ile Ala Lys Glu Leu Ile Gln Asn Glu	405	410	415
Pro Glu Leu Lys	Glu His Asn Lys Ile Ile Gln Glu Cys Lys Lys	420	425	430

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

760

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

```

Met Leu Tyr Ala Ser Lys Ala Arg Leu Phe Leu Gln Ile Lys Gly Lys
1           5           10           15
Phe Met Leu Arg Ile Leu Ile Pro Leu Leu Ile Ile Val Trp Val Leu
          20           25           30
Trp Arg Leu Phe Leu Arg Gln Lys Pro His Lys Asp Asp His Arg Asp
          35           40           45
Asn His Ser Tyr Thr Gln Gln Thr Pro Lys Glu Leu Glu Asp His Met
          50           55           60
Ile Val Cys Ser Lys Cys Gln Thr Tyr Val Ser Ser Lys Asp Ala Ile
65           70           75           80
Tyr Ser Gly Ala Val Ala Tyr Cys Ser Glu Thr Cys Leu Lys Asp Lys
          85           90           95
Gly

```

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 479 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

```

Met Lys Asn Ser Ala Pro Leu Lys Asn Lys Val Phe Cys Gly Leu Tyr
1           5           10           15
Val Leu Ser Leu Ser Ala Ser Val Gln Ala Phe Asp Tyr Lys Ile Glu
          20           25           30
Val Leu Ala Glu Ser Phe Ser Lys Val Gly Phe Asn Lys Lys Lys Ile
          35           40           45
Asp Ile Ala Arg Gly Ile Tyr Pro Thr Glu Thr Phe Val Thr Ala Val
          50           55           60
Gly Gln Gly Asn Ile Tyr Ala Asp Phe Leu Ser Lys Ser Leu Lys Asp
65           70           75           80
Gln Gly His Val Leu Glu Gly Lys Val Gly Gly Thr Ile Gly Gly Ile
          85           90           95
Ala Tyr Asp Ser Thr Lys Phe Asn Gln Gly Gly Ser Val Ile Tyr Asn
          100          105          110

```

. 761

```

Tyr Ile Gly Tyr Trp Asp Gly Tyr Leu Gly Gly Lys Arg Ala Leu Leu
    115                      120                      125
Asp Gly Thr Ser Ile His Glu Cys Ala Leu Gly Ser Asp Gly Lys Val
    130                      135                      140
Ile Asp Ser Ile Ala Cys Gly Asn Ala Arg Ala Asn Lys Ile Arg Arg
    145                      150                      155                      160
Asn Tyr Leu Met Asn Asn Ala Phe Leu Glu Tyr Arg Tyr Lys Asp Ile
    165                      170                      175
Phe Ala Ala Lys Gly Gly Arg Tyr Gln Ser Asn Ala Pro Tyr Met Ser
    180                      185                      190
Ser Tyr Thr Gln Gly Phe Glu Ile Ser Ala Lys Ile Lys Asp Lys Asn
    195                      200                      205
Glu Gly Ser His Lys Leu Trp Trp Phe Ser Ser Trp Gly Arg Ala Phe
    210                      215                      220
Ala Tyr Gly Glu Trp Ile Tyr Asp Phe Tyr Ser Pro Arg Thr Val Ile
    225                      230                      235                      240
Lys Asn Gly Arg Thr Leu Asn Tyr Gly Ile His Leu Val Asp Tyr Thr
    245                      250                      255
Tyr Glu Arg Lys Gly Val Ser Val Ser Pro Phe Phe Gln Phe Ser Pro
    260                      265                      270
Gly Thr Tyr Tyr Ser Pro Gly Val Ala Val Gly Tyr Asp Ser Asn Pro
    275                      280                      285
Asn Phe Asn Gly Val Gly Phe Arg Ser Glu Thr Lys Ala Tyr Ile Leu
    290                      295                      300
Leu Pro Val His Ala Pro Leu Lys Arg Asp Thr Tyr Arg Tyr Ala Val
    305                      310                      315                      320
Lys Ala Gly Thr Ala Gly Gln Ser Leu Leu Ile Arg Gln Arg Phe Asp
    325                      330                      335
Tyr Asn Glu Phe Asn Phe Gly Gly Ala Phe Tyr Lys Val Trp Lys Asn
    340                      345                      350
Ala Asn Ala Tyr Ile Gly Thr Thr Gly Asn Pro Leu Gly Ile Asp Phe
    355                      360                      365
Trp Thr Asn Ser Val Tyr Asp Ile Gly Gln Ala Leu Ser His Val Val
    370                      375                      380
Thr Ala Asp Ala Val Ser Gly Trp Val Phe Gly Gly Gly Val His Lys
    385                      390                      395                      400
Lys Trp Leu Trp Gly Thr Leu Trp Arg Trp Thr Ser Gly Ala Leu Ala
    405                      410                      415
Asn Glu Ala Ser Ala Ala Val Asn Val Gly Tyr Lys Ile Ser Lys Ser
    420                      425                      430
Leu Thr Ala Ser Val Lys Leu Glu Tyr Leu Gly Val Met Thr His Ser
    435                      440                      445
Gly Phe Thr Val Gly Ser Tyr Arg Pro Thr Pro Gly Ser Lys Ala Leu
    450                      455                      460
Tyr Ser Asp Arg Ser His Leu Met Thr Thr Leu Ser Ala Lys Phe
    465                      470                      475

```

(2) INFORMATION FOR SEQ ID NO:856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

```

Met Lys Asn Ser Ala Pro Leu Lys Asn Lys Val Phe Cys Gly Leu Tyr
1          5          10          15
Val Leu Ser Leu Ser Ala Ser Val Gln Ala Phe Asp Tyr Lys Ile Glu
20          25          30
Val Leu Ala Glu Ser Phe Ser Lys Val Gly Phe Asn Lys Lys Lys Ile
35          40          45
Asp Ile Ala Arg Gly Ile Tyr Pro Thr Glu Thr Phe Val Thr Ala Val
50          55          60
Gly Gln Gly Asn Ile Tyr Ala Asp Phe Leu Ser Lys Ser Leu Lys Asp
65          70          75          80
Gln Gly His Val Leu Glu Gly Lys Val Gly Gly Thr Ile Gly Gly Ile
85          90          95
Ala Tyr Asp Ser Thr Lys Phe Asn Gln Gly Gly Ser Val Ile Tyr Asn
100         105         110
Tyr Ile Gly Tyr Trp Asp Gly Tyr Leu Gly Gly Lys Arg Ala Leu Leu
115         120         125
Asp Gly Thr Ser Ile His Glu Cys Ala Leu Gly Ser Asp Gly Lys Val
130         135         140
Ile Asp Ser Ile Ala Cys Gly Asn Ala Arg Ala Asn Lys Ile Arg Arg
145         150         155         160
Asn Tyr Leu Met Asn Asn Ala Phe Leu Glu Tyr Arg Tyr Lys Asp Ile
165         170         175
Phe Ala Ala Lys Gly Gly Arg Tyr Gln Ser Asn Ala Pro Tyr Met Ser
180         185         190
Ser Tyr Thr Gln Gly Phe Glu Ile Ser Ala Lys Ile Lys Asp Lys Asn
195         200         205
Glu Gly Ser His Lys Leu Trp Trp Phe Ser Ser Trp Gly Arg Ala Phe
210         215         220
Ala Tyr Gly Glu Trp Ile Tyr Asp Phe Tyr Ser Pro Arg Thr Val Ile
225         230         235         240
Lys Asn Gly Arg Thr Leu Asn Tyr Gly Ile His Leu Val Asp Tyr Thr
245         250         255
Tyr Glu Arg Lys Gly Val Ser Val Ser Pro Phe Phe Gln Phe Ser Pro
260         265         270
Gly Thr Tyr Tyr Ser Pro Gly Val Ala Val Gly Tyr Asp Ser Asn Pro
275         280         285
Asn Phe Asn Gly Val Gly Phe Arg Ser Glu Thr Lys Ala Tyr Ile Leu
290         295         300
Leu Pro Val His Ala Pro Leu Lys Arg Asp Thr Tyr Arg Tyr Ala Val
305         310         315         320
Lys Ala Gly Thr Ala Gly Gln Ser Leu Leu Ile Arg Gln Arg Phe Asp
325         330         335
Tyr Asn Glu Phe Asn Phe Gly Gly Ala Phe Tyr Lys Val Trp Lys Asn
340         345         350
Ala Asn Ala Tyr Ile Gly Thr Thr Gly Asn Pro Leu Gly Ile Asp Phe
355         360         365
Trp Thr Asn Ser Val Tyr Asp Ile Gly Gln Ala Leu Ser His Val Val

```


763

370	375	380
Thr Ala Asp Ala Val Ser Gly Trp Val Phe Gly Gly Gly Val His Lys		
385	390	395
Lys Trp Leu Trp Gly Thr Leu Trp Arg Trp Thr Ser Gly Ala Leu Ala		
	405	410
Asn Glu Ala Ser Ala Ala Val Asn Val Gly Tyr Lys Ile Ser Lys Ser		
	420	425
Leu Thr Ala Ser Val Lys Leu Glu Tyr Leu Gly Val Met Thr His Ser		
	435	440
Gly Phe Thr Val Gly Ser Tyr Arg Pro Thr Pro Gly Ser Lys Ala Leu		
	450	455
Tyr Ser Asp Arg Ser His Leu Met Thr Thr Leu Ser Ala Lys Phe		
465	470	475

(2) INFORMATION FOR SEQ ID NO:857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

Met Gly Leu Lys Asn Leu Ser Thr Leu Leu Val Phe Leu Phe Phe Cys		
1	5	10
Leu Gly Cys Val Ser Asn Phe Asn Glu Asp Thr Tyr Thr Leu Asp Leu		
	20	25
Val Leu Glu Lys Lys Ile Gln Ala Ser Arg Lys Gly Glu Ile Thr Gln		
	35	40
Asp Asn Val Pro Ile Ile Thr Ala Ile Ala Thr His Leu Asn Asp Val		
	50	55
Asp Ser Gly Thr Tyr Tyr Asp His Glu Tyr Phe Leu Val Glu Ile Phe		
65	70	75
Thr Gln Asn Asn Asp Trp Ile Asp Asp Gly Tyr Ile Ser Tyr Glu Leu		
	85	90
Phe Gly Thr Lys Pro Thr Gly Ser Glu Pro Leu Trp Val Arg Glu Ile		
	100	105
Thr Arg Asp Glu Phe Asp Gly Ile Leu Glu Thr Thr Asn Arg Trp Ser		
	115	120
Arg Ala Phe Leu Ile Ala Phe Asp Lys Leu Asp Tyr Leu Ala Val Gln		
	130	135
Glu Ala Lys Leu Glu Leu Asp Ala Tyr Ser Leu Gly Lys Ile Val Phe		
145	150	155
Asn Phe Ala Tyr Gln Val Pro Leu Pro Gln Phe		
	165	170

(2) INFORMATION FOR SEQ ID NO:858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

Val	Asn	Lys	Lys	His	Arg	Leu	Ala	Phe	Leu	Gly	Leu	Ile	Val	Gly	Val
1				5					10					15	
Leu	Phe	Phe	Phe	Ser	Ala	Cys	Gln	His	Arg	Leu	His	Met	Gly	Tyr	Tyr
			20					25					30		
Ser	Glu	Val	Thr	Gly	Asp	Tyr	Leu	Phe	Asn	Tyr	Asn	Ser	Thr	Ile	Val
		35					40					45			
Val	Ala	Tyr	Asp	Arg	Ser	Asp	Ala	Met	Thr	Ser	Tyr	Tyr	Ile	Asn	Val
	50					55					60				
Ile	Val	Tyr	Glu	Leu	Gln	Lys	Leu	Gly	Phe	Tyr	Asn	Val	Phe	Thr	Gln
65					70					75					80
Ala	Asn	Ser	Arg												

(2) INFORMATION FOR SEQ ID NO:859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

Met	Gln	Tyr	Lys	Lys	Asn	Lys	Lys	Arg	Tyr	Tyr	His	Leu	Ala	Leu	Gly
1				5					10					15	
Ile	Leu	Phe	Cys	Asn	Gly	Leu	Ser	Leu	Lys	Ala	Leu	Glu	Ile	Ala	Val
			20					25					30		

765

```

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

```

(2) INFORMATION FOR SEQ ID NO:860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

```

Met Val Gln Lys Ile Gly Ile Leu Gly Ala Met Arg Glu Glu Ile Thr
1           5           10           15
Pro Ile Leu Glu Leu Phe Gly Val Asp Phe Glu Glu Ile Pro Leu Gly
    20           25           30
Gly Asn Val Phe His Lys Gly Val Tyr His Asn Lys Glu Ile Ile Val
    35           40           45
Ala Tyr Ser Lys Ile Gly Lys Val His Ser Thr Leu Thr Thr Thr Ser
    50           55           60

```

766

```

Met Ile Leu Ala Phe Gly Val Gln Lys Val Leu Phe Ser Gly Val Ala
65          70          75          80
Gly Ser Leu Val Lys Asp Leu Lys Ile Asn Asp Leu Leu Val Ala Thr
          85          90          95
Gln Leu Val Gln His Asp Val Asp Leu Ser Ala Phe Asp His Pro Leu
          100          105          110
Gly Phe Ile Pro Glu Ser Ala Ile Phe Ile Glu Thr Ser Gly Ser Leu
          115          120          125
Asn Ala Leu Ala Lys Lys Ile Ala Asn Glu Gln His Ile Ala Leu Lys
          130          135          140
Glu Gly Val Ile Ala Ser Gly Asp Gln Phe Val His Ser Lys Glu Arg
145          150          155          160
Lys Glu Phe Leu Val Ser Glu Phe Lys Ala Ser Ala Val Glu Met Glu
          165          170          175
Gly Ala Ser Val Ala Phe Val Cys Gln Lys Phe Gly Val Pro Cys Cys
          180          185          190
Val Leu Arg Ser Ile Ser Asp Asn Ala Asp Glu Lys Ala Gly Met Ser
          195          200          205
Phe Asp Glu Phe Leu Glu Lys Ser Ala His Thr Ser Ala Lys Phe Leu
          210          215          220
Lys Ser Met Val Asp Glu Leu
225          230

```

(2) INFORMATION FOR SEQ ID NO:861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

```

Met Arg Ala Thr Ala Ile Lys Ile Phe Ser Phe Ser Ser Ala Leu Ala
1          5          10          15
Leu Leu Leu Gln Gly Cys Leu Ser Ile Asn Leu Lys Gln Met Leu Pro
          20          25          30
Glu Ile Arg Thr Tyr Asp Leu Asn Ala Ser Ser Phe Glu Met Thr Gln
          35          40          45
Cys Pro Lys Pro Leu Thr Glu Val Arg Leu Ile Ser Ile Leu Ser Ala
          50          55          60
Asp Leu Phe Asn Thr Lys Glu Ile Val Phe Lys Ala Gln Asp Gly Gln
65          70          75          80
Ile Thr His Gly Lys His Gln Lys Trp Ile Asp Leu Pro Arg Asn Met
          85          90          95
Leu Lys Thr Met Phe Met Gln Glu Ala Gln Lys Ala Cys Leu Gly Val
          100          105          110

```

767

Ala Leu Pro Pro Tyr Gly Ala Gly Ala Pro Thr Tyr Ala Val Arg Phe
 115 120 125
 Thr Ile Leu Ser Phe Ser Leu Leu Glu Lys Glu Asn Ser Thr Tyr Arg
 130 135 140
 Ala Glu Phe Ala Leu Gly Tyr Asp Ile Ser Val Lys Gly Asp Ser His
 145 150 155 160
 Ser Gly Val Ile Ile Lys His Glu Asn Ile Ser Ser Leu Glu Asn Lys
 165 170 175
 Thr Thr Lys Thr Ser Lys Asn Gly Ser Gln Asp Phe Gln Glu Ser Ala
 180 185 190
 Ile Gln Ser Leu Gln His Val Ser Thr Gln Ala Met Gln Glu Ala Ile
 195 200 205
 Ser Leu Ile Lys Lys Ala Val Glu Ala Gln Ser Val Ser Pro Leu Lys
 210 215 220
 Lys
 225

(2) INFORMATION FOR SEQ ID NO:862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

Leu Glu Arg His Val Asn Tyr Thr Leu Ile Gly Gly Leu Phe Phe Leu
 1 5 10 15
 Cys Leu Val Cys Met Val Gly Phe Ile Leu Trp Leu Gly His Leu Gly
 20 25 30
 Leu Asp Asp Gly Lys Tyr Tyr Glu Tyr Val Val Tyr Thr Asp Lys Asp
 35 40 45
 Leu Gly Gly Ile Ala Thr Asn Ser Pro Ile Asn Tyr Lys Gly Ile Gln
 50 55 60
 Val Gly Asn Val Ile Lys Val Gly Phe Ala Lys Asp Lys Val Gly Val
 65 70 75 80
 Val Arg Leu Asp Leu Met Ile Lys Ser Ser Val Lys Ile Arg Lys Asp
 85 90 95
 Ser Lys Val Ala Val Ser Ser Arg Gly Phe Met Gly Leu Lys Phe Leu
 100 105 110
 Ala Leu Glu Gln Ser His Asn Glu Phe Tyr Gly Ser Gly Asp Lys
 115 120 125
 Gly Glu Arg Ile Leu Ile Phe Lys Glu Gly Leu Met Asp Arg Leu Ser
 130 135 140
 Gly Asp Ala Asn Gln Val Val Gln Glu Val Met Lys Ala Ile Arg Asn
 145 150 155 160

768

```

Val Asn Arg Ile Leu Asp Asp Glu Asn Val Glu Lys Phe Lys His Ile
      165                      170                      175
Leu Ala Ser Val Asp Asp Leu Ile Ala Asn Leu Asp Ser Arg Lys Thr
      180                      185                      190
Gln Phe Asp Ser Leu Ile Asn Asn Ala Asn Asn Leu Val Ser Asn Val
      195                      200                      205
Asn Asn Val Ala Leu Asp Val Asp Lys Arg Val Lys Gln Gly Gln Tyr
      210                      215                      220
Asp Phe Lys Ala Met Phe Thr Pro Leu Ile Met Gln Ala Gln Leu Ser
      225                      230                      235                      240
Leu Arg Asn Ile Asp Asn Phe Val Glu Lys Gly Ser Ala Leu Ile Asp
      245                      250                      255
Lys Phe Asp Ala Asn Pro Tyr Lys Thr Ile Phe Gly Glu Arg Lys
      260                      265                      270

```

(2) INFORMATION FOR SEQ ID NO:863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

```

Met Lys Lys Thr Ile Leu Leu Ser Ala Leu Leu Ala Phe Ser Cys Ala
1      5      10      15
His Ala Leu Ser Asp Met Asp Leu Ile Lys Lys Ala Lys Glu Ser Gln
      20      25      30
Leu Glu Pro Met Pro Met Gly Lys Ala Leu Lys Glu Tyr Gln Ile Lys
      35      40      45
Lys Thr Arg Asp Val Gly Ile Gly Ala Lys Asn Ser Glu Ile Met Thr
      50      55      60
Ser Ala Gln Val Glu Leu Gly Lys Met Leu Tyr Phe Asp Pro Arg Ile
      65      70      75      80
Ser Thr Ser Tyr Leu Val Ser Cys Asn Thr Cys His Asn Leu Gly Leu
      85      90      95
Gly Gly Val Asp Leu Ile Pro Ser Ala Ile Gly Ser Gln Trp Lys Lys
      100     105     110
Asn Pro His Leu Leu Ser Ser Pro Thr Val Tyr Asn Ser Val Phe Asn
      115     120     125
Asp Val Gln Phe Trp Asp Gly Arg Val Thr His Leu Asn Glu Gln Ala
      130     135     140
Gln Gly Pro Ile Gln Ser Ser Phe Glu Met Gly Ala Asp Pro Lys Val
      145     150     155     160
Val Val Glu Lys Ile Asn Ser Ile Pro Gly Tyr Val Lys Leu Phe Arg
      165     170     175

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.769

```

Lys Ala Tyr Gly Ser Lys Val Lys Ile Asp Phe Lys Leu Ile Ala Asp
      180                      185                      190
Ser Ile Ala Met Phe Glu Ala Thr Leu Ile Thr Pro Ser Arg Tyr Asp
      195                      200                      205
Asp Phe Leu Arg Gly Asn Pro Lys Ala Leu Ser Lys Ala Glu Lys Glu
      210                      215                      220
Gly Leu Asp Leu Phe Ile Ser Lys Gly Cys Val Ala Cys His Asn Gly
      225                      230                      235                      240
Ile Asn Leu Gly Gly Thr Met Gln Pro Phe Gly Val Val Lys Pro Tyr
      245                      250                      255
Lys Phe Ala Asn Val Gly Asp Phe Lys Gly Asp Lys Asn Gly Leu Val
      260                      265                      270
Lys Val Pro Thr Leu Arg Asn Ile Thr Glu Thr Met Pro Tyr Phe His
      275                      280                      285
Asn Gly Gln Phe Trp Asp Val Lys Asp Ala Ile Lys Glu Met Gly Ser
      290                      295                      300
Ile Gln Leu Gly Ile Glu Ile Ser Asp Ala Glu Ala Lys Lys Ile Glu
      305                      310                      315                      320
Thr Phe Phe Glu Ala Leu Lys Gly Lys Lys Pro Lys Ile Ile Tyr Pro
      325                      330                      335
Glu Leu Pro Val Met Thr Asp Lys Thr Pro Lys Pro Ser Phe
      340                      345                      350

```

(2) INFORMATION FOR SEQ ID NO:864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

```

Met Met Asp Leu Glu Ser Leu Arg Gly Phe Ala Tyr Ala Phe Phe Thr
1          5          10          15
Ile Leu Phe Thr Leu Phe Leu Tyr Ala Tyr Ile Phe Ser Met Tyr Arg
      20          25          30
Lys Gln Lys Lys Gly Ile Val Asp Tyr Glu Arg Tyr Gly Tyr Leu Ala
      35          40          45
Leu Asn Asp Ala Leu Glu Asp Glu Leu Ile Glu Pro Arg His Lys Glu
      50          55          60
Val His Asp Lys Gly Ile Lys Glu Ser
      65          70

```

(2) INFORMATION FOR SEQ ID NO:865:

(i) SEQUENCE CHARACTERISTICS:

770

(A) LENGTH: 275 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

```

Leu Leu Asp Val Lys Ala Asn Ser Pro Ala Tyr Gln Ala Val Leu Leu
1           5           10           15
Ala Leu Asn Ala Ala Val Gly Leu Trp Gln Val Thr Ser Tyr Ala Phe
20           25           30
Thr Ala Cys Gly Pro Gly Ser Asn Glu Asn Ala Asn Gly Gly Ile Gln
35           40           45
Thr Phe Asn Asn Val Pro Gly Gln Asn Thr Thr Thr Ile Thr Cys Asn
50           55           60
Ser Tyr Tyr Glu Pro Gly His Gly Gly Pro Ile Ser Thr Glu Asn Tyr
65           70           75           80
Ala Ile Ile Asn Lys Ala Tyr Gln Ile Ile Gln Lys Ala Leu Thr Ala
85           90           95
Asn Gly Glu Gly Ile Pro Val Leu Ser Asn Thr Thr Thr Lys Leu Asp
100          105          110
Phe Thr Ile Asn Gly Asp Lys Arg Thr Gly Gly Glu Pro Asn Lys Lys
115          120          125
Leu Val Tyr Pro Trp Ser His Gly Lys Pro Ile Ser Thr Ser Trp Asn
130          135          140
Ala Thr Ile Thr Val Pro Thr Thr Glu Asn Ile Asn Thr Thr Asn Ser
145          150          155          160
Ala Gln Glu Leu Leu Lys Gln Ala Ser Ile Ile Ile Thr Thr Leu Asn
165          170          175
Ser Ala Cys Pro Asn Phe Gln Asn Gly Gly Ser Gly Tyr Trp Ala Gly
180          185          190
Ile Ser Gly Asn Gly Thr Met Cys Gly Met Phe Lys Asn Glu Ile Ser
195          200          205
Ala Ile Gln Gly Met Ile Ala Asn Ala Gln Glu Ala Val Ala Gln Ala
210          215          220
Lys Ile Val Ser Glu Asn Thr Gln Asn Gln Asn Ser Leu Asp Ala Glu
225          230          235          240
Asn His Ser Thr Pro Thr Gln Thr Leu Val Leu Leu Lys Ala Cys Ser
245          250          255
Lys Thr Arg Ser Pro Ser Gly Asp Phe Lys Pro Ser Arg Thr Ser Gly
260          265          270
Glu Lys Leu
275

```

(2) INFORMATION FOR SEQ ID NO:866:

(i) SEQUENCE CHARACTERISTICS:

771

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

```

Met Leu Thr Ile Glu Thr Ser Lys Lys Phe Asp Lys Asp Leu Lys Ile
1           5           10           15
Leu Val Lys Asn Gly Phe Asp Leu Lys Leu Leu Tyr Lys Val Val Gly
          20           25           30
Asn Leu Ala Thr Glu Gln Pro Leu Glu Pro Lys Tyr Lys Asp His Pro
          35           40           45
Leu Lys Gly Ala Leu Lys Asp Phe Arg Glu Cys His Leu Lys Pro Asp
          50           55           60
Leu Leu Leu Val Tyr Gln Ile Lys Lys Gln Glu Asn Thr Leu Phe Leu
65           70           75           80
Val Arg Leu Gly Ser His Ser Glu Leu Phe
          85           90

```

(2) INFORMATION FOR SEQ ID NO:867:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

```

Met Leu Glu Ile Glu Leu Lys Lys Lys Phe Thr Lys Asp Leu Lys Lys
1           5           10           15
His Ile Leu Asn Gln Lys Ile Glu Leu Glu Val Phe Asp Leu Val Val
          20           25           30
Glu Asn Leu Arg Asn Gln Ile Pro Leu Asp Lys Arg Phe Lys Asp His
          35           40           45
Ala Leu Ser Gly Thr Tyr Lys Gly Cys Arg Glu Arg His Ile Lys Pro

```

772

```

      50              55              60
Asp Val Leu Leu Val Tyr Arg Val Lys Gly Asn Val Leu Thr Leu Val
65              70              75              80
Arg Leu Gly Ser His Ser Glu Leu Phe Cys Lys Pro Pro Thr Pro Leu
      85              90              95
Ile Thr Leu Lys
      100

```

(2) INFORMATION FOR SEQ ID NO:868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

```

Leu Val Val Ser Gly Ser Leu Gln Asn Ile Val Arg Ser Phe Leu Arg
1              5              10              15
Arg Ile Ser Val Phe Phe Ile Ile Asp Phe Ile Asn Phe Ile Phe Val
      20              25              30
Ile Asp Gln Ile Ile His Phe Phe Gly Asp Phe Phe Ile Phe Phe Phe
      35              40              45
Met Leu Asn Leu Phe Tyr Ile Leu Ile Arg Leu Ile Asp Leu Ile Val
      50              55              60
Leu Ser Gly Phe Ser Val Val Leu Val Arg Leu Gly Arg Phe Phe Arg
65              70              75              80
Leu Ile Phe Ala Gly Ala Gln His Ala
      85

```

(2) INFORMATION FOR SEQ ID NO:869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

```

Met Lys Lys Ser Leu Cys Leu Ser Phe Phe Leu Thr Phe Ser Asn Pro
1      5      10      15
Leu Gln Ala Leu Val Ile Glu Leu Leu Glu Glu Ile Lys Thr Ser Pro
      20      25      30
His Lys Gly Thr Phe Lys Ala Lys Val Leu Asp Ser Lys Glu Pro Arg
      35      40      45
Gln Val Leu Gly Val Tyr Asn Ile Ser Pro His Lys Lys Leu Thr Leu
      50      55      60
Thr Ile Thr His Ile Ser Thr Ala Ile Val Tyr Gln Pro Leu Asp Glu
65      70      75      80
Lys Leu Ser Leu Glu Thr Thr Leu Ser Pro Asn Arg Pro Thr Ile Pro
      85      90      95
Arg Asn Thr Gln Ile Val Phe Ser Ser Lys Glu Leu Lys Glu Pro His
      100     105     110
Ser Asn Pro Ile Pro Ser Leu Asn Ala Pro Met Gln Lys Pro Gln Asn
      115     120     125
Lys Pro Ser Ser Ser Gln Gln Ser Pro Gln Asn Phe Ser Tyr Pro Glu
      130     135     140
Ser Lys Leu Gly Ser Lys Asn Ser Lys Asn Ser Leu Leu Gln Pro Leu
145     150     155     160
Val Thr Pro Ser Lys Val Ser Pro Thr Asn Glu Val Lys Thr Pro Thr
      165     170     175
Asn Asp Ala Asn Pro Pro Leu Lys His Ser Ser Gln Asp Gln Glu Asn
      180     185     190
Asn Leu Phe Val Ala Pro Pro Thr Glu Lys Thr Leu Pro Asn Asn Thr
      195     200     205
Ser Ser Ala Asp Ala Ser Glu Asn Asn Glu Ser Asn Glu Asn Arg Asp
      210     215     220
Asn Val Glu Lys Gln Ala Ile Arg Asp Pro Asn Ile Lys Glu Phe Ala
225     230     235     240
Cys Gly Lys Trp Val Tyr Asp Asp Glu Asn Leu Gln Ala Tyr Arg Pro
      245     250     255
Ser Ile Leu Lys Arg Val Asp Lys Asp Lys Glu Ile Thr Thr Asp Ile
      260     265     270
Thr Pro Cys Asp Tyr Ser Thr Ala Glu Asn Lys Ser Gly Lys Ile Ile
      275     280     285
Thr Pro Tyr Thr Lys Ile Ser Val His Lys Thr Glu Pro Leu Glu Asp
      290     295     300
Pro Gln Thr Phe Glu Ala Lys Asn Asn Phe Ala Ile Leu Gln Ala Arg
305     310     315     320
Ser Ser Thr Glu Lys Cys Lys Arg Ala Arg Ala Arg Lys Asp Gly Thr
      325     330     335
Thr Arg Gln Cys Tyr Leu Ile Glu Glu Pro Leu Lys Gln Ala Trp Glu
      340     345     350
Ser Glu Tyr Glu Ile Thr Thr Gln Leu Val Lys Ala Ile Tyr Glu Arg
      355     360     365
Pro Lys Gln Asp Asp Gln Val Glu Pro Thr Phe Tyr Glu Thr Ser Glu
      370     375     380
Leu Ala Tyr Ser Ser Thr Arg Lys Ser Glu Ile Thr Arg Asn Glu Leu
385     390     395     400
Asn Leu Asn Glu Lys Phe Met Glu Phe Val Glu Val Tyr Glu Gly His
      405     410     415
Tyr Leu Asn Asp Ile Ile Lys Glu Ser Ser Glu Tyr Lys Glu Trp Val

```

	420		425		430										
Lys	Asn	His	Val	Arg	Phe	Lys	Glu	Gly	Val	Cys	Met	Ala	Leu	Glu	Ile
	435						440					445			
Glu	Glu	Gln	Pro	Arg	Ala	Lys	Ser	Thr	Pro	Leu	Ser	Ile	Glu	Asn	Ser
	450						455					460			
Arg	Val	Val	Cys	Val	Lys	Lys	Gly	Asn	Tyr	Leu	Phe	Asn	Glu	Val	
465					470					475					

(2) INFORMATION FOR SEQ ID NO:870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

Met	Lys	Lys	Ser	Leu	Cys	Leu	Ser	Phe	Phe	Leu	Thr	Phe	Ser	Asn	Pro
1				5					10					15	
Leu	Gln	Ala	Leu	Val	Ile	Glu	Leu	Leu	Glu	Glu	Ile	Lys	Thr	Ser	Pro
			20					25					30		
His	Lys	Gly	Thr	Phe	Lys	Ala	Lys	Val	Leu	Asp	Ser	Lys	Glu	Pro	Arg
		35					40					45			
Gln	Val	Leu	Gly	Val	Tyr	Asn	Ile	Ser	Pro	His	Lys	Lys	Leu	Thr	Leu
	50					55					60				
Thr	Ile	Thr	His	Ile	Ser	Thr	Ala	Ile	Val	Tyr	Gln	Pro	Leu	Asp	Glu
65				70						75				80	
Lys	Leu	Ser	Leu	Glu	Thr	Thr	Leu	Ser	Pro	Asn	Arg	Pro	Thr	Ile	Pro
			85					90					95		
Arg	Asn	Thr	Gln	Ile	Val	Phe	Ser	Ser	Lys	Glu	Leu	Lys	Glu	Pro	His
			100					105					110		
Ser	Asn	Pro	Ile	Pro	Ser	Leu	Asn	Ala	Pro	Met	Gln	Lys	Pro	Gln	Asn
		115					120					125			
Lys	Pro	Ser	Ser	Ser	Gln	Gln	Ser	Pro	Gln	Asn	Phe	Ser	Tyr	Pro	Glu
	130					135					140				
Ser	Lys	Leu	Gly	Ser	Lys	Asn	Ser	Lys	Asn	Ser	Leu	Leu	Gln	Pro	Leu
145				150						155				160	
Val	Thr	Pro	Ser	Lys	Val	Ser	Pro	Thr	Asn	Glu	Val	Lys	Thr	Pro	Thr
			165					170					175		
Asn	Asp	Ala	Asn	Pro	Pro	Leu	Lys	His	Ser	Ser	Gln	Asp	Gln	Glu	Asn
		180						185					190		
Asn	Leu	Phe	Val	Ala	Pro	Pro	Thr	Glu	Lys	Thr	Leu	Pro	Asn	Asn	Thr
	195						200					205			
Ser	Ser	Ala	Asp	Ala	Ser	Glu	Asn	Asn	Glu	Ser	Asn	Glu	Asn	Arg	Asp
	210					215					220				
Asn	Val	Glu	Lys	Gln	Ala	Ile	Arg	Asp	Pro	Asn	Ile	Lys	Glu	Phe	Ala

775

```

225          230          235          240
Cys Gly Lys Trp Val Tyr Asp Asp Glu Asn Leu Gln Ala Tyr Arg Pro
          245          250          255
Ser Ile Leu Lys Arg Val Asp Lys Asp Lys Glu Ile Thr Thr Asp Ile
          260          265          270
Thr Pro Cys Asp Tyr Ser Thr Ala Glu Asn Lys Ser Gly Lys Ile Ile
          275          280          285
Thr Pro Tyr Thr Lys Ile Ser Val His Lys Thr Glu Pro Leu Glu Asp
          290          295          300
Pro Gln Thr Phe Glu Ala Lys Asn Asn Phe Ala Ile Leu Gln Ala Arg
305          310          315          320
Ser Ser Thr Glu Lys Cys Lys Arg Ala Arg Ala Arg Lys Asp Gly Thr
          325          330          335
Thr Arg Gln Cys Tyr Leu Ile Glu Glu Pro Leu Lys Gln Ala Trp Glu
          340          345          350
Ser Glu Tyr Glu Ile Thr Thr Gln Leu Val Lys Ala Ile Tyr Glu Arg
          355          360          365
Pro Lys Gln Asp Asp Gln Val Glu Pro Thr Phe Tyr Glu Thr Ser Glu
          370          375          380
Leu Ala Tyr Ser Ser Thr Arg Lys Ser Glu Ile Thr Arg Asn Glu Leu
385          390          395          400
Asn Leu Asn Glu Lys Phe Met Glu Phe Val Glu Val Tyr Glu Gly His
          405          410          415
Tyr Leu Asn Asp Ile Ile Lys Glu Ser Ser Glu Tyr Lys Glu Trp Val
          420          425          430
Lys Asn His Val Arg Phe Lys Glu Gly Val Cys Met Ala Leu Glu Ile
          435          440          445
Glu Glu Gln Pro Arg Ala Lys Ser Thr Pro Leu Ser Ile Glu Asn Ser
          450          455          460
Arg Val Val Cys Val Lys Lys Gly Asn Tyr Leu Phe Asn Glu Val
465          470          475

```

(2) INFORMATION FOR SEQ ID NO:871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

```

Met Arg Lys Thr Ile Ser Ala Leu Phe Leu Ser Ala Cys Ile Gly Leu
1          5          10          15
Ser Ser Val His Ala Ser Asn Ala Leu Ile Leu Gln Thr Asp Phe Ser
          20          25          30
Leu Lys Asp Gly Ala Val Ser Ala Met Lys Gly Val Ala Phe Ser Val

```

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...156

(xi) SEQUENCE DESCRIPTION: SEO ID NO:872:

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

777

20						25						30					
Lys	Ser	Leu	Thr	Ala	Tyr	Leu	Asn	Ala	Tyr	Leu	Glu	Gln	Arg	Pro	Asn		
35						40						45					
Ile	Glu	Gly	Met	Gly	Ile	Ile	Gly	Val	Pro	Phe	Lys	Cys	Glu	Arg	Phe		
50						55						60					
Phe	Lys	Ile	Ala	Cys	Val	Ser	Lys	Glu	Leu	Arg	Phe	Leu	Asp	Pro	Gln		
65			70						75			80					
Asn	Ser	Pro	Ile	Met	Asp	Phe	Lys	Asn	Leu	Lys	Ile	Lys	Leu	His	Ser		
			85						90			95					
Leu	Asp	Lys	Ser	Ser	Leu	Thr	Leu	Ser	Ile	His	Ser	Gln	Ile	Gln	Ser		
			100						105			110					
Pro	Ile	Leu	Glu	Gln	Ser	Ile	Gln	Gln	Lys	Ile	Ser	Gln	Ile	Pro	Leu		
115						120						125					
Lys	Asn	Leu	Asn	Ala	Leu	Leu	Glu	Lys	Phe	Lys	Pro	Thr	Arg	Leu	Asn		
130						135						140					
Cys	Ser	Leu	Thr	Phe	Asn	Ala	Leu	Asp	Glu	Lys	Thr						
145			150						155								

(2) INFORMATION FOR SEQ ID NO:873:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

Met	Gln	Asp	Phe	Ile	Lys	Ile	Phe	Ile	Gln	Glu	Val	Val	Ser	Thr	Leu
1				5					10					15	
Glu	Gly	Leu	Val	Gly	Lys	Ala	Pro	Ser	Val	Gly	Leu	Glu	Lys	Glu	Val
			20					25					30		
Ser	Asn	Asn	Glu	Glu	Ala	Ser	Leu	Ile	Ser	Thr	Pro	Tyr	Ala	Arg	Val
		35					40					45			
Lys	Ile	Ser	Ala	Ile	Glu	Lys	Asn	Glu	Ser	Pro	Ile	Glu	Leu	Leu	Ala
	50					55					60				
Pro	Val	Asp	Leu	Val	Thr	Ala	Leu	Ser	Asp	Leu	Met	Leu	Gly	Gly	Glu
65					70					75					80
Gly	Ala	Ser	Lys	Glu	Glu	Met	Asp	Asn	Asp	Asp	Leu	Asp	Ala	Phe	Lys
				85					90					95	
Glu	Met	Ala	Ser	Asn	Ile	Phe	Gly	Ala	Ile	Ala	Thr	Ser	Leu	Lys	Ser
			100					105					110		
Gln	Glu	Leu	Leu	Pro	Lys	Leu	Asn	Phe	Thr	Thr	Thr	Asn	Ala	Glu	Ile
		115					120					125			
Ala	Lys	Glu	Leu	Pro	Lys	Lys	Glu	Asp	Tyr	Ala	Lys	Ala	Met	Val	Phe
	130					135					140				
Ser	Phe	Lys	Met	Glu	Ala	Ile	Lys	Glu	Ser	Gln	Ile	Val	Leu	Leu	Ile

778

```

145          150          155          160
Thr Ser Ala Phe Glu Gly Gln Phe Glu Lys Thr His Lys Glu Glu Lys
          165          170          175
Glu Glu Thr Thr Lys Ser Ala Thr Glu Glu Thr Lys Thr His Asp Ala
          180          185          190
Ser Leu Glu Asn Ile Glu Ile Arg Asn Ile Ser Met Leu Leu Asp Val
          195          200          205
Lys Leu Asn Val Lys Val Arg Ile Gly Gln Lys Lys Met Ile Leu Lys
          210          215          220
Asp Val Val Ser Met Asp Ile Gly Ser Val Val Glu Leu Asp Gln Leu
225          230          235          240
Val Asn Asp Pro Leu Glu Ile Leu Val Asp Asp Lys Val Ile Ala Lys
          245          250          255
Gly Glu Val Val Ile Val Asp Gly Asn Phe Gly Ile Gln Ile Thr Asp
          260          265          270
Ile Gly Thr Lys Lys Glu Arg Leu Glu Gln Leu Lys Asn
          275          280          285

```

(2) INFORMATION FOR SEQ ID NO:874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

```

Met Thr Thr Lys Arg Val Asn Thr Ala Thr Asn Lys Ile Met Thr Leu
1          5          10          15
Asn Thr Phe Leu Asp Thr Cys Phe Leu Phe Phe Ile Ser Ile Leu Phe
          20          25          30
Tyr Leu Ser Ile Pro Ile Tyr Pro Asn Lys Val Val Val Pro Gln
          35          40          45
Gly Ser Leu Lys Lys Val Phe Phe Ser Leu Lys Glu Gln Gly Val Asp
          50          55          60
Ile Asn Ala Leu Asp Leu Leu Leu Leu Arg Leu Met Gly Met Pro Lys
65          70          75          80
Lys Gly Tyr Ile Asp Met Gly Asp Gly Ala Leu Arg Lys Gly Asp Phe
          85          90          95
Leu Val Arg Leu Ile Lys Ala Lys Thr Ala Gln Lys Ser Val Thr Leu
          100          105          110
Ile Pro Gly Glu Thr Arg Tyr Phe Phe Thr Gln Ile Leu Ser Glu Thr
          115          120          125
Tyr Gln Leu Glu Thr Ser Asp Leu Asn Glu Ala Tyr Glu Ser Ile Ala
          130          135          140
Pro Arg Leu Asn Gly Ala Val Ile Glu Asp Gly Val Ile Trp Pro Asp

```


779

```

145          150          155          160
Thr Tyr His Leu Pro Leu Gly Glu Asp Ala Phe Lys Ile Met Gln Thr
          165          170          175
Leu Ile Gly Gln Ser Met Lys Lys His Glu Ala Leu Ser Lys Gln Trp
          180          185          190
Leu Gly Tyr Tyr His Lys Glu Glu Trp Phe Glu Lys Ile Ile Leu Ala
          195          200          205
Ser Ile Val Gln Lys Glu Ala Ala Asn Val Glu Glu Met Pro Leu Ile
          210          215          220
Ala Ser Val Ile Phe Asn Arg Leu Lys Lys Gly Met Pro Leu Gln Met
225          230          235          240
Asp Gly Ala Leu Asn Tyr Gln Glu Phe Ser His Ala Lys Val Thr Lys
          245          250          255
Glu Arg Ile Lys Thr Asp Asn Thr Pro Tyr Asn Thr Tyr Lys Phe Lys
          260          265          270
Gly Leu Pro Lys Asn Pro Val Gly Ser Val Ser Leu Glu Ala Val Arg
          275          280          285
Ala Val Val Phe Pro Lys Lys Thr Asp Phe Leu Tyr Phe Val Lys Met
          290          295          300
Pro Asp Lys Lys His Ala Phe Ser Ala Thr Tyr Lys Glu His Leu Lys
305          310          315          320
Asn Ile Asn Ile Ser Asn Asn His Phe
          325

```

(2) INFORMATION FOR SEQ ID NO:875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

```

Met Arg Leu Leu Phe Leu Leu Leu Ser Ala Thr Leu Met Leu Leu Ala
1          5          10          15
Glu Glu Lys Ile Pro Leu Ser Asp Asp Ala Pro Ile Lys Leu Val His
          20          25          30
Trp Gln Asn Ala Leu Lys Glu Val Gln Pro Asp Ser Asn Ala Pro Ala
          35          40          45
Thr Pro Pro Ile Lys Ala Val Gln Thr Thr Leu Thr Phe Glu Thr Pro
          50          55          60
Phe Asn Lys Thr Pro Lys Ile Met Glu Val Glu Gly Gln Lys Val Ile
65          70          75          80
Val Leu Lys Asn Ala Gln Leu Asp Ser Lys Lys Thr Met Asp Phe Lys
          85          90          95
Glu Ala Ser Leu Asn Ala Leu Glu Met Phe Ser Tyr Gln Asn Asp Ile

```

```

          100              105              110
Tyr Leu Leu Ser Lys Lys Ala Lys Ala Gly Leu Glu Ile Gln Ala Ser
          115              120              125
Ser Ser Lys Asp Lys Lys Gln Leu Ala Phe Phe Phe Tyr Pro Lys Val
          130              135              140
Phe Ile
145

```

(2) INFORMATION FOR SEQ ID NO:876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

```

Met Leu Lys Lys Ile Phe Tyr Gly Phe Ile Val Leu Phe Leu Ile Ile
1           5           10           15
Val Gly Leu Leu Ala Val Leu Val Ala Gln Val Trp Val Thr Thr Asp
          20           25           30
Lys Asp Ile Ala Lys Ile Lys Asp Tyr Arg Pro Ser Val Ala Ser Gln
          35           40           45
Ile Leu Asp Arg Lys Gly Arg Leu Ile Ala Asn Ile Tyr Asp Lys Glu
          50           55           60
Phe Arg Phe Tyr Ala Arg Phe Glu Glu Ile Pro Pro Arg Phe Val Glu
65           70           75           80
Ser Leu Leu Ala Val Glu Asp Thr Leu Phe Phe Glu His Gly Gly Ile
          85           90           95
Asn Leu Asp Ala Val Met Arg Ala Met Ile Lys Asn Ala Lys Ser Gly
          100          105          110
Arg Tyr Thr Glu Gly Gly Ser Thr Leu Thr Gln Gln Leu Val Lys Asn
          115          120          125
Met Val Leu Thr Arg Glu Lys Thr Leu Thr Arg Lys Leu Lys Glu Ala
          130          135          140
Ile Ile Ser Ile Arg Ile Glu Lys Val Leu Ser Lys Glu Glu Ile Leu
145          150          155          160
Glu Arg Tyr Leu Asn Gln Thr Phe Phe Gly His Gly Tyr Tyr Gly Val
          165          170          175
Lys Thr Ala Ser Leu Gly Tyr Phe Lys Lys Pro Leu Asp Lys Leu Thr
          180          185          190
Leu Lys Glu Ile Thr Met Leu Val Ala Leu Pro Arg Ala Pro Ser Phe
          195          200          205
Tyr Asp Pro Thr Lys Asn Leu Glu Phe Ser Leu Ser Arg Ala Asn Asp
210          215          220
Ile Leu Arg Arg Leu Tyr Ser Leu Gly Trp Ile Ser Ser Asn Glu Leu

```

781

225		230		235		240
Lys Ser Ala Leu Asn Glu Val Pro Ile Val Tyr Asn Gln Thr Ser Thr						
	245			250		255
Gln Asn Ile Ala Pro Tyr Val Val Asp Glu Val Leu Lys Gln Leu Asp						
	260			265		270
Gln Leu Asp Gly Leu Lys Thr Gln Gly Tyr Thr Ile Lys Leu Thr Ile						
	275			280		285
Asp Leu Asp Tyr Gln Arg Leu Ala Leu Glu Ser Leu Arg Phe Gly His						
	290			295		300
Gln Lys Ile Leu Glu Lys Ile Ala Lys Glu Lys Pro Lys Thr Asn Ala						
305		310			315	320
Ser Asn Asp Lys Asp Glu Asp Asn Leu Asn Ala Ser Met Ile Val Thr						
	325			330		335
Glu Thr Ser Thr Gly Lys Ile Leu Ala Leu Val Gly Gly Ile Asp Tyr						
	340			345		350
Lys Lys Ser Ala Phe Asn Arg Ala Thr Gln Ala Lys Arg Gln Phe Gly						
	355			360		365
Ser Ala Ile Lys Pro Phe Val Tyr Gln Ile Ala Phe Asp Asn Gly Tyr						
	370			375		380
Ser Thr Thr Ser Lys Ile Pro Asp Thr Ala Arg Asn Phe Glu Asn Gly						
385		390			395	400
Asn Tyr Ser Lys Asn Ser Val Gln Asn His Ala Trp His Pro Ser Asn						
	405			410		415
Tyr Thr Arg Lys Phe Leu Gly Leu Val Thr Leu Gln Glu Ala Leu Ser						
	420			425		430
His Ser Leu Asn Leu Ala Thr Ile Asn Leu Ser Asp Gln Leu Gly Phe						
	435			440		445
Glu Lys Ile Tyr Gln Ser Leu Ser Asp Met Gly Phe Lys Asn Leu Pro						
	450			455		460
Lys Asp Leu Ser Ile Val Leu Gly Ser Phe Ala Ile Ser Pro Ile Asp						
465		470			475	480
Ala Ala Glu Lys Tyr Ser Leu Phe Ser Asn Tyr Gly Thr Met Leu Lys						
	485			490		495
Pro Met Leu Ile Glu Ser Ile Thr Asn Gln Gln Asn Glu Val Lys Thr						
	500			505		510
Phe Thr Pro Ile Glu Thr Lys Lys Ile Thr Ser Lys Glu Gln Ala Phe						
	515			520		525
Leu Thr Leu Ser Ala Leu Met Asp Ala Val Glu Asn Gly Thr Gly Ser						
	530			535		540
Leu Ala Arg Ile Lys Gly Leu Glu Ile Ala Gly Lys Thr Gly Thr Ser						
545		550			555	560
Asn Asn Asn Ile Asp Ala Trp Phe Ile Gly Phe Thr Pro Thr Leu Gln						
	565			570		575
Ser Val Ile Trp Phe Gly Arg Asp Asp Asn Thr Pro Ile Gly Lys Gly						
	580			585		590
Ala Thr Gly Gly Val Val Ser Ala Pro Val Tyr Ser Tyr Phe Met Arg						
	595			600		605
Asn Ile Leu Ala Ile Glu Pro Ser Leu Lys Arg Lys Phe Asp Val Pro						
	610			615		620
Lys Gly Leu Arg Lys Glu Ile Val Asp Lys Ile Pro Tyr Tyr Ser Ser						
625		630			635	640
Pro Asn Ser Ile Thr Pro Thr Pro Lys Lys Thr Asp Asp Ser Glu Glu						
	645			650		655
Arg Leu Leu Phe						
	660					

(2) INFORMATION FOR SEQ ID NO:877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

```

Met Ala Lys Met Asn Ala Pro Asp Gly Val Ala Val Trp Val Asn Glu
1           5           10           15
Asp Arg Cys Lys Gly Cys Asp Ile Cys Val Ser Val Cys Pro Ala Gly
          20           25           30
Val Leu Gly Met Gly Ile Glu Lys Glu Arg Val Leu Gly Lys Val Ala
          35           40           45
Lys Val Ala Tyr Pro Glu Ser Cys Ile Gly Cys Val Gln Cys Glu Leu
          50           55           60
His Cys Pro Asp Phe Ala Ile Tyr Val Ala Asp Arg Lys Asp Phe Lys
65           70           75           80
Phe Ala Lys Val Ser Lys Glu Ala Gln Glu Arg Ser Glu Lys Val Lys
          85           90           95
Ala Asn Lys Tyr Met Leu Leu Glu Glu Thr Ile Leu Glu Gly Arg Gly
          100          105          110
Lys

```

(2) INFORMATION FOR SEQ ID NO:878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

```

Met Ile Phe Ile Asp Ala Cys Phe Arg Lys Glu Thr Pro Tyr Thr Pro

```

783

1		5		10		15									
Ile	Trp	Met	Met	Arg	Gln	Ala	Gly	Arg	Tyr	Leu	Ser	Glu	Tyr	Gln	Glu
		20						25					30		
Ser	Arg	Lys	Lys	Ala	Gly	Ser	Phe	Leu	Glu	Leu	Cys	Lys	Asn	Ser	Asp
		35					40					45			
Leu	Ala	Thr	Glu	Val	Thr	Leu	Gln	Pro	Val	Glu	Ile	Leu	Gly	Val	Asp
	50					55					60				
Ala	Ala	Ile	Leu	Phe	Ser	Asp	Ile	Leu	Val	Val	Pro	Leu	Glu	Met	Gly
65					70					75					80
Leu	Asn	Leu	Glu	Phe	Ile	Pro	Lys	Lys	Gly	Pro	His	Phe	Leu	Glu	Thr
				85					90					95	
Ile	Thr	Asp	Leu	Lys	Ser	Val	Glu	Ser	Leu	Lys	Val	Gly	Val	Tyr	Lys
			100					105					110		
Gln	Leu	Asn	Tyr	Val	Tyr	Asp	Thr	Ile	Ser	Gln	Thr	Arg	Gln	Lys	Leu
		115					120					125			
Ser	Lys	Glu	Lys	Ala	Leu	Ile	Gly	Phe	Cys	Gly	Ser	Pro	Trp	Thr	Leu
		130				135					140				
Ala	Thr	Tyr	Met	Ile	Glu	Gly	Glu	Gly	Ser	Lys	Ser	Tyr	Ala	Lys	Ser
145					150					155					160
Lys	Lys	Met	Leu	Tyr	Ser	Glu	Pro	Glu	Val	Leu	Lys	Ala	Leu	Leu	Glu
			165					170					175		
Lys	Leu	Ser	Leu	Glu	Leu	Ile	Glu	Tyr	Leu	Ser	Leu	Gln	Ile	Gln	Ala
			180					185					190		
Gly	Val	Asn	Ala	Val	Met	Ile	Phe	Asp	Ser	Trp	Ala	Ser	Ala	Leu	Glu
		195					200				205				
Lys	Glu	Ala	Tyr	Leu	Glu	Phe	Ser	Trp	Asp	Tyr	Leu	Lys	Lys	Ile	Ser
	210					215				220					
Lys	Glu	Leu	Lys	Lys	Arg	Tyr	Ala	His	Ile	Pro	Val	Ile	Leu	Phe	Pro
225				230						235					240
Lys	Gly	Ile	Gly	Ala	Tyr	Leu	Asp	Ser	Ile	Asp	Gly	Glu	Phe	Asp	Val
			245					250					255		
Phe	Gly	Val	Asp	Trp	Gly	Thr	Pro	Leu	Thr	Ala	Ala	Lys	Lys	Ile	Leu
		260						265					270		
Gly	Gly	Lys	Tyr	Val	Leu	Gln	Gly	Asn	Leu	Glu	Pro	Thr	Arg	Leu	Tyr
		275				280						285			
Asp	Lys	Asn	Ala	Leu	Glu	Glu	Gly	Val	Glu	Lys	Ile	Leu	Lys	Val	Met
	290					295				300					
Gly	Asn	Gln	Gly	His	Ile	Phe	Asn	Leu	Gly	His	Gly	Met	Leu	Pro	Asp
305				310						315					320
Leu	Pro	Arg	Glu	Asn	Ala	Lys	Tyr	Leu	Val	Gln	Leu	Val	His	Ala	Lys
			325					330					335		
Thr	Arg	Arg													

(2) INFORMATION FOR SEQ ID NO:879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

```

Val Leu Glu Lys Ser Phe Leu Lys Ser Lys Gln Leu Val Leu Cys Gly
1      5      10      15
Leu Gly Val Leu Met Leu Gln Ala Cys Thr Cys Pro Asn Thr Ser Gln
      20      25      30
Arg Asn Ser Phe Leu Gln Asp Val Pro Tyr Trp Met Leu Gln Asn Arg
      35      40      45
Ser Gln Tyr Leu Thr Gln Gly Val Asp Ser Ser His Ile Val Asp Gly
      50      55      60
Lys Ala Thr Glu Glu Ile Glu Lys Ile Ala Thr Lys Arg Ala Thr Ile
65      70      75      80
Arg Val Ala Gln Asn Ile Val His Lys Leu Lys Glu Ala Tyr Leu Ser
      85      90      95
Lys Ser Asn Arg Ile Lys Gln Lys Ile Thr Asn Glu Met Phe Ile Gln
      100     105     110
Met Thr Lys Pro Ile Phe Asp Ser Leu Met Asn Val Asp Arg Leu Gly
      115     120     125
Ile Tyr Ile Asn Pro Asn Asn Glu Glu Val Phe Ala Leu Val Arg Ala
      130     135     140
Arg Ser Phe Asp Lys Asp Ala Leu Ser Glu Gly Leu His Lys Met Ser
145     150     155     160
Leu Asp Asp Gln Ala Val Ser Ile Leu Val Ser Lys Val Glu Glu Ile
      165     170     175
Phe Lys Asp Ser Ile Asn Tyr Gly Asp Val Lys Val Pro Ile Ala Met
      180     185     190

```

(2) INFORMATION FOR SEQ ID NO:880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

```

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

```

785

35	40	45
Arg Lys Glu Leu Gln Gln Arg Gln Ser Asn Gln Ile Arg Asp Ile Phe		
50	55	60
Arg Thr Arg Ala Asp Val Asn Val Ala Ser Gly Gly Leu Met Ala Gln		
65	70	75
Lys Ile Tyr Val Arg Gly Ile Glu Ser Arg Leu Leu Arg Val Thr Ile		80
	85	90
Asp Gly Val Ala Gln Asn Gly Asn Ile Phe His His Asp Ala		95
100	105	110

(2) INFORMATION FOR SEQ ID NO:881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

Val Met Lys Lys Ile Val Val Ser Leu Cys Val Ala Leu Gly Phe Leu	
1	15
Ser Ala Asp Pro Ala Gln Ala Asn Lys Ala Ile Ser Asp Ala Asp Leu	
20	30
Ile Glu Glu Ile Arg Asp Leu Lys Lys Ile Ile Ser Ala Gln Asn Thr	
35	45
Glu Ile Asn Gln Leu Arg Lys Val Gln Glu Val Leu Ser Gly Gln Leu	
50	60
Gly Asp Met Arg Lys Asp Ile Leu Ser Thr Arg Asp Tyr Cys Ile Ser	
65	80
Leu Arg Pro Tyr Ile Tyr Asn Trp Arg	
85	

(2) INFORMATION FOR SEQ ID NO:882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

```

Leu Asn Lys Phe Gly Trp Arg Ala Cys Phe Leu Thr Leu Phe Phe Ser
1          5          10          15
Gly Tyr Ser Lys Lys Ala Pro Gly Thr Ile Gly Ser Leu Val Ala Leu
20          25          30
Leu Leu Gly Leu Pro Ile Leu Ile Phe Ser Ala Asn Thr Leu Phe Leu
35          40          45
Gly Ala Ile Phe Val Gly Leu Ile Ala Ile Thr Gln Ile Asp Lys Glu
50          55          60
Glu Glu Glu Thr Lys Arg His Asp Ser Ser Tyr Ile Val Ile Asp Glu
65          70          75          80
Leu Val Gly Met Trp Leu Ala Met Ala Ile Ser Gly Leu Ser Leu Val
85          90          95
Gly Val Ile Leu Ser Phe Ile Phe Phe Arg Ile Tyr Asp Ile Thr Lys
100         105         110
Pro Ser Leu Ile Gly Lys Ile Asp Lys Glu Val Lys Gly Gly Leu Gly
115         120         125
Val Val Ala Asp Asp Ala Leu Ala Gly Val Leu Ala Gly Leu Ser Thr
130         135         140
Leu Leu Ala Ile Asn Ile Leu Gly Phe Phe Asn Ile Lys Phe
145         150         155

```

(2) INFORMATION FOR SEQ ID NO:883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

```

Met Glu Leu Ile Lys Lys Leu Glu Lys Glu Ser Glu Val Leu Lys Lys
1          5          10          15
Asp Leu Gln Gln His Ser Asn Glu Leu Phe Lys Met Leu Ile Ile Asp
20          25          30
Asn Glu Asp Leu Phe Lys Glu Gln Phe Glu Ile Met Phe Lys Ala Trp
35          40          45
Val Glu Ile Val Lys Met Met Phe Glu Leu Thr Lys Lys Thr Lys Phe
50          55          60
Asp Gly Glu Met Ile Gly Tyr Thr Glu Glu Leu Leu Thr Phe Leu Val
65          70          75          80

```


787

Arg Asp Phe Phe Asn Gly Ile Phe Lys Ser Lys Val Ile Pro Lys Met
 85 90 95
 Pro Ile Phe Cys Gly Asp Val Lys Cys Glu Asp Phe Asn Ala Leu Arg
 100 105 110
 Ser Leu Val Tyr Leu Ser Val Leu Glu Leu Glu Glu Thr Ile Asn Pro
 115 120 125
 Asn Lys Ile Pro Phe
 130

(2) INFORMATION FOR SEQ ID NO:884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

Met Glu Leu Ile Lys Lys Leu Glu Lys Glu Ser Glu Val Leu Lys Lys
 1 5 10 15
 Asp Leu Gln Gln His Ser Asn Glu Leu Phe Lys Met Leu Ile Ile Asp
 20 25 30
 Asn Glu Asp Leu Phe Lys Glu Gln Phe Glu Ile Met Phe Lys Ala Trp
 35 40 45
 Val Glu Ile Val Lys Met Met Phe Glu Leu Thr Lys Lys Thr Lys Phe
 50 55 60
 Asp Gly Glu Met Ile Gly Tyr Thr Glu Glu Leu Leu Thr Phe Leu Val
 65 70 75 80
 Arg Asp Phe Phe Asn Gly Ile Phe Lys Ser Lys Val Ile Pro Lys Met
 85 90 95
 Pro Ile Phe Cys Gly Asp Val Lys Cys Glu Asp Phe Asn Ala Leu Arg
 100 105 110
 Ser Leu Val Tyr Leu Ser Val Leu Glu Leu Glu Glu Thr Ile Asn Pro
 115 120 125
 Asn Lys Ile Pro Phe
 130

(2) INFORMATION FOR SEQ ID NO:885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

788

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

```

Met Lys Lys Leu Ala Ala Leu Phe Leu Val Ser Ala Leu Gly Val Met
 1              5              10              15
Ser Leu Asn Ala Trp Glu Gln Thr Leu Lys Ala Asn Asp Leu Glu Val
      20              25              30
Lys Ile Lys Ser Val Gly Asn Pro Ile Lys Gly Asp Asn Thr Phe Val
      35              40              45
Leu Ser Pro Thr Leu Lys Gly Lys Ala Leu Glu Lys Ala Ile Val Arg
      50              55              60
Val Gln Phe Met Met Pro Glu Met Pro Gly Met Pro Ala Met Lys Glu
      65              70              75              80
Met Ala Gln Val Ser Glu Lys Asn Gly Leu Tyr Glu Ala Lys Thr Asn
      85              90              95
Leu Ser Met Asn Gly Thr Trp Gln Val Arg Val Asp Ile Lys Ser Lys
      100             105             110
Glu Gly Gln Val Tyr Arg Thr Lys Thr Ser Leu Asp Leu
      115             120             125

```

(2) INFORMATION FOR SEQ ID NO:886:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

```

Met Lys Arg Leu Leu Leu Ala Leu Ala Leu Phe Phe Ser Leu Ser
 1              5              10              15
Cys Thr Asn Ala Gln Glu Ile Lys Glu Thr Gln Glu Thr Lys Lys Thr
      20              25              30
Lys Glu Thr Lys Ser Gln Thr Arg Phe Asn Ile Ser Thr Thr Lys Val
      35              40              45
Ile Glu Lys Glu Phe Ser Gln Ser Arg Arg Tyr Tyr Ala Leu Leu Glu
      50              55              60
Pro Asn Glu Ala Leu Ile Phe Ser Gln Thr Leu Arg Phe Asp Gly Tyr

```

789

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

(2) INFORMATION FOR SEQ ID NO:887:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

Met Gly Val Ala Val Val Leu Phe Leu Thr Leu Ile Leu Leu Phe Leu

790

```

1           5           10           15
Val Leu Arg Asp Phe Gly Leu Ala Ser Pro Lys Gln Lys Ile Leu Ala
                20                25                30
Phe Leu Ile Val Gly Ile Ile Gly Ala Ser Ile Ser Val Tyr Thr Tyr
                35                40                45
Lys Gln Asn Gln Gln Asn Gln Gln Glu Ile Ala Leu Gln Arg Ala Phe
                50                55                60
Leu Arg Gly Glu Thr Leu Leu Cys Lys Gly Ile Lys Val Asn Asn Gln
65                70                75                80
Thr Phe Asn Leu Val Ser Gly Thr Leu Ser Phe Leu Gly Lys Lys Gln
                85                90                95
Thr Pro Met Lys Asp Val Leu Val Asp Leu Asp Ser Cys Gln Thr Leu
                100                105                110
Gln Lys Asp Pro Leu Ile Gln Pro
                115                120

```

(2) INFORMATION FOR SEQ ID NO:888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

```

Met Arg Phe Phe Ile Leu Phe Phe Met Gly Met Leu Gly Val Gly Phe
1           5           10           15
Ser Gln Thr Glu Leu Asp Leu Lys Asp Leu Glu Lys Lys Pro Ala Gly
                20                25                30
Ile Val Arg Asp Tyr Tyr Leu Trp Arg Tyr Ile Ser Asp Lys Lys Thr
                35                40                45
Ser Leu Glu Asn Ala Lys Lys Ala Tyr Glu Leu Thr Gln Asn Lys Asn
50                55                60
Ser Ala Leu Gln Lys Ala Met Gln Glu Lys Gly Val Glu Asn Ser Asp
65                70                75                80
Lys Ser Pro Asp Ala Lys Met Pro Glu Asp Ile Tyr Cys Lys Gln Ile
                85                90                95
Thr Leu Glu Ser Met Leu Glu Thr Thr Asp Ala Phe Gln Ala Ser Cys
                100                105                110
Ile Ala Ile Ala Leu Lys Ser Lys Ile Arg Asp Phe Asp Lys Ile Pro
                115                120                125
Ile Gln Thr Phe Lys Pro Leu Gln Glu Lys Ile Lys Glu Ala Tyr Pro
130                135                140
Ile Leu Tyr Glu Glu Leu Glu Ile Leu Gln Ser Lys Asn Val Ser Ala
145                150                155                160
Ser Leu Phe Lys Ala Asn Ala Gln Val Phe Ser Ala Leu Phe Asn His

```

791

```

                165                170                175
Leu Ser Tyr Glu Lys Lys Leu Gln Ile Phe Glu Lys His Ile Pro Ile
                180                185                190
Lys Glu Leu Asn Arg Leu Leu Asp Glu Asp Tyr Pro Ala Phe Asn Arg
                195                200                205
Leu Ile Tyr Gln Val Ile Leu Asp Pro Lys Leu Asp His Phe Lys Asp
                210                215                220
Ala Leu Ala Lys Ser Asn Ala Thr Gln Ser Asn Ala Gln Thr Phe Phe
225                230                235                240
Ile Leu Gly Ile Asn Glu Ile Leu His Lys Lys Thr Ser Lys Ala Leu
                245                250                255
Lys Tyr Phe Glu Arg Ser Glu Ala Val Val Lys Asp Asp Asp Phe Ser
                260                265                270
Lys Asp Arg Ala Ile Phe Trp Gln Tyr Leu Ala Ser Lys Lys Lys Lys
275                280                285
Thr Leu Glu His Leu Ser Gln Ser Pro Ala Leu Asn Leu Tyr Ser Leu
290                295                300
Tyr Ala Ser Arg Lys Pro Gln Asn His Ala Gln Leu Ser His His Phe
305                310                315                320
Ser Tyr Pro Lys Phe Lys Pro Arg Glu Pro Ser Phe
                325                330

```

(2) INFORMATION FOR SEQ ID NO:889:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

```

Val His Leu Ala His Tyr Leu Lys Arg Asn Phe Ser Phe Phe Pro Ser
1                5                10                15
Val Asp Ile Val Asp Gly Gly Thr Met Ala Gln Gln Leu Ile Pro Leu
20                25                30
Ile Thr Ser Tyr Glu Lys Val Leu Ile Leu Asp Cys Val Ser Ala Lys
35                40                45
Gly Val Glu Ile Gly Ser Val Tyr Ala Phe Asp Phe Lys Asp Ala Pro
50                55                60
Lys Glu Ile Thr Trp Ala Gly Ser Ala His Glu Val Glu Met Leu His
65                70                75                80
Thr Leu Arg Leu Thr Glu Phe Leu Gly Asp Leu Pro Lys Thr Phe Ile
85                90                95
Val Gly Leu Val Pro Phe Val Ile Gly Ser Glu Thr Thr Phe Lys Leu
100               105               110
Ser Ser Glu Met Leu Asn Ala Leu Glu Thr Ala Leu Lys Ala Ile Glu

```

	115		120		125										
Thr	Gln	Leu	Asn	Ala	Trp	Gly	Val	Lys	Met	Gln	Arg	Thr	Asp	His	Ile
	130				135						140				
Ala	Leu	Asp	Cys	Ile	Ala	Glu	Leu	Ser	Tyr	Lys	Gly	Phe			
145					150					155					

(2) INFORMATION FOR SEQ ID NO:890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

Met	Lys	Lys	Val	Leu	Leu	Leu	Thr	Leu	Ser	Leu	Ser	Leu	Ser	Phe	Trp
1				5					10					15	
Leu	His	Ala	Glu	Arg	Asn	Gly	Phe	Tyr	Leu	Gly	Leu	Asn	Phe	Ala	Glu
			20					25					30		
Gly	Ser	Tyr	Ile	Gln	Gly	Gln	Gly	Ser	Ile	Gly	Glu	Lys	Ala	Ser	Ala
		35					40						45		
Glu	Asn	Ala	Leu	Asn	Gln	Ala	Ile	Asn	Asn	Ala	Lys	Asn	Ser	Leu	Phe
	50					55					60				
Pro	Asn	Thr	Lys	Ala	Ile	Arg	Asp	Val	Gln	Asn	Ala	Leu	Asn	Ala	Val
65				70					75					80	
Lys	Asp	Ser	Asn	Lys	Ile	Ala	Asn	Arg	Phe	Ala	Gly	Asn	Gly	Gly	Ser
			85						90					95	
Gly	Gly	Ile	Phe	Asn	Glu	Leu	Ser	Leu	Gly	Tyr	Lys	Tyr	Phe	Leu	Gly
		100						105					110		
Lys	Lys	Arg	Ile	Ile	Gly	Phe	Arg	His	Ser	Leu	Phe	Phe	Gly	Tyr	Gln
		115					120					125			
Leu	Gly	Gly	Val	Gly	Ser	Val	Pro	Gly	Ser	Gly	Leu	Ile	Ala	Phe	Leu
	130					135					140				
Pro	Tyr	Gly	Phe	Asn	Thr	Asp	Leu	Leu	Ile	Asn	Trp	Thr	Asn	Asp	Lys
145				150						155				160	
Arg	Ala	Ser	Gln	Glu	Tyr	Val	Glu	Arg	Arg	Val	Lys	Gly	Leu	Ser	Ile
			165						170					175	
Phe	Tyr	Lys	Asp	Met	Thr	Gly	Arg	Thr	Leu	Asp	Ala	Asp	Thr	Leu	Lys
		180					185						190		
Arg	Ala	Ser	Arg	His	Ile	Ile	Arg	Lys	Ser	Ser	Gly	Leu	Val	Ile	Gly
		195					200					205			
Met	Glu	Leu	Gly	Ala	Ser	Thr	Trp	Phe	Ala	Ser	Asn	Asn	Leu	Thr	Pro
	210						215				220				
Phe	Asn	Gln	Val	Lys	Ser	Arg	Thr	Ile	Phe	Gln	Leu	Gln	Gly	Lys	Phe
225				230						235				240	
Gly	Val	Arg	Phe	Ser	Ser	Asp	Glu	Tyr	Asp	Ile	Asp	Arg	Tyr	Gly	Asp

793

				245					250					255					
Glu	Asn	Tyr	Leu	Gly	Gly	Ser	Ser	Val	Glu	Leu	Gly	Val	Lys	Val	Pro				
			260					265					270						
Ala	Phe	Lys	Val	Asn	Tyr	Tyr	Ser	Asp	Asp	Tyr	Gly	Asp	Lys	Leu	Asp				
		275					280					285							
Tyr	Lys	Arg	Val	Val	Ser	Val	Tyr	Leu	Asn	Tyr	Thr	Tyr	Asn	Phe	Lys				
	290					295					300								
Asn	Lys	His																	
305																			

(2) INFORMATION FOR SEQ ID NO:891:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 578 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

Met	Ser	Lys	Lys	Ile	Val	Val	Asp	Pro	Ile	Thr	Arg	Ile	Glu	Gly	His				
1				5					10					15					
Leu	Arg	Ile	Glu	Val	Ile	Val	Asp	Asp	Asp	Asn	Val	Ile	Thr	Asp	Ala				
			20					25					30						
Phe	Ser	Ser	Ser	Thr	Leu	Phe	Arg	Gly	Leu	Glu	Thr	Ile	Ile	Lys	Gly				
		35					40					45							
Arg	Asp	Pro	Arg	Asp	Ala	Gly	Phe	Ile	Ala	Gln	Arg	Ile	Cys	Gly	Val				
	50					55				60									
Cys	Thr	Tyr	Ser	His	Tyr	Lys	Ala	Gly	Val	Thr	Ala	Val	Glu	Asn	Ala				
65				70					75					80					
Leu	Gly	Ile	Thr	Pro	Pro	Leu	Asn	Ala	Gln	Leu	Val	Arg	Ser	Leu	Met				
			85					90					95						
Asn	Met	Ala	Leu	Phe	His	Asp	His	Val	Val	His	Phe	Tyr	Thr	Leu					
		100					105					110							
His	Gly	Leu	Asp	Trp	Cys	Asp	Ile	Leu	Ser	Thr	Leu	Lys	Ala	Asp	Pro				
	115					120					125								
Ile	Gln	Ala	Ala	Lys	Leu	Ser	Phe	Lys	Tyr	Ser	Pro	Tyr	Pro	Ile	Asn				
	130				135					140									
Thr	Gly	Ala	Gly	Glu	Leu	Lys	Ala	Val	Gln	Lys	Arg	Leu	Asn	Asp	Phe				
145				150					155					160					
Ala	Lys	Ser	Gly	Ser	Leu	Gly	Pro	Phe	Ser	Asn	Gly	Tyr	Tyr	Gly	His				
		165					170					175							
Lys	Thr	Tyr	Arg	Leu	Asn	Pro	Glu	Gln	Asn	Leu	Ile	Val	Leu	Ser	His				
		180				185						190							
Tyr	Leu	Lys	Leu	Leu	Glu	Ile	Gln	Arg	Glu	Ala	Ala	Lys	Met	Thr	Ala				
	195					200					205								
Ile	Phe	Gly	Ala	Lys	Gln	Pro	His	Pro	Gln	Ser	Leu	Thr	Val	Gly	Gly				

794

210		215		220
Val Thr Ser Val Met Asp Ile Leu Asp Pro Thr Arg Leu Ala Glu Trp				
225		230		240
Lys Ser Lys Phe Glu Val Val Ala Asn Phe Ile Asn His Ala Tyr Tyr				
	245		250	255
Pro Asp Leu Val Met Ala Gly Glu Met Phe Ala Asn Glu Pro Ser Val				
	260		265	270
Ile Lys Gly Cys Gly Leu Arg Asn Phe Ile Ala Tyr Glu Glu Val Leu				
	275		280	285
Leu Gly Lys Asp Lys Tyr Leu Leu Ser Ser Gly Val Val Leu Asp Gly				
	290		295	300
Asp Ile Ser Lys Leu His Pro Ile Asp Glu Ser Leu Ile Lys Glu Glu				
305		310		320
Val Thr His Ser Trp Tyr Gln Tyr Glu Asp Thr Lys Glu Val Gln Leu				
	325		330	335
His Pro Tyr Asp Gly Gln Thr Asn Pro His Tyr Thr Gly Leu Lys Asp				
	340		345	350
Gly Glu Ser Val Gly Ile Glu Asn Lys Ile Ile Pro Ala Lys Val Leu				
	355		360	365
Asp Thr Lys Asp Lys Tyr Ser Trp Ile Lys Ser Pro Arg Tyr Asp Ser				
	370		375	380
Lys Pro Met Glu Val Gly Pro Leu Ser Ser Val Val Val Gly Leu Ala				
385		390		400
Ala Lys Asn Pro Tyr Val Thr Glu Val Ala Thr Lys Phe Leu Lys Asp				
	405		410	415
Thr Lys Leu Pro Leu Glu Ala Leu Phe Ser Thr Leu Gly Arg Thr Ala				
	420		425	430
Ala Arg Cys Ile Glu Ala Lys Thr Ile Ala Asp Asn Gly Leu Leu Ala				
	435		440	445
Phe Asp Ala Leu Val Glu Asn Leu Lys Ser Asp Gln Ser Thr Cys Ala				
	450		455	460
Pro Tyr His Ile Asp Lys Asn Gln Glu Tyr Lys Gly Arg Tyr Ile Gly				
465		470		480
Gln Val Pro Arg Gly Met Leu Ser His Trp Val Arg Ile Lys Asn Gly				
	485		490	495
Val Val Glu Asn Tyr Gln Ala Val Val Pro Ser Thr Trp Asn Ala Gly				
	500		505	510
Pro Arg Asp Ser Lys Asn Gln Arg Gly Ala Tyr Glu Met Ser Leu Ile				
	515		520	525
Gly Thr Lys Ile Ala Asp Leu Thr Gln Pro Leu Glu Ile Ile Arg Thr				
	530		535	540
Ile His Ser Phe Asp Pro Cys Ile Ala Cys Ser Val His Val Met Asp				
545		550		560
Phe Lys Gly Gln Ser Leu Asn Glu Phe Lys Val Glu Pro Asn Phe Ala				
	565		570	575
Lys Phe				

(2) INFORMATION FOR SEQ ID NO:892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

795

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

```

Met Asn Ser Ser Asn Leu Lys Asn Trp Leu Phe Pro Thr Ile Cys Phe
1           5           10           15
Phe Leu Phe Cys Tyr Ile Leu Ile Phe Leu Ile Phe Phe Met Phe Lys
          20           25           30
Asn Leu Gln Ser Gln Ser Phe Gly Ser Val Ala Glu Thr Gly Lys Lys
          35           40           45
Pro Ile Thr Thr Thr Lys Lys Phe Gly Lys Glu Leu Gln Lys Gln Ile
          50           55           60
Ser Lys Ile His
65

```

(2) INFORMATION FOR SEQ ID NO:893:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...53

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

```

Val Val Leu Pro Lys Glu Thr Leu Ser Ser Ile Ala Lys Arg Tyr Gln
1           5           10           15
Val Ser Ile Ser Ser Ile Gln Leu Ala Asn Asn Leu Lys Asp Ser Asn
          20           25           30
Ile Phe Ile His Gln Arg Leu Ile Ile Pro Thr Asn Lys Lys Leu Leu
          35           40           45
Ala Thr Arg Glu Phe
50

```

(2) INFORMATION FOR SEQ ID NO:894:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

```

Leu Tyr Phe Leu Asn Gly Gly Tyr Asn Arg Leu His Lys Ser Tyr Glu
1      5      10      15
Arg Ile Val Met Leu Ile Ala Arg Phe Lys Lys Ala Leu Ile Ser Tyr
      20      25      30
Ser Leu Gly Val Leu Leu Val Ser Ser Leu Leu Gly Val Ala Asn Ala
      35      40      45
Ser Asn Gln Glu Ile Gln Val Lys Asp Tyr Phe Gly Glu Gln Thr Ile
      50      55      60
Lys Leu Pro Val Ser Lys Ile Ile Tyr Leu Gly Ser Phe Ala Glu Val
65      70      75      80
Pro Ala Met Phe Asn Thr Trp Asp Arg Val Val Gly Ile Ser Asp Tyr
      85      90      95
Ala Phe Lys Ser Asp Ile Val Lys Ala Thr Leu Lys Asp Pro Glu Arg
      100     105     110
Ile Lys Pro Met Ser Ser Asp His Val Ala Ala Leu Asn Val Glu Leu
      115     120     125
Leu Lys Lys Leu Ser Pro Asp Leu Val Val Thr Phe Val Gly Asn Pro
      130     135     140
Lys Ala Val Glu His Ala Lys Lys Phe Gly Ile Ser Phe Leu Ser Phe
145     150     155     160
Gln Glu Lys Thr Ile Val Glu Val Met Glu Asp Ile Asp Ala Gln Ala
      165     170     175
Lys Ala Leu Glu Val Asp Ala Ser Lys Lys Leu Ala Lys Met Gln Glu
      180     185     190
Thr Leu Asp Phe Ile Lys Glu Arg Leu Lys Asn Val Lys Lys Lys
      195     200     205
Gly Val Glu Leu Phe His Lys Ala Asn Lys Ile Ser Gly His Gln Ala
      210     215     220
Leu Asp Ser Asp Ile Leu Glu Lys Gly Gly Ile Asp Asn Phe Gly Leu
225     230     235     240
Lys Tyr Val Lys Phe Gly Arg Ala Asp Ile Ser Val Glu Lys Ile Val
      245     250     255
Lys Glu Asn Pro Glu Ile Ile Phe Ile Trp Trp Ile Ser Pro Leu Ser
      260     265     270
Pro Glu Asp Val Leu Asn Asn Pro Lys Phe Ser Thr Ile Lys Ala Ile
      275     280     285
Lys Asn Lys Gln Val Tyr Lys Leu Pro Thr Met Asp Ile Gly Gly Pro
      290     295     300
Arg Ala Pro Leu Ile Ser Leu Phe Ile Ala Leu Lys Ala His Pro Glu
305     310     315     320
Ala Phe Lys Gly Val Asp Ile Asn Ala Ile Ile Lys Asp Tyr Tyr Lys
      325     330     335
Val Val Phe Asp Leu Asn Asp Ala Glu Val Glu Pro Phe Leu Trp His

```

340

345

350

(2) INFORMATION FOR SEQ ID NO:895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

```

Met Lys Cys Ser Ser Phe Thr Ser Asn Ser Val Leu Asn Phe Phe Val
1      5      10      15
Val Leu Ser Phe Ile Thr Ile Gly Leu Val Phe Phe Phe Leu Arg Ser
20      25      30
Gln Pro Thr Ser Val Val Ser Lys Glu Asn Ile Pro Lys Ile Glu Leu
35      40      45
Glu Asn Phe Lys Ala Phe Gln Ile Asn Asp Lys Ile Leu Asp Leu Ser
50      55      60
Ile Glu Gly Lys Lys Ala Leu Gln Tyr Asp Asp His Glu Ile Phe Phe
65      70      75      80
Asp Ser Lys Ile Lys Arg Tyr Asp Glu Asp Thr Ile Glu Ser Val Glu
85      90      95
Ser Pro Glu Ala Lys Arg Gln Gln Asp Leu Tyr Phe Phe Pro Asn Gly
100     105     110
Val Thr Tyr Lys Arg Ser Asp Asp Ser Ser Phe Trp Ser Glu Thr Gly
115     120     125
Ile Tyr Asn His Lys Glu Gln Asn Phe Lys Gly Lys Gly Arg Phe Ile
130     135     140
Leu Thr Ser Lys Asp Ser Lys Val Glu Gly Leu Asp Ile Ser Tyr Ser
145     150     155     160
His Ala Leu Ala Ile Ile Glu Ala Gln Ser Ile Gln Ala Asn Leu Phe
165     170     175
Leu Asp Glu Ile Lys Gln Ser Gln Lys Glu Lys Lys Lys Phe Pro Thr
180     185     190
Phe Lys Gly Gly Phe
195

```

(2) INFORMATION FOR SEQ ID NO:896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

```

Met Arg Trp Trp Cys Phe Leu Val Cys Cys Leu Ser Val Leu Ser Val
1           5           10           15
Met Asp Ala Lys Lys Leu Glu Asn Lys Gly Leu Lys Lys Glu Arg Glu
20           25           30
Leu Leu Glu Ile Thr Gly Asn Gln Phe Val Ala Asn Asp Lys Thr Lys
35           40           45
Thr Ala Val Ile Gln Gly Asn Val Gln Ile Lys Lys Gly Lys Asp Arg
50           55           60
Leu Phe Ala Asp Lys Val Ser Val Phe Leu Asn Asp Lys Arg Lys Pro
65           70           75           80
Glu Arg Tyr Glu Ala Thr Gly Asn Thr His Phe Asn Ile Phe Thr Glu
85           90           95
Asp Asn Arg Glu Ile Ser Gly Ser Thr Asp Lys Leu Ile Tyr Asn Ala
100          105          110
Leu Asn Gly Glu Tyr Lys Leu Leu Gln Asn Ala Val Val Arg Glu Val
115          120          125
Gly Lys Ser Asn Val Ile Thr Gly Asp Glu Ile Ile Leu Asn Lys Thr
130          135          140
Lys Gly Tyr Ala Asp Val Leu Gly Ser Ala Lys Arg Pro Ala Lys Phe
145          150          155          160
Val Phe Asp Met Glu Asp Ile Asn Glu Glu Asn Arg Lys Ala Lys Leu
165          170          175
Lys Lys Lys Gly Ala Lys Glu Lys Pro
180          185

```

(2) INFORMATION FOR SEQ ID NO:897:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

799

```

Leu Ile Gln Gln Asn Phe Lys Thr Leu Lys Glu Leu Tyr Met Leu Val
1           5           10           15
Thr Lys Leu Ala Pro Asp Phe Lys Ala Pro Ala Val Leu Gly Asn Asn
          20           25           30
Glu Val Asp Glu His Phe Glu Leu Ser Lys Asn Leu Gly Lys Asn Gly
          35           40           45
Val Ile Leu Phe Phe Trp Pro Lys Asp Phe Thr Phe Val Cys Pro Thr
          50           55           60
Glu Ile Ile Ala Phe Asp Lys Arg Val Lys Asp Phe His Glu Lys Gly
65           70           75           80
Phe Asn Val Ile Gly Val Ser Ile Asp Ser Glu Gln Val His Phe Ala
          85           90           95
Trp Lys Asn Thr Pro Val Glu Lys Gly Gly Ile Gly Gln Val Ser Phe
          100          105          110
Pro Met Val Ala Asp Ile Thr Lys Ser Ile Ser Arg Asp Tyr Asp Val
          115          120          125
Leu Phe Glu Glu Ala Ile Ala Leu Arg Gly Ala Phe Leu Ile Asp Lys
          130          135          140
Asn Met Lys Val Arg His Ala Val Ile Asn Asp Leu Pro Leu Gly Arg
145          150          155          160
Asn Ala Asp Glu Met Leu Arg Met Val Asp Ala Leu Leu His Phe Glu
          165          170          175
Glu His Gly Glu Val Cys Pro Ala Gly Trp Arg Lys Gly Asp Lys Gly
          180          185          190
Met Lys Ala Thr His Gln Gly Val Ala Glu Tyr Leu Lys Glu Asn Ser
          195          200          205
Ile Lys Leu
          210

```

(2) INFORMATION FOR SEQ ID NO:898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

```

Val Pro Leu Trp Ile Met Val Val Gly Ala Ala Gly Ile Ala Leu Gly
1           5           10           15
Leu Ser Leu Tyr Gly Pro Lys Leu Ile Lys Thr Val Gly Ser Glu Ile
          20           25           30
Thr Glu Leu Asp Lys Met Gln Ala Phe Cys Ile Ala Leu Ser Ala Val
          35           40           45
Ile Thr Val Leu Leu Ala Ser Gln Leu Gly Leu Pro Val Ser Ser Thr
          50           55           60

```

800

```

His Ile Val Val Gly Ala Val Phe Gly Val Gly Phe Leu Arg Glu Arg
65          70          75          80
Leu Arg Glu Gln Ser Arg Arg Arg Phe Ala Arg Ile Arg Asp Asn Ile
          85          90          95
Val Ala Ala His Phe Gly Glu Asp Leu Glu Glu Ile Glu Gly Phe Leu
          100         105         110
Glu Arg Phe Asp Lys Ala Asn Leu Lys Glu Lys Ser Leu Met Leu Glu
          115         120         125
Ser Leu Lys Lys Ser Lys Asn Thr Ala Ile Ala Leu Glu Leu Lys Lys
          130         135         140
Lys Glu Lys Lys Ser Leu Lys Lys Val Tyr Lys Glu Glu Val Ile Lys
145          150          155          160
Arg Ser Ile Leu Lys Lys Ile Val Thr Ala Trp Leu Val Thr Val Pro
          165          170          175
Val Ser Ala Leu Leu Gly Ala Leu Leu Phe Val Ala Leu Gly Phe Ile
          180          185          190
Glu Lys Tyr Phe
          195

```

(2) INFORMATION FOR SEQ ID NO:899:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

```

Met Ser Asn Ser Met Leu Asp Lys Asn Lys Ala Ile Leu Thr Gly Gly
1          5          10          15
Gly Ala Leu Leu Leu Gly Leu Ile Val Leu Phe Tyr Leu Ala Tyr Arg
          20          25          30
Pro Lys Ala Glu Val Leu Gln Gly Phe Leu Glu Ala Arg Glu Tyr Ser
          35          40          45
Val Ser Ser Lys Val Pro Gly Arg Ile Glu Lys Val Phe Val Lys Lys
          50          55          60
Gly Asp Arg Ile Lys Lys Gly Asp Leu Val Phe Ser Ile Ser Ser Pro
65          70          75          80
Glu Leu Glu Ala Lys Leu Ala Gln Ala Glu Ala Gly His Lys Ala Ala
          85          90          95
Lys Ala Val Ser Asp Glu Val Lys Arg Gly Ser Arg Asp Glu Thr Ile
          100         105         110
Asn Ser Ala Arg Asp Val Trp Gln Ala Ala Lys Ser Gln Ala Asn Leu
          115         120         125
Ala Lys Glu Thr Tyr Lys Arg Val Gln Asp Leu Tyr Asp Asn Gly Val
130          135          140

```

800

```

His Ile Val Val Gly Ala Val Phe Gly Val Gly Phe Leu Arg Glu Arg
65              70              75              80
Leu Arg Glu Gln Ser Arg Arg Arg Phe Ala Arg Ile Arg Asp Asn Ile
              85              90              95
Val Ala Ala His Phe Gly Glu Asp Leu Glu Glu Ile Glu Gly Phe Leu
              100             105             110
Glu Arg Phe Asp Lys Ala Asn Leu Lys Glu Lys Ser Leu Met Leu Glu
              115             120             125
Ser Leu Lys Lys Ser Lys Asn Thr Ala Ile Ala Leu Glu Leu Lys Lys
              130             135             140
Lys Glu Lys Lys Ser Leu Lys Lys Val Tyr Lys Glu Glu Val Ile Lys
145             150             155             160
Arg Ser Ile Leu Lys Lys Ile Val Thr Ala Trp Leu Val Thr Val Pro
              165             170             175
Val Ser Ala Leu Leu Gly Ala Leu Leu Phe Val Ala Leu Gly Phe Ile
              180             185             190
Glu Lys Tyr Phe
              195

```

(2) INFORMATION FOR SEQ ID NO:899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

```

Met Ser Asn Ser Met Leu Asp Lys Asn Lys Ala Ile Leu Thr Gly Gly
1              5              10              15
Gly Ala Leu Leu Gly Leu Ile Val Leu Phe Tyr Leu Ala Tyr Arg
              20              25              30
Pro Lys Ala Glu Val Leu Gln Gly Phe Leu Glu Ala Arg Glu Tyr Ser
              35              40              45
Val Ser Ser Lys Val Pro Gly Arg Ile Glu Lys Val Phe Val Lys Lys
              50              55              60
Gly Asp Arg Ile Lys Lys Gly Asp Leu Val Phe Ser Ile Ser Ser Pro
65              70              75              80
Glu Leu Glu Ala Lys Leu Ala Gln Ala Glu Ala Gly His Lys Ala Ala
              85              90              95
Lys Ala Val Ser Asp Glu Val Lys Arg Gly Ser Arg Asp Glu Thr Ile
              100             105             110
Asn Ser Ala Arg Asp Val Trp Gln Ala Ala Lys Ser Gln Ala Asn Leu
              115             120             125
Ala Lys Glu Thr Tyr Lys Arg Val Gln Asp Leu Tyr Asp Asn Gly Val
130             135             140

```

801

Ala Ser Leu Gln Lys Arg Asp Glu Ala Tyr Ala Ala Met Lys Ala Pro
 145 150 155 160
 Asn Thr Thr Arg Ala Arg Leu Thr Lys Ser Ile Lys Trp Leu
 165 170

(2) INFORMATION FOR SEQ ID NO:900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

Met Glu Phe Leu Ser Gly Tyr Phe Leu Trp Val Lys Ala Phe His Val
 1 5 10 15
 Ile Ala Val Ile Ser Trp Met Ala Ala Leu Phe Tyr Leu Pro Arg Leu
 20 25 30
 Phe Val Tyr His Ala Glu Asn Ala His Lys Lys Glu Phe Val Gly Val
 35 40 45
 Val Gln Ile Gln Glu Lys Lys Leu Tyr Ser Phe Ile Ala Ser Pro Ala
 50 55 60
 Met Gly Phe Thr Leu Ile Thr Gly Ile Leu Met Leu Leu Ile Ala Pro
 65 70 75 80
 Glu Met Phe Lys Ser Gly Gly Trp Leu His Ala Lys Leu Ala Leu Val
 85 90 95
 Val Leu Leu Leu Ile Tyr His Phe Tyr Cys Lys Lys Cys Met Arg Glu
 100 105 110
 Leu Glu Lys Asp Pro Thr Gly Lys Asn Ala Arg Phe Tyr Arg Val Phe
 115 120 125
 Asn Glu Ile Pro Thr Ile Leu Met Ile Leu Ile Val Ile Leu Val Val
 130 135 140
 Val Lys Pro Phe
 145

(2) INFORMATION FOR SEQ ID NO:901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

802

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

```

Met Lys Pro Ile Phe Leu Leu Ile Phe Leu Leu Leu Ala Ser Leu Ile
1           5           10           15
Ala Arg Glu Lys Asp Ala Ser Ser Asn Leu Phe Asp Leu Ile Asp Lys
20           25           30
Gly Ile Asn Arg Glu Gln Glu Leu Lys Glu Gln Glu Gln Lys Thr Arg
35           40           45
Leu Lys Leu Ala Gln Ser Pro Leu Val Ala Leu Glu Ile Val Pro Gln
50           55           60
Glu Thr Pro Tyr Leu Glu Trp Gln Gly Ala Arg Glu Ser Tyr Tyr Leu
65           70           75           80
Lys Val Ser Ala Val Val Glu Ser Val Val Ile Leu Lys Ile Asp Ile
85           90           95
Asn Gln Gly Arg Ser Cys Ser Leu Tyr Pro Thr Pro Lys Ser Val Ser
100          105          110
Leu Val Arg Asn Gln Ser Val Ala Tyr Glu Ile Leu Cys Glu Asn Gln
115          120          125
Pro Leu Trp Ile Glu Val Ser Thr Asn Leu Gly Lys Arg Thr Phe Gln
130          135          140
Phe
145

```

(2) INFORMATION FOR SEQ ID NO:902:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

```

Met Ala Lys Lys Asn Lys Pro Thr Glu Cys Pro Ala Gly Glu Lys Trp
1           5           10           15
Ala Val Pro Tyr Ala Asp Phe Leu Ser Leu Leu Leu Ala Leu Phe Ile
20           25           30
Ala Leu Tyr Ala Ile Ser Ala Val Asn Lys Ser Lys Val Glu Ala Leu
35           40           45
Lys Thr Glu Phe Ile Lys Ile Phe Asn Tyr Ala Pro Lys Pro Glu Ala

```

803

```

      50              55              60
Met Gln Pro Val Val Val Ile Pro Pro Asp Ser Gly Lys Glu Glu Glu
65              70              75              80
Gln Met Ala Ser Glu Ser Ser Lys Pro Ala Ser Gln Asn Thr Glu Thr
      85              90              95
Lys Ala Thr Ile Ala Arg Lys Gly Glu Gly Ser Val Leu Glu Gln Ile
      100              105              110
Asp Gln Gly Ser Val Leu Lys Leu Pro Ser Ser Leu Leu Phe Glu Asn
      115              120              125
Ala Thr Ser Asp Ala Ile Asn Gln Asp Met Met Leu Tyr Ile Glu Arg
      130              135              140
Ile Ala Lys Ile Ile Gln Lys Leu Pro Lys Arg Val His Ile Asn Val
145              150              155              160
Arg Gly Phe Thr Asp Asn Thr Pro Leu Asn Lys Thr Arg Phe Lys Ser
      165              170              175
His Tyr Glu Leu Ala Ala Asn Arg Ala Tyr Arg Val Met Lys Val Leu
      180              185              190
Ile Gln Tyr Gly Val Asp Pro Asn Gln Leu Ser Phe Ser Ser Tyr Gly
      195              200              205
Ser Thr Asn Pro Ile Ala Pro Asn Asp Ser Leu Glu Asn Arg Met Lys
      210              215              220
Asn Asn Arg Val Glu Ile Phe Phe Ser Thr Asp Ala Asn Asp Leu Ser
225              230              235              240
Lys Ile His Ser Ile Leu Asp Glu Glu Phe Asn Pro His Lys Gln Gln
      245              250              255
Glu

```

(2) INFORMATION FOR SEQ ID NO:903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

```

Met Arg Lys Val Ile Ile Met Asn Gly Tyr Leu Arg Val Lys Thr Pro
1              5              10              15
Tyr Phe Leu Ala Ser Val Val Leu Thr Phe Trp Thr Phe Asn Ser Phe
      20              25              30
Met Ser Ala Lys Asp Lys His His Phe Leu Lys Lys Val Thr Thr Thr
      35              40              45
Glu Gln Lys Phe Ser Ser Ser Ala Pro Ile Ser Trp Gln Ser Glu Glu
      50              55              60
Val Arg Asn Ser Thr Ser Ser Arg Thr Val Ile Ser Asn Lys Glu Leu

```

804

65					70					75				80	
Lys	Lys	Thr	Gly	Asn	Leu	Asn	Ile	Glu	Asn	Ala	Leu	Gln	Asn	Val	Pro
				85					90					95	
Gly	Ile	Gln	Ile	Arg	Asp	Ala	Thr	Gly	Thr	Gly	Val	Leu	Pro	Lys	Ile
			100					105					110		
Ser	Val	Arg	Gly	Phe	Gly	Gly	Gly	Gly	Asn	Gly	His	Ser	Asn	Thr	Asn
			115				120					125			
Met	Ile	Leu	Val	Asn	Gly	Ile	Pro	Ile	Tyr	Gly	Ala	Pro	Tyr	Ser	Asn
			130				135				140				
Ile	Glu	Leu	Ala	Ile	Phe	Pro	Val	Thr	Phe	Gln	Ser	Val	Asp	Arg	Ile
145					150					155					160
Asp	Val	Ile	Lys	Gly	Gly	Thr	Ser	Val	Gln	Tyr	Gly	Pro	Asn	Thr	Phe
				165					170					175	
Gly	Gly	Val	Val	Asn	Val	Ile	Thr	Lys	Glu	Ile	Pro	Lys	Glu	Trp	Glu
			180					185					190		
Asn	Gln	Ala	Ala	Glu	Arg	Ile	Thr	Phe	Trp	Gly	Arg	Ser	Ser	Asn	Gly
		195					200					205			
Asn	Phe	Val	Asp	Pro	Lys	Glu	Lys	Gly	Lys	Pro	Leu	Ala	Gln	Thr	Leu
		210				215					220				
Gly	Asn	Gln	Met	Leu	Phe	Asn	Thr	Tyr	Gly	Arg	Thr	Ala	Gly	Met	Leu
225					230					235					240
Gly	Lys	Tyr	Ile	Gly	Ile	Ser	Ala	Gln	Gly	Asn	Trp	Ile	Asn	Gly	Gln
				245					250					255	
Gly	Phe	Arg	Gln	Asn	Ser	Pro	Thr	Lys	Val	Gln	Asn	Tyr	Leu	Leu	Asp
			260					265					270		
Ala	Ile	Tyr	Lys	Ile	Asn	Ala	Thr	Asn	Thr	Phe	Lys	Ala	Tyr	Tyr	Gln
			275				280					285			
Tyr	Tyr	Gln	Tyr	Asn	Ser	Tyr	His	Pro	Gly	Thr	Leu	Ser	Ala	Gln	Asp
		290				295					300				
Tyr	Ala	Tyr	Asn	Arg	Phe	Ile	Asn	Glu	Arg	Pro	Asp	Asn	Gln	Asp	Gly
305					310					315					320
Gly	Arg	Ala	Lys	Arg	Phe	Gly	Ile	Val	Tyr	Gln	Asn	Tyr	Phe	Gly	Asp
				325					330					335	
Pro	Asp	Arg	Lys	Val	Gly	Gly	Asp	Phe	Lys	Phe	Thr	Tyr	Phe	Thr	His
			340					345					350		
Asp	Met	Ser	Arg	Asp	Phe	Gly	Phe	Ser	Asn	Gln	Tyr	Gln	Ser	Val	Tyr
		355				360					365				
Met	Ser	Gly	Gln	Asn	Lys	Ile	Leu	Pro	Phe	Lys	Gly	Lys	Gly	Glu	Ile
		370				375					380				
Ser	Ala	Lys	Asn	Pro	Asn	Cys	Gly	Leu	Tyr	Ser	Tyr	Ser	Asp	Thr	Asn
385					390					395					400
Ser	Pro	Cys	Trp	Gln	Phe	Phe	Asp	Asn	Ile	Arg	Arg	Ser	Val	Val	Asn
				405					410					415	
Ala	Phe	Glu	Pro	Lys	Leu	Asn	Leu	Ile	Val	Asn	Thr	Gly	Lys	Val	Lys
			420					425					430		
Gln	Thr	Phe	Asn	Met	Gly	Met	Arg	Phe	Leu	Thr	Glu	Asp	Leu	Tyr	Arg
		435					440					445			
Arg	Ser	Thr	Thr	Arg	Lys	Asn	Pro	Ser	Met	Pro	Asn	Asn	Gly	Ser	Gly
		450				455					460				
Phe	Asp	Ala	Gly	Thr	Ser	Leu	Asn	Asn	Phe	Asn	Asn	Tyr	Thr	Ala	Val
465					470					475					480
Tyr	Ala	Ser	Asp	Glu	Ile	Asn	Phe	Asn	Asn	Gly	Met	Leu	Thr	Ile	Thr
				485					490					495	
Pro	Gly	Leu	Arg	Tyr	Thr	Phe	Leu	Asn	Tyr	Glu	Lys	Lys	Asp	Ala	Pro
			500					505					510		
Pro	Phe	Lys	Val	Gly	Gln	Thr	Pro	Lys	Thr	Thr	Lys	Glu	Arg	Tyr	Asn
			515				520						525		

805

```

Gln Trp Asn Pro Ala Val Asn Val Gly Tyr Lys Pro Ile Lys Glu Leu
530                    535                    540
Leu Phe Tyr Phe Asn Tyr Gln Arg Ser Tyr Ile Pro Pro Gln Phe Ser
545                    550                    555                    560
Asn Ile Gly Asn Phe Val Gly Thr Ser Thr Asp Tyr Phe Gln Ile Phe
                    565                    570                    575
Asn Val Met Glu Gly Gly Ser Arg Tyr Tyr Phe Asn His Gln Val Ser
                    580                    585                    590
Phe Asn Ala Asn Tyr Phe Val Ile Phe Ala Asn His Tyr Phe Thr Gly
                    595                    600                    605
Arg Tyr Gly Asp Asn Arg Glu Pro Val Asn Ala Arg Ser Gln Gly Val
610                    615                    620
Glu Leu Glu Leu Tyr Tyr Thr Pro Ile Arg Gly Leu Asn Phe His Ala
625                    630                    635                    640
Ala Tyr Thr Phe Ile Asp Ala Asn Ile Thr Ser His Thr Met Val Thr
                    645                    650                    655
Asn Pro Ala Asn Pro Lys Gly Pro Lys Lys Asp Ile Phe Gly Lys Lys
                    660                    665                    670
Leu Pro Phe Val Ser Pro His Gln Phe Ile Leu Asp Ala Ser Tyr Thr
675                    680                    685
Tyr Ala Lys Thr Thr Ile Gly Leu Ser Ser Phe Phe Tyr Ser Arg Ala
690                    695                    700
Tyr Ser Asp Val Leu Asn Thr Val Pro Phe Thr Glu Tyr Ala Pro Thr
705                    710                    715                    720
Ile Lys Asn Gly Ala Ile Val Thr Lys Thr Ala Gly Met Thr Pro Tyr
                    725                    730                    735
Tyr Trp Val Trp Asn Leu Gln Ile Ser Thr Thr Leu Trp Glu Arg Lys
740                    745                    750
Asn Gln Ser Val Asn Ala Ser Leu Gln Ile Asn Asn Ile Phe Asn Met
755                    760                    765
Lys Tyr Trp Phe Ser Gly Ile Gly Thr Ser Pro Asn Gly Lys Glu Ala
770                    775                    780
Ala Pro Pro Arg Ser Ile Thr Ala Tyr Val Ser Tyr Asn Phe
785                    790                    795

```

(2) INFORMATION FOR SEQ ID NO:904:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 798 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

```

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

```

Tyr Phe Leu Ala Ser Val Val Leu Thr Phe Trp Thr Phe Asn Ser Phe
 20 25 30
 Met Ser Ala Lys Asp Lys His His Phe Leu Lys Lys Val Thr Thr Thr
 35 40 45
 Glu Gln Lys Phe Ser Ser Ser Ala Pro Ile Ser Trp Gln Ser Glu Glu
 50 55 60
 Val Arg Asn Ser Thr Ser Ser Arg Thr Val Ile Ser Asn Lys Glu Leu
 65 70 75 80
 Lys Lys Thr Gly Asn Leu Asn Ile Glu Asn Ala Leu Gln Asn Val Pro
 85 90 95
 Gly Ile Gln Ile Arg Asp Ala Thr Gly Thr Gly Val Leu Pro Lys Ile
 100 105 110
 Ser Val Arg Gly Phe Gly Gly Gly Gly Asn Gly His Ser Asn Thr Asn
 115 120 125
 Met Ile Leu Val Asn Gly Ile Pro Ile Tyr Gly Ala Pro Tyr Ser Asn
 130 135 140
 Ile Glu Leu Ala Ile Phe Pro Val Thr Phe Gln Ser Val Asp Arg Ile
 145 150 155 160
 Asp Val Ile Lys Gly Gly Thr Ser Val Gln Tyr Gly Pro Asn Thr Phe
 165 170 175
 Gly Gly Val Val Asn Val Ile Thr Lys Glu Ile Pro Lys Glu Trp Glu
 180 185 190
 Asn Gln Ala Ala Glu Arg Ile Thr Phe Trp Gly Arg Ser Ser Asn Gly
 195 200 205
 Asn Phe Val Asp Pro Lys Glu Lys Gly Lys Pro Leu Ala Gln Thr Leu
 210 215 220
 Gly Asn Gln Met Leu Phe Asn Thr Tyr Gly Arg Thr Ala Gly Met Leu
 225 230 235 240
 Gly Lys Tyr Ile Gly Ile Ser Ala Gln Gly Asn Trp Ile Asn Gly Gln
 245 250 255
 Gly Phe Arg Gln Asn Ser Pro Thr Lys Val Gln Asn Tyr Leu Leu Asp
 260 265 270
 Ala Ile Tyr Lys Ile Asn Ala Thr Asn Thr Phe Lys Ala Tyr Tyr Gln
 275 280 285
 Tyr Tyr Gln Tyr Asn Ser Tyr His Pro Gly Thr Leu Ser Ala Gln Asp
 290 295 300
 Tyr Ala Tyr Asn Arg Phe Ile Asn Glu Arg Pro Asp Asn Gln Asp Gly
 305 310 315 320
 Gly Arg Ala Lys Arg Phe Gly Ile Val Tyr Gln Asn Tyr Phe Gly Asp
 325 330 335
 Pro Asp Arg Lys Val Gly Gly Asp Phe Lys Phe Thr Tyr Phe Thr His
 340 345 350
 Asp Met Ser Arg Asp Phe Gly Phe Ser Asn Gln Tyr Gln Ser Val Tyr
 355 360 365
 Met Ser Gly Gln Asn Lys Ile Leu Pro Phe Lys Gly Lys Gly Glu Ile
 370 375 380
 Ser Ala Lys Asn Pro Asn Cys Gly Leu Tyr Ser Tyr Ser Asp Thr Asn
 385 390 395 400
 Ser Pro Cys Trp Gln Phe Phe Asp Asn Ile Arg Arg Ser Val Val Asn
 405 410 415
 Ala Phe Glu Pro Lys Leu Asn Leu Ile Val Asn Thr Gly Lys Val Lys
 420 425 430
 Gln Thr Phe Asn Met Gly Met Arg Phe Leu Thr Glu Asp Leu Tyr Arg
 435 440 445
 Arg Ser Thr Thr Arg Lys Asn Pro Ser Met Pro Asn Asn Gly Ser Gly
 450 455 460
 Phe Asp Ala Gly Thr Ser Leu Asn Asn Phe Asn Asn Tyr Thr Ala Val

807

465		470		475		480									
Tyr	Ala	Ser	Asp	Glu	Ile	Asn	Phe	Asn	Asn	Gly	Met	Leu	Thr	Ile	Thr
			485						490					495	
Pro	Gly	Leu	Arg	Tyr	Thr	Phe	Leu	Asn	Tyr	Glu	Lys	Lys	Asp	Ala	Pro
		500						505					510		
Pro	Phe	Lys	Val	Gly	Gln	Thr	Pro	Lys	Thr	Thr	Lys	Glu	Arg	Tyr	Asn
		515					520					525			
Gln	Trp	Asn	Pro	Ala	Val	Asn	Val	Gly	Tyr	Lys	Pro	Ile	Lys	Glu	Leu
	530					535					540				
Leu	Phe	Tyr	Phe	Asn	Tyr	Gln	Arg	Ser	Tyr	Ile	Pro	Pro	Gln	Phe	Ser
545				550					555					560	
Asn	Ile	Gly	Asn	Phe	Val	Gly	Thr	Ser	Thr	Asp	Tyr	Phe	Gln	Ile	Phe
			565					570					575		
Asn	Val	Met	Glu	Gly	Gly	Ser	Arg	Tyr	Tyr	Phe	Asn	His	Gln	Val	Ser
		580						585					590		
Phe	Asn	Ala	Asn	Tyr	Phe	Val	Ile	Phe	Ala	Asn	His	Tyr	Phe	Thr	Gly
	595					600						605			
Arg	Tyr	Gly	Asp	Asn	Arg	Glu	Pro	Val	Asn	Ala	Arg	Ser	Gln	Gly	Val
	610					615					620				
Glu	Leu	Glu	Leu	Tyr	Tyr	Thr	Pro	Ile	Arg	Gly	Leu	Asn	Phe	His	Ala
625				630					635					640	
Ala	Tyr	Thr	Phe	Ile	Asp	Ala	Asn	Ile	Thr	Ser	His	Thr	Met	Val	Thr
			645					650					655		
Asn	Pro	Ala	Asn	Pro	Lys	Gly	Pro	Lys	Lys	Asp	Ile	Phe	Gly	Lys	Lys
		660				665							670		
Leu	Pro	Phe	Val	Ser	Pro	His	Gln	Phe	Ile	Leu	Asp	Ala	Ser	Tyr	Thr
	675					680						685			
Tyr	Ala	Lys	Thr	Thr	Ile	Gly	Leu	Ser	Ser	Phe	Phe	Tyr	Ser	Arg	Ala
	690				695						700				
Tyr	Ser	Asp	Val	Leu	Asn	Thr	Val	Pro	Phe	Thr	Glu	Tyr	Ala	Pro	Thr
705				710					715					720	
Ile	Lys	Asn	Gly	Ala	Ile	Val	Thr	Lys	Thr	Ala	Gly	Met	Thr	Pro	Tyr
			725					730						735	
Tyr	Trp	Val	Trp	Asn	Leu	Gln	Ile	Ser	Thr	Thr	Leu	Trp	Glu	Arg	Lys
		740				745							750		
Asn	Gln	Ser	Val	Asn	Ala	Ser	Leu	Gln	Ile	Asn	Asn	Ile	Phe	Asn	Met
	755					760						765			
Lys	Tyr	Trp	Phe	Ser	Gly	Ile	Gly	Thr	Ser	Pro	Asn	Gly	Lys	Glu	Ala
	770				775						780				
Ala	Pro	Pro	Arg	Ser	Ile	Thr	Ala	Tyr	Val	Ser	Tyr	Asn	Phe		
785					790					795					

(2) INFORMATION FOR SEQ ID NO:905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

```

Met Lys Thr Asn Gly Leu Phe Lys Met Trp Gly Leu Phe Leu Val Leu
1      5      10      15
Ile Ala Leu Val Phe Asn Ala Cys Ser Asp Ser His Lys Glu Lys Lys
20      25      30
Asp Ala Leu Glu Val Ile Lys Gln Arg Gly Val Leu Lys Val Gly Val
35      40      45
Phe Ser Asp Lys Pro Pro Phe Gly Ser Val Asp Ser Lys Gly Asn Tyr
50      55      60
Gln Gly Tyr Asp Val Val Ile Ala Lys Arg Met Ala Leu Asp Leu Leu
65      70      75      80
Gly Asp Glu Asn Lys Ile Glu Phe Ile Pro Val Glu Ala Ser Ala Arg
85      90      95
Val Glu Phe Leu Lys Ala Asn Lys Val Asp Ile Ile Met Ala Asn Phe
100     105     110
Thr Arg Thr Lys Glu Arg Glu Lys Val Val Asp Phe Ala Asn Pro Tyr
115     120     125
Met Lys Val Ala Leu Gly Val Ile Ser Lys Asp Gly Val Ile Lys Asn
130     135     140
Ile Glu Glu Leu Lys Asp Lys Glu Leu Ile Val Asn Lys Gly Thr Thr
145     150     155     160
Ala Asp Phe Tyr Phe Thr Lys Asn Tyr Pro Asn Ile Lys Leu Leu Lys
165     170     175
Phe Glu Gln Asn Thr Glu Thr Phe Leu Ala Leu Leu Asn Asn Lys Ala
180     185     190
Ile Ala Leu Ala His Asp Asn Thr Leu Leu Leu Ala Trp Val Lys Gln
195     200     205
His Pro Glu Phe Lys Leu Gly Ile Thr Ser Leu Gly Asp Lys Asp Val
210     215     220
Ile Ala Pro Ala Ile Lys Lys Gly Asn Pro Lys Leu Leu Glu Trp Leu
225     230     235     240
Asn Asn Glu Ile Asp Ser Leu Ile Ser Ser Asp Phe Leu Lys Glu Ala
245     250     255
Tyr Gln Glu Thr Leu Glu Pro Ile Tyr Gly Asp Gly Ile Lys Pro Glu
260     265     270
Glu Ile Ile Phe Glu
275

```

(2) INFORMATION FOR SEQ ID NO:906:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

809

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

```

Leu Asp Asn Phe Ile Ser Gln Tyr Ala Gln Arg Leu Ile Val Thr Asn
1          5          10          15
Leu Ser Gln Ala Ile Arg Ile Tyr Gly Tyr Glu Val Gly Gly Thr Phe
20          25          30
Arg Tyr Lys Gly Val Ser Leu Asn Val Gly Ile Ser Arg Thr Trp Pro
35          40          45
Thr Thr Arg Gly Tyr Leu Met Ala Asp Ser Tyr Glu Leu Ala Ala Ser
50          55          60
Thr Gly Asn Val Phe Ile Ile Lys Leu Asp Tyr Thr Ile Pro Lys Thr
65          70          75          80
Gly Ile Asn Leu Ala Trp Leu Ser Arg Phe Val Thr Gly Leu Asp Tyr
85          90          95
Cys Gly Phe Asp Ile Tyr Leu Pro Asp Tyr Gly Thr Ala Glu Lys Pro
100         105         110
Lys Thr Pro Thr Asp Leu Ala Lys Cys Gly Ser Gln Leu Gly Leu Val
115         120         125
His Met His Lys Pro Gly Tyr Gly Val Ser Asn Phe Tyr Ile Asn Trp
130         135         140
Ser Pro Lys Thr Lys Ser His Trp Lys Gly Leu Leu Leu Ser Ala Val
145         150         155         160
Phe Asn Asn Val Phe Asn Lys Phe Tyr Val Asp Gln Thr Ser Pro Tyr
165         170         175
Val Met Ser Pro Asp Met Pro Gly Thr Asp Ala Ile Lys Arg Ala Ile
180         185         190
Ala Glu Pro Gly Phe Asn Ala Arg Phe Glu Val Ala Tyr Lys Trp
195         200         205

```

(2) INFORMATION FOR SEQ ID NO:907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

```

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

```


810

35	40	45
Ile Glu Val Lys Pro Asp Ala Gly Tyr Val Val Leu Lys Asp Ile Asn		
50	55	60
Gly Pro Leu Gln Tyr Leu Leu Met Pro Thr Thr His Ile Ser Gly Ile		
65	70	75
Glu Asn Pro Leu Leu Leu Asp Pro Ser Thr Pro Asn Phe Phe Tyr Leu		
85	90	95
Ser Trp Gln Ala Arg Asp Phe Met Ser Lys Lys Tyr Gly Lys Pro Ile		
100	105	110
Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn Ser Lys Lys Gly Arg Ser		
115	120	125
Gln Asn His Phe His Ile His Ile Ser Cys Ile Ser Leu Asp Val Arg		
130	135	140
Lys Gln Leu Asp Asn Asn Leu Lys Asn Ile Asn Ser Arg Trp Ser Pro		
145	150	155
Leu Ser Gly Gly Leu Asn Gly His Lys Tyr Leu Ala Arg Arg Val Thr		
165	170	175
Glu Ser Glu Leu Ala Gln Lys Ser Pro Phe Val Met Leu Ala Lys Glu		
180	185	190
Val Pro Asn Ala His Lys Arg Met Gly Asp Tyr Gly Leu Ala Val Val		
195	200	205
Gln Gln Ser Asp Asn Ser Phe Val Leu Leu Ala Thr Gln Phe Asn Pro		
210	215	220
Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu Ile Gln Asp His Glu Cys		
225	230	235
Ala Ile Leu Arg		240

(2) INFORMATION FOR SEQ ID NO:908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

Met Val Phe Asp Arg Thr Thr Ser Val Arg Glu Lys Lys Ala Ala Lys
1 5 10 15
Ala Leu Gly Ile Val Gly Ile Val Phe Phe Ile Leu Phe Gly Ile Val
20 25 30
Ile Ser Gly Val Ala Ser Gln Lys Glu Trp Val Gln Gln Leu Asp Leu
35 40 45
Phe Phe Ile Asp Leu Ile Arg Asn Pro Ala Pro Ile Gln Gly Ser Thr
50 55 60
Trp Leu Ser Phe Val Phe Phe Ser Thr Trp Phe Ala Gln Ser Lys Leu

811

```

65          70          75          80
Thr Thr Pro Ile Ala Leu Leu Ile Gly Leu Trp Phe Gly Phe Gln Lys
      85          90          95
Arg Ile Ala Leu Gly Val Trp Phe Phe Ser Ile Leu Leu Gly Glu
      100         105         110
Phe Thr Leu Lys Ser Leu Lys Leu Leu Val Ala Arg Pro Arg Pro Val
      115         120         125
Thr Asn Gly Glu Leu Val Phe Ala His Gly Phe Ser Phe Pro Ser Gly
      130         135         140
His Ala Leu Ala Ser Ala Leu Phe Tyr Gly Ser Leu Ala Leu Leu Leu
145         150         155         160
Cys Tyr Ser Asn Ala Asn Asn Arg Ile Lys Thr Ile Gly Ala Ile Ile
      165         170         175
Leu Leu Phe Trp Ile Phe Leu Met Ala Tyr Asp Arg Val Tyr Leu Gly
      180         185         190
Val His Tyr Pro Ser Asp Val Leu Gly Gly Phe Leu Leu Gly Ile Ala
      195         200         205
Trp Ser Cys Cys Ser Leu Ala Leu Tyr Leu Gly Phe Leu Lys Arg Pro
      210         215         220
Tyr Lys Ala Ala
225

```

(2) INFORMATION FOR SEQ ID NO:909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

```

Met Lys Lys Phe Gly Leu Gly Val Tyr Leu Leu Leu Leu Gly Ile Leu
1      5      10      15
Gly Gly Ser Leu Ile Ile Leu Gly Ala Ile Val Ala Pro Ile Val Phe
      20      25      30
Lys Ala Ser Ser Ile Leu Pro Glu Leu Asn Leu Thr Pro Phe Glu Ser
      35      40      45
Gly Lys Leu Met Ala Gln Ile Phe Val Arg Phe Asn Tyr Val Leu Gly
      50      55      60
Ala Ile Gly Phe Val Val Leu Leu Tyr Glu Ile Ile Ser Phe Ile Tyr
65      70      75      80
Tyr Lys Arg Ser Leu Val Tyr Leu Ile Leu Gly Val Ala Ile Gly Ala
      85      90      95
Leu Cys Leu Leu Phe Val Phe Tyr Tyr Thr Pro Tyr Ile Leu Asn Ala
      100     105     110
Gln Lys Val Gly Glu Val Ala Leu Gln Ser Ala Glu Phe Ala Arg Ser

```

812

	115		120		125
His	Ala	Gln	Ser	Glu	Trp
			Leu	Phe	Lys
				Glu	Leu
					Phe
					Val
					Leu
					Val
					Cys
	130		135		140
Ala	Leu	Phe	Phe	Trp	Arg
			Leu	Phe	Gly
				Lys	Asn
					Ala
					Leu
145			150		155

(2) INFORMATION FOR SEQ ID NO:910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

Leu	Ile	Asn	Leu	Leu	Pro	His	His	Tyr	His	Lys	Phe	Pro	Pro	Asn	Ile
1			5					10						15	
Asn	Pro	Ser	Leu	Ile	Ser	Leu	Lys	Asp	Arg	Phe	Leu	Pro	His	Glu	Lys
			20				25						30		
His	Ser	Gln	Lys	Val	Lys	Lys	Glu	Cys	Val	Asn	Leu	Phe	Glu	Val	Leu
		35				40						45			
Ser	Pro	Leu	His	Lys	Ile	Asp	Glu	Lys	Tyr	Leu	Phe	His	Leu	Lys	Ile
		50			55					60					
Ala	Gly	Glu	Leu	Ala	Ser	Met	Gly	Lys	Ile	Leu	Ser	Val	Tyr	Leu	Ala
65				70					75					80	
His	Lys	His	Ser	Ala	Tyr	Phe	Ile	Leu	Asn	Ala	Leu	Ser	Tyr	Gly	Phe
			85				90							95	
Ser	His	Gln	Asp	Arg	Ala	Ile	Ile	Cys	Leu	Leu	Gly	Ala	Ile		
		100					105						110		

(2) INFORMATION FOR SEQ ID NO:911:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

```

Met Lys Ser Phe Leu Lys Leu Phe Ala Gln Pro Leu Leu Val Val Leu
1           5           10           15
Ala Phe Met Leu Leu Tyr Ala Leu Ala His Ala Val Leu Gly Phe Tyr
          20           25           30
Val Lys Lys Asp Ser Ala Pro Met Ser Pro Asn Val Glu Lys Ser Glu
          35           40           45
Thr Glu Arg Gln Asn Ser Thr Phe Ser Pro Lys Glu Glu Ala Asn Ala
          50           55           60
Thr Thr Thr Ala Thr Glu Gln Asn Pro Thr Lys Asp Thr Val Pro Pro
65           70           75           80
Leu Asp Thr Ala Thr Gln Lys Gln Glu Ile Lys Gln Glu Ile Lys Gln
          85           90           95
Glu Ile Lys Gln Glu Ile Lys Gln Glu Ile Lys Gln Glu Ile Lys Gln
          100          105          110
Glu Ile Lys Gln Glu Thr Lys Gln Glu Gln Glu Lys Glu Asn Lys Pro
          115          120          125
Lys Gln Asn Ser Val Ser Pro Val Gln Asn Asp Gln Lys Thr Pro Thr
          130          135          140
Thr Pro Leu Met Gly Lys Lys Pro Leu Glu Tyr Lys Val Ala Val Ser
145          150          155          160
Gly Val Asn Val Arg Ala Phe Pro Ser Thr Lys Gly Lys Ile Ile Gly
          165          170          175
Ser Leu Ile Lys Asn Lys Ser Val Lys Val Leu Glu Ile Gln Asn Asp
          180          185          190
Trp Ala Glu Ile Glu Phe Ser His Glu Thr Lys Gly Tyr Val Phe Leu
          195          200          205
Lys Leu Leu Lys Lys Ala Glu
          210          215

```

(2) INFORMATION FOR SEQ ID NO:912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

```

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

```

814

```

Met Phe Pro Trp Ala Ile Asp Phe Lys Lys Leu Gly Leu Phe Gly Leu
   35          40          45
Val Glu Met Leu Gly Phe Val Phe Phe Leu Ala Ile Gly Phe Ile Tyr
   50          55          60
Ala Leu Lys Arg Asn Ala Leu Ser Trp Gln Lys Leu Glu Val Lys
   65          70          75

```

(2) INFORMATION FOR SEQ ID NO:913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

```

Met Cys Gly Met Phe Lys Asn Glu Ile Ser Ala Ile Gln Gly Met Ile
1      5      10      15
Ala Asn Ala Gln Glu Ala Val Ala Gln Ala Lys Ile Val Ser Glu Asn
   20      25      30
Thr Gln Asn Gln Asn Ser Leu Asp Ala Gly Lys Pro Phe Asn Pro Tyr
   35      40      45
Thr Asp Ala Ser Phe Ala Glu Ser Met Leu Lys Asn Ala Gln Ala Gln
   50      55      60
Ala Glu Ile Leu Asn Gln Ala Glu Gln Val Val Lys Asn Phe Glu Lys
   65      70      75      80
Ile Pro Thr Ala Phe Val Asn Asp Ser Leu Gly Val Cys Tyr Glu Val
   85      90      95
Gln Gly Gly Glu Arg Arg Gly Thr Asn Pro Gly Gln Thr Thr Ser Asn
   100     105     110
Thr Trp Gly Ala Gly Cys Ala Tyr Val Gly Gln Thr Ile Thr Asn Leu
   115     120     125
Lys Asn Ser Ile Ala His Phe Gly Thr Gln Glu Gln Gln Ile Gln Gln
   130     135     140
Ala Glu Asn Ile Ala Asp Thr Leu Val Asn Phe Lys Ser Arg Tyr Ser
   145     150     155     160
Glu Leu Gly Asn Thr Tyr Asn Ser Ile Thr Thr Ala Leu Ser Asn Ile
   165     170     175
Pro Asn Ala Gln Ser Leu Gln Asn Ala Val Ser Lys Lys Asn Asn Pro
   180     185     190
Tyr Ser Pro Gln Gly Ile Asp Thr Asn Tyr Tyr Leu Asn Gln Asn Ser
   195     200     205
Tyr Asn Gln Ile Gln Thr Ile Asn Gln Glu Leu Gly Arg Asn Pro Phe
   210     215     220
Arg Lys Val Gly Ile Val Ser Ser Gln Thr Asn Asn Gly Ala Met Asn
   225     230     235     240

```

815

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

(2) INFORMATION FOR SEQ ID NO:914:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) **FEATURE:**

(A) NAME/KEY: misc_feature

(B) LOCATION 1...114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

Met	Ala	Thr	Ile	Gln	Pro	Phe	Asn	His	Ser	Thr	Ile	Gln	Pro	Phe	Asn
1				5					10					15	
His	Ser	Thr	Ile	Gln	Pro	Phe	Asn	His	Ser	Ile	Ile	Gln	Ser	Phe	Asn
			20					25					30		
His	Ser	Thr	Ile	Gln	Ala	Thr	Leu	Pro	Tyr	Phe	Tyr	Asn	Tyr	Leu	Ser
			35				40					45			
Phe	Tyr	Lys	Asn	Leu	Phe	Lys	Asn	Pro	Leu	Phe	Phe	Ile	Ile	Pro	Pro
	50					55					60				
Phe	Ile	Asn	Pro	Phe	Ile	Asn	Pro	Phe	Ile	Asn	Pro	Phe	Ile	Asn	Pro
65					70					75					80
Phe	Ile	Asn	Pro	Phe	Ile	Asn	Pro	Phe	Ile	Asn	Pro	Phe	Ile	Asn	Pro
				85					90					95	
Phe	Ile	Asn	Pro	Phe	Ile	Asn	Pro	Phe	Ile	Asn	Pro	Phe	Ile	Asn	Pro
			100					105						110	

Phe Ile

(2) INFORMATION FOR SEQ ID NO:915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

```

Leu Val Ser Glu Tyr Trp Leu Lys Phe Phe Thr Arg Ser Phe Ser Lys
1          5          10          15
Ser Thr Met Leu Phe Lys Thr Leu Leu Arg Ser Phe Phe Thr Phe Pro
          20          25          30
Val Glu Leu Ser Glu Asn Ile Thr Leu Gly Ser Thr Val Val Leu Ile
          35          40          45
Val Ala Glu Ala Val Ser Ala Leu Asn Lys Lys Val Val Ala Ala Lys
          50          55          60
Lys Asn Lys Ile Arg Phe Thr Pro Asn Ser Tyr Ile His Asn Arg Asn
65          70          75          80
Lys Asn Arg Arg Tyr Ser Ser Leu Ser Pro Leu Leu Lys Ser Ser Ser
          85          90          95
Ile Tyr Lys Asn Pro Pro Arg Ile Gln Ala Ile Leu Ile Ile Leu Lys
          100          105          110
Tyr Arg Leu Ser Lys Gly Ile Tyr His Leu Gly Met Ile Leu
          115          120          125

```

(2) INFORMATION FOR SEQ ID NO:916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

Met	Lys	Lys	Ser	Val	Ile	Val	Gly	Ala	Ile	Ser	Leu	Ala	Met	Thr	Ser
1				5					10					15	
Leu	Leu	Ser	Ala	Glu	Thr	Pro	Lys	Gln	Glu	Lys	Ala	Ile	Lys	Thr	Ser
			20					25					30		
Pro	Thr	Lys	Lys	Gly	Glu	Arg	Asn	Ala	Ala	Phe	Ile	Gly	Ile	Asp	Tyr
		35					40					45			
Gln	Leu	Gly	Met	Leu	Ser	Thr	Thr	Ala	Gln	Asn	Cys	Ser	His	Gly	Asn
	50					55					60				
Cys	Asn	Gly	Asn	Gln	Ser	Gly	Ala	Tyr	Gly	Ser	Asn	Thr	Pro	Asn	Met
65					70					75				80	
Pro	Thr	Ala	Ser	Asn	Pro	Thr	Gly	Gly	Leu	Thr	His	Gly	Ala	Leu	Gly
			85					90						95	
Thr	Arg	Gly	Tyr	Lys	Gly	Leu	Ser	Asn	Gln	Gln	Tyr	Ala	Ile	Asn	Gly
	100							105					110		
Phe	Gly	Phe	Val	Val	Gly	Tyr	Lys	His	Phe	Phe	Lys	Lys	Ala	Pro	Gln
	115						120					125			
Phe	Gly	Met	Arg	Tyr	Tyr	Gly	Phe	Phe	Asp	Phe	Ala	Ser	Ser	Tyr	Tyr
	130					135					140				
Lys	Tyr	Tyr	Thr	Tyr	Asn	Asp	Tyr	Gly	Met	Arg	Asp	Ala	Arg	Lys	Gly
145					150					155				160	
Ser	Gln	Ser	Phe	Met	Phe	Gly	Tyr	Gly	Ala	Gly	Thr	Asp	Val	Leu	Phe
			165					170						175	
Asn	Pro	Ala	Ile	Phe	Asn	Arg	Glu	Asn	Leu	His	Leu	Gly	Phe	Phe	Leu
			180					185					190		
Gly	Val	Ala	Ile	Gly	Gly	Thr	Ser	Trp	Gly	Pro	Thr	Asn	Tyr	Tyr	Phe
	195					200						205			
Lys	Asp	Leu	Ala	Glu	Glu	Tyr	Arg	Gly	Ser	Phe	His	Pro	Ser	Asn	Phe
	210					215					220				
Gln	Val	Leu	Val	Asn	Gly	Gly	Ile	Arg	Leu	Gly	Thr	Lys	His	Gln	Gly
225				230						235				240	
Phe	Glu	Ile	Gly	Leu	Lys	Ile	Gln	Thr	Ile	Arg	Asn	Asn	Tyr	Tyr	Thr
			245					250					255		
Ala	Ser	Ala	Asp	Asn	Val	Pro	Glu	Gly	Thr	Thr	Tyr	Arg	Phe	Thr	Phe
			260					265					270		
His	Arg	Pro	Tyr	Ala	Phe	Tyr	Trp	Arg	Tyr	Ile	Val	Ser	Phe		
	275						280					285			

(2) INFORMATION FOR SEQ ID NO:917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

```

Val Lys Arg Ile Leu Phe Phe Leu Ala Ala Thr Thr Phe Leu Leu Arg
1           5           10           15
Ala Glu Thr Ala Ser Ala Thr Ile Asn Thr Thr Val Asp Pro Asn Val
20           25           30
Met Phe Ser Glu Ser Ser Thr Gly Asn Val Lys Lys Asp Arg Lys Arg
35           40           45
Val Leu Lys Ser Met Val Asp Leu Glu Lys Glu Arg Val Lys Asn Phe
50           55           60
Asn Gln Tyr Ser Glu Thr Lys Met Ser Lys Gly Asp Leu Ser Ala Phe
65           70           75           80
Gly Ala Phe Phe Lys Gly Ser Leu Glu Asp Cys Val Glu Gln Lys Ile
85           90           95
Cys Tyr Tyr Glu His Arg Asn Gly Lys Val Ser Phe Val Val Asn Asp
100          105          110
Arg Glu Lys Phe Tyr Lys His Val Leu Lys Asp Leu Gly Thr Glu Leu
115          120          125
Ser Leu Pro Leu Phe Asn Trp Leu Tyr Lys Gly Ser Asp Phe Gly Ala
130          135          140
Leu His Glu Gln Phe Gly Asp Met Tyr Asp Gly Tyr Ile Lys Tyr Leu
145          150          155          160
Ile Ser Met Val Arg Val Ser Gln Lys Glu Lys Ala Arg Lys Val Asp
165          170          175
Ala Ile Val Leu Lys Lys Met Glu Glu Gln Ala Glu Lys Asp Thr Lys
180          185          190
Ala Ala Phe Gln Lys Arg Ser Ser Gly Glu Leu Glu Ser His Thr Asp
195          200          205
Ser Pro Glu Phe Ile Ser Ser Ser Lys Thr Gln Asn Ser Ser Asn Pro
210          215          220
Asp Leu Asp Pro Met Thr Asn Ala Asn Thr Leu Lys Glu Thr Ala Ser
225          230          235          240
Lys Glu Pro Glu Thr Ser Ser Lys Lys Glu Lys Lys Pro Lys Lys Lys
245          250          255
Arg Arg Leu Ser Lys Lys Glu Lys Gln Gln Ala Leu Gln Gln Glu
260          265          270
Phe Glu Lys Gln Ile Ser Asp Ser Ser Lys Ser Glu Lys
275          280          285

```

(2) INFORMATION FOR SEQ ID NO:918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:

```

Met Pro Lys Glu Asn Thr Thr His Glu Asp Ala Leu Ala Lys Cys Phe
1           5           10           15
Ala Pro Ala Ile Phe Lys Ala Ile Met Leu Asn Lys Leu Ile Leu Ala
          20           25           30
Val Val Ala Ala Pro Ile Ile Lys Met Leu Lys Leu Ser Lys Glu Ile
          35           40           45
Trp Trp Lys Lys Met Gly Lys Lys His Ala Ile Asp Phe Lys Met Arg
          50           55           60
Ile Lys Ile Leu Ala Ser Leu Ala Pro Ser Phe
65           70           75

```

(2) INFORMATION FOR SEQ ID NO:919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

```

Met Cys Gln Ile Gln Cys Leu Leu Ile Leu Leu Ser Ile Asn Ile Val
1           5           10           15
Ser Ala Ile Ile Val Tyr Phe Phe Gln Ala Phe Gln Gly Val Leu Asn
          20           25           30
Phe Glu Gly Gly Phe Leu Gly Phe Phe Ile Val Ala Leu Ser Ser Tyr
          35           40           45
Tyr Gly Val Lys Lys Arg Leu Asp Leu Arg Lys Gln Asp Ser Lys Glu
          50           55           60
Lys Glu Glu Lys Gln Lys Phe Gln Lys Phe Ala Leu Gly Leu Glu Met
65           70           75           80
Ser Phe Asn Val Trp Arg Leu Gly Gly Tyr Gly Val Leu Leu Gly Ile
          85           90           95
Leu Gly Val Leu Leu Phe Leu His Leu Phe Asn Gly Leu Pro Phe Leu
          100          105          110
Ile Gly Val Phe Val Ser Ser Leu Ser Ser Ala Leu Leu Arg Phe Leu
          115          120          125
Asn Asn Asn Gly Lys Phe
130

```

(2) INFORMATION FOR SEQ ID NO:920:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids

820

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

```

Met Ala Cys Glu Phe Leu Lys Lys Pro Lys Tyr Tyr Lys Phe Ile Glu
 1             5             10             15
Gly Ala Asn Tyr Leu Ser Leu Gly Leu Ser Met Val Val Ala Ile Leu
 20             25             30
Met Gly Val Ala Ile Gly Tyr Gly Leu Lys Lys Leu Thr His Ile Ser
 35             40             45
Trp Leu Phe Trp Leu Gly Val Ile Trp Gly Val Leu Ala Ser Phe Leu
 50             55             60
Asn Val Tyr Lys Ala Tyr Lys Asn Met Gln Lys Asp Tyr Glu Glu Leu
 65             70             75             80
Ala Lys Asp Pro Lys Tyr Thr Gln Asn Lys Thr Lys
 85             90

```

(2) INFORMATION FOR SEQ ID NO:921:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

```

Met Glu Asp Phe Leu Tyr Asn Thr Leu Tyr Phe Ile Glu Asp Tyr Lys
 1             5             10             15
Leu Val Val Ile Phe Ser Phe Ile Gly Leu Ile Ala Leu Phe Phe Leu
 20             25             30
Tyr Lys Phe Ile Lys Thr Gln Lys Lys Val Phe Lys Asp Lys Ala Asn
 35             40             45
Gln Pro Gln Lys Lys Lys Ser Phe Lys Glu Ile Ile Ile Asp Gly Leu
 50             55             60

```

821

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

(2) INFORMATION FOR SEQ ID NO:922:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

Met Ala Ile Asp Leu Ala Glu Val Thr Gly Ala Lys Ala Ala Gln Glu
 1 5 10 15
 Arg Lys Lys Glu Gln Pro Thr Ile Ala Asn Gly Leu Asp Lys Asn Ala
 20 25 30
 Phe Met Lys Leu Phe Leu Glu Gln Leu Lys Asn Gln Asp Pro Thr Ala
 35 40 45
 Pro Met Glu Thr Asp Lys Ile Ile Thr Gln Thr Ala Gln Leu Thr Gln
 50 55 60
 Val Glu Met Gln Glu Glu Asn Lys Lys Thr Met Gln Glu Val Ala Ser
 65 70 75 80
 Ala Met Lys Ser Asn Lys Glu Thr Asn Glu Ser Leu Lys Asp Phe Gln
 85 90 95
 Gly Ala Leu Lys Asp Thr Met Glu Asn Leu Asn Lys Gly Met Asp Asp
 100 105 110
 Ser Leu Lys Ala Asn Asn Ala Leu Arg Glu Val Ser Ala Leu Asn Ser
 115 120 125
 Val Ser Met Ile Gly Lys Ile Ala Glu Thr Asp Val Ser Gly Ala Asn
 130 135 140
 Phe Asp Gly Asn Asn Lys Leu Ser Phe Ser Leu Phe Phe Asp Glu Lys
 145 150 155 160
 Ile Asp Ala Ser Lys Gly Val Pro Ala Ile Gln Ile Leu Asn Glu Asn
 165 170 175
 Asn Glu Leu Val Lys Thr Ile Pro Leu Lys Asp Tyr Asn Gly Gln Lys
 180 185 190
 Gly Tyr Ile Asn Phe Glu Trp Asp Gly Thr Asn Glu Lys Gly Glu Lys
 195 200 205
 Val Pro Lys Gly Asn Tyr Lys Ile Lys Ala Glu Tyr Asn Leu Asp Ser
 210 215 220
 Gln Ser Lys Gln Tyr Leu Gln Thr Arg Ile Gly Arg Gly Glu Val Glu
 225 230 235 240
 Ser Val Ile Phe Asp Lys Gly Lys Pro Met Leu Arg Met Gly Glu Met
 245 250 255
 Ile Leu Pro Ile Asp Ser Ala Ile Glu Phe Tyr Lys Pro Asp Gln Lys
 260 265 270

822

Pro Leu Asp Gln Lys Leu Ser Asp Gln Lys Pro Gln Lys Leu Ser Glu
 275 280 285
 Gln Lys Ala Leu Glu Gln Lys Ile Ser Glu Gln Lys Pro Gln Glu Pro
 290 295 300
 Leu Asp Gln Lys Leu Ser Asp Gln Lys Pro Gln Lys Pro Leu Glu Gln
 305 310 315 320
 Lys Ile Ser Glu Gln Lys Pro Leu Asp Gln Lys Leu Ser Asp Gln Lys
 325 330 335
 Pro Gln Lys Pro Leu Glu Gln Lys Ile Ser Glu Gln Lys Pro Leu Asp
 340 345 350
 Gln Lys Pro Gln Thr Pro Pro Lys Glu Thr Ala
 355 360

(2) INFORMATION FOR SEQ ID NO:923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

Leu Lys His Leu Ala Pro Leu Ile His Ile Pro Phe Lys Ala Leu Trp
 1 5 10 15
 Leu Gly Thr Ala Leu Ser Met Phe Leu Ser Leu Asn Leu Asn Ala Glu
 20 25 30
 Glu Asn Pro Thr Lys Thr Glu Pro Lys Pro Ala Lys Gly Val Lys Asn
 35 40 45
 Lys Pro Lys Ser Pro Val Thr Asn Val Met Met Thr Asn Cys Asp Asn
 50 55 60
 Leu Lys Asp Phe Asn Ala Lys Gln Lys Glu Val Leu Lys Ala Ala Tyr
 65 70 75 80
 Gln Phe Gly Ser Lys Glu Asn Leu Gly Tyr Glu Met Ala Gly Ile Ala
 85 90 95
 Trp Lys Glu Ser Cys Ala Gly Thr Tyr Lys Ile Asn Phe Ser Asn Pro
 100 105 110
 Ser Ala Gly Ile Tyr His Ala Tyr Ile Pro Ser Val Leu Lys Ser Tyr
 115 120 125
 Gly His Asn Asn Ser Pro Phe Leu Arg Asn Val Met Gly Glu Leu Leu
 130 135 140
 Ile Lys Asp Asp Ala Phe Ala Ser Glu Val Ala Leu Lys Glu Leu Leu
 145 150 155 160
 Tyr Trp Lys Thr Arg Tyr His Asp Asn Leu Lys Asp Met Ile Lys Ser
 165 170 175
 Tyr Asn Lys Gly Ser Arg Trp Glu Lys Asn Glu Lys Ala Asn Ala Asp
 180 185 190

823

Ala Glu Lys Tyr Tyr Glu Glu Ile Gln Asp Arg Ile Arg Arg Leu Lys
 195 200 205
 Glu Ser Lys Ile Phe Glu Leu Ala Val
 210 215

(2) INFORMATION FOR SEQ ID NO:924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

Met Gln Phe Gln Lys Thr Leu Leu Ser Leu Ser Leu Leu Phe Leu Ser
 1 5 10 15
 Tyr Cys Ile Ala Glu Glu Asn Gly Ala Tyr Ala Ser Val Gly Phe Glu
 20 25 30
 Tyr Ser Ile Ser His Ala Val Glu His Asn Asn Pro Phe Leu Asn Gln
 35 40 45
 Glu Arg Ile Gln Thr Ile Ser Asn Ala Gln Asn Lys Ile Tyr Lys Leu
 50 55 60
 Asn Gln Val Lys Asn Glu Ile Thr Asn Met Pro Asn Thr Phe Asn Tyr
 65 70 75 80
 Ile Asn Asn Ala Leu Lys Asn Asn Ala Lys Leu Thr Pro Thr Glu Lys
 85 90 95
 Gln Ala Glu Thr Tyr Tyr Leu Gln Ser Thr Leu Gln Asn Ile Glu Lys
 100 105 110
 Ile Val Met Leu Ser Gly Gly Val Ala Ser Asn Pro Lys Leu Ala Gln
 115 120 125
 Ala Leu Glu Lys Met Gln Glu Pro Ile Thr Asn Pro Leu Glu Leu Val
 130 135 140
 Glu Asn Leu Lys Asn Leu Glu Leu Gln Phe Ser Gln Ser Gln Asn Ser
 145 150 155 160
 Met Leu Ser Ser Leu Ser Ser Gln Ile Ala Gln Ile Ser Asn Ser Leu
 165 170 175
 Asn Ala Leu Asp Pro Ser Ser Tyr Ser Lys Asn Val Ser Ser Met Tyr
 180 185 190
 Gly Val Gly Leu Ser Val Gly Tyr Lys His Phe Phe Thr Lys Lys Lys
 195 200 205
 Asn Gln Gly Phe Arg Tyr Tyr Leu Phe Tyr Asp Tyr Gly Tyr Thr Asn
 210 215 220
 Phe Gly Phe Val Gly Asn Gly Phe Asp Gly Leu Gly Lys Met Asn Asn
 225 230 235 240
 His Leu Tyr Gly Leu Gly Ile Asp Tyr Leu Phe Asn Phe Ile Asp Asn
 245 250 255

824

```

Ala Gln Lys His Ser Ser Val Gly Phe Tyr Val Gly Phe Ala Leu Ala
      260      265      270
Gly Ser Ser Trp Val Gly Ser Gly Leu Gly Met Trp Val Ser Gln Met
      275      280      285
Asp Phe Ile Asn Asn Tyr Leu Thr Asp Tyr Arg Ala Lys Met His Thr
      290      295      300
Ser Phe Phe Gln Ile Pro Leu Asn Phe Gly Val Arg Val Asn Val Asp
305      310      315      320
Arg His Asn Gly Phe Glu Met Gly Leu Lys Ile Pro Leu Ala Val Asn
      325      330      335
Ser Phe Tyr Glu Thr His Gly Lys Gly Leu Asn Ala Ser Leu Phe Phe
      340      345      350
Lys Arg Leu Val Met Phe Asn Val Ser Tyr Val Tyr Ser Phe
      355      360      365

```

(2) INFORMATION FOR SEQ ID NO:925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

```

Met Gln Phe Gln Lys Thr Leu Leu Ser Leu Ser Leu Leu Phe Leu Ser
1      5      10      15
Tyr Cys Ile Ala Glu Glu Asn Gly Ala Tyr Ala Ser Val Gly Phe Glu
      20      25      30
Tyr Ser Ile Ser His Ala Val Glu His Asn Asn Pro Phe Leu Asn Gln
      35      40      45
Glu Arg Ile Gln Thr Ile Ser Asn Ala Gln Asn Lys Ile Tyr Lys Leu
      50      55      60
Asn Gln Val Lys Asn Glu Ile Thr Asn Met Pro Asn Thr Phe Asn Tyr
65      70      75      80
Ile Asn Asn Ala Leu Lys Asn Asn Ala Lys Leu Thr Pro Thr Glu Lys
      85      90      95
Gln Ala Glu Thr Tyr Tyr Leu Gln Ser Thr Leu Gln Asn Ile Glu Lys
      100     105     110
Ile Val Met Leu Ser Gly Gly Val Ala Ser Asn Pro Lys Leu Ala Gln
      115     120     125
Ala Leu Glu Lys Met Gln Glu Pro Ile Thr Asn Pro Leu Glu Leu Val
      130     135     140
Glu Asn Leu Lys Asn Leu Glu Leu Gln Phe Ser Gln Ser Gln Asn Ser
145     150     155     160
Met Leu Ser Ser Leu Ser Ser Gln Ile Ala Gln Ile Ser Asn Ser Leu
      165     170     175

```

825

```

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

```

(2) INFORMATION FOR SEQ ID NO:926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

```

Leu Asn Thr Met Asn Ser Val Leu Glu Cys Lys Glu Leu Ala Leu Tyr
1           5           10           15
Gly Gly Ser Phe Asp Pro Leu His Lys Ala His Leu Ala Ile Glu
      20           25           30
Gln Thr Leu Glu Leu Leu Pro Phe Val Gln Leu Ile Val Leu Pro Ala
      35           40           45
Tyr Gln Asn Pro Phe Lys Lys Pro Cys Phe Leu Asp Ala Lys Thr Arg
      50           55           60
Phe Lys Glu Leu Glu Arg Ala Leu Lys Gly Met Pro Arg Val Leu Leu
      65           70           75           80
Ser Asp Phe Glu Ile Lys Gln Glu Arg Ala Val Pro Thr Ile Glu Ser
      85           90           95

```


826

```

Val Leu His Phe Gln Lys Leu Tyr Arg Pro Lys Thr Leu Tyr Leu Val
      100      105      110
Ile Gly Ala Asp Cys Leu Arg His Leu Ser Ser Trp Thr Asn Ala Lys
      115      120      125
Glu Leu Leu Lys Arg Val Glu Leu Val Val Phe Glu Arg Ile Gly Tyr
      130      135      140
Glu Glu Ile Gln Phe Lys Gly Arg Tyr His Pro Leu Lys Gly Ile Asp
      145      150      155      160
Ala Pro Ile Ser Ser Ser Ala Ile Arg Ala Ser Leu Gly Val
      165      170

```

(2) INFORMATION FOR SEQ ID NO:927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

```

Met Arg Phe Phe Cys Phe Phe Leu Phe Phe Leu Thr Phe Ser Asn Ala
1      5      10      15
Gln Ile Met Met Thr Phe Asp Ser Gln Thr Asn Ala Lys Leu Ser Arg
      20      25      30
Ser Asn Glu Gln Leu Ser Asp Met Leu Tyr Lys Leu Asn Glu Ser Leu
      35      40      45
Arg Ile Tyr Gln Asn Val Leu Ser Asn Asn Gln Asp Gln Leu Lys Glu
      50      55      60
Ile Lys Lys Ala Asn Ser Thr Leu Thr Ser Gln Arg Arg Phe Phe Asn
      65      70      75      80
Ala Ser Gln Ile Arg Leu Met Asp Thr Asp Ala Leu Leu Lys Gln Ser
      85      90      95
Ala Leu Glu Leu Glu Lys Leu Gln Ala Leu Glu Lys His Leu Lys Glu
      100     105     110
Ser Met Glu His Glu Arg Leu Ile Lys Glu Ser Gln Ala Leu Phe Leu
      115     120     125
Gln Glu His Cys Pro Tyr Leu Ser Gly Val Lys Asn Leu Glu Glu Ala
      130     135     140
Ser Asn Ala Leu Glu Val Gln Glu Lys Asn Asn Ala Leu Phe Leu Leu
      145     150     155     160
Lys Glu Pro Lys Leu Phe His Leu Leu Ser Arg Leu Asp Leu Met Ser
      165     170     175
Ala Leu Asn Ala Leu Cys Asp Gln Val Leu Glu Asn Glu Ile Gln Asp
      180     185     190
Gln Gln Ser His Asn Lys Thr Leu Glu Tyr Asn Ala Leu Met Asn His
      195     200     205

```

827

```

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

```

(2) INFORMATION FOR SEQ ID NO:928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

```

Val Lys Gly Glu Lys Asn Ala Trp Tyr Leu Gly Ile Ser Tyr Gln Val
1          5          10          15
Gly Gln Ala Ser Gln Ser Val Lys Asn Pro Pro Lys Ser Ser Glu Phe
                20                25                30
Asn Tyr Pro Lys Phe Pro Val Gly Lys Thr Asp Tyr Leu Ala Val Met
                35                40                45
Gln Gly Leu Gly Leu Thr Val Gly Tyr Lys Gln Phe Phe Gly Glu Lys
50          55          60
Arg Trp Phe Gly Ala Arg Tyr Tyr Gly Phe Met Asp Tyr Gly His Ala
65          70          75          80
Val Phe Gly Ala Asn Ala Leu Thr Ser Asp Asn Gly Gly Val Cys Lys
                85                90                95
Leu Asn Glu Pro Cys Ala Thr Lys Val Gly Thr Met Gly Asn Leu Ser
100        105        110

```

828

```

Asp Met Phe Thr Tyr Gly Val Gly Ile Asp Thr Leu Tyr Asn Val Ile
      115                      120                      125
Asn Lys Glu Asp Ala Ser Phe Gly Phe Phe Phe Gly Ala Gln Ile Ala
      130                      135                      140
Gly Asn Ser Trp Gly Asn Thr Thr Gly Ala Phe Leu Glu Thr Lys Ser
      145                      150                      155                      160
Pro Tyr Lys His Thr Ser Tyr Ser Leu Asp Pro Ala Ile Phe Gln Phe
      165                      170                      175
Leu Phe Asn Leu Gly Ile Arg Thr His Ile Gly Gln His Gln Glu Phe
      180                      185                      190
Asp Phe Gly Val Lys Ile Pro Thr Ile Asn Val Tyr Tyr Phe Asn His
      195                      200                      205
Gly Asn Leu Ser Phe Thr Tyr Arg Arg Gln Tyr Ser Leu Tyr Val Gly
      210                      215                      220
Tyr Arg Tyr Asn Phe
      225

```

(2) INFORMATION FOR SEQ ID NO:929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

```

Leu Lys Asn His Ser Phe Lys Lys Thr Ile Ala Leu Ser Leu Leu Ala
1      5      10      15
Ser Met Ser Leu Cys Asn Ala Glu Glu Asp Gly Ala Phe Phe Val Ile
      20      25      30
Asp Tyr Gln Thr Ser Leu Ala Arg Gln Glu Leu Lys Asn Pro Gly Phe
      35      40      45
Thr Gln Ala Gln Glu Leu Lys Gln Leu Ile Arg Asp Gly Ala Val Arg
      50      55      60
Leu Gln Thr Ser Ala Ile Pro Leu Ser Tyr Tyr Leu Asp Ile Leu Gly
      65      70      75      80
Asn Lys Thr Lys Thr Leu Leu Ser Glu Ser Leu Lys Asn Asn Pro Gln
      85      90      95
Gln Pro Asn Gly Gln Pro Asn Gln Ala Leu Val Asn Leu Glu Gln Ser
      100     105     110
Leu Gly Ile Leu Gly Lys Leu Leu Asp Leu Ser Gln Gln Tyr Ala Ser
      115     120     125
Glu Gly Val Ile Lys Pro Leu Val Val Asp Val Gly Lys Glu Gln Ile
      130     135     140
Gly Ile Thr Asp Ser Met Leu Leu Val Ala Gln Asn Ile Val Leu Ala
      145     150     155     160

```

829

```

Leu Gly Gln Val Asp Leu Ser Lys Ile Gln Gln Asn Asn Gly Asn Gln
      165      170      175
Gln Leu Tyr Glu Asn Ile Met Lys Val Met Leu Leu Gly Thr Gly Gly
      180      185      190
Thr Asn Gly Ala Tyr Asn Gly Val Ser Val Gly Asp Ile Ala Thr Gly
      195      200      205
Met Gln Asn Phe Pro Ser Gln Thr Gly Leu Ile Gly Ala Asn Ser Thr
      210      215      220
Val Ser Glu Leu Asn Ala Leu Ile Lys Ser Gly Ile Ser Leu Asp Arg
      225      230      235      240
Glu Thr Leu Gly Leu Gly Ser Phe Ile Glu Lys Asn Ile Cys Ser Gly
      245      250      255
Ala Ser Ser Cys Phe Ser Gly Asn Gln Leu Ile Tyr Lys Lys Gly Leu
      260      265      270
Asp Arg Thr Ile Asn Ile Ile Asn Ala Val Leu Gly Gln Phe Glu Ser
      275      280      285
Ser Ala Ser Ser Leu Tyr Lys Ile Ser Tyr Ile Pro Asn Leu Phe Ser
      290      295      300
Leu Lys Asp Tyr Gln Ser Ala Ser Met Asn Gly Phe Gly Ala Lys Met
      305      310      315      320
Gly Tyr Lys Gln Phe Phe Thr His Lys Lys Asn Ile Gly Leu Arg Tyr
      325      330      335
Tyr Gly Phe Leu Asp Tyr Gly Tyr Ala Asn Phe Gly Asp Thr Asn Leu
      340      345      350
Lys Val Gly Ala Asn Leu Val Thr Tyr Gly Val Gly Thr Asp Phe Leu
      355      360      365
Tyr Asn Val Tyr Glu Arg Ser Arg Arg Arg Glu Arg Thr Thr Ile Gly
      370      375      380
Leu Phe Phe Gly Ala Gln Ile Ala Gly Gln Thr Trp Ser Thr Asn Val
      385      390      395      400
Thr Asn Leu Leu Ser Gly Gln Arg Pro Asp Val Lys Ser Ser Ser Phe
      405      410      415
Gln Phe Leu Phe Asp Leu Gly Val Arg Thr Asn Phe Ala Lys Thr Asn
      420      425      430
Phe Asn Lys His Arg Leu Asp Gln Gly Ile Glu Phe Gly Val Lys Ile
      435      440      445
Pro Val Ile Ala His Lys Tyr Phe Ala Thr Gln Gly Ser Ser Ala Ser
      450      455      460
Tyr Met Arg Asn Phe Ser Phe Tyr Val Gly Tyr Ser Val Gly Phe
      465      470      475

```

(2) INFORMATION FOR SEQ ID NO:930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

```

Met Ala Ser Leu Ala Phe Val Gln Ala Phe Leu Glu Ser Phe Lys Gly
1      5      10      15
Phe Leu Ser Gln Ala Thr Leu Ile Ser Val Leu Ile Ala Ser Val Leu
20      25      30
Ile Leu Phe Cys Ala Ile Leu Leu Leu Leu Ala Leu Leu Leu Arg Asn
35      40      45
Arg Trp Ala Ser Tyr Ile Thr Thr Ala Ala Phe Leu Gly Ala Phe Leu
50      55      60
Ser Met Pro Phe Val Leu Asn Val Leu Leu Thr Gln Ala Ile Tyr Pro
65      70      75      80
Ile Glu Thr Arg Ile Leu His Ala Asn Pro Leu Ser Tyr Ser Asn Ala
85      90      95
Phe Ser Leu Gln Val Gly Val Lys Asn Ile Ser Lys Phe Ser Leu Asn
100     105     110
Lys Cys Val Leu Arg Leu Glu Val Leu Lys Asn Pro His Asn Phe Val
115     120     125
Glu Glu Arg Ala Phe Lys Trp Phe Val Lys Lys Ser Tyr Glu Lys Thr
130     135     140
Phe Lys Glu Lys Ile Leu Pro Glu Glu Ser Lys Val Phe Ser Phe Phe
145     150     155     160
Ile Asp Asp Tyr Pro Tyr Ser Lys Thr Ala Pro Tyr Gln Val Ser Leu
165     170     175
Phe Cys Leu

```

(2) INFORMATION FOR SEQ ID NO:931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

```

Leu Gly Glu Leu Leu Gln Ala Ser Ala Pro Tyr Ala Ile Ala Pro Val
1      5      10      15
Glu Leu Ile Val Val Phe Tyr Lys Asn Glu Tyr Lys Arg Lys Lys Gln
20      25      30
Thr Ser Thr Met Ser Arg Glu Glu Phe Leu Leu Tyr Thr Asn Gly Leu
35      40      45
Trp Asn Phe Ser Gly Glu Ser Lys Lys Arg Leu Lys His Pro Ala Pro
50      55      60

```

831

```

Phe Pro Arg Glu Leu Pro Arg Arg Cys Ile Gln Leu Phe Ser Phe Leu
65          70          75          80
Glu Asp Thr Ile Phe Asp Pro Phe Ser Gly Ser Gly Thr Thr Ile Leu
          85          90          95
Glu Ala Asn Ala Leu Gly Arg Phe Ser Val Gly Leu Glu Ile Glu Lys
          100         105         110
Glu Tyr Cys Glu Leu Ser Lys Lys Arg Ile Leu Glu Ser Leu Ser Leu
          115         120         125
Val

```

(2) INFORMATION FOR SEQ ID NO:932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

```

Val Leu Lys Gly Leu Lys Lys Ala Phe Lys Glu Arg Phe Cys Ser Gln
1          5          10         15
Val Tyr Ile Ser Phe Asn Val Asp His Asn Leu Leu Ser Ala Gln Val
          20         25         30
Leu Arg Val Lys Asn His Arg Ile Lys Glu Lys Phe Phe Lys Thr Phe
          35         40         45
Glu Thr Lys Val Glu Thr Lys Asn Gly Glu Val Pro Ile Gln Ala Leu
          50         55         60
Lys Ile Ala Arg Thr Tyr Ser Gln Lys Tyr Pro Tyr Thr Tyr Phe Ser
65          70          75          80
Ala Met Ser Lys Ala Lys Glu Val Leu Cys Glu Lys Gln Ala Phe Glu
          85          90          95
Gln Ile Lys Gln Glu Asn Gln Asp Tyr Gln Ala Cys Glu Val Asn Gln
          100         105         110
Lys Tyr Cys Val Tyr Val Glu Ser Lys Asp Phe Leu Lys Asp Phe Lys
          115         120         125
Arg Phe Lys Ile Gln Asp Val Asp Phe Leu Phe Ser Pro Phe Ser Leu
          130         135         140
Ile Tyr Asp Phe Val Arg Asp Asn Leu Glu Asn Lys Pro Leu Leu Tyr
145          150         155         160
Leu Leu Leu Glu Arg Ser Arg Phe Tyr Phe Leu Ile Ala Asp Lys Lys
          165         170         175
Glu Ile Phe Leu Ala Lys Ser Val Phe Leu Glu Glu Gln Pro Glu Glu
          180         185         190
Phe Ile Glu Ser Lys Glu Glu Asp Ser Met Gly Met Asp Asn Glu Ala
          195         200         205

```

832

```

Val Asp Leu Phe Leu Ser Glu Ile Gln Glu Asp Ile Asp Ser Leu Glu
  210                      215                      220
Glu Ala Ile Gly Leu Asp Ser Ser Lys Asp Asn Ser Glu Lys Ile Thr
  225                      230                      235                      240
Glu Asp Ala Tyr Ser Leu Ile Glu Gly Met Thr Asn Ile Pro Leu Ile
                      245                      250                      255
Ala Asp Val Leu Gln Glu Gly Leu Arg Gly Val Tyr His Ser Arg Glu
                      260                      265                      270
Ile Asp Phe Val Glu Lys Val Val Val Leu Asp Ser Cys Gln Ile His
                      275                      280                      285
His Lys Ala Leu Met His Leu Gln Glu Thr Leu Met Ile Glu Val Asp
                      290                      295                      300
Arg Leu Asp Phe Ser Leu Val Glu Arg Leu Asn Val Leu Ala Arg Met
  305                      310                      315                      320
Glu Asn Glu Lys His Ala Phe
                      325

```

(2) INFORMATION FOR SEQ ID NO:933:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:

```

Met Asn Ile Gln Thr Lys Lys Arg Phe Leu Ala Asn Leu Leu Leu Phe
  1                      5                      10                      15
Ser Leu Phe Ser Cys Leu Lys Ala Glu Thr Leu Ser Glu Asp His Gln
                      20                      25                      30
Ile Leu Leu Ser Ser Asp Ala Phe His Arg Gly Asp Phe Ala Thr Ala
                      35                      40                      45
Gln Lys Gly Tyr Met Asn Leu Tyr Lys Gln Thr Asn Lys Val Val Tyr
                      50                      55                      60
Ala Lys Glu Ala Ala Ile Ser Ala Ala Ser Leu Gly Asp Ile Lys Thr
  65                      70                      75                      80
Ala Met His Leu Ala Met Leu Tyr Gln Lys Ile Thr Asn Asn Arg Asn
                      85                      90                      95
Asp Val Ser Ile Asn Lys Ile Leu Val Asp Gly Tyr Ala Gln Met Gly
                      100                      105                      110
Gln Ile Asp Lys Ala Ile Glu Leu Leu His Lys Ile Arg Lys Glu Glu
                      115                      120                      125
Lys Thr Ile Ala Thr Asp Asn Val Leu Gly Thr Leu Tyr Leu Thr Gln
                      130                      135                      140
Lys Arg Leu Asp Lys Ala Phe Pro Leu Leu Asn Lys Phe Tyr Asn Gln
  145                      150                      155                      160

```

833

```

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

```

(2) INFORMATION FOR SEQ ID NO:934:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 414 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:

```

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

```


834

```

Val Val Phe Leu Gly Lys Ile Ile Leu His Lys Val Phe Ile Met Glu
      20                      25                      30
Ala Leu Glu Cys Leu Lys Arg Ile Glu Lys Glu Ser Ile Gln Thr Ile
      35                      40                      45
Tyr Ile Asp Pro Pro Tyr Asn Thr Lys Ser Ser Asn Phe Glu Tyr Glu
      50                      55                      60
Asp Ala His Ala Asp Tyr Glu Lys Trp Ile Glu Glu His Leu Ile Leu
      65                      70                      75                      80
Ala Lys Ala Val Leu Lys Gln Ser Gly Cys Ile Phe Ile Ser Met Asp
      85                      90                      95
Asp Asn Lys Met Ala Glu Val Lys Ile Ile Ala Asn Glu Ile Phe Gly
      100                     105                     110
Thr Arg Asn Phe Leu Gly Thr Phe Ile Thr Lys Gln Ala Thr Arg Ser
      115                     120                     125
Asn Ala Lys His Ile Asn Ile Thr His Glu Tyr Val Leu Ser Tyr Ala
      130                     135                     140
Lys Asn Lys Ala Phe Ala Pro Gly Phe Lys Ile Leu Arg Thr Leu Leu
      145                     150                     155                     160
Pro Ile Tyr Ala Lys Ala Leu Lys Asp Leu Met Arg Thr Ile Lys Asn
      165                     170                     175
Val Phe Lys Gln Lys Gly Gln Ala Gln Ala Gln Leu Ile Leu Lys Glu
      180                     185                     190
Gln Ile Lys Glu Leu Ser Gln Lys Glu His Phe Asn Phe Leu Lys Asn
      195                     200                     205
Tyr Asn Leu Val Asp Glu Lys Gly Glu Ile Tyr Phe Ala Lys Asp Leu
      210                     215                     220
Ser Thr Pro Ser Asn Pro Arg Ser Val Ala Ile Gln Glu Ile Asn Leu
      225                     230                     235                     240
Phe Leu Glu Pro Leu Lys Ser Arg Gly Trp Ser Ser Asp Glu Lys Leu
      245                     250                     255
Lys Glu Leu Tyr Tyr Gln Asn Arg Leu Ile Phe Lys Asn Asn Arg Pro
      260                     265                     270
Tyr Glu Lys Tyr Tyr Leu Lys Glu Ser Gln Asp Asn Cys Leu Ser Val
      275                     280                     285
Leu Asp Phe Tyr Ser Arg Gln Gly Thr Lys Asp Leu Glu Lys Leu Gly
      290                     295                     300
Leu Lys Gly Leu Phe Lys Thr Pro Lys Pro Val Ala Leu Ile Lys Tyr
      305                     310                     315                     320
Leu Leu Leu Cys Ser Thr Pro Lys Asp Ser Ile Ile Leu Asp Phe Phe
      325                     330                     335
Ala Gly Ser Gly Thr Thr Ala Gln Ala Val Ile Glu Val Asn Lys Asp
      340                     345                     350
Tyr Tyr Leu Asn Trp Ser Phe Tyr Leu Cys Gln Lys Glu Glu Lys Ile
      355                     360                     365
Lys Asn Asn Pro Gln Ala Val Ser Ile Leu Lys Asn Lys Gly Tyr Lys
      370                     375                     380
Asn Thr Ile Ser Asp Ile Met Leu Leu Arg Leu Glu Lys Ile Ile Lys
      385                     390                     395                     400
Arg Ser Glu Tyr Glu Ile Leu Lys Thr Lys Ser Ile Leu Phe
      405                     410

```

(2) INFORMATION FOR SEQ ID NO:935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

835

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...166
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

Leu	Glu	Ile	Asp	Lys	Thr	Glu	Cys	Ser	Thr	Leu	Leu	Ala	Ser	Ile	Gln
1				5				10						15	
Lys	Gln	Gln	Leu	Val	Ile	Pro	Val	Val	Gly	Asn	Phe	Ser	Ala	Gly	Lys
			20					25					30		
Ser	Thr	Leu	Leu	Asn	Arg	Phe	Leu	Gly	Ser	Ser	Val	Leu	Pro	Thr	Gly
			35				40						45		
Ile	Thr	Pro	Glu	Thr	Ser	Leu	Ala	Thr	Glu	Leu	His	Tyr	Ser	Ala	Asn
			50				55				60				
Glu	Arg	Ile	Glu	Ala	Phe	Ser	Ser	Asn	Asp	Glu	Lys	Thr	Glu	Ser	Phe
65					70					75					80
Glu	Leu	Asn	Glu	Gln	Ser	Phe	Glu	Ala	Ile	Lys	Glu	Asn	Ala	Ala	Lys
				85					90					95	
Tyr	Ser	Tyr	Leu	Lys	Val	Tyr	Leu	Asn	Asn	Glu	Ala	Leu	Lys	Asp	Ser
			100					105					110		
Ala	Pro	Leu	Val	Phe	Val	Asp	Met	Pro	Gly	Phe	Asp	Ser	Pro	Ile	Ser
			115				120					125			
Ser	His	Thr	His	Ala	Ile	Leu	Glu	Tyr	Leu	Glu	Arg	Gly	Val	His	Phe
			130				135				140				
Val	Ile	Leu	Thr	Ser	Val	Glu	Glu	Gly	Asn	Leu	Thr	Lys	Arg	Met	Val
145					150					155					160
Arg	Glu	Leu	Lys	Thr	Phe										
					165										

(2) INFORMATION FOR SEQ ID NO:936:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...251
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

836

```

Met Lys Leu Pro Val Val Glu Ser Phe Phe Ser Leu Gln Gly Glu Gly
1      5      10      15
Lys Arg Ile Gly Lys Pro Ser Leu Phe Leu Arg Leu Gly Gly Cys Asn
20      25      30
Leu Ser Cys Lys Gly Phe Asn Cys Lys Thr Leu Phe Asn Asp Glu Ile
35      40      45
Leu Thr Gly Cys Asp Ser Leu Tyr Ala Val His Pro Lys Phe Lys Thr
50      55      60
Ser Trp Asp Tyr Tyr Asn Glu Pro Lys Pro Leu Ile Glu Arg Leu Val
65      70      75      80
Asn Leu Ala Pro Asn Tyr Lys Asp Phe Asp Phe Ile Leu Thr Gly Gly
85      90      95
Glu Pro Ser Leu Tyr Phe Asn Asn Pro Ile Leu Leu Ser Val Leu Glu
100     105     110
His Phe Tyr His Lys Lys Ile Pro Leu Phe Val Glu Ser Asn Gly Ser
115     120     125
Ile Phe Phe Glu Phe Ser Pro Ile Leu Lys Glu Leu His Phe Thr Leu
130     135     140
Ser Val Lys Leu Ser Phe Ser Leu Glu Gln Glu Ser Lys Arg Ile Asn
145     150     155     160
Leu Lys Ala Leu Gln Asn Ile Leu Asn Asn Ala Lys Ser Val His Phe
165     170     175
Lys Phe Val Leu Glu Ser Gln Asn Ala Ala His Ser Ile Ala Glu Ile
180     185     190
Gln Ser Leu Leu Lys Gln Leu Ser Leu Lys Asn Asn Glu Ile Phe Leu
195     200     205
Met Pro Leu Gly Thr Thr Asn Asn Glu Leu Asp Lys Asn Leu Lys Thr
210     215     220
Leu Ala Pro Leu Ala Ile Glu His Gly Phe Arg Leu Ser Asp Arg Leu
225     230     235     240
His Ile Arg Leu Trp Asp Asn Lys Lys Gly Phe
245     250

```

(2) INFORMATION FOR SEQ ID NO:937:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

```

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

```

837

```

Val Pro Leu Tyr Glu Phe Ser Asn Thr Gly Glu His Ala Val Ile Gln
    35                      40                      45
Val Arg Lys Ser Gly Leu Ser Thr Leu Glu Met Leu Gln Ile Phe Ser
    50                      55                      60
Gln Ile Leu Gly Val Lys Ile Ala Glu Leu Gly Tyr Ala Gly Leu Lys
    65                      70                      75                      80
Asp Lys Asn Ala Leu Thr Thr Gln Phe Ile Ser Leu Pro Lys Lys Tyr
                      85                      90                      95
Ala Pro Leu Leu Glu Lys Asn Thr Ser Asn Phe Gln Glu Arg Asn Leu
                      100                      105                      110
Lys Ile Leu Ser Leu Asn Tyr His His Asn Lys Ile Lys Leu Gly His
                      115                      120                      125
Leu Lys Gly Asn Arg Phe Phe Met Arg Phe Lys Lys Met Thr Pro Leu
                      130                      135                      140
Asn Ala Gln Lys Thr Glu Gln Val Leu Glu Gln Ile Ala Gln Phe Gly
    145                      150                      155                      160
Met Pro Asn Tyr Phe Gly Ser Gln Arg Phe Gly Lys Phe Asn Asp Asn
                      165                      170                      175
His Lys Glu Gly Leu Lys Ile Leu Gln Asn Glu Thr Lys Phe Ala His
                      180                      185                      190
Gln Lys Leu Asn Ala Phe Leu Ile Ser Ser Tyr Gln Ser Tyr Leu Phe
    195                      200                      205
Asn Ser Leu Leu Ser Lys Arg Leu Glu Ile Ser Lys Ile Ile Ser Ala
    210                      215                      220
Phe Ser Val Lys Glu Ser Leu Glu Phe Phe Lys Gln Lys Asn Leu Ser
    225                      230                      235                      240
Val His Ser Asn Ala Leu Lys Ala Leu Lys Asn Gln Ala His Pro Phe
                      245                      250                      255
Lys Ile Leu Glu Gly Asp Val Met Arg His Tyr Pro Tyr Gly Lys Phe
    260                      265                      270
Phe Asp Ala Leu Glu Leu Glu Lys Glu Ser Glu Arg Phe Leu Asn Lys
    275                      280                      285
Glu Ala Val Pro Thr Gly Leu Leu Asp Gly Lys Lys Ala Leu Tyr Ala
    290                      295                      300
Lys Asn Leu Ser Leu Glu Ile Glu Lys Gly Phe Gln His Asn Leu Leu
    305                      310                      315                      320
Ser Gly His Ala Lys Thr Leu Gly Ser Arg Arg Phe Phe Trp Val Phe
                      325                      330                      335
Val Glu Asn Ile Thr Ser Gln Tyr Ile Lys Glu Lys Ala Gln Phe Glu
                      340                      345                      350
Leu Glu Phe Tyr Leu Pro Lys Gly Ser Tyr Ala Ser Ala Leu Leu Lys
    355                      360                      365
Glu Ile Lys His Glu Lys Gly Glu Asn Asn Asp Glu Phe
    370                      375                      380

```

(2) INFORMATION FOR SEQ ID NO:938:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

```

Leu Gln Asn Phe Val Phe Asn Lys Lys Trp Leu Ile Tyr Ser Ser Leu
1           5           10           15
Leu Pro Leu Phe Phe Leu Asn Pro Leu Met Ala Glu Asp Asp Gly Phe
20           25           30
Phe Met Gly Val Ser Tyr Gln Thr Ser Leu Ala Val Gln Arg Val Asp
35           40           45
Asn Ser Gly Leu Asn Ala Ser Gln Asp Ala Ser Thr Tyr Ile Arg Gln
50           55           60
Asn Ala Ile Ala Leu Glu Ser Ala Ala Val Pro Leu Ala Tyr Tyr Leu
65           70           75           80
Glu Ala Met Gly Gln Gln Thr Arg Val Leu Met Gln Met Leu Cys Pro
85           90           95
Asp Pro Ser Lys Arg Cys Leu Leu Tyr Ala Gly Gly Tyr Gln Asn Gly
100          105          110
Gln Asn Asn Asn Gly Asp Thr Gly Asn Asn Pro Pro Arg Gly Asn Val
115          120          125
Asn Ala Thr Phe Asp Met Gln Ser Leu Val Asn Asn Leu Asn Lys Leu
130          135          140
Thr Gln Leu Ile Gly Glu Thr Leu Ile Arg Asn Pro Glu Asn Leu Pro
145          150          155          160
Asn Ser Lys Val Phe Asn Val Lys Phe Gly Asn Gln Ser Thr Val Ile
165          170          175
Ala Leu Pro Glu Gly Leu Ala Asn Thr Met Asp Ala Leu Asn Asn Asp
180          185          190
Ile Thr Asn Ala Leu Thr Thr Leu Trp Tyr Asn Gln Thr Leu Thr Asn
195          200          205
Lys Ser Phe Ser Thr Pro Ser Asn Thr Ser Val Asn Phe Ser Pro Gln
210          215          220
Val Leu Gln His Leu Leu Gln Asp Gly Leu Ala Thr Ala Asn Asn Asn
225          230          235          240
Gln Thr Ile Cys Ser Thr Gln Asn Gln Cys Thr Ala Thr Asn Glu Ala
245          250          255
Lys Ser Ile Ala Gln Asn Ala Gln Asn Ile Phe Gln Ala Leu Met Gln
260          265          270
Ala Gly Ile Leu Gly Gly Leu Ala Asn Glu Lys Gln Phe Gly Phe Thr
275          280          285
Tyr Asn Lys Ala Pro Asn Gly Ser Asp Ser Gln Gln Gly Tyr Gln Ser
290          295          300
Phe Ser Gly Pro Gly Tyr Tyr Thr Lys Asn Asp Asn Thr Thr Gln Ala
305          310          315          320
Pro Leu Lys Ala Leu Pro Ala Gly Ala Thr Ile Gly Ser Gly Asn Gly
325          330          335
Gln Tyr Thr Tyr His Pro Ser Ser Ala Val Tyr Tyr Leu Ala Asp Ser
340          345          350
Ile Ile Ala Asn Gly Ile Thr Ala Ser Met Ile Phe Ser Gly Met Gln
355          360          365
Asn Phe Ala Asn Lys Ala Ala Lys Leu Ile Gly Thr Ser Ser Tyr Asn
370          375          380
Gln Met Gln Asp Val Ile Asn Tyr Gly Glu Ser Leu Leu Ser Asn Thr

```

839

```

385          390          395          400
Val Ala Tyr Gly Asp Phe Ile Thr Asn Trp Val Ala Pro Tyr Leu Asp
          405          410          415
Leu Asn Asn Lys Gly Leu Asn Phe Leu Pro Asn Tyr Gly Gly Gln Leu
          420          425          430
Asn Gly Ala Asn Asn Gln Thr Pro Gln Leu Thr Pro Gln Gln Ala Gln
          435          440          445
Gln Glu Gln Lys Val Ile Met Asn Gln Leu Glu Gln Ala Thr Asn Ala
          450          455          460
Pro Thr Pro Ala Gln Ile Asn Arg Ile Leu Ala Asn Pro Tyr Ser Pro
465          470          475          480
Thr Ala Lys Thr Leu Met Ala Tyr Gly Leu Tyr Arg Ser Lys Ala Val
          485          490          495
Ile Gly Gly Val Ile Asp Glu Met Gln Thr Lys Val Asn Gln Val Tyr
          500          505          510
Gln Met Gly Phe Ala Arg Asn Phe Leu Glu His Asn Ser Asn Ser Asn
          515          520          525
Asn Met Asn Gly Phe Gly Val Lys Met Gly Tyr Lys Gln Phe Phe Gly
          530          535          540
Lys Lys Arg Met Phe Gly Leu Arg Tyr Tyr Gly Phe Tyr Asp Phe Gly
545          550          555          560
Tyr Ala Gln Phe Gly Thr Glu Ser Ser Leu Val Lys Ala Thr Leu Ser
          565          570          575
Ser Tyr Gly Ala Gly Thr Asp Phe Leu Tyr Asn Val Phe Thr Arg Lys
          580          585          590
Arg Gly Thr Glu Ala Ile Asp Ile Gly Phe Phe Ala Gly Ile Gln Leu
          595          600          605
Ala Gly Gln Thr Trp Lys Thr Asn Phe Leu Asp Gln Val Asp Gly Asn
          610          615          620
His Leu Lys Pro Lys Asp Thr Ser Phe Gln Phe Leu Phe Asp Leu Gly
625          630          635          640
Ile Arg Thr Asn Phe Ser Lys Ile Ala His Gln Lys Arg Ser Arg Phe
          645          650          655
Ser Gln Gly Ile Glu Phe Gly Leu Lys Ile Pro Val Leu Tyr His Thr
          660          665          670
Tyr Tyr Gln Ser Glu Gly Val Thr Ala Lys Tyr Arg Arg Ala Phe Ser
          675          680          685
Phe Tyr Val Gly Tyr Asn Ile Gly Phe
          690          695

```

(2) INFORMATION FOR SEQ ID NO:939:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

Leu	Gln	Asn	Phe	Val	Phe	Asn	Lys	Lys	Trp	Leu	Ile	Tyr	Ser	Ser	Leu	1	5	10	15
Leu	Pro	Leu	Phe	Phe	Leu	Asn	Pro	Leu	Met	Ala	Glu	Asp	Asp	Gly	Phe	20	25	30	
Phe	Met	Gly	Val	Ser	Tyr	Gln	Thr	Ser	Leu	Ala	Val	Gln	Arg	Val	Asp	35	40	45	
Asn	Ser	Gly	Leu	Asn	Ala	Ser	Gln	Asp	Ala	Ser	Thr	Tyr	Ile	Arg	Gln	50	55	60	
Asn	Ala	Ile	Ala	Leu	Glu	Ser	Ala	Ala	Val	Pro	Leu	Ala	Tyr	Tyr	Leu	65	70	75	80
Glu	Ala	Met	Gly	Gln	Gln	Thr	Arg	Val	Leu	Met	Gln	Met	Leu	Cys	Pro	85	90	95	
Asp	Pro	Ser	Lys	Arg	Cys	Leu	Leu	Tyr	Ala	Gly	Gly	Tyr	Gln	Asn	Gly	100	105	110	
Gln	Asn	Asn	Asn	Gly	Asp	Thr	Gly	Asn	Asn	Pro	Pro	Arg	Gly	Asn	Val	115	120	125	
Asn	Ala	Thr	Phe	Asp	Met	Gln	Ser	Leu	Val	Asn	Asn	Leu	Asn	Lys	Leu	130	135	140	
Thr	Gln	Leu	Ile	Gly	Glu	Thr	Leu	Ile	Arg	Asn	Pro	Glu	Asn	Leu	Pro	145	150	155	160
Asn	Ser	Lys	Val	Phe	Asn	Val	Lys	Phe	Gly	Asn	Gln	Ser	Thr	Val	Ile	165	170	175	
Ala	Leu	Pro	Glu	Gly	Leu	Ala	Asn	Thr	Met	Asp	Ala	Leu	Asn	Asn	Asp	180	185	190	
Ile	Thr	Asn	Ala	Leu	Thr	Thr	Leu	Trp	Tyr	Asn	Gln	Thr	Leu	Thr	Asn	195	200	205	
Lys	Ser	Phe	Ser	Thr	Pro	Ser	Asn	Thr	Ser	Val	Asn	Phe	Ser	Pro	Gln	210	215	220	
Val	Leu	Gln	His	Leu	Leu	Gln	Asp	Gly	Leu	Ala	Thr	Ala	Asn	Asn	Asn	225	230	235	240
Gln	Thr	Ile	Cys	Ser	Thr	Gln	Asn	Gln	Cys	Thr	Ala	Thr	Asn	Glu	Ala	245	250	255	
Lys	Ser	Ile	Ala	Gln	Asn	Ala	Gln	Asn	Ile	Phe	Gln	Ala	Leu	Met	Gln	260	265	270	
Ala	Gly	Ile	Leu	Gly	Gly	Leu	Ala	Asn	Glu	Lys	Gln	Phe	Gly	Phe	Thr	275	280	285	
Tyr	Asn	Lys	Ala	Pro	Asn	Gly	Ser	Asp	Ser	Gln	Gln	Gly	Tyr	Gln	Ser	290	295	300	
Phe	Ser	Gly	Pro	Gly	Tyr	Tyr	Thr	Lys	Asn	Asp	Asn	Thr	Thr	Gln	Ala	305	310	315	320
Pro	Leu	Lys	Ala	Leu	Pro	Ala	Gly	Ala	Thr	Ile	Gly	Ser	Gly	Asn	Gly	325	330	335	
Gln	Tyr	Thr	Tyr	His	Pro	Ser	Ser	Ala	Val	Tyr	Tyr	Leu	Ala	Asp	Ser	340	345	350	
Ile	Ile	Ala	Asn	Gly	Ile	Thr	Ala	Ser	Met	Ile	Phe	Ser	Gly	Met	Gln	355	360	365	
Asn	Phe	Ala	Asn	Lys	Ala	Ala	Lys	Leu	Ile	Gly	Thr	Ser	Ser	Tyr	Asn	370	375	380	
Gln	Met	Gln	Asp	Val	Ile	Asn	Tyr	Gly	Glu	Ser	Leu	Leu	Ser	Asn	Thr	385	390	395	400
Val	Ala	Tyr	Gly	Asp	Phe	Ile	Thr	Asn	Trp	Val	Ala	Pro	Tyr	Leu	Asp	405	410	415	
Leu	Asn	Asn	Lys	Gly	Leu	Asn	Phe	Leu	Pro	Asn	Tyr	Gly	Gly	Gln	Leu	420	425	430	

841

```

Asn Gly Ala Asn Asn Gln Thr Pro Gln Leu Thr Pro Gln Gln Ala Gln
    435                      440                      445
Gln Glu Gln Lys Val Ile Met Asn Gln Leu Glu Gln Ala Thr Asn Ala
    450                      455                      460
Pro Thr Pro Ala Gln Ile Asn Arg Ile Leu Ala Asn Pro Tyr Ser Pro
465                      470                      475                      480
Thr Ala Lys Thr Leu Met Ala Tyr Gly Leu Tyr Arg Ser Lys Ala Val
    485                      490                      495
Ile Gly Gly Val Ile Asp Glu Met Gln Thr Lys Val Asn Gln Val Tyr
    500                      505                      510
Gln Met Gly Phe Ala Arg Asn Phe Leu Glu His Asn Ser Asn Ser Asn
    515                      520                      525
Asn Met Asn Gly Phe Gly Val Lys Met Gly Tyr Lys Gln Phe Phe Gly
    530                      535                      540
Lys Lys Arg Met Phe Gly Leu Arg Tyr Tyr Gly Phe Tyr Asp Phe Gly
545                      550                      555                      560
Tyr Ala Gln Phe Gly Thr Glu Ser Ser Leu Val Lys Ala Thr Leu Ser
    565                      570                      575
Ser Tyr Gly Ala Gly Thr Asp Phe Leu Tyr Asn Val Phe Thr Arg Lys
    580                      585                      590
Arg Gly Thr Glu Ala Ile Asp Ile Gly Phe Phe Ala Gly Ile Gln Leu
    595                      600                      605
Ala Gly Gln Thr Trp Lys Thr Asn Phe Leu Asp Gln Val Asp Gly Asn
    610                      615                      620
His Leu Lys Pro Lys Asp Thr Ser Phe Gln Phe Leu Phe Asp Leu Gly
625                      630                      635                      640
Ile Arg Thr Asn Phe Ser Lys Ile Ala His Gln Lys Arg Ser Arg Phe
    645                      650                      655
Ser Gln Gly Ile Glu Phe Gly Leu Lys Ile Pro Val Leu Tyr His Thr
    660                      665                      670
Tyr Tyr Gln Ser Glu Gly Val Thr Ala Lys Tyr Arg Arg Ala Phe Ser
    675                      680                      685
Phe Tyr Val Gly Tyr Asn Ile Gly Phe
    690                      695

```

(2) INFORMATION FOR SEQ ID NO:940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1237 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

```

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

```


Leu Leu Ala Glu Asp Asn Gly Trp Tyr Met Ser Val Gly Tyr Gln Ile
 20 25 30
 Gly Gly Thr Gln Gln Phe Ile Asn Asn Lys Gln Leu Leu Glu Asn Gln
 35 40 45
 Asn Ile Ile Asn Ser Ile Thr Gln Ser Ala Ile Asn Ile Ala Gly Pro
 50 55 60
 Thr Thr Gly Leu Ile Thr Leu Ser Ser Gln Ser Val Ile Asp Ala Leu
 65 70 75 80
 Gly Tyr Gly Val Ser Asn Thr Val Gly Asn Gln Leu Glu Gly Ile Ser
 85 90 95
 Asn Ile Leu Asn Gln Ile Gly Lys Arg Lys Asp Phe Tyr Ser Ser Arg
 100 105 110
 Gln Ile Ser Ser Ile Ser Gln Gln Ile Ile Gly Leu Lys Gly Ser Ser
 115 120 125
 Asp Pro Leu Lys Ala His Ser Ser Gln Ile Thr Ala Lys Leu Leu Ser
 130 135 140
 Asn Thr Gln Ser Ala Phe Asp Gln Gly Ile Ala Leu Ser Ser Asn Ile
 145 150 155 160
 Ile Ser Ala Val Asn Ser Leu Asn Pro Ser Asn Asn Ser Gln Glu Val
 165 170 175
 Lys Ala Gln Leu Gln Asn Thr Ala Gln Ser Met Thr Glu Leu Leu Gln
 180 185 190
 Gln Ile Glu His Ser Ile Thr Lys Thr Thr Ser Thr Thr Tyr Ala Gln
 195 200 205
 Ser Leu Leu Ser Asn Leu Thr Asp Ala Val Asn Ala Ser Ser Asn Asn
 210 215 220
 Thr Thr Tyr Val Ser Ala Leu Val Asn Ala Leu Asn Thr Leu Gly Val
 225 230 235 240
 Gly Val Phe Pro Thr Thr Thr Ser Thr His Val Val Leu Asn Pro Pro
 245 250 255
 Gly Gln Val Val Phe Tyr Pro Thr Asn Ser Leu Leu Gly Ser Thr Ser
 260 265 270
 Ser Asn Ser Asn Asn Gln Gln Gln Tyr Asn Asn Thr Leu Leu Met Asn
 275 280 285
 Thr Leu Gln Gly Glu Leu Ser Thr Asn Asn Gln Asn Asn Pro Asn Gly
 290 295 300
 Cys Ala Asn Gln Ile Gln Cys Leu Glu Gln Phe Ile Gln Asn Leu Thr
 305 310 315 320
 Pro Leu Ala Ala Thr Pro Thr Ser Thr Asn Gln Ala Asn Gln Gln Val
 325 330 335
 Gln Ala Ile Ala Gln Lys Leu Gln Ser Val Ala Ile Asn Ala Leu Asp
 340 345 350
 Asn Asn Ala Ile Asn Asn Thr Thr Tyr Asn Leu Asn Asn Leu His Asn
 355 360 365
 Ala Leu Asn Phe Gln Ala Tyr Gln Ser Thr Ile Glu Gln Tyr Asn Asn
 370 375 380
 Ala Leu Lys Gln Ile Ser Trp Ile Ser Phe Ser Glu Pro Lys Asn Leu
 385 390 395 400
 Leu Lys Asn Thr Ser Asn Asn Tyr Gln Ile Gly Thr Val Thr Asn Asp
 405 410 415
 Gln Gly Gln Asn Ile Ser Ala Tyr Asp Cys Thr Ser Ala Thr Gly Ser
 420 425 430
 Leu Ser Ser Asp Ala Ser Ser Gly Ile Ser Cys Ser Ala Thr Ser Ser
 435 440 445
 Thr Asn Asn Thr Asn Ser Phe Asp Asn Ser Leu Val Ala Thr Ser Lys
 450 455 460
 Val Gln Thr Ile Asn Gly Lys Glu Gln Ile Gly Val Asn Ser Phe Asn

843

465					470					475				480	
Leu	Val	Ser	Gln	Val	Trp	Ser	Val	Tyr	Asn	Ser	Leu	Lys	Thr	Ser	Glu
				485					490					495	
Glu	Asn	Leu	Gln	Lys	Asn	Ala	Lys	Ile	Leu	Cys	Asn	Asn	Gly	Ser	Gln
			500					505					510		
Ser	Gly	Thr	Ser	Pro	Cys	Asn	Ser	Ser	Ser	Gly	Gly	Leu	Ser	Ile	Ser
		515					520					525			
Gly	Asn	Ala	Gln	Leu	Gln	Asn	Ile	Leu	Ser	Pro	Thr	Asn	Gly	Thr	Thr
	530					535					540				
Thr	Asn	Thr	Gln	Ala	Lys	Ser	Asn	Ala	Ser	Lys	Leu	Lys	Ala	Met	Val
545					550					555					560
Met	Val	Asn	Asn	Glu	Glu	Glu	Ala	Lys	Thr	Thr	Asn	Phe	Asn	Gln	Ser
				565					570					575	
Ser	Gly	Pro	Thr	Thr	Gln	Ser	Ser	Asn	Ser	Thr	Val	Met	Gly	Ala	Leu
			580					585					590		
Asn	Thr	Val	Leu	Gln	Asn	Val	Ser	Asn	Phe	Gln	Gln	Ser	Ile	Gln	Ser
		595					600					605			
Ala	Phe	Gln	Asn	Gln	Glu	Asn	Asn	Ile	Gln	Ala	Trp	Ala	Asn	Ala	Leu
	610					615					620				
Tyr	Asn	Thr	Ser	Asn	Pro	Asn	Gly	Asn	Gln	Ser	Gln	Asn	Leu	Thr	Thr
625					630					635					640
Asn	Asn	Asn	Gln	Asp	Leu	Arg	Ile	Gln	Leu	Arg	Ala	Asn	Phe	Tyr	Gln
				645					650					655	
Leu	Ile	Asn	Thr	Ile	Asn	Gln	Gln	Val	Pro	Thr	Asp	Met	Asn	Ala	Leu
			660					665					670		
Ile	Asn	Gln	Ser	Gln	Gln	Thr	Gln	Gln	Thr	Ser	Gly	Ser	Ala	Ser	Thr
		675					680					685			
Thr	Asn	Asn	Ala	Cys	Ala	Ser	Gly	Met	Gly	Ser	Ser	Gly	Asn	Trp	Cys
	690					695					700				
Tyr	Gln	Gln	Trp	Ser	Asp	Ser	Lys	Ala	Tyr	Tyr	Ser	Gly	Leu	Gln	Ser
705					710					715					720
Ala	Leu	Gly	Tyr	Gln	Thr	Gln	Ala	Thr	Thr	Gln	Asn	Gly	Ser	Ser	Gly
				725					730					735	
Gly	Ser	Asn	Ile	Thr	Tyr	Asn	Val	Gln	Gln	Ile	Thr	Leu	Thr	Ser	Gly
			740					745					750		
Gly	Leu	Leu	Asn	Gln	Ile	Ile	Thr	Asn	Leu	Lys	Ser	Val	Asn	Gly	Gly
		755					760					765			
Ser	Asn	Gly	Gly	Ser	Ser	Gly	Asn	Gly	Thr	Ser	Gln	Ile	Asn	Thr	Ala
	770					775					780				
Tyr	Gln	Met	Leu	Thr	Asp	Ala	Ser	Asp	Gly	Lys	Leu	Gly	Thr	Tyr	Asn
785					790					795					800
Ser	Ser	Asn	Ser	Ser	Asn	Ser	Ser	Asn	Ser	Gly	Asn	Asn	Asn	Gly	Tyr
				805					810					815	
Thr	Pro	Cys	Asn	Ser	Thr	Asn	Gly	Ser	Asn	Gly	Thr	Ser	Gly	Ser	Asn
			820					825					830		
Cys	Tyr	Glu	Pro	Asn	Lys	Gln	Gln	Asn	Ala	Thr	Thr	Ala	Thr	Thr	Thr
		835					840					845			
Thr	Asp	Ser	Asn	Leu	Gln	Lys	Val	Tyr	Asn	Asp	Ala	Gln	Lys	Ile	Ala
	850					855					860				
Asn	Ile	Ile	Ala	Ser	Ser	Gly	Asn	Asn	Lys	Gly	Val	Glu	Asn	Gly	Leu
865					870					875					880
Lys	Gln	Phe	Phe	Glu	Ala	Leu	Lys	Ser	Asn	Ser	Ser	Ser	Leu	Ser	Asn
				885					890					895	
Leu	Cys	Gly	Asn	Gly	Ser	Ser	Gly	Ser	Ser	Ser	Thr	Cys	Ser	Gly	Gly
			900					905					910		
Leu	Ile	Asn	Leu	Leu	Gly	Ala	Ile	Pro	Thr	Asn	Gly	Val	Ser	Asp	Thr
		915					920					925			

844

```

Asn Asn Leu Ile Asn Leu Leu Thr Glu Phe Ile Lys Thr Ala Gly Phe
 930                      935                      940
Ile Gln Asn Asn Asp Ser Asn Val Ser Thr Ser Leu Thr Ser Ala Phe
945                      950                      955                      960
Gln Ala Ile Thr Ser Ala Ile Ser Gln Gly Phe Gln Ala Leu Gln Asn
                      965                      970                      975
Asp Ile Ser Pro Asn Ala Ile Leu Thr Leu Leu Gln Glu Ile Thr Ser
                      980                      985                      990
Asn Thr Thr Thr Ile Gln Ser Phe Ser Gln Thr Leu Arg Gln Leu Leu
                      995                      1000                      1005
Gly Asp Lys Thr Phe Phe Met Val Gln Gln Lys Leu Ile Asp Ala Met
1010                      1015                      1020
Ile Asn Ala Arg Asn Gln Val Gln Asn Ala Gln Asn Gln Ala Asn Asn
1025                      1030                      1035                      1040
Tyr Gly Ser Gln Pro Val Leu Ser Gln Tyr Ala Ala Gly Lys Ser Thr
                      1045                      1050                      1055
Gln His Gly Met Ser Asn Gly Leu Gly Val Gly Ile Gly Tyr Lys Tyr
                      1060                      1065                      1070
Phe Phe Gly Lys Ala Arg Lys Leu Gly Leu Arg His Tyr Phe Phe Phe
                      1075                      1080                      1085
Asp Tyr Gly Phe Ser Glu Ile Gly Leu Ala Asn Gln Ser Val Lys Ala
1090                      1095                      1100
Asn Ile Phe Ala Tyr Gly Val Gly Thr Asp Phe Leu Trp Asn Leu Phe
1105                      1110                      1115                      1120
Arg Arg Thr Tyr Asn Thr Lys Ala Leu Asn Phe Gly Leu Phe Ala Gly
                      1125                      1130                      1135
Val Gln Leu Gly Gly Ala Thr Trp Leu Ser Ser Leu Arg Gln Gln Ile
                      1140                      1145                      1150
Ile Asp Asn Trp Gly Asn Ala Asn Asp Ile His Ser Thr Asn Phe Gln
                      1155                      1160                      1165
Val Ala Leu Asn Phe Gly Val Arg Thr Asn Phe Ala Glu Phe Lys Arg
1170                      1175                      1180
Phe Ala Lys Lys Phe His Asn Gln Gly Val Ile Ser Gln Lys Ser Val
1185                      1190                      1195                      1200
Glu Phe Gly Ile Lys Val Pro Leu Ile Asn Gln Ala Tyr Leu Asn Ser
                      1205                      1210                      1215
Ala Gly Ala Asp Val Ser Tyr Arg Arg Leu Tyr Thr Phe Tyr Ile Asn
                      1220                      1225                      1230
Tyr Ile Met Gly Phe
1235

```

(2) INFORMATION FOR SEQ ID NO:941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

845

(B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

```

Met Glu Lys Leu Pro Lys Lys Arg Val Ser Lys Thr Lys Ser Gln Lys
1           5           10           15
Leu Ile His Ser Leu Thr Thr Gln Lys Asn Arg Ala Phe Leu Gln Lys
          20           25           30
Thr Ser Ala Asn Glu Met Leu Leu Glu Leu Glu Lys Gly Ala Phe Lys
          35           40           45
Lys Asn Glu Ala Tyr Phe Ile Ser Asp Glu Glu Asp Lys Asn Tyr Val
          50           55           60
Leu Val Pro Asp Asn Val Ile Ser Leu Leu Ala Glu Asn Ala Arg Lys
65           70           75           80
Ala Phe Glu Ala Arg Leu Arg Ala Glu Leu Glu Arg Asp Ile Ile Thr
          85           90           95
Gln Ala Pro Ile Asp Phe Glu Asp Val Arg Glu Val Ser Leu Gln Leu
          100          105          110
Leu Glu Asn Leu Arg Gln Lys Asp Gly Asn Leu Pro Asn Ile Asn Thr
          115          120          125
Leu Asn Phe Val Lys Gln Ile Lys Lys Glu His Pro Asn Leu Phe Phe
          130          135          140
Asn Phe Asp Asn Met Phe Lys Gln Pro Pro Phe Asn Glu Asn Asn Phe
145          150          155          160
Glu Asn Phe Asp Asn Ser Asp Glu Glu Asn Phe
          165          170

```

(2) INFORMATION FOR SEQ ID NO:942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

```

Met Lys Lys Ile Leu Ile Thr Leu Ile Thr Leu Leu Leu Gly Val Phe
1           5           10           15
Met Gly Leu Gln Ala Ser Ala Leu Thr His Gln Glu Ile Asn Gln Ala
          20           25           30
Lys Val Pro Val Ile Tyr Glu Glu Asn His Leu Leu Pro Met Gly Phe
          35           40           45
Ile His Leu Ala Phe Arg Gly Gly Gly Ser Leu Ser Asp Lys Asn Gln
          50           55           60
Leu Gly Leu Ala Lys Leu Phe Ala Gln Val Leu Asn Glu Gly Thr Lys
65           70           75           80

```

846

Glu Leu Gly Ala Val Gly Phe Ala Gln Leu Leu Glu Gln Lys Ala Ile
 85 90 95
 Ser Leu Asn Val Asp Thr Ser Ala Glu Asp Leu Gln Ile Thr Leu Glu
 100 105 110
 Phe Leu Lys Glu Tyr Glu Asp Glu Ala Ile Met Arg Leu Lys Glu Leu
 115 120 125
 Leu Lys Ser Pro Asn Phe Thr Gln Asn Ala Leu Glu Lys Val Lys Thr
 130 135 140
 Arg Met Leu Ala Gln Leu Leu Gln Lys Glu Ser Asp Phe Asp Tyr Leu
 145 150 155 160
 Ala Lys Leu Thr Leu Lys Gln Glu Leu Phe Ala Asn Thr Pro Leu Ala
 165 170 175
 Asn Ala Ala Leu Gly Thr Lys Glu Ser Leu Gln Lys Ile Lys Leu Asp
 180 185 190
 Asp Leu Lys Gln Gln Phe Ala Lys Val Phe Glu Leu Asn Lys Leu Val
 195 200 205
 Val Val Leu Gly Gly Asp Leu Lys Val Asn Gln Thr Leu Asn Arg Leu
 210 215 220
 Asn Asn Ala Leu Asn Phe Leu Pro Gln Gly Lys Ala Tyr Glu Glu Pro
 225 230 235 240
 Tyr Phe Glu Ala Ser Asp Lys Lys Ser Glu Lys Val Leu Tyr Lys Asp
 245 250 255
 Thr Glu Gln Ala Phe Val Tyr Phe Gly Val Pro Phe Lys Ile Lys Asp
 260 265 270
 Leu Lys Gln Asp Leu Ala Lys Ser Lys Val Met Met Phe Val Leu Gly
 275 280 285
 Gly Gly Phe Gly Ser Arg Leu Met Glu Lys Ile Arg Val Gln Glu Gly
 290 295 300
 Leu Ala Tyr Ser Val Tyr Ile Arg Ser Asn Phe Ser Lys Val Ala His
 305 310 315 320
 Phe Ala Ser Gly Tyr Leu Gln Thr Lys Leu Ser Thr Gln Ala Lys Ser
 325 330 335
 Val Ala Leu Val Lys Lys Ile Ile Lys Glu Phe Ile Glu Lys Gly Met
 340 345 350
 Thr Gln Gln Glu Leu Asp Asp Ala Lys Lys Phe Leu Leu Gly Ser Glu
 355 360 365
 Pro Leu Arg Asn Glu Thr Ile Ser Ser Arg Leu Asn Thr Thr Tyr Asn
 370 375 380
 Tyr Phe Tyr Leu Gly Leu Pro Leu Asp Phe Asn Gln Thr Leu Leu Asn
 385 390 395 400
 Gln Ile Gln Lys Met Ser Leu Lys Glu Ile Asn Asp Phe Ile Lys Glu
 405 410 415
 His Thr Glu Ile Asn Asp Leu Thr Phe Ala Ile Val Ser Asn Lys Lys
 420 425 430
 Lys Asp Lys
 435

(2) INFORMATION FOR SEQ ID NO:943:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

```

Leu Ala Ser Pro Lys Glu Thr Pro Lys Glu Ala Gln Lys Asn Glu Ala
1      5      10      15
Gln Asn Glu Thr Ser Gln Ser Asn Gln Thr Pro Lys Glu Met Lys Val
20     25     30
Lys Ser Ile Ser Tyr Val Gly Leu Ser Tyr Met Ser Asp Met Leu Ala
35     40     45
Asn Glu Ile Ala Lys Ile Arg Val Gly Asp Met Val Asp Ser Lys Lys
50     55     60
Ile Asp Thr Ala Val Leu Ala Leu Phe Asn Gln Gly Tyr Phe Lys Asp
65     70     75     80
Val Tyr Ala Thr Phe Glu Asn Gly Ile Leu Glu Phe His Phe Asp Glu
85     90     95
Lys Ala Arg Ile Ala Gly Val Glu Ile Lys Gly Tyr Gly Thr Glu Lys
100    105    110
Glu Lys Asp Gly Leu Lys Ser Gln Met Gly Ile Lys Lys Gly Asp Thr
115    120    125
Phe Asp Glu Gln Lys Leu Glu His Ala Lys Thr Ala Leu Lys Thr Ala
130    135    140
Leu Glu Gly Gln Gly Tyr Tyr Gly Ser Val Val Glu Val Arg Thr Glu
145    150    155    160
Lys Val Ser Glu Gly Ala Leu Leu Ile Val Phe Asp Val Asn Arg Gly
165    170    175
Asp Ser Ile Tyr Ile Lys Gln Ser Ile Tyr Glu Gly Ser Asp Lys Leu
180    185    190
Lys Arg Arg Val Ile Glu Ser Leu Ser Ala Asn Lys Gln Arg Asp Phe
195    200    205
Met Gly Trp Met Trp Gly Leu Asn Asp Gly Lys Leu Arg Leu Asp Gln
210    215    220
Leu Glu Tyr Asp Ser Leu Arg Ile Gln Asp Val Tyr Met Arg Arg Gly
225    230    235    240
Tyr Leu Asp Ala His Ile Ser Ser Pro Phe Leu Lys Thr Asp Phe Ser
245    250    255
Thr His Asp Ala Lys Leu His Tyr Lys Val Lys Glu Gly Ile Gln Tyr
260    265    270
Arg Ile Ser Asp Ile Leu Ile Glu Ile Asp Asn Pro Val Val Pro Leu
275    280    285
Lys Thr Leu Glu Lys Ala Leu Lys Val Lys Arg Lys Asp Val Phe Asn
290    295    300
Ile Glu His Leu Arg Ala Asp Ala Gln Ile Leu Lys Thr Glu Ile Ala
305    310    315    320
Asp Lys Gly Tyr Ala Phe Ala Val Val Lys Pro Asp Leu Asp Lys Asp
325    330    335
Glu Lys Asn Gly Leu Val Lys Val Ile Tyr Arg Ile Glu Val Gly Asp
340    345    350
Met Val His Ile Asn Asp Val Ile Ser Gly Asn Gln Arg Thr Ser
355    360    365
Asp Arg Ile Ile Arg Arg Glu Leu Leu Gly Pro Lys Asp Lys Tyr

```

```

370          375          380
Asn Leu Thr Lys Leu Arg Asn Ser Glu Asn Ser Leu Arg Arg Leu Gly
385          390          395          400
Phe Phe Ser Lys Val Lys Ile Glu Glu Lys Arg Val Asn Ser Ser Leu
          405          410          415
Met Asp Leu Leu Val Ser Val Glu Glu Gly Arg Thr Gly Gln Leu Gln
          420          425          430
Phe Gly Leu Gly Tyr Gly Ser Tyr Gly Gly Leu Met Leu Asn Gly Ser
          435          440          445
Val Ser Glu Arg Asn Leu Phe Gly Thr Gly Gln Ser Met Ser Leu Tyr
          450          455          460
Ala Asn Ile Ala Thr Gly Gly Arg Ser Tyr Pro Gly Met Pro Lys
465          470          475          480
Gly Ala Gly Arg Met Phe Ala Gly Asn Leu Ser Leu Thr Asn Pro Arg
          485          490          495
Ile Phe Asp Ser Trp Tyr Ser Ser Thr Ile Asn Leu Tyr Ala Asp Tyr
          500          505          510
Arg Ile Ser Tyr Gln Tyr Ile Gln Gln Gly Gly Gly Phe Gly Val Asn
          515          520          525
Val Gly Arg Met Leu Gly Asn Arg Thr His Val Ser Leu Gly Tyr Asn
          530          535          540
Leu Asn Val Thr Lys Leu Leu Gly Phe Ser Ser Pro Leu Tyr Asn Arg
545          550          555          560
Tyr Tyr Ser Ser Val Asn Glu Val Ala Ser Pro Arg Gln Cys Ser Thr
          565          570          575
Pro Ala Ser Val Ile Ile Asn Arg Leu Ser Gly Gly Arg Thr Pro Leu
          580          585          590
Val Pro Glu Ser Cys Ser Ser Pro Gly Ala Ile Thr Ile Phe Thr Arg
          595          600          605
Asn Lys Arg Tyr Leu Gly
610

```

(2) INFORMATION FOR SEQ ID NO:944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

```

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

```

35	40	45
Val Pro Gly Leu Arg Tyr Ala Phe Val Gln Tyr Asn Asn Glu Asn Ala		
50	55	60
Ser Asn Trp Met Gln Ile Pro Glu Lys Asp Leu Arg Lys Ile Lys His		
65	70	75
Met Asn Asn Trp Met Pro Ser Thr Asn Ile Gly Phe Ile Pro Val Gln		
85	90	95
Gly Asp His Asn Val Leu Thr Tyr Phe Asn Tyr Gln Arg Ser Phe Val		
100	105	110
Pro Pro Gln Leu Asp Val Leu Ser Tyr Gly Gly Ala Glu Tyr Phe Thr		
115	120	125
Gln His Phe Asp Thr Val Glu Ala Gly Ala Arg Tyr Thr Tyr Lys Asp		
130	135	140
Lys Phe Ser Phe Asn Ala Asp Tyr Phe Arg Ile Trp Ala Arg Asp Phe		
145	150	155
Ala Thr Gly Gln Tyr Ser Val Tyr Thr Ser Gly Pro Met Lys Gly Asn		
165	170	175
Val Arg Pro Ile Asn Gly Tyr Ser Gln Gly Val Glu Leu Glu Leu Tyr		
180	185	190
Tyr Arg Pro Ile Arg Gly Leu Gln Phe His Ala Ala Phe Asn Tyr Ile		
195	200	205
Asp Thr Arg Val Thr Ser His Gly Pro Leu Thr Asp Leu Asn Gly Asp		
210	215	220
Val Leu Lys Gly Thr Ser Tyr Asn Lys His Phe Pro Phe Val Ser Pro		
225	230	235
Phe Gln Phe Ile Phe Asp Ala Arg Tyr Asn Trp Arg Lys Thr Thr Ile		
245	250	255
Gly Ile Ser Ser Tyr Phe Tyr Ser Arg Ala Tyr Ser Gly Ile Ser Asn		
260	265	270
Ser Ala Ala Gly Gly Tyr Tyr Gly Met Gln Tyr Tyr Ser Gly Gly Asn		
275	280	285
Asn Tyr Glu Ser Val Leu Asn Ser Gly Tyr Gln Cys Glu Ala Trp Cys		
290	295	300
Met Thr Gln His Glu Gly Leu Leu Pro Trp Tyr Trp Val Trp Asn Ile		
305	310	315
Gln Val Ser Gln Ile Phe Trp Glu Asn Gly Arg His Arg Val Thr Gly		
325	330	335
Ser Leu Gln Ile Asn Asn Ile Phe Asn Met Lys Tyr Tyr Phe Thr Gly		
340	345	350
Ile Gly Ser Ser Pro Ala Gly Leu Gln Pro Ala Pro Gly Arg Ser Val		
355	360	365
Thr Ala Tyr Leu Asn Tyr Thr Phe		
370	375	

(2) INFORMATION FOR SEQ ID NO:945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

```

Leu His Ala Glu Asp Asn Gly Phe Phe Val Ser Ala Gly Tyr Gln Ile
1      5      10      15
Gly Glu Ala Val Gln Met Val Lys Asn Thr Gly Glu Leu Lys Asn Leu
20      25      30
Asn Asp Lys Tyr Glu Gln Leu Ser Gln Ser Leu Ala Gln Leu Ala Ser
35      40      45
Leu Lys Lys Ser Ile Gln Thr Ala Asn Asn Ile Gln Ala Val Asn Asn
50      55      60
Ala Leu Ser Asp Leu Lys Ser Phe Ala Ser Asn Asn His Thr Asn Lys
65      70      75      80
Glu Thr Ser Pro Ile Tyr Asn Thr Ala Gln Ala Val Ile Thr Ser Val
85      90      95
Leu Ala Phe Trp Ser Leu Tyr Ala Gly Asn Ala Leu Ser Phe His Val
100     105     110
Thr Gly Leu Asn Asp Gly Ser Asn Ser Pro Leu Gly Arg Ile His Arg
115     120     125
Asp Gly Asn Cys Thr Gly Leu Gln Gln Cys Phe Met Ser Lys Glu Thr
130     135     140
Tyr Asp Lys Met Lys Thr Leu Ala Glu Asn Leu Gln Lys Ala Gln Gly
145     150     155     160
Asn Leu Cys Ala Leu Ser Glu Cys Ser Ser Asn Gln Ser Asn Gly Gly
165     170     175
Lys Thr Ser Met Thr Thr Ala Leu Gln Thr Ala Gln Gln Leu Met Asp
180     185     190
Leu Ile Glu Gln Thr Lys Val Ser Met Val Trp Lys Asn Ile Val Ile
195     200     205
Ala Gly Val Thr Asn Lys Pro Asn Gly Ala Gly Ala Ile Thr Ser Thr
210     215     220
Gly His Val Thr Asp Tyr Ala Val Phe Asn Asn Ile Lys Ala Met Leu
225     230     235     240
Pro Ile Leu Gln Gln Ala Leu Thr Leu Ser Gln Ser Asn His Thr Leu
245     250     255
Ser Thr Gln Leu Gln Ala Arg Ala Met Gly Ser Gln Thr Asn Arg Glu
260     265     270
Phe Ala Lys Asp Ile Tyr Ala Leu Ala Gln Asn Gln Lys Gln Ile Leu
275     280     285
Ser Asn Ala Ser Ser Ile Phe Asn Leu Phe Asn Ser Ile Pro Lys Asp
290     295     300
Gln Leu Lys Tyr Leu Glu Asn Ala Tyr Leu Lys Val Pro His Leu Gly
305     310     315     320
Lys Thr Pro Thr Asn Pro Tyr Arg Gln Asn Val Asn Leu Asn Lys Glu
325     330     335
Ile Asn Ala Val Gln Asp Asn Val Ala Asn Tyr Gly Asn Arg Leu Asp
340     345     350
Ser Ala Leu Ser Val Ala Lys Asp Val Tyr Asn Leu Lys Ser Asn Gln
355     360     365
Thr Glu Ile Val Thr Thr Tyr Asn Asp Ala Lys Asn Leu Ser Glu Glu
370     375     380
Ile Ser Lys Leu Pro Tyr Asn Gln Val Asn Val Thr Asn Ile Val Met
385     390     395     400

```

851

```

Ser Pro Lys Asp Ser Thr Ala Gly Gln Tyr Gln Ile Asn Pro Glu Gln
      405                      410                      415
Gln Ser Asn Leu Asn Gln Ala Leu Ala Ala Met Ser Asn Asn Pro Phe
      420                      425                      430
Lys Lys Val Gly Met Ile Ser Ser Gln Asn Asn Asn Gly Ala Leu Asn
      435                      440                      445
Gly Leu Gly Val Gln Val Gly Tyr Lys Gln Phe Phe Gly Glu Ser Lys
      450                      455                      460
Arg Trp Gly Leu Arg Tyr Tyr Gly Phe Phe Asp Tyr Asn His Gly Tyr
      465                      470                      475                      480
Ile Lys Ser Ser Phe Phe Asn Ser Ser Ser Asp Ile Trp Thr Tyr Gly
      485                      490                      495
Gly Gly Ser Asp Leu Leu Val Asn Phe Ile Asn Asp Ser Ile Thr Arg
      500                      505                      510
Lys Asn Asn Lys Leu Ser Val Gly Leu Phe Gly Gly Ile Gln Leu Ala
      515                      520                      525
Gly Thr Thr Trp Leu Asn Ser Gln Tyr Met Asn Leu Thr Ala Phe Asn
      530                      535                      540
Asn Pro Tyr Ser Ala Lys Val Asn Ala Ser Asn Phe Gln Phe Leu Phe
      545                      550                      555                      560
Asn Leu Gly Leu Arg Thr Asn Leu Ala Thr Ala Lys Lys Lys Asp Ser
      565                      570                      575
Glu Arg Ser Ala Gln His Gly Val Glu Leu Gly Ile Lys Ile Pro Thr
      580                      585                      590
Ile Asn Thr Asn Tyr Tyr Ser Phe Leu Gly Thr Lys Leu Glu Tyr Arg
      595                      600                      605
Arg Leu Tyr Ser Val Tyr Leu Asn Tyr Val Phe Ala Tyr
      610                      615                      620

```

(2) INFORMATION FOR SEQ ID NO:946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

```

Met Met Arg Glu Ile Leu Thr Asn Arg Phe Phe Pro Ser Leu Phe Lys
1      5      10      15
Lys Arg Leu Asp Phe Ser Asn Arg Val Val Leu Gly Leu Gly Ser Asn
      20      25      30
Leu Lys Asn Pro Leu Lys Ile Leu Lys Ser Cys Phe Leu Tyr Phe Lys
      35      40      45
Asn His Ser Lys Ile Gly Lys Ile Phe Ser Ser Pro Ile Tyr Ile Asn
      50      55      60

```

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

Met	Gln	Asp	Phe	Ile	Lys	Ile	Phe	Ile	Gln	Glu	Val	Val	Ser	Thr	Leu
1				5					10					15	
Glu	Gly	Leu	Val	Gly	Lys	Ala	Pro	Ser	Val	Gly	Leu	Glu	Lys	Glu	Val
			20					25					30		
Ser	Asn	Asn	Glu	Glu	Ala	Ser	Leu	Ile	Ser	Thr	Pro	Tyr	Ala	Arg	Val
		35					40					45			
Lys	Ile	Ser	Ala	Ile	Glu	Lys	Asn	Glu	Ser	Pro	Ile	Glu	Leu	Leu	Ala
	50					55					60				
Pro	Val	Asp	Leu	Val	Thr	Ala	Leu	Ser	Asp	Leu	Met	Leu	Gly	Gly	Glu
65					70					75					80
Gly	Ala	Ser	Lys	Glu	Glu	Met	Asp	Asn	Asp	Asp	Leu	Asp	Ala	Phe	Lys
				85					90					95	
Glu	Met	Ala	Ser	Asn	Ile	Phe	Gly	Ala	Ile	Ala	Thr	Ser	Leu	Lys	Ser
			100					105					110		
Gln	Glu	Leu	Leu	Pro	Lys	Leu	Asn	Phe	Thr	Thr	Thr	Asn	Ala	Glu	Ile
		115					120					125			
Ala	Lys	Glu	Leu	Pro	Lys	Lys	Glu	Asp	Tyr	Ala	Lys	Ala	Met	Val	Phe
	130					135					140				
Ser	Phe	Lys	Met	Glu	Ala	Ile	Lys	Glu	Ser	Gln	Ile	Val	Leu	Leu	Ile
145					150					155					160
Thr	Ser	Ala	Phe	Glu	Gly	Gln	Phe	Glu	Lys	Thr	His	Lys	Glu	Glu	Lys
				165					170						175

853

Glu	Glu	Thr	Thr	Lys	Ser	Ala	Thr	Glu	Glu	Thr	Lys	Thr	His	Asp	Ala
			180					185					190		
Ser	Leu	Glu	Asn	Ile	Glu	Ile	Arg	Asn	Ile	Ser	Met	Leu	Leu	Asp	Val
		195					200					205			
Lys	Leu	Asn	Val	Lys	Val	Arg	Ile	Gly	Gln	Lys	Lys	Met	Ile	Leu	Lys
		210				215					220				
Asp	Val	Val	Ser	Met	Asp	Ile	Gly	Ser	Val	Val	Glu	Leu	Asp	Gln	Leu
225					230					235				240	
Val	Asn	Asp	Pro	Leu	Glu	Ile	Leu	Val	Asp	Asp	Lys	Val	Ile	Ala	Lys
			245					250						255	
Gly	Glu	Val	Val	Ile	Val	Asp	Gly	Asn	Phe	Gly	Ile	Gln	Ile	Thr	Asp
		260					265						270		
Ile	Gly	Thr	Lys	Lys	Glu	Arg	Leu	Glu	Gln	Leu	Lys	Asn			
		275					280					285			

(2) INFORMATION FOR SEQ ID NO:948:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

Met	Lys	Ile	Leu	Val	Ile	Gln	Gly	Pro	Asn	Leu	Asn	Met	Leu	Gly	His
1			5					10					15		
Arg	Asp	Pro	Arg	Leu	Tyr	Gly	Met	Val	Thr	Leu	Asp	Gln	Ile	His	Glu
		20					25					30			
Ile	Met	Gln	Thr	Phe	Val	Lys	Gln	Gly	Asn	Leu	Asp	Val	Glu	Leu	Glu
		35				40					45				
Phe	Phe	Gln	Thr	Asn	Phe	Glu	Gly	Glu	Ile	Ile	Asp	Lys	Ile	Gln	Glu
	50				55					60					
Ser	Val	Gly	Ser	Asp	Tyr	Glu	Gly	Ile	Ile	Ile	Asn	Pro	Gly	Ala	Phe
65				70					75				80		
Ser	His	Thr	Ser	Ile	Ala	Ile	Ala	Asp	Ala	Ile	Met	Leu	Ala	Gly	Lys
			85					90					95		
Pro	Val	Ile	Glu	Val	His	Leu	Thr	Asn	Ile	Gln	Ala	Arg	Glu	Glu	Phe
		100						105					110		
Arg	Lys	Asn	Ser	Tyr	Thr	Gly	Ala	Ala	Cys	Gly	Gly	Val	Ile	Met	Gly
		115				120						125			
Phe	Gly	Pro	Leu	Gly	Tyr	Asn	Met	Ala	Leu	Met	Ala	Met	Val	Asn	Ile
	130					135				140					
Leu	Ala	Glu	Met	Lys	Ala	Phe	Gln	Glu	Ala	Gln	Lys	Asn	Asn	Pro	Asn
145				150					155					160	
Asn	Pro	Asn	Asn	Pro	Ile	Asn	Asn	Gln	Lys						
			165					170							

(2) INFORMATION FOR SEQ ID NO:949:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

```

Met Arg Gly Leu Glu Arg Glu Ser His Phe Thr Leu Asn Glu Asn Ala
1      5      10      15
Met Phe Phe Glu Cys Ala Tyr Ser Cys Asp Asn Ala Leu Phe Leu Gln
      20      25      30
Leu Asp Asp Arg Ser Phe Phe Ile Thr Asp Ser Arg Tyr Thr Gln Glu
      35      40      45
Ala Lys Glu Ser Leu Gln Pro Lys Lys Gly Val Leu Val Glu Val Ile
      50      55      60
Glu Ser Ser Asp Leu Val Gln Ser Ala Ile Asp Leu Ile Thr Lys Ser
      65      70      75      80
Ser Val Lys Lys Leu Phe Phe Asp Pro Asn Gln Val Asn Leu Gln Thr
      85      90      95
Tyr Lys Arg Leu Asp Ser Ala Val Gly Asn Lys Val Val Leu Glu Gly
      100     105     110
Val Pro Ser Tyr His Arg Gln Lys Arg Ile Ile Lys Asn Glu His Glu
      115     120     125
Ile Gln Leu Leu Lys Lys Ser Gln Ala Leu Asn Val Glu Ala Phe Glu
      130     135     140
Asn Phe Ala Glu Tyr Val Lys Lys Ile Phe Asp Glu Lys Glu Ser Leu
      145     150     155     160
Ser Glu Arg Tyr Leu Gln His Lys Val Lys Asp Phe Leu Thr Lys Glu
      165     170     175
Gly Val Tyr Asp Leu Ser Phe Glu Pro Ile Leu Ala Leu Asn Ala Asn
      180     185     190
Ala Ser Lys Pro His Ala Leu Pro Ser Ala Lys Asp Phe Leu Lys Ala
      195     200     205
Asp His Ser Ile Leu Leu Asp Met Gly Ile Lys Tyr Glu Arg Tyr Cys
      210     215     220
Ser Asp Arg Thr Arg Thr Ala Phe Phe Asp Pro Lys Asp Phe Val Phe
      225     230     235     240
Lys Arg Glu Gln Ser Phe Lys Asp Lys Glu Arg Gln Lys Ile Tyr Asp
      245     250     255
Ile Val Lys Glu Ala Gln Glu Lys Ala Ile Ser Gly Ile Arg Ala Gly
      260     265     270
Met Thr Gly Lys Glu Ala Asp Ser Leu Ala Arg Gly Val Ile Ser Asp
      275     280     285

```

855

```

Tyr Gly Tyr Gly Gln Tyr Phe Thr His Ser Thr Gly His Gly Ile Asp
 290          295          300
Leu Asp Ile His Glu Leu Pro Tyr Ile Ser Ser Arg Ser Glu Thr Ile
305          310          315          320
Leu Glu Glu Gly Met Val Phe Ser Val Glu Pro Gly Ile Tyr Ile Pro
          325          330          335
Gly Phe Phe Gly Val Arg Ile Glu Asp Leu Val Val Ile Lys Asn Ser
          340          345          350
Arg Ala Glu Leu Leu
          355

```

(2) INFORMATION FOR SEQ ID NO:950:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

```

Met Lys Asp Ser Phe Leu Phe Thr Ser Glu Ser Val Thr Glu Gly His
1          5          10          15
Pro Asp Lys Met Ala Asp Gln Ile Ser Asp Ala Val Leu Asp Tyr Ile
          20          25          30
Ile Glu Arg Asp Lys Lys Ala Lys Val Ala Cys Glu Thr Leu Val Ser
          35          40          45
Asn Gly Phe Cys Met Ile Thr Gly Glu Leu Lys Thr Ser Val Tyr Ala
          50          55          60
Pro Met Gln Glu Ile Ala Arg Glu Val Val Lys Lys Ile Gly Tyr Thr
          65          70          75          80
Asp Ala Leu Tyr Gly Phe Asp Tyr Arg Ser Ala Ala Val Leu Asn Gly
          85          90          95
Ile Gly Glu Gln Ser Pro Asp Ile Asn Gln Gly Val Asp Arg Glu Asp
          100          105          110
Gly Glu Ile Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Cys
          115          120          125
Lys Glu Thr Glu Thr Leu Met Pro Leu Pro Ile His Leu Ala His Gln
          130          135          140
Leu Ala Phe Ala Leu Ala Gln Lys Arg Lys Asp Asn Thr Leu Pro Phe
          145          150          155          160
Leu Arg Pro Asp Gly Lys Ser Gln Val Ser Val Arg Tyr Glu Asn Asn
          165          170          175
Lys Pro Val Ser Val Asp Thr Ile Val Ile Ser Thr Gln His Ser Pro
          180          185          190
Glu Val Ser Gln Lys His Leu Lys Glu Ala Val Ile Glu Glu Ile Val
          195          200          205

```

856

```

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

```

(2) INFORMATION FOR SEQ ID NO:951:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

```

Val Leu Asp Ser Phe Glu Ile Leu Lys Ala Leu Lys Ser Leu Asp Leu
1          5          10          15
Leu Lys Asn Ala Pro Ala Trp Trp Trp Pro Asn Ala Leu Lys Phe Glu
20          25          30
Ala Leu Leu Gly Ala Val Leu Thr Gln Asn Thr Lys Phe Glu Ala Val
35          40          45
Leu Lys Ser Leu Glu Asn Leu Lys Asn Ala Phe Ile Leu Glu Asn Asp
50          55          60
Asp Glu Ile Asn Leu Lys Lys Ile Ala Tyr Ile Glu Phe Ser Lys Leu
65          70          75          80
Ala Glu Cys Val Arg Pro Ser Gly Phe Tyr Asn Gln Lys Ala Lys Arg
85          90          95

```

857

```

Leu Ile Asp Leu Ser Lys Asn Ile Leu Lys Asp Phe Gln Ser Phe Glu
      100      105      110
Asn Phe Lys Gln Glu Val Thr Lys Glu Trp Leu Leu Asp Gln Lys Gly
      115      120      125
Ile Gly Lys Glu Ser Ala Asp Ala Ile Leu Cys Tyr Val Cys Ala Lys
      130      135      140
Glu Val Met Val Val Asp Lys Tyr Ser Tyr Leu Phe Leu Lys Lys Leu
      145      150      155      160
Gly Ile Glu Ile Glu Asp Tyr Asp Glu Leu Gln His Phe Phe Glu Lys
      165      170      175
Gly Val Gln Glu Asn Leu Asn Ser Ala Leu Ala Leu Tyr Glu Asn Thr
      180      185      190
Ile Ser Leu Ala Gln Leu Tyr Ala Arg Phe His Gly Lys Ile Val Glu
      195      200      205
Phe Ser Lys Gln Lys Leu Glu Leu Lys Leu
      210      215

```

(2) INFORMATION FOR SEQ ID NO:952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

```

Met Lys Gln Leu Phe Leu Ile Ile Gly Ala Pro Gly Ser Gly Lys Thr
1      5      10      15
Thr Asp Ala Glu Leu Ile Ala Lys Asn Asn Ser Glu Thr Ile Ala His
      20      25      30
Phe Ser Thr Gly Asp Leu Leu Arg Ala Glu Ser Ala Lys Lys Thr Glu
      35      40      45
Arg Gly Leu Leu Ile Glu Lys Phe Thr Ser Gln Gly Glu Leu Val Pro
      50      55      60
Leu Glu Ile Val Val Glu Thr Ile Leu Ser Ala Ile Lys Ser Ser Ser
      65      70      75      80
Lys Gly Ile Ile Leu Ile Asp Gly Tyr Pro Arg Ser Val Glu Gln Met
      85      90      95
Gln Ala Leu Asp Lys Glu Leu Asn Ala Pro Asn Glu Val Ile Leu Lys
      100      105      110
Ser Val Ile Glu Val Glu Val Ser Glu Asn Thr Ala Lys Glu Arg Val
      115      120      125
Leu Gly Gln Phe
      130

```

(2) INFORMATION FOR SEQ ID NO:953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

```

Met His Tyr Ser Tyr Glu Ala Phe Leu Lys Asp Ser Leu Glu Leu Ala
1      5      10      15
Lys Gln Val Glu Arg Leu Cys Gly Ile Pro Glu Ala Leu Val Cys Val
20     25     30
Met Arg Gly Gly Met Thr Leu Val His Phe Leu Ser Leu His Trp Asn
35     40     45
Leu Arg Glu Val Tyr Gly Ile Asn Ala Ile Ser Tyr Asp Thr Thr Lys
50     55     60
Arg Gln Asn Ala Leu Lys Ile Glu Asn Thr Pro Thr Ile Lys Asp His
65     70     75     80
Leu Lys Thr Ile Leu Val Val Asp Glu Ile Val Asp Ser Gly Asn Ser
85     90     95
Leu Glu Ala Val Leu Lys Val Leu Gln Asp Lys His Pro Asp Lys Lys
100    105    110
Phe Tyr Ser Ala Ser Leu Phe Gln Lys Thr Ser Ala Lys Tyr Lys Ala
115    120    125
Asp Ala Phe Leu Lys Asp Ala Pro Glu Trp Ile Asp Phe Phe Trp Glu
130    135    140
Val Asp Leu Lys Asn Leu Lys Ser His
145    150

```

(2) INFORMATION FOR SEQ ID NO:954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

```

Leu Ser Glu Pro Ile Asp Arg Phe Thr Arg Ile Arg Trp Leu Phe Lys
1      5      10      15
Asn Asp Phe Glu Lys Ile Arg Gln Gln Arg Val Leu Ile Cys Gly Val
20     25     30
Gly Gly Val Gly Gly Phe Ala Leu Asp Ser Leu Tyr Arg Val Gly Ile
35     40     45
Gly Gln Ile Thr Ile Ile Asp Lys Asp Met Phe Asp Val Thr Asn Gln
50     55     60
Asn Arg Gln Ile Gly Ser Glu Arg Ile Gly Glu Ser Lys Val Leu Val
65     70     75     80
Leu Gln Asp Leu Tyr Lys Gly Ile Gln Ala Leu Asn Cys Arg Ile Asp
85     90     95
Glu Ala Phe Leu Asn Ser Phe Asn Phe Arg Asp Tyr Asp Tyr Ile Leu
100    105    110
Asp Cys Met Asp Asp Leu Pro Ile Lys Thr Ser Leu Ala Ile Lys Cys
115    120    125
Gln Asn Phe Ala Tyr Gly Lys Phe Ile Ser Ser Met Gly Ser Ala Lys
130    135    140
Arg Leu Asn Pro Lys His Ile Gln Val Gly Ser Val Trp Glu Ser Tyr
145    150    155    160
Gly Asp Lys Phe Gly Arg Lys Phe Arg Asp Phe Leu Lys Lys Arg Arg
165    170    175
Phe Lys Gly Asp Phe Lys Val Val Phe Ser Pro Glu Val Pro His Cys
180    185    190
Ile Glu Leu Gly Ser Phe Asn Ala Val Thr Ala Ser Phe Gly Leu Gln
195    200    205
Ile Ala Ser Glu Val Val Gln Asp Ile Ile Lys Asn Glu Arg Gln Trp
210    215    220
Asn Glu Arg Leu Arg Arg Arg Ile Gly Arg Phe
225    230    235

```

(2) INFORMATION FOR SEQ ID NO:955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

```

Met Gln Val Lys Glu Asn Lys Gln Leu Cys Leu Ile Ser Leu Gly Cys
1      5      10      15
Ser Lys Asn Leu Val Asp Ser Glu Val Met Leu Gly Lys Leu Tyr Asn

```

20										25					30				
Tyr	Thr	Leu	Thr	Asn	Asp	Ala	Lys	Lys	Ala	Asp	Val	Ile	Leu	Ile	Asn				
		35					40					45							
Thr	Cys	Gly	Phe	Ile	Glu	Ser	Ala	Lys	Gln	Glu	Ser	Ile	Gln	Thr	Ile				
	50					55					60								
Leu	Asn	Ala	Ala	Lys	Asp	Lys	Lys	Glu	Gly	Ala	Ile	Leu	Ile	Ala	Ser				
65					70					75					80				
Gly	Cys	Leu	Ser	Glu	Arg	Tyr	Lys	Asp	Glu	Ile	Lys	Glu	Leu	Ile	Pro				
				85					90					95					
Glu	Val	Asp	Ile	Phe	Thr	Gly	Val	Gly	Asp	Tyr	Asp	Lys	Ile	Asp	Ile				
			100					105					110						
Leu	Ile	Ala	Lys	Lys	Gln	Asn	Gln	Phe	Ser	Glu	Gln	Val	Phe	Leu	Ser				
		115					120					125							
Glu	His	Tyr	Asn	Ala	Arg	Ile	Ile	Thr	Gly	Ser	Ser	Val	His	Ala	Tyr				
	130					135						140							
Val	Lys	Ile	Ser	Glu	Gly	Cys	Asn	Gln	Lys	Cys	Ser	Phe	Cys	Ala	Ile				
145					150					155					160				
Pro	Ser	Phe	Lys	Gly	Lys	Leu	Gln	Ser	Arg	Glu	Leu	Asp	Ser	Ile	Leu				
				165					170					175					
Lys	Glu	Val	Glu	Asp	Leu	Ala	Leu	Lys	Gly	Tyr	Lys	Asp	Met	Thr	Phe				
			180					185					190						
Ile	Ala	Gln	Asp	Ser	Ser	Ser	Phe	Leu	Tyr	Asp	Lys	Gly	Gln	Lys	Asp				
		195					200					205							
Gly	Leu	Ile	Gln	Leu	Ile	Arg	Ala	Ile	Asp	Lys	Gln	Gln	Ala	Leu	Lys				
	210					215					220								
Ser	Ala	Arg	Ile	Leu	Tyr	Leu	Tyr	Pro	Ser	Ser	Thr	Thr	Leu	Glu	Leu				
225					230					235					240				
Ile	Gly	Ala	Ile	Glu	Asp	Ser	Pro	Ile	Phe	Gln	Asn	Tyr	Phe	Asp	Met				
				245					250					255					
Pro	Ile	Gln	His	Ile	Ser	Asp	Ser	Met	Leu	Lys	Lys	Met	Arg	Arg	Asn				
			260					265					270						
Ser	Ser	Gln	Ala	His	His	Leu	Lys	Leu	Leu	Asn	Ala	Met	Lys	Gln	Val				
		275					280					285							
Lys	Glu	Ser	Phe	Ile	Arg	Ser	Thr	Ile	Ile	Val	Gly	His	Pro	Glu	Glu				
	290					295					300								
Asn	Glu	Ser	Glu	Phe	Glu	Glu	Leu	Ser	Ala	Phe	Leu	Asp	Glu	Phe	Arg				
305					310					315					320				
Phe	Asp	Arg	Leu	Asn	Ile	Phe	Ala	Phe	Ser	Ala	Glu	Glu	Asn	Thr	His				
				325					330					335					
Ala	Tyr	Ser	Leu	Glu	Lys	Val	Pro	Lys	Lys	Ile	Ile	Asn	Ala	Arg	Ile				
			340					345					350						
Lys	Ala	Leu	Asn	Lys	Ile	Ala	Leu	Lys	His	Gln	Asn	His	Ser	Phe	Lys				
		355					360					365							

(i) SEQUENCE CHARACTERISTICS:

861

- (A) LENGTH: 667 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

```

Lys Lys Pro Phe Tyr Ser Leu Ser Leu Ala Ser Ser Leu Leu Asn Ala
1      5      10      15
Glu Asp Asn Gly Phe Phe Ile Ser Ala Gly Tyr Gln Ile Gly Glu Ala
      20      25      30
Ala Gln Met Val Lys Asn Thr Gly Glu Leu Lys Lys Leu Ser Asp Thr
      35      40      45
Tyr Glu Asn Leu Ser Asn Leu Leu Thr Asn Phe Asn Asn Leu Asn Gln
      50      55      60
Ala Val Thr Asn Ala Ser Ser Pro Ser Glu Ile Asn Ala Ala Ile Asp
65      70      75      80
Asn Leu Lys Ala Asn Thr Gln Gly Leu Ile Gly Glu Lys Thr Asn Ser
      85      90      95
Pro Ala Tyr Gln Ala Val Tyr Leu Ala Leu Asn Ala Ala Val Gly Leu
      100     105     110
Trp Asn Val Ile Ala Tyr Asn Val Gln Cys Gly Pro Gly Asn Ser Gly
      115     120     125
Gln Gln Ser Val Thr Phe Glu Gly Gln Pro Gly His Asn Ser Ser Ser
      130     135     140
Ile Asn Cys Asn Leu Thr Gly Tyr Asn Asn Gly Val Ser Gly Pro Leu
145     150     155     160
Ser Ile Glu Asn Phe Lys Lys Leu Asn Gln Ala Tyr Gln Thr Ile Gln
      165     170     175
Gln Ala Leu Lys Gln Asp Ser Gly Phe Pro Val Leu Asp Ser Ala Gly
      180     185     190
Lys Gln Val Thr Ile Thr Ile Thr Thr Gln Thr Asn Gly Ala Asn Lys
      195     200     205
Ser Glu Thr Thr Thr Thr Thr Thr Thr Thr Asn Asp Ala Gln Thr Leu
      210     215     220
Leu Gln Glu Ala Ser Lys Met Ile Ser Val Leu Thr Thr Asn Cys Pro
225     230     235     240
Trp Val Asn His Asn Gln Gly Gln Asn Gly Gly Ala Pro Trp Gly Leu
      245     250     255
Asp Thr Ala Gly Asn Val Cys Gln Val Phe Ala Thr Glu Phe Ser Ala
      260     265     270
Val Thr Ser Met Ile Lys Asn Ala Gln Glu Ile Val Thr Gln Ala Gln
      275     280     285
Ser Leu Asn Gln Gln Asn Asn Gln Asn Ala Pro Gln Asp Phe Asn Pro
      290     295     300
Tyr Thr Ser Ala Asp Arg Ala Phe Ala Gln Asn Met Leu Asn His Ala
305     310     315     320

```

Gln	Ala	Gln	Ala	Lys	Ile	Leu	Glu	Leu	Ala	Asp	Gln	Met	Lys	Lys	Asp
				325					330					335	
Leu	Asn	Thr	Ile	Pro	Ser	Gln	Phe	Ile	Thr	Asn	Tyr	Leu	Ala	Ala	Cys
			340					345					350		
His	Asn	Gly	Gly	Gly	Thr	Leu	Pro	Asp	Ala	Gly	Val	Thr	Asn	Asn	Thr
		355				360						365			
Trp	Gly	Ala	Gly	Cys	Ala	Tyr	Val	Glu	Glu	Thr	Ile	Thr	Ala	Leu	Asn
	370					375					380				
Asn	Ser	Leu	Ala	His	Phe	Gly	Thr	Gln	Ala	Glu	Gln	Ile	Lys	Gln	Ser
385				390					395					400	
Glu	Leu	Leu	Ala	Arg	Thr	Ile	Leu	Asp	Phe	Arg	Gly	Ser	Leu	Ser	Asn
			405					410					415		
Leu	Asn	Asn	Thr	Tyr	Asn	Ser	Ile	Thr	Thr	Thr	Ala	Ser	Asn	Thr	Pro
	420						425						430		
Asn	Ser	Pro	Phe	Leu	Lys	Asn	Leu	Ile	Ser	Gln	Ser	Thr	Asn	Pro	Asn
	435					440						445			
Asn	Pro	Gly	Gly	Leu	Gln	Ala	Val	Tyr	Gln	Val	Asn	Gln	Ser	Ala	Tyr
	450				455						460				
Ser	Gln	Leu	Leu	Ser	Ala	Thr	Gln	Glu	Leu	Gly	His	Asn	Pro	Phe	Arg
465				470					475					480	
Arg	Val	Gly	Leu	Ile	Ser	Ser	Gln	Thr	Asn	Asn	Gly	Ala	Met	Asn	Gly
			485					490					495		
Ile	Gly	Val	Gln	Val	Gly	Tyr	Lys	Gln	Phe	Phe	Gly	Glu	Lys	Arg	Arg
		500						505				510			
Trp	Gly	Leu	Arg	Tyr	Tyr	Gly	Phe	Phe	Asp	Tyr	Asn	His	Ala	Tyr	Ile
	515					520						525			
Lys	Ser	Ser	Phe	Phe	Asn	Ser	Ala	Ser	Asp	Val	Phe	Thr	Tyr	Gly	Val
	530				535						540				
Gly	Thr	Asp	Val	Leu	Tyr	Asn	Phe	Ile	Asn	Asp	Lys	Thr	Thr	Lys	Asn
545				550					555					560	
Ser	Lys	Ile	Ser	Phe	Gly	Val	Phe	Gly	Gly	Ile	Ala	Leu	Ala	Gly	Thr
			565					570					575		
Ser	Trp	Leu	Asn	Ser	Gln	Tyr	Val	Asn	Leu	Ala	Thr	Phe	Asn	Asn	Phe
		580					585					590			
Tyr	Ser	Ala	Lys	Met	Asn	Val	Ala	Asn	Phe	Gln	Phe	Leu	Phe	Asn	Leu
	595				600						605				
Gly	Leu	Arg	Met	Asn	Leu	Ala	Lys	Asn	Lys	Lys	Lys	Ala	Ser	Asp	His
	610				615						620				
Ala	Ala	Gln	His	Gly	Val	Glu	Leu	Gly	Val	Lys	Ile	Pro	Thr	Ile	Asn
625				630					635					640	
Thr	Asn	Tyr	Tyr	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Gln	Tyr	Arg	Arg	Leu
			645					650					655		
Tyr	Ser	Val	Tyr	Leu	Asn	Tyr	Val	Phe	Ala	Tyr					
		660					665								

(2) INFORMATION FOR SEQ ID NO:957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

863

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...87

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:

```

Met Phe Ile Leu Phe Lys Phe Gly Arg Val Leu Gly Lys Ala Tyr Ser
1           5           10           15
Leu Tyr Leu Tyr Ile Tyr Glu Ser Leu Ile Cys Gln Ala Phe Gly Leu
          20           25           30
Ser Leu Ser Cys Asn Asn Ser Met Leu Phe Ser Thr Phe Leu Ile Asn
          35           40           45
Leu Pro Leu Pro His Asn Glu Ser Leu Cys Cys Cys Arg Asp Ile Leu
          50           55           60
Ala Tyr Ser Asn Ser Ser Ser Leu Lys Thr Tyr Ser Leu Glu Ser Asn
65           70           75           80
Phe Ser Phe Asn Ser Leu Phe
          85

```

(2) INFORMATION FOR SEQ ID NO:958:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

```

Met Phe Met Ala Ser Ile Arg Thr Leu Thr His Met Thr Asn Ala Asp
1           5           10           15
Gly Thr Ile Thr Cys Gly Asp Thr Thr Pro Ala Ser Cys Asn Val Gly
          20           25           30
Ile Asn Pro Asn Ser Val Tyr Thr Thr Gly Lys Leu Asn Ala Lys Val
          35           40           45
Asn His Thr Ile Phe Gln Phe Leu Val Asn Val Gly Ile Arg Thr Asn
          50           55           60
Ile Phe Glu His His Gly Ile Glu Phe Gly Ile Lys Ile Pro Thr Leu
65           70           75           80
Pro Asn Tyr Phe Phe Lys Gly Ser Thr Thr Ile Arg Ala Lys Lys Gln
          85           90           95
Gly Pro Leu Glu Asn Gly Asn Pro Thr Thr Ile Thr Gly Ala Glu Thr
          100          105          110
Asn Phe Ser Leu Thr Gln Thr Leu Arg Arg Gln Tyr Ser Met Tyr Leu
          115          120          125

```

864

Arg Tyr Val Tyr Thr Phe
130

(2) INFORMATION FOR SEQ ID NO:959:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

Leu	Asn	Lys	Leu	Leu	Lys	Lys	Gly	Phe	Leu	Ala	Phe	Phe	Leu	Ser	Val	1	5	10	15
Tyr	Leu	Arg	Ala	Asp	Asp	Leu	Val	Thr	Tyr	Thr	Ile	Ala	Lys	Glu	Glu	20	25	30	
Asp	Leu	Gly	Tyr	Gln	Arg	Phe	Leu	Ala	Lys	Lys	Cys	Leu	Arg	Gly	Lys	35	40	45	
Thr	His	Pro	Pro	Cys	Phe	Thr	Ala	Ser	Lys	Lys	Pro	Lys	Arg	Lys	Pro	50	55	60	
Phe	Asn	Ile	Asp	Lys	Ser	Ser	His	Tyr	Tyr	Gly	Thr	Ser	Val	Val	Gln	65	70	75	80
Met	Ser	Trp	Leu	Gln	Ser	Arg	Glu	Lys	Phe	Glu	Asn	His	Ser	Lys	Tyr	85	90	95	
Arg	Asn	Ile	Pro	Phe	Ala	Glu	Val	Ser	Leu	Ile	Tyr	Gly	Tyr	Lys	Gln	100	105	110	
Phe	Phe	Pro	Lys	Lys	Glu	His	Tyr	Gly	Phe	Arg	Phe	Tyr	Val	Ser	Leu	115	120	125	
Asp	Tyr	Ala	Tyr	Gly	Phe	Phe	Leu	Lys	Asn	Lys	Gly	Ala	Leu	Gly	Asp	130	135	140	
Ser	Leu	Arg	Ala	Ser	Ser	Gln	Ile	Pro	Lys	Ser	Tyr	Arg	Glu	Lys	Leu	145	150	155	160
Gln	Arg	Lys	Glu	Thr	Phe	Ile	Asn	Ala	Ile	Phe	Tyr	Gly	Val	Gly	Ala	165	170	175	
Asp	Phe	Leu	Tyr	Lys	Arg	Ala	Phe	Gly	Thr	Leu	Ile	Leu	Gly	Val	Asn	180	185	190	
Phe	Val	Gly	Glu	Thr	Trp	Phe	Tyr	Glu	Thr	Lys	Ile	Phe	Lys	Gln	Trp	195	200	205	
Ala	Lys	Asp	Ser	Leu	Asn	Thr	Tyr	Arg	Pro	Asn	Met	Phe	Gln	Val	Met	210	215	220	
Leu	Asn	Val	Gly	Tyr	Arg	Tyr	Arg	Phe	Ser	Arg	Tyr	Lys	Asn	Trp	Ala	225	230	235	240
Ile	Glu	Phe	Gly	Ala	Arg	Ile	Pro	Phe	Leu	Ile	Asn	Asp	Tyr	Phe	Lys	245	250	255	
Thr	Pro	Leu	Tyr	Thr	Leu	His	Phe	Lys	Arg	Asn	Ile	Ser	Val	Tyr	Leu	260	265	270	

Thr Ser Thr Tyr Asp Phe
275

(2) INFORMATION FOR SEQ ID NO:960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

Met	Lys	Leu	Lys	Lys	Arg	Lys	Val	Ala	Ala	Thr	Leu	Leu	Lys	Arg	Leu	1	5	10	15
Thr	Leu	Pro	Leu	Leu	Phe	Thr	Thr	Gly	Ser	Leu	Gly	Ala	Val	Thr	Tyr	20	25	30	
Glu	Val	His	Gly	Asp	Phe	Ile	Asn	Phe	Ser	Lys	Val	Gly	Phe	Asn	Arg	35	40	45	
Ser	Pro	Ile	Asn	Pro	Val	Lys	Gly	Ile	Tyr	Pro	Thr	Glu	Thr	Phe	Val	50	55	60	
Asn	Leu	Thr	Gly	Lys	Leu	Glu	Gly	Ser	Val	His	Leu	Gly	Arg	Gly	Trp	65	70	75	80
Thr	Val	Asn	Val	Gly	Gly	Val	Leu	Gly	Gly	Gln	Val	Tyr	Asp	Asn	Thr	85	90	95	
Arg	Tyr	Asp	Arg	Trp	Ala	Lys	Asp	Phe	Thr	Pro	Pro	Ser	Tyr	Trp	Asp	100	105	110	
Lys	Thr	Ser	Cys	Gly	Thr	Asp	Ser	Leu	Ser	Leu	Cys	Met	Asn	Ala	Thr	115	120	125	
Lys	Met	Trp	Gln	Gln	Gln	Gly	Pro	Gly	Gly	Ile	Ile	Asp	Pro	Arg	Gly	130	135	140	
Ile	Gly	Tyr	Met	Tyr	Met	Gly	Glu	Trp	Asn	Gly	Leu	Phe	Pro	Asn	Tyr	145	150	155	160
Tyr	Pro	Ala	Asn	Ala	Tyr	Leu	Pro	Gly	His	Ser	Arg	Arg	Tyr	Glu	Val	165	170	175	
Tyr	Lys	Ala	Asn	Leu	Thr	Tyr	Asp	Ser	Asp	Arg	Val	His	Met	Val	Met	180	185	190	
Gly	Arg	Phe	Asp	Val	Thr	Glu	Gln	Glu	Gln	Met	Asp	Trp	Ile	Tyr	Gln	195	200	205	
Leu	Phe	Gln	Gly	Phe	Tyr	Gly	Thr	Phe	Lys	Leu	Thr	Lys	Asn	Met	Lys	210	215	220	
Phe	Leu	Leu	Phe	Ser	Ser	Trp	Gly	Arg	Gly	Ile	Ala	Asp	Gly	Gln	Trp	225	230	235	240
Leu	Phe	Pro	Ile	Tyr	Arg	Glu	Lys	Pro	Trp	Gly	Ile	His	Lys	Ala	Gly	245	250	255	
Ile	Ile	Tyr	Arg	Pro	Thr	Lys	Asn	Leu	Met	Ile	His	Pro	Tyr	Val	Tyr	260	265	270	

866

```

Leu Ile Pro Met Val Gly Thr Leu Pro Gly Ala Lys Ile Glu Tyr Asp
    275                      280                      285
Thr Asn Pro Glu Phe Ser Gly Arg Gly Ile Arg Asn Lys Thr Thr Phe
    290                      295                      300
Tyr Val Leu Tyr Asp Tyr Arg Trp Asn Asn Ala Glu Tyr Gly Arg Tyr
305                      310                      315                      320
Ala Pro Ala Arg Tyr Asn Thr Trp Asp Pro Phe Leu Asp Asn Gly Lys
    325                      330                      335
Trp Arg Gly Leu Gln Gly Pro Gly Gly Ala Thr Leu Tyr Leu His His
    340                      345                      350
His Ile Asp Ile Asn Asn Tyr Phe Val Val Gly Gly Ala Tyr Leu Asn
    355                      360                      365
Ile Gly Asn Pro Asn Met Asn Leu Gly Thr Trp Gly Asn Pro Val Ala
    370                      375                      380
Leu Asp Gly Ile Glu Gln Trp Val Gly Gly Ile Tyr Ser Leu Gly Phe
385                      390                      395                      400
Ala Gly Ile Asp Asn Ile Thr Asp Ala Asp Ala Phe Thr Glu Tyr Val
    405                      410                      415
Lys Gly Gly Gly Lys His Gly Lys Phe Ser Trp Ser Val Tyr Gln Arg
    420                      425                      430
Phe Thr Thr Ala Pro Arg Ala Leu Glu Tyr Gly Ile Gly Met Tyr Leu
    435                      440                      445
Asp Tyr Gln Phe Ser Lys His Val Lys Ala Gly Leu Lys Leu Val Trp
    450                      455                      460
Leu Glu Phe Gln Ile Arg Ala Gly Tyr Asn Pro Gly Thr Gly Phe Leu
465                      470                      475                      480
Gly Pro Asn Gly Gln Pro Leu Asn Leu Asn Asn Gly Leu Phe Glu Ser
    485                      490                      495
Ser Ala Phe

```

(2) INFORMATION FOR SEQ ID NO:961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

```

Leu Lys Glu Lys Phe Asp Phe Phe Lys Gly Lys Asn Phe Lys Ile Val
1           5           10           15
Tyr Cys Ile Gly Glu Asp Leu Thr Thr Arg Glu Lys Gly Phe Arg Ala
    20           25           30
Val Lys Glu Phe Leu Ser Glu Gln Leu Glu Asn Ile Asp Leu Asn Tyr
    35           40           45

```

Ser Asn Leu Ile Val Ala Tyr Glu Pro Ile Trp Ala Ile Gly Thr Lys
 50 55 60
 Lys Ala Arg Phe
 65

(2) INFORMATION FOR SEQ ID NO:962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

Met	Ser	Lys	Ser	Ala	Ile	Phe	Val	Leu	Ser	Gly	Phe	Leu	Ala	Phe	Leu	1	5	10	15
Leu	Tyr	Ala	Leu	Leu	Tyr	Gly	Leu	Leu	Glu	Arg	His	Asn	Lys			20	25	30	
Glu	Ala	Glu	Lys	Ile	Leu	Leu	Asp	Leu	Asn	Lys	Lys	Asp	Glu	Gln	Ala	35	40	45	
Ile	Asp	Leu	Asn	Leu	Glu	Asp	Leu	Pro	Ser	Glu	Lys	Lys	Asn	Glu	Lys	50	55	60	
Ile	Glu	Lys	Val	Thr	Glu	Lys	Gln	Gly	Asp	Phe	Leu	Glu	Pro	Lys	Glu	65	70	75	80
Glu	Pro	Lys	Glu	Glu	Pro	Glu	Glu	Ser	Leu	Glu	Asp	Ile	Phe	Ser	Ser	85	90	95	
Leu	Asn	Asp	Phe	Gln	Glu	Lys	Thr	Asp	Lys	Asn	Ala	Gln	Lys	Asp	Glu	100	105	110	
Gln	Lys	Asn	Glu	Gln	Glu	Glu	Gln	Arg	Arg	Leu	Arg	Glu	Gln	Gln	Arg	115	120	125	
Leu	Lys	Gln	Asn	Gln	Glu	Asn	Gln	Glu	Met	Leu	Lys	Gly	Leu	Gln	Gln	130	135	140	
Asn	Leu	Asn	Gln	Phe	Thr	Gln	Lys	Leu	Glu	Ser	Val	Lys	Asn	Lys	Thr	145	150	155	160
Leu	Asp	Leu	Gln	Ile	Pro	Lys	Gln	Asp	Gly	Val	Asp	Glu	Lys	Ala	Tyr	165	170	175	
Gln	Glu	Trp	Tyr	Ala	Gln	Ile	Tyr	Gln	Ile	Leu	Tyr	Lys	Gly	Trp	Arg	180	185	190	
Gly	Val	Phe	Tyr	His	Lys	Ala	Ser	Val	Ser	Val	Leu	Ile	Met	Ile	Thr	195	200	205	
Lys	Asp	Gly	Glu	Phe	Asp	Tyr	Thr	Ile	Leu	Ser	Tyr	Ser	Asp	Phe	Lys	210	215	220	
Asp	Tyr	Asn	Lys	Ser	Val	Met	Thr	Leu	Leu	Asp	Asp	Leu	Lys	Lys	Val	225	230	235	240
Asp	Phe	Pro	Pro	Tyr	Pro	Gly	Gly	Asn	Met	Ile	Ser	Ile	Lys	Val	Asn	245	250	255	

Phe Thr Thr Lys Glu Glu Gln
260

(2) INFORMATION FOR SEQ ID NO:963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

Met	Glu	Gln	Pro	Val	Ile	Lys	Glu	Gly	Thr	Leu	Ala	Leu	Ile	Asp	Thr	1	5	10	15
Phe	Ala	Tyr	Leu	Phe	Arg	Ser	Tyr	Tyr	Met	Ser	Ala	Lys	Asn	Lys	Pro	20	25	30	
Leu	Thr	Asn	Asp	Lys	Gly	Phe	Pro	Thr	Gly	Leu	Leu	Thr	Gly	Leu	Val	35	40	45	
Gly	Met	Val	Lys	Lys	Phe	Tyr	Lys	Asp	Arg	Lys	Asn	Met	Pro	Phe	Ile	50	55	60	
Val	Phe	Ala	Leu	Glu	Ser	Gln	Thr	Lys	Thr	Lys	Arg	Ala	Glu	Lys	Leu	65	70	75	80
Gly	Glu	Tyr	Lys	Gln	Asn	Arg	Lys	Asp	Ala	Pro	Lys	Glu	Met	Leu	Leu	85	90	95	
Gln	Ile	Pro	Ile	Ala	Leu	Glu	Trp	Leu	Gln	Lys	Met	Gly	Phe	Thr	Cys	100	105	110	
Val	Glu	Val	Gly	Gly	Phe	Glu	Ala	Asp	Asp	Val	Ile	Ala	Ser	Leu	Ala	115	120	125	
Thr	Leu	Ser	Pro	Tyr	Lys	Thr	Arg	Ile	Tyr	Ser	Lys	Asp	Lys	Asp	Phe	130	135	140	
Asn	Gln	Leu	Leu	Ser	Asp	Lys	Ile	Ala	Leu	Phe	Asp	Gly	Lys	Thr	Glu	145	150	155	160
Phe	Leu	Ala	Lys	Asp	Cys	Val	Glu	Lys	Tyr	Gly	Ile	Leu	Pro	Ser	Gln	165	170	175	
Phe	Thr	Asp	Tyr	Gln	Gly	Ile	Val	Gly	Asp	Ser	Ser	Asp	Asn	Tyr	Lys	180	185	190	
Gly	Val	Lys	Gly	Ile	Gly	Ser	Lys	Asn	Ala	Lys	Glu	Leu	Leu	Gln	Arg	195	200	205	
Leu	Gly	Ser	Leu	Glu	Lys	Ile	Tyr	Glu	Asn	Leu	Asp	Leu	Ala	Lys	Asn	210	215	220	
Leu	Leu	Ser	Pro	Lys	Met	Tyr	Gln	Ala	Leu	Ile	Gln	Asp	Lys	Gly	Ser	225	230	235	240
Ala	Phe	Leu	Ser	Lys	Glu	Leu	Ala	Thr	Leu	Glu	Arg	Gly	Cys	Ile	Lys	245	250	255	
Glu	Phe	Asp	Phe	Leu	Ser	Cys	Ala	Phe	Pro	Ser	Glu	Asn	Pro	Leu	Leu	260	265	270	

869

Lys Ile Lys Asp Glu Leu Lys Glu Tyr Gly Phe Ile Ser Thr Leu Arg
 275 280 285
 Asp Leu Glu Asn Ser Pro Phe Ile Val Glu Asn Val Pro Ile Leu Asn
 290 295 300
 Ser Thr Pro Ile Leu Asp Asn Thr Pro Ala Leu Asp Asn Ala Pro Lys
 305 310 315 320
 Lys Ser Arg Met Ile Val Leu Glu Ser Ala Glu Pro Leu Ser Met Phe
 325 330 335
 Leu Glu Lys Leu Glu Asn Pro Asn Ala Arg Val Phe Met Arg Leu Val
 340 345 350
 Leu Asp Lys Asp Lys Lys Ile Leu Ala Leu Ala Phe Leu Leu Gln Asp
 355 360 365
 Gln Gly Tyr Phe Leu Pro Leu Glu Glu Ala Leu Phe Ser Pro Phe Ser
 370 375 380
 Leu Glu Phe Leu Gln Asn Ala Phe Ser Gln Met Leu Gln His Ala Cys
 385 390 395 400
 Ile Ile Gly His Asp Leu Lys Pro Leu Leu Ser Phe Leu Lys Ala Lys
 405 410 415
 Tyr Gln Val Pro Leu Glu Asn Ile Arg Ile Gln Asp Thr Gln Ile Leu
 420 425 430
 Ala Phe Leu Lys Asn Pro Glu Lys Val Gly Phe Asp Glu Val Leu Lys
 435 440 445
 Glu Tyr Leu Lys Glu Asp Leu Ile Pro His Glu Lys Ile Lys Asp Phe
 450 455 460
 Lys Thr Lys Ser Lys Ala Glu Lys Ser Glu Leu Leu Ser Met Glu Leu
 465 470 475 480
 Asn Ala Leu Lys Arg Leu Cys Glu Tyr Phe Glu Lys Gly Gly Leu Glu
 485 490 495
 Glu Asp Leu Leu Thr Leu Ala Arg Asp Ile Glu Thr Pro Phe Val Lys
 500 505 510
 Val Leu Met Gly Met Glu Phe Gln Gly Phe Lys Ile Asp Ala Pro Tyr
 515 520 525
 Phe Lys Arg Leu Glu Gln Glu Phe Lys Asn Glu Leu Asn Val Leu Glu
 530 535 540
 Arg Gln Ile Leu Asp Leu Ile Gly Val Asp Phe Asn Leu Asn Ser Pro
 545 550 555 560
 Lys Gln Leu Gly Glu Val Leu Tyr Asp Lys Leu Gly Leu Pro Lys Asn
 565 570 575
 Lys Ser His Ser Thr Asp Glu Lys Asn Leu Leu Lys Ile Leu Asp Lys
 580 585 590
 His Pro Ser Ile Pro Leu Ile Leu Glu Tyr Arg Glu Leu Asn Lys Leu
 595 600 605
 Phe Asn Thr Tyr Thr Thr Pro Leu Leu Arg Leu Lys Asp Lys Asp Asp
 610 615 620
 Lys Ile His Thr Thr Phe Ile Gln Thr Gly Thr Ala Thr Gly Arg Leu
 625 630 635 640
 Ser Ser His Ser Pro Asn Leu Gln Asn Ile Pro Val Arg Ser Pro Lys
 645 650 655
 Gly Leu Leu Ile Arg Lys Gly Phe Ile Ala Ser Ser Lys Glu Tyr Cys
 660 665 670
 Leu Leu Gly Val Asp Tyr Ser Gln Ile Glu Leu Arg Leu Leu Ala His
 675 680 685
 Phe Ser Gln Asp Lys Asp Leu Met Glu Ala Phe Leu Lys Gly Arg Asp
 690 695 700
 Ile His Leu Glu Thr Ser Lys Ala Leu Phe Gly Glu Asp Leu Ala Lys
 705 710 715 720
 Glu Lys Arg Ser Ile Ala Lys Ser Ile Asn Phe Gly Leu Val Tyr Gly

870

	725		730		735
Met Gly Ser Lys Lys Leu Ser Glu Thr Leu Ser Ile Pro Leu Ser Glu					
	740		745		750
Ala Lys Ser Tyr Ile Glu Ala Tyr Phe Lys Arg Phe Pro Ser Ile Lys					
	755		760		765
Asp Tyr Leu Asn Gly Met Arg Glu Glu Ile Leu Lys Thr Ser Lys Ala					
	770		775		780
Phe					
785					

(2) INFORMATION FOR SEQ ID NO:964:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

Val Ser Glu Ser Glu Lys Gln Glu Ile Glu Asn Lys Ile Glu Glu Arg	
1	5 10 15
Lys Arg Ala Lys Glu Gln Lys Asp Phe Leu Lys Ala Asp Ser Ile Arg	
	20 25 30
Glu Glu Leu Leu Gln Gln Lys Ile Ala Leu Met Asp Thr Pro Gln Gly	
	35 40 45
Thr Ile Trp Glu Lys Leu Phe	
50	55

(2) INFORMATION FOR SEQ ID NO:965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

Leu	Pro	Ser	Val	Gln	Ile	Trp	Gly	Ser	Tyr	Thr	Asn	Ser	Phe	Lys	Gln
1				5					10					15	
Thr	Phe	Ser	Ala	Ser	Asn	Ser	Asn	Leu	Val	Ile	Gly	Tyr	Asn	Ala	Thr
			20					25					30		
Trp	Thr	Asp	Pro	Asn	Val	Ser	Ser	Ser	Asp	Thr	Val	Ala	Phe	Gly	Asp
		35					40					45			
Pro	Ser	Gly	Ser	Ala	Leu	Asn	Gly	His	Cys	Gly	Pro	Trp	Pro	Tyr	Tyr
	50					55					60				
Gln	Cys	Thr	Gly	Thr	Thr	Asn	Gly	Thr	Tyr	Ser	Ala	Tyr	His	Val	Tyr
65					70					75				80	
Ile	Thr	Ala	Asn	Leu	Arg	Ser	Gly	Asn	Arg	Ile	Gly	Thr	Gly	Gly	Ala
			85						90					95	
Ala	Asn	Leu	Ile	Phe	Asn	Gly	Val	Asp	Ser	Ile	Asn	Ile	Ala	Asn	Ala
		100						105					110		
Thr	Ile	Thr	Gln	His	Asn	Ala	Gly	Ala	Tyr	Ser	Ser	Ser	Met	Thr	Phe
	115						120					125			
Ser	Thr	Gln	Asn	Met	Asp	Asn	Ser	Gln	Asn	Leu	Asn	Gly	Leu	Asn	Ser
	130					135					140				
Asn	Gly	Lys	Leu	Leu	Val	Tyr	Gly	Thr	Thr	Phe	Thr	Asn	Gln	Ala	Lys
145					150					155				160	
Asp	Gly	Lys	Phe	Ile	Phe	Asn	Ala	Gly	Gln	Ala	Thr	Phe	Glu	Asn	Thr
			165						170				175		
Asn	Phe	Asn	Gly	Gly	Ser	Tyr	Gln	Phe	Ser	Gly	Asp	Ser	Leu	Asn	Phe
	180						185					190			
Ser	Asn	Asn	Asn	Gln	Phe	Asn	Ser	Gly	Ser	Phe	Glu	Ile	Gly	Ala	Lys
	195						200				205				
Asn	Thr	Ile	Phe	Asn	Asn	Ala	Asn	Phe	Asn	Asn	Ser	Thr	Ser	Phe	Asn
	210					215					220				
Phe	Asn	Asn	Ser	Ser	Ala	Thr	Thr	Ser	Phe	Val	Gly	Asp	Phe	Thr	Asn
225					230					235				240	
Ala	Asn	Ser	Asn	Leu	Gln	Ile	Ala	Gly	Asn	Ala	Val	Phe	Gly	Asn	Ser
			245						250				255		
Thr	Asn	Gly	Ser	Gln	Asn	Thr	Ala	Asn	Phe	Asn	Asn	Thr	Gly	Ser	Val
		260						265					270		
Asn	Ile	Ala	Gly	Asn	Ala	Thr	Phe	Asp	Asn	Val	Val	Phe	Asn	Ser	Pro
	275						280					285			
Thr	Asn	Thr	Ser	Val	Lys	Gly	Lys	Val	Thr	Leu	Asn	Asn	Ile	Thr	Leu
	290					295					300				
Lys	Asn	Leu	Asn	Ala	Pro	Leu	Ser	Phe	Gly	Asp	Gly	Thr	Ile	Val	Phe
305					310					315				320	
Ser	Ala	His	Ser	Val	Ile	Asn	Ile	Gly	Glu	Ala	Ile	Thr	Asn	Gly	Asn
			325						330				335		
Pro	Ile	Thr	Leu	Val	Ser	Ser	Ser	Lys	Ala	Ile	Glu	Tyr	Asn	Asp	Ala
		340						345					350		
Phe	Ser	Lys	Asn	Leu	Trp	Gln	Leu	Ile	Asn	Tyr	Gln	Gly	His	Gly	Ala
	355						360					365			
Ser	Ser	Glu	Lys	Leu	Val	Ser	Ser	Ala	Gly	Asn	Gly	Val	Tyr	Asp	Val
	370					375					380				
Val	Tyr	Ser	Leu	Asn	Asn	Gln	Thr	Tyr	Asn	Phe	Gln	Glu	Val	Phe	Ser
385					390					395				400	
Pro	Asn	Ser	Ile	Ser	Ile	Arg	Arg	Leu	Gly	Val	Gly	Met	Val	Phe	Asp
			405						410					415	
Tyr	Val	Asp	Met	Glu	Lys	Ser	Asp	Arg	Leu	Tyr	Tyr	Gln	Asn	Ala	Leu
		420						425					430		
Gly	Phe	Met	Thr	Tyr	Met	Pro	Asn	Ser	Tyr	Asn	Asn	Asn	Leu	Gly	Asn

```

      435              440              445
Leu Asn Asn Thr Ile Tyr Tyr Tyr Asp Asn Ser Ile Asp Phe Tyr Ala
  450              455              460
Ser Gly Lys Thr Leu Phe Thr Lys Ala Glu Phe Ser Gln Thr Phe Thr
465              470              475              480
Gly Gln Asn Ser Ala Ile Val Phe Gly Ala Lys Asn Ile Trp Thr Ser
      485              490              495
Val Ser Asp Ala Pro Gln Ser Asn Val Ile Ile Arg Phe Gly Asp Asn
      500              505              510
Lys Gly Ala Gly Ser Asn Asp Ala Ser Gly His Cys Trp Asn Leu Gln
      515              520              525
Cys Ile Gly Phe Ile Thr Gly His Tyr Glu Ala Gln Lys Ile Tyr Ile
      530              535              540
Thr Gly Ser Ile Glu Ser Gly Asn Arg Ile Ser Ser Gly Gly Ala Arg
545              550              555              560
Ala Leu Ile Leu Thr Gly Phe Lys Ala Phe Phe
      565              570

```

(2) INFORMATION FOR SEQ ID NO:966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

```

Met Val Val Leu Gly Ser Thr Gly Ser Ile Gly Lys Asn Ala Leu Lys
 1              5              10              15
Ile Ala Lys Lys Phe Gly Val Lys Ile Glu Ala Leu Ser Cys Gly Lys
      20              25              30
Asn Ile Ala Leu Ile Asn Glu Gln Ile Lys Val Phe Lys Pro Lys Lys
      35              40              45
Val Ala Ile Leu Asp Pro Asn Asp Leu Asn Asn Leu Glu Pro Leu Gly
      50              55              60
Ala Glu Val Phe Val Gly Leu Asp Gly Ile Asp Ala Met Ile Glu Glu
65              70              75              80
Cys Val Ser Asn Leu Val Ile Asn Ala Ile Val Gly Val Ala Gly Leu
      85              90              95
Lys Ala Ser Phe Lys Ser Leu Gln Arg Asn Lys Lys Leu Ala Leu Ala
      100              105              110
Asn Lys Glu Ser Leu Val Ser Ala Gly His Leu Leu Asp Ile Ser Gln
      115              120              125
Ile Thr Pro Val Asp Ser Glu His Phe Gly Leu Trp Ala Leu Leu Gln
      130              135              140
Asn Lys Thr Leu Lys Pro Lys Ser Leu Ile Ile Ser Ala Ser Gly Gly

```

873

```

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

```

(2) INFORMATION FOR SEQ ID NO:967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

```

Met Lys Thr Thr Glu Asn Thr Asp Glu Thr His Leu Arg Glu Thr Lys
1          5          10          15
Asn Lys Leu Gly Arg Lys Pro Lys Ala Asp Ala Asn Lys Lys Thr Arg
          20          25          30
Ala Val Ser Leu Tyr Phe Ser Asp Glu Gln Tyr Gln Lys Leu Glu Lys
          35          40          45
Met Ala Asn Glu Glu Glu Glu Ser Val Gly Ser Tyr Ile Lys Arg Tyr
          50          55          60
Ile Leu Lys Ala Leu Arg Lys Ile Glu Gln Gly Gly Gly Phe Ile Ala

```


65	70	75	80
Phe Asn Leu Phe Leu Ile			
	85		

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Helicobacter pylori*

{A} NAME/KEY: misc_feature

- (B) LOCATION 1...803

(xi) SEQUENCE DESCRIPTION: SEO ID NO:968:

Leu	Trp	Leu	Lys	Ser	Lys	Phe	Phe	Leu	Leu	Met	Gly	Val	Gly	Leu	Leu
1				5				10						15	
Ser	His	Ser	Leu	Asn	Ala	Leu	Ser	Leu	Thr	Leu	Thr	Gln	Gly	Lys	Glu
			20					25					30		
Glu	Gly	Glu	Asp	Phe	Ser	Val	Leu	Thr	Leu	Arg	Asn	Asp	Lys	Ala	Phe
			35				40					45			
Ser	Cys	Ser	Tyr	Ala	Asn	Glu	Lys	Pro	Pro	Ser	Gly	Ile	Glu	Ala	Ser
	50					55					60				
Leu	Ser	Ile	Ile	His	Ala	Lys	Arg	Pro	Ile	Glu	Cys	Val	Ile	Asp	Ser
65				70						75					80
Ile	Pro	Lys	Glu	Gly	Phe	Thr	Pro	Leu	Glu	Asn	Ala	Phe	Phe	Asn	Ile
				85					90					95	
Thr	Tyr	Ser	Met	Arg	Gln	Gln	Gln	Phe	Ile	Leu	His	Ile	Lys	Pro	Lys
			100					105					110		
Val	Met	Arg	Arg	Leu	Thr	Leu	Phe	Ser	Phe	Asp	Arg	Asp	Tyr	Lys	Lys
			115				120					125			
Ala	Ile	Pro	Leu	Phe	Val	Glu	Asn	Asp	Ala	Lys	Ala	Lys	Met	Trp	Gln
			130			135					140				
Ile	Ile	Gly	Tyr	Asp	Gln	Lys	Ile	Pro	Phe	Leu	Ser	Glu	Lys	Asp	Asn
145				150						155					160
Ala	Gln	Lys	Gly	Leu	Asn	Phe	Pro	Ile	Ile	Ile	Lys	Asp	Ala	Gln	Thr
				165					170					175	
Pro	Ile	Ile	Gln	Glu	Leu	Asp	Val	Asn	Asn	Lys	Pro	Leu	Leu	Thr	Thr
			180					185					190		
Lys	Gly	Tyr	Asp	Leu	Asn	Ala	Tyr	Leu	Glu	Ala	Lys	Lys	Gln	Met	Asp
			195				200					205			
Ser	Gln	Ala	Tyr	Phe	Asp	Ala	Leu	Arg	Thr	Ile	Ser	Arg	Ala	Phe	Lys
	210					215					220				
Asn	Tyr	Pro	Gln	Thr	Ile	Phe	Lys	Lys	Asp	Leu	Tyr	Leu	Leu	Glu	Ile
225				230						235					240
Ile	Ala	Leu	Gly	Lys	Leu	Gly	Ile	Lys	Lys	Ser	Leu	Leu	Ile	Asp	Ile
				245					250					255	
Gly	Thr	Gln	Trp	Ile	Lys	Asn	Tyr	Pro	Thr	Asp	Pro	Asn	Ile	Pro	Glu

										260											265											270			
Ala	Leu	Tyr	Tyr	Val	Ala	Lys	Ala	Lys	Ala	Leu	Asp	Glu	Asn	Asn	Asn	Tyr	Lys	Ala	Leu	Asp	Glu	Asn	Asn	Asn	Tyr	Lys	Ala	Leu	Asp	Glu	Asn	Asn	Asn	Tyr	Lys
										275											280											285			
Gln	Ala	Val	Arg	Tyr	Tyr	Lys	Arg	Ile	Leu	Leu	Glu	Tyr	Lys	Asn	Ser		Gln	Ala	Val	Arg	Tyr	Tyr	Lys	Arg	Ile	Leu	Leu	Glu	Tyr	Lys	Asn	Ser			
										290											295											300			
Arg	Tyr	Ala	Pro	Leu	Ala	Gln	Met	Arg	Leu	Ala	Ile	Glu	Ala	Ala	Glu		Arg	Tyr	Ala	Pro	Leu	Ala	Gln	Met	Arg	Leu	Ala	Ile	Glu	Ala	Ala	Glu			
305											310											315											320		
Gly	Ser	Asp	Leu	Ser	Asn	Ala	Asn	Met	Leu	Phe	Lys	Glu	Ala	Phe	Ser		Gly	Ser	Asp	Leu	Ser	Asn	Ala	Asn	Met	Leu	Phe	Lys	Glu	Ala	Phe	Ser			
										325											330											335			
Asn	Ala	Lys	Asp	Lys	Glu	Ser	Ala	Ser	Glu	Ile	Ala	Leu	Asn	Trp	Ala		Asn	Ala	Lys	Asp	Lys	Glu	Ser	Ala	Ser	Glu	Ile	Ala	Leu	Asn	Trp	Ala			
										340											345											350			
Glu	Ala	Glu	Ile	Asn	Tyr	Gln	Asn	Phe	Asn	Asn	Ala	Lys	Tyr	Leu	Ile		Glu	Ala	Glu	Ile	Asn	Tyr	Gln	Asn	Phe	Asn	Asn	Ala	Lys	Tyr	Leu	Ile			
										355											360											365			
Asp	Lys	Val	Val	Gln	Ser	Asn	Pro	Asp	Tyr	Leu	Ser	Met	His	Ser	Glu		Asp	Lys	Val	Val	Gln	Ser	Asn	Pro	Asp	Tyr	Leu	Ser	Met	His	Ser	Glu			
										370											375											380			
Leu	Ala	Leu	Glu	Leu	Leu	Lys	Leu	Leu	Lys	Lys	Asn	Gln	Met	Asn	Glu		Leu	Ala	Leu	Glu	Leu	Leu	Lys	Leu	Leu	Lys	Lys	Asn	Gln	Met	Asn	Glu			
385											390											395											400		
Ser	Ala	Ile	Glu	Ile	Ala	His	Leu	Leu	Leu	Asn	Gln	Asp	Asp	Asp	Leu		Ser	Ala	Ile	Glu	Ile	Ala	His	Leu	Leu	Leu	Asn	Gln	Asp	Asp	Asp	Leu			
										405											410											415			
Lys	Ala	Lys	Glu	Gln	Ala	Leu	Tyr	Asp	Leu	Gly	Ala	Leu	Tyr	Ala	Arg		Lys	Ala	Lys	Glu	Gln	Ala	Leu	Tyr	Asp	Leu	Gly	Ala	Leu	Tyr	Ala	Arg			
										420											425											430			
Ile	Lys	Asp	Phe	Lys	Asn	Ala	His	Leu	Tyr	Asn	Leu	Gln	Tyr	Leu	Gln		Ile	Lys	Asp	Phe	Lys	Asn	Ala	His	Leu	Tyr	Asn	Leu	Gln	Tyr	Leu	Gln			
										435											440											445			
Asp	His	Ala	Glu	Leu	Glu	Arg	Ala	Ser	Val	Val	Arg	Ala	Arg	Asp	Glu		Asp	His	Ala	Glu	Leu	Glu	Arg	Ala	Ser	Val	Val	Arg	Ala	Arg	Asp	Glu			
										450											455											460			
Lys	Ala	Leu	Phe	Ser	Met	Glu	Gly	Asn	Thr	Gln	Glu	Lys	Ile	Ala	His		Lys	Ala	Leu	Phe	Ser	Met	Glu	Gly	Asn	Thr	Gln	Glu	Lys	Ile	Ala	His			
465											470											475											480		
Tyr	Asp	Lys	Ile	Ile	Gln	Asn	Phe	Pro	Asn	Ser	Asn	Glu	Ala	Gln	Lys		Tyr	Asp	Lys	Ile	Ile	Gln	Asn	Phe	Pro	Asn	Ser	Asn	Glu	Ala	Gln	Lys			
										485											490											495			
Ala	Leu	Glu	Leu	Lys	Ala	Gln	Leu	Leu	Phe	Asp	Asn	Lys																							

Met	Ile	Leu	Arg	Ala	Ser	Val	Leu	Ser	Ala	Leu	Leu	Leu	Val	Gly	Leu
1				5					10					15	
Gly	Ala	Ala	Pro	Lys	His	Ser	Val	Ser	Ala	Ser	Asp	Lys	Arg	Met	Gln
			20					25					30		
Asp	Asn	Leu	Val	Ser	Val	Ile	Glu	Lys	Gln	Thr	Asn	Lys	Lys	Val	Arg
		35					40					45			
Ile	Leu	Glu	Ile	Lys	Pro	Leu	Lys	Ser	Ser	Gln	Asp	Leu	Lys	Met	Val
	50					55					60				
Val	Ile	Glu	Asp	Pro	Asp	Thr	Lys	Tyr	Asn	Ile	Pro	Leu	Val	Val	Ser
65					70					75					80
Lys	Asp	Gly	Asn	Ser	Val	Ile	Gly	Leu	Ser	Asn	Ile	Phe	Phe	Ser	Asn
			85						90					95	
Lys	Ser	Asp	Asp	Val	Lys	Leu	Val	Ala	Glu	Thr	Asn	Gln	Lys	Ile	Gln
			100					105					110		
Ala	Leu	Asn	Ala	Thr	Gln	Gln	Asn	Ser	Ala	Lys	Leu	Asn	Ala	Ile	Phe
		115					120					125			
Asn	Glu	Ile	Pro	Ala	Asp	Tyr	Ala	Ile	Glu	Leu	Pro	Ser	Thr	Asn	Ala
	130					135					140				
Glu	Asn	Lys	Asp	Lys	Ile	Leu	Tyr	Ile	Val	Ser	Asp	Pro	Met	Cys	Pro
145					150					155					160
His	Cys	Gln	Lys	Glu	Leu	Thr	Lys	Leu	Arg	Asp	His	Leu	Lys	Glu	Asn
				165					170					175	
Thr	Val	Arg	Met	Val	Val	Val	Gly	Trp	Leu	Gly	Val	Asn	Ser	Ala	Lys
			180					185					190		

877

```

Lys Ala Ala Leu Ile Gln Glu Glu Met Ala Lys Ala Arg Ala Arg Gly
    195                      200                      205
Ala Ser Val Glu Asp Lys Ile Ser Ile Leu Glu Lys Ile Tyr Ser Thr
    210                      215                      220
Gln Tyr Asp Ile Asn Ala Gln Lys Glu Pro Glu Asp Leu Arg Thr Lys
    225                      230                      235                      240
Val Glu Asn Thr Thr Lys Lys Ile Phe Glu Ser Gly Val Ile Lys Gly
                      245                      250                      255
Val Pro Phe Leu Tyr His Tyr Lys Ala
                      260                      265

```

(2) INFORMATION FOR SEQ ID NO:970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

```

Leu Asp Phe Lys Ala Ile Glu His Gly Glu Glu Thr Leu Lys Asn Glu
1          5          10          15
Thr Leu Arg Ala Leu Ser Asp Phe Ala Lys Ser Ser Asp Thr His Ile
    20          25          30
Val Ala Cys Ser Ile Glu Lys Asn Asn Lys Lys Leu Tyr Asp Ser Ala
    35          40          45
Tyr Ile Ile Pro Pro Lys Gly Lys Ile Val Gly Lys His Arg Lys Ile
    50          55          60
Tyr Leu Trp Gly Asp Glu Lys Ser Arg Phe Lys Arg Gly Lys Lys Tyr
    65          70          75          80
Glu Val Phe Thr Leu Asp Phe Gly Asp Phe Ser Ala Lys Val Gly Leu
    85          90          95
Gln Ile Cys Tyr Glu Thr Gly Phe Gly Val Gly Ala Asn Leu Leu Val
    100          105          110
Leu Gln Gly Ala Glu Val Leu Ile Tyr Pro Ser Ala Phe Gly Lys Ala
    115          120          125
Arg Ala Tyr Asn Trp Asp Leu Leu Ser Lys Ala Arg Ala Leu Glu Asn
    130          135          140
Gly Cys Phe Val Cys Ala Cys Asn His Ser Gly Glu Glu Thr Asn Ala
    145          150          155          160
Lys Leu Lys Gln Thr Leu Glu Phe Ala Gly Asp Ser Arg Ile Ile Ala
    165          170          175
Pro Asn Gly Lys Ile Ile Ala Gln Ala Thr Lys Leu Asn Glu Val Ile
    180          185          190
Ile Ala Glu Met Asp Leu Asn Glu Val Ala Leu Gln Arg Gln Lys Ile
    195          200          205

```

Pro Tyr Leu Gln Asp Phe Asp Thr Lys Leu Thr Lys Lys Gly Phe Gly
 210 215 220
 Lys Leu Thr
 225

(2) INFORMATION FOR SEQ ID NO:971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

Met Ala Lys Glu Ile Leu Val Ala Tyr Gly Val Asp Ile Asp Ala Val
 1 5 10 15
 Ala Gly Trp Leu Gly Ser Tyr Gly Gly Glu Asp Ser Pro Asp Asp Ile
 20 25 30
 Ser Arg Gly Leu Phe Ala Gly Glu Val Gly Ile Pro Arg Leu Leu Lys
 35 40 45
 Leu Phe Lys Lys Tyr His Leu Pro Ala Thr Trp Phe Ala Pro Gly His
 50 55 60
 Ser Ile Glu Thr Phe Pro Glu Pro Met Lys Met Ile Val Asp Ala Gly
 65 70 75 80
 His Glu Val Gly Ala His Gly Tyr Ser His Glu Asn Pro Ile Ala Met
 85 90 95
 Thr Ala Lys Gln Glu Glu Asp Val Leu Leu Lys Ser Val Glu Leu Ile
 100 105 110
 Lys Asp Leu Thr Gly Lys Ala Pro Thr Gly Tyr Val Ala Pro Trp Trp
 115 120 125
 Glu Phe Ser Asn Ile Thr Asn Glu Leu Leu Leu Lys His Gly Phe Lys
 130 135 140
 Tyr Asp His Ser Leu Met His Asn Asp Phe Thr Pro Tyr Phe Val Arg
 145 150 155 160
 Val Gly Asp Ser Trp Ser Lys Ile Asp Tyr Ser Leu Glu Ala Lys Asp
 165 170 175
 Trp Met Lys Pro Leu Ile Arg Gly Val Glu Thr Asn Leu Val Glu Ile
 180 185 190
 Pro Ala Asn Trp Tyr Leu Asp Asp Leu Pro Pro Met Met Phe Ile Lys
 195 200 205
 Lys Ser Pro Asn Ser Phe Gly Phe Val Ser Pro Arg Asp Ile Gly Gln
 210 215 220
 Met Trp Ile Asp Gln Phe Asp Trp Val Tyr Arg Glu Met Asp Tyr Ala
 225 230 235 240
 Val Phe Ser Met Thr Ile His Pro Asp Val Ser Ala Arg Pro Gln Val
 245 250 255

879

Leu Leu Met His Glu Lys Ile Ile Glu His Ile Asn Gln His Glu Gly
 260 265 270
 Val Arg Trp Val Thr Phe Asn Glu Ile Ala Asp Asp Phe Leu Lys Arg
 275 280 285
 Asn Pro Arg Lys Lys
 290

(2) INFORMATION FOR SEQ ID NO:972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

Val Cys Gly Val Leu Ser Leu Gln Ala Arg Leu Ser Phe Glu Asn Cys
 1 5 10 15
 Ser Lys Pro Leu Asp Cys Ser Leu Phe Ala Thr Thr Cys Thr Pro Gln
 20 25 30
 Asn Pro Ile Gly Ser Cys Met Val Ser Ser Gln Gly Gly Val Cys Gly
 35 40 45
 Val Leu Ser Leu Gln Ala Arg Leu Ser Phe Glu Asn Cys Ser Lys Pro
 50 55 60
 Leu Asp Cys Ser Leu Phe Ala Thr Thr Cys Thr Pro Gln Asn Pro Ile
 65 70 75 80
 Gly Ser Cys Met Val Ser Ser Gln Gly Gly Val Arg Gly Val Leu Ser
 85 90 95
 Leu Gln Ala Arg Leu Ser Phe Lys Asn Cys Phe Leu Val Lys Ser Leu
 100 105 110
 Lys Pro Ser Gln Leu Thr Leu Met Leu Thr Gly Phe Leu Gly Gly Phe
 115 120 125
 Ser Phe Leu Thr Thr Gly Phe Trp
 130 135

(2) INFORMATION FOR SEQ ID NO:973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

880

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

```

Met Asn Gly Phe Cys Ala Arg Leu Arg Ala Ile Thr Phe Asn Glu Arg
1           5           10           15
Leu Lys Met Lys Ile Ala Val Leu Leu Ser Gly Gly Val Asp Ser Ser
20           25           30
Tyr Ser Ala Tyr Ser Leu Lys Glu Gln Gly His Glu Leu Val Gly Ile
35           40           45
Tyr Leu Lys Leu His Ala Ser Glu Lys Lys His Asp Leu Tyr Ile Lys
50           55           60
Asn Ala Gln Lys Ala Cys Glu Phe Leu Gly Ile Pro Leu Glu Val Leu
65           70           75           80
Asp Phe Gln Lys Asp Phe Lys Ser Ala Val Tyr Asp Glu Phe Ile Asn
85           90           95
Ala Tyr Glu Glu Gly Gln Thr Pro Asn Pro Cys Ala Leu Cys Asn Pro
100          105          110
Leu Met Lys Phe Gly Leu Ala Leu Asp His Ala Leu Lys Leu Gly Cys
115          120          125
Glu Lys Ile Ala Thr Gly His Tyr Ala Arg Val Lys Glu Ile Asp Lys
130          135          140
Val Ser Tyr Ile Gln Glu Ala Leu Asp Lys Thr Lys Asp Gln Ser Tyr
145          150          155          160
Phe Leu Tyr Ala Leu Glu His Glu Val Ile Ala Lys Leu Val Phe Pro
165          170          175
Leu Gly Asp Leu Leu Lys Lys Asp Ile Lys Pro Leu Ala Leu Asn Ala
180          185          190
Met Pro Phe Leu Gly Thr Leu Glu Thr Tyr Lys Glu Ser Gln Glu Ile
195          200          205
Cys Phe Val Glu Lys Ser Tyr Ile Asp Thr Leu Lys Lys His Val Glu
210          215          220
Val Glu Lys Glu Gly Val Val Lys Asn Leu Gln Gly Glu Val Ile Gly
225          230          235          240
Thr His Lys Gly Tyr Met Gln Tyr Thr Ile Gly Lys Arg Lys Gly Phe
245          250          255
Ser Val Lys Gly Ala Leu Glu Pro His Phe Val Val Gly Ile Asp Ala
260          265          270
Lys Lys Asn Glu Leu Ile Val Gly Lys Lys Glu Asp Leu Ala Thr His
275          280          285
Ser Leu Lys Ala Lys Asn Lys Ser Leu Thr Lys Asp Phe Lys Asp Gly
290          295          300
Glu Tyr Phe Ile Lys Ala Arg Tyr Arg Ser Val Pro Thr Lys Ala Phe
305          310          315          320
Val Ser Leu Lys Asp Gly Met Ile Glu Val Glu Phe Lys Glu Pro Phe
325          330          335
Tyr Gly Val Ala Lys Gly Gln Ala Leu Val Val Tyr Lys Asp Asp Ile
340          345          350
Leu Leu Gly Gly Gly Val Ile Val
355          360

```

(2) INFORMATION FOR SEQ ID NO:974:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 357 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...357
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

```

Met Lys Ala Ser Ile Tyr Asp Phe Thr Leu Asp Glu Leu Ser Gln Leu
1      5      10      15
Leu Lys Pro Ser Phe Arg Ala Lys Gln Leu Tyr Leu Trp Leu Tyr Ala
20     25     30
Lys Tyr Lys Thr Ser Phe Lys Asp Met Gln Asn Asn Phe Ser Lys Asp
35     40     45
Phe Ile Ala Tyr Leu Glu Gln Glu Phe Thr Leu Arg Thr Ile Glu Ile
50     55     60
Ala His Val Arg Glu Ser Val Asp Gly Ser Lys Lys Tyr Leu Phe Lys
65     70     75     80
Ser Leu Arg Asp Asn His Thr Phe Glu Ala Val Leu Leu Lys Met Lys
85     90     95
Asp Lys Lys Ile Asp Glu Glu Thr Asn Ala Val Leu Glu Gly Glu Lys
100    105    110
Tyr Thr Val Cys Val Ser Cys Gln Ile Gly Cys Gln Val Gly Cys Ser
115    120    125
Phe Cys Phe Thr Gln Lys Gly Gly Phe Val Arg Asp Leu Lys Ala Ser
130    135    140
Glu Ile Ile Gln Gln Ala Leu Leu Ile Lys Glu Ala Asn Asn Leu Pro
145    150    155    160
Ile Glu Lys Ala Leu Asn Ile Val Phe Met Gly Met Gly Glu Pro Leu
165    170    175
Asn Asn Leu Asp Glu Val Cys Lys Ala Val Glu Ile Phe Asn Thr Gly
180    185    190
Met Gln Ile Ser Pro Lys Arg Ile Thr Ile Ser Thr Ser Gly Val Ala
195    200    205
Asp Lys Ile Pro Ile Leu Ala Gly Lys Asn Leu Gly Val Gln Leu Ala
210    215    220
Ile Ser Leu His Ala Val Asp Asp Lys Thr Arg Ser Ser Leu Met Pro
225    230    235    240
Leu Asn Lys Lys Tyr Asn Ile Glu Cys Val Leu Asn Glu Val Arg Lys
245    250    255
Trp Pro Leu Glu Gln Arg Lys Arg Val Met Phe Glu Tyr Leu Leu Ile
260    265    270
Lys Asp Leu Asn Asp Ser Leu Asp Cys Ala Lys Lys Leu Leu Lys Leu
275    280    285
Leu Asn Gly Ile Lys Ser Lys Val Asn Leu Ile Leu Phe Asn Pro His
290    295    300

```


Glu Gly Ser Lys Phe Glu Arg Pro Ser Leu Glu Ser Ala Arg Met Phe
 305 310 315 320
 Ala Asp Phe Leu Asn Ala Lys Gly Leu Leu Cys Thr Ile Arg Glu Ser
 325 330 335
 Lys Ala Leu Asp Ile Glu Ala Ala Cys Gly Gln Leu Arg Glu Lys Lys
 340 345 350
 Leu Gln Gln Lys Ile
 355

(2) INFORMATION FOR SEQ ID NO:975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

Met Ala Glu Trp Lys Thr Asp Thr Glu Glu Val Lys Lys Val Val Gly
 1 5 10 15
 Arg Cys Arg Glu Phe Lys Arg Ser Leu Gln Glu Glu Lys Cys Ser Pro
 20 25 30
 Phe Ile Lys Asp Leu Asp Ser Tyr Ala Leu Lys Ile Ile Val Glu Arg
 35 40 45
 Arg Lys Thr Glu Met Gln Leu Glu Lys Ala Ile Gly Glu Leu Lys Lys
 50 55 60
 Ala Lys Ser Asn Glu Asp Asp Ala Lys Val Ala Leu Arg Val Leu Gln
 65 70 75 80
 Gly Ala Ser Val Val Ser Trp Ile Trp Pro Pro Ala Arg Ile Ala Ala
 85 90 95
 Thr Ala Ala Ile Val Ala Ala Glu Ala Val Leu Lys Phe Met Lys Glu
 100 105 110
 Asp Thr Glu Lys Cys Lys Arg Asn Val Glu Leu Leu Glu Arg Met Leu
 115 120 125
 Glu Ile Tyr Ser Asn Gln Ala Lys Ala Ser Ala Asn Leu Met Asn Gln
 130 135 140
 Ala Trp Glu Gly Ile Lys Lys Arg Leu His Phe Tyr Thr Asp Lys His
 145 150 155 160
 Gln Glu Phe Ile Arg Arg Leu Lys Gln Ala Ser Asp Ala Ile Asp Asn
 165 170 175
 Glu Tyr Asn Phe Pro Thr Pro Gly Val Leu Leu Glu Tyr Asp Phe Glu
 180 185 190
 Arg Pro Ala Ile Ser Tyr Thr Pro Lys Lys Ser Val Phe Asn Glu Arg
 195 200 205
 Leu Lys Asp Leu Arg Glu Asn Phe Ser Ala Ser Leu Tyr Ala Asp Leu
 210 215 220

883

Lys Asp Lys Ile His His Asn Ala Leu Ser Asn Asp Asp Leu Glu Arg
 225 230 235 240
 Met Ile Ala Phe Arg Glu Gln Glu Phe Glu Lys Ser Leu Glu Asp Trp
 245 250 255
 Met Gly Ala Tyr Ser Tyr Asp Glu Asn Pro Asn Asp Glu Leu Asp Arg
 260 265 270
 Met Ala Ile Ser Lys Glu Gln Glu Leu Glu Lys Ser Leu Glu Asp Leu
 275 280 285
 Met Pro Ser Val Leu Gly Val Pro Ser Tyr Asn Glu Ser Leu Thr Leu
 290 295 300
 Ala Lys Asn Arg Cys Val Lys Asn Phe Lys Glu Ala Leu Glu Gly Phe
 305 310 315 320
 Thr Glu Lys Ile Lys Glu Ser Pro Asn Asp Ser Asn Ala Ile Asn Glu
 325 330 335
 Ala Phe Asp Asn Leu Glu Thr Glu Leu Glu Arg Ala Thr Glu Asn Leu
 340 345 350
 Ser Gln Lys Ile Asp Pro Val Leu Glu Arg Asn Glu Asn Tyr Thr Gln
 355 360 365
 Lys Ala Leu Glu Tyr Arg Glu Phe Leu Glu Ser Arg Lys Glu Ser Phe
 370 375 380
 Ile Val Asp Glu Lys Asn Pro Tyr Pro Glu Glu Val Ser Phe Asn Glu
 385 390 395 400
 Trp Arg Trp Ala Glu Phe Asp Ser Val Phe Ser Ala Ile Val Pro Leu
 405 410 415
 Glu Asp Leu Asn Lys Thr Ala Cys Ala His His Ala Leu Lys Ala Leu
 420 425 430
 Gln Ala Thr Leu Lys Thr Thr Ile Trp Ala Leu Met Arg Gln Ser Trp
 435 440 445
 Asn Arg Ser Gln Lys Asp Ser Ser Leu Gly Gly Ile Cys Gly Ile Leu
 450 455 460
 Thr Arg Met Phe
 465

(2) INFORMATION FOR SEQ ID NO:976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

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

884

```

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

```

(2) INFORMATION FOR SEQ ID NO:977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

```

Leu Leu Ser Asn Lys Thr Leu Pro Lys Arg Phe Ala Thr Tyr Ser Leu
1           5           10           15
Gln Glu Val Gly Val Ile Phe Leu Thr Thr Gln Ile Leu Ser Ile Met
20           25           30
Arg Lys Thr Arg Cys Ser Lys Thr Leu Phe Phe Ile Thr Arg Gly Arg
35           40           45

```

885

```

Glu Ser Phe Arg Tyr Gln Leu Cys Asp His Tyr Lys Gln Lys Arg His
 50          55          60
Gln Phe Asp Glu Asp Phe Arg Ser Leu Leu Lys Ala Leu Lys Ile Ala
65          70          75          80
Leu Val Glu Lys Tyr Pro Leu Lys Lys Gly Ala Lys Ile Gln Gly Glu
          85          90          95
His Cys Phe Glu Tyr Glu Ala Asp Asp Ile Ile Ser Phe Tyr Lys Lys
          100          105          110
Lys Asp Pro Asn Asn Tyr Val Ile Ala Ser Met Asp Lys Asp Ile Leu
          115          120          125
Tyr Ser Asn Arg Gly Ser His Phe Asn Leu Lys Thr Asn Ala Phe Phe
          130          135          140
Asn Val Ser Gln Lys Glu Ala His Phe Phe Ala Tyr Tyr Gln Cys Val
          145          150          155          160
Val Gly Asp Lys Gly Asp Asn Ile Lys Gly Val Lys Gly Ile Gly Gly
          165          170          175
Phe Asn Tyr Lys Asp Phe Leu Asn Glu Asp Ala Lys Glu His Glu Leu
          180          185          190
Trp Glu Gln Ile Ile Gln Ala Phe Lys Ile Lys Glu Asp Leu Ser Asp
          195          200          205
Ser Glu Ala Lys Glu Lys Ala Leu Leu Asn Met Arg Leu Val Asn Met
          210          215          220
His Gln Met Thr His His Gly Val Ile Lys Leu Trp Glu Pro Glu Phe
          225          230          235          240
Lys Lys Ala Phe Phe Pro Lys Lys Pro Gln Arg Pro Asp Phe Lys Arg
          245          250          255
Ile Ser

```

(2) INFORMATION FOR SEQ ID NO:978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

```

Leu Cys Leu Lys Leu Leu Ile Trp Asn Phe Lys Glu His Ser Leu Lys
1          5          10          15
Val Asn Phe Phe Ala Thr Cys Leu Gly Ala Ala Ile Tyr Ser Asn Ala
          20          25          30
Ser Leu Asn Ala Ile Lys Leu Leu Arg Lys Glu Asn Leu Glu Val Val
          35          40          45
Phe Lys Lys Asp Gln Thr Cys Cys Gly Gln Pro Ser Tyr Asn Ser Gly
          50          55          60

```

886

```

Tyr Tyr Glu Glu Thr Lys Lys Val Val Leu Tyr Asn Ile Lys Leu Tyr
65          70          75          80
Ser Asn Asn Asp Tyr Pro Ile Ile Leu Pro Ser Gly Ser Cys Thr Gly
          85          90          95
Met Met Arg His Asp Tyr Leu Glu Leu Phe Glu Gly His Ala Glu Phe
          100         105         110
Asn Met Val Lys Asp Phe Cys Ser Arg Val Tyr Glu Leu Ser Glu Phe
          115         120         125
Leu Asp Lys Lys Leu Gln Val Lys Tyr Glu Asp Lys Gly Glu Pro Leu
          130         135         140
Lys Ile Thr Trp His Ser Asn Cys His Ala Leu Arg Val Ala Lys Val
145          150         155         160
Ile Asp Ser Ala Lys Asn Leu Ile Arg Gln Leu Lys Asn Val Glu Leu
          165         170         175
Ile Glu Leu Glu Lys Glu Glu Glu Cys Cys Gly Phe Gly Gly Thr Phe
          180         185         190
Ser Val Lys Glu Pro Glu Ile Ser Ala Val Met Val Lys Glu Lys Ile
          195         200         205
Lys Asp Ile Glu Ser Arg His Val Asp Val Ile Val Ser Ala Asp Ala
          210         215         220
Gly Cys Leu Met Asn Ile Ser Thr Ala Met Gln Lys Met Gly Ser Leu
225          230         235         240
Thr Lys Pro Met His Phe Tyr Asp Phe Leu Ala Ser Arg Leu Gly Leu
          245         250         255

```

(2) INFORMATION FOR SEQ ID NO:979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

```

Leu Lys Ile Phe Val Leu Leu Met Ser Val Ile Leu Gly Ile Ser Leu
1          5          10          15
Thr Gly Cys Ile Gly Tyr Arg Met Asp Leu Glu His Phe Asn Thr Leu
          20          25          30
Tyr Tyr Glu Glu Ser Pro Lys Lys Ala Tyr Glu Tyr Ser Lys Gln Phe
          35          40          45
Thr Lys Lys Lys Lys Asn Ala Leu Leu Trp Asp Leu Gln Asn Gly Leu
          50          55          60
Ser Ala Leu Tyr Ala Arg Asp Tyr Lys Thr Ser Leu Gly Val Leu Asp
65          70          75          80
Gln Ala Glu Gln Arg Phe Asp Lys Thr Gln Ser Ala Phe Thr Arg Gly
          85          90          95

```

887

Ala Gly Tyr Val Gly Ala Thr Met Ile Asn Asp Asn Val Arg Ala Tyr
 100 105 110
 Gly Gly Asn Ile Tyr Glu Gly Val Leu Ile Asn Tyr Tyr Lys Ala Ile
 115 120 125
 Asp Tyr Met Leu Leu Asn Asp Ser Ala Lys Ala Arg Val Gln Phe Asn
 130 135 140
 Arg Ala Asn Glu Arg Gln Arg Arg Ala Lys Glu Phe Tyr Tyr Glu Glu
 145 150 155 160
 Val Gln Lys Ala Ile Lys Glu Ile Asp Ser Ser Lys Lys His Asn Ile
 165 170 175
 Asn Met Glu Arg Ser Arg Ala Glu Val Ser Glu Ile Leu Asn Asn Thr
 180 185 190
 Tyr Ser Asn Leu Asp Lys Tyr Glu Ala Tyr Gln Gly Leu Leu Asn Pro
 195 200 205
 Ala Val Ser Tyr Leu Ser Gly Leu Phe Tyr Ala Leu Asn Gly Asp Lys
 210 215 220
 Asn Lys Gly Leu Gly Tyr Leu Asn Glu Ala Tyr Gly Ile Ser Gln Ser
 225 230 235 240
 Pro Phe Val Ala Gln Asp Leu Val Phe Phe Lys Asn Pro Asn Arg Ser
 245 250 255
 His Phe Thr Trp Ile Ile Ile Glu Asp Gly Lys Glu Pro Gln Lys Ser
 260 265 270
 Glu Phe Lys Ile Asp Val Pro Ile Phe Met Ile Asp Ser Val Tyr Asn
 275 280 285
 Val Ser Val Ala Leu Pro Lys Leu Glu Lys Gly Glu Ala Phe Tyr Gln
 290 295 300
 Asn Phe Thr Leu Lys Asp Gly Glu Lys Val Thr Pro Phe Asp Thr Leu
 305 310 315 320
 Ala Ser Ile Asp Ala Val Val Ala Ser Glu Phe Arg Lys Gln Leu Pro
 325 330 335
 Tyr Ile Ile Thr Arg Ala Ile Leu Ser Ala Thr Phe Lys Val Gly Met
 340 345 350
 Gln Ala Val Ala Asn Tyr Tyr Leu Gly Phe Val Gly Gly Leu Val Thr
 355 360 365
 Ser Leu Tyr Ser Gly Val Ser Thr Phe Ala Asp Thr Arg Asn Thr Ser
 370 375 380
 Ile Phe Ala His Lys Ile Tyr Leu Met Arg Ile Lys Asn Lys Ala Phe
 385 390 395 400
 Glu Ser Tyr Glu Val Arg Ala Asp Ser Ile Asp Ala Phe Ser Phe Ser
 405 410 415
 Leu Lys Pro Cys Lys Arg Ser Leu Glu Ser Pro Lys Ile Ile Asp Ala
 420 425 430
 Arg Glu Leu Leu Ser Gly Phe Val Thr Ala Pro Gln Val Phe Cys Ser
 435 440 445
 Asn Arg His Asn Ile Leu Tyr Val Arg Ser Phe Lys Asn Gly Phe Val
 450 455 460
 Leu Ser His Leu Lys
 465

(2) INFORMATION FOR SEQ ID NO:980:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

```

Met Lys Gln Ile Lys Ala Leu Ala Leu Phe Ser Gly Gly Leu Asp Ser
1           5           10           15
Leu Leu Ser Met Lys Leu Leu Ile Asp Gln Gly Ile Glu Val Thr Ala
20           25           30
Leu His Phe Asn Ile Gly Phe Gly Gly Asn Lys Asp Lys Arg Glu Tyr
35           40           45
Phe Glu Asn Ala Thr Ala Gln Ile Gly Ala Lys Leu Leu Val Cys Asp
50           55           60
Ile Arg Glu Gln Phe Phe Asn Asp Val Leu Phe Lys Pro Lys Tyr Gly
65           70           75           80
Tyr Gly Lys Tyr Phe Asn Pro Cys Ile Asp Cys His Ala Asn Met Phe
85           90           95
Arg Asn Ala Phe Tyr Lys Met Leu Glu Leu Asp Ala Asp Phe Val Leu
100          105          110
Ser Gly Glu Val Leu Gly Gln Arg Pro Lys Ser Gln Arg Lys Glu Ala
115          120          125
Leu Asn Gln Val Arg Lys Leu Val Arg Glu Val Gly Glu Glu Ala Arg
130          135          140
Phe Asp Leu Ile Leu Asp Arg Thr Gln Ala Ser Gly Glu Lys Pro Gln
145          150          155          160
Phe Leu Asp Glu Leu Leu Leu Arg Pro Met Ser Ala Lys Leu Leu Glu
165          170          175
Pro Thr Phe Met Glu Lys Lys Gly Trp Val Asp Arg Glu Lys Leu Leu
180          185          190
Asp Val Ser Gly Arg Gly Arg Ala Arg Gln Leu Gln Met Ile Lys Asp
195          200          205
Tyr Gly Leu Lys Tyr Tyr Glu Lys Pro Gly Gly Gly Cys Leu Leu Thr
210          215          220
Asp Ile Gln Val Ser Asn Lys Ile Lys Asn Leu Lys Glu Tyr Arg Glu
225          230          235          240
Met Val Phe Glu Asp Gly Val Ile Val Lys Asn Gly Arg Tyr Phe Val
245          250          255
Leu Pro His Asn Ala Arg Leu Val Val Ala Arg Asn Glu Glu Glu Asn
260          265          270
His Lys Leu Asp Ile Glu His Pro Leu Met Asp Lys Ile Glu Leu Leu
275          280          285
Gly Cys Lys Gly Pro Leu Ser Leu Val Asp Lys Asn Ala Ser Gln Glu
290          295          300
Asp Lys Glu Leu Ala Gly Arg Ile Ala Leu Gly Tyr Ala Lys Thr Leu
305          310          315          320
Lys Asn Gln Ala Tyr Leu Ile Gln Ile Gly Asn Glu Lys Arg Glu Leu
325          330          335
Tyr Pro Leu Asp Lys Glu Asn Ala Arg Glu Tyr Leu Phe Ala
340          345          350

```

(2) INFORMATION FOR SEQ ID NO:981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

```

Met Lys Lys Tyr Ser Ala Ile Pro Thr Pro Cys Tyr Ala Leu Glu Ser
 1          5          10          15
Glu Arg Leu Glu Lys Asn Ala Lys Ile Leu Glu Ile Val Arg Gln Gln
          20          25          30
Ser Gly Ala Lys Val Leu Leu Ala Leu Lys Gly Tyr Ala Phe Trp Arg
          35          40          45
Glu Phe Gly Ile Leu Arg Gln Lys Leu Asn Gly Cys Cys Ala Ser Gly
          50          55          60
Leu Tyr Glu Ala Lys Leu Ala Phe Glu Glu Phe Gly Gly Arg Glu Ser
65          70          75          80
His Lys Glu Ile Cys Val Tyr Ser Pro Ala Phe Lys Glu Ala Glu Met
          85          90          95
Ser Ala Ile Leu Pro Leu Ala Thr Ser Ile Ile Phe Asn Ser Phe His
          100          105          110
Gln Tyr Ala Thr Tyr Lys Asp Arg Ile Leu Asp Lys Asn Lys Gln Leu
          115          120          125
Glu Asn Leu Gly Leu Ser Pro Ile Lys Met Gly Leu Arg Ile Asn Pro
          130          135          140
Leu Tyr Ser Glu Val Thr Pro Ala Ile Tyr Asn Pro Cys Ser Lys Met
145          150          155          160
Ser Arg Leu Gly Ile Thr Pro Ser Gly Phe Glu Lys Gly Val Lys Glu
          165          170          175
His Gly Leu Glu Gly Val Ser Gly Leu His Phe His Thr His Cys Glu
          180          185          190
Gln Asn Ala Asp Ala Leu Cys Arg Thr Leu Glu His Val Glu Arg His
          195          200          205
Phe Lys Pro Tyr Leu Glu Asn Met Ala Trp Val Asn Phe Gly Gly Gly
210          215          220
His His Ile Thr Arg Ser Asp Tyr Asp Val Asn Leu Leu Ile Gln Thr
225          230          235          240
Ile Lys Asp Phe Lys Glu Arg Tyr His Asn Thr Glu Val Ile Leu Glu
          245          250          255
Pro Gly Glu Ala Ile Gly Trp Gln Cys Gly Phe Leu Ile Ala Ser Val
          260          265          270
Ile Asp Ile Val Gln Asn Asp Gln Glu Ile Ala Ile Leu Asp Ala Ser
          275          280          285
Phe Ser Ala His Met Pro Asp Cys Leu Glu Met Pro Tyr Arg Pro Ser

```


890

```

      290              295              300
Ile Leu Lys Val Ser Val Glu Asn Asp Glu Glu Ile Ile Glu Val Glu
305              310              315              320
Lys Gly Glu Asn Gln Gly Ala Phe Ser Tyr Phe Leu Gly Gly Pro Thr
      325              330              335
Cys Leu Ala Gly Asp Phe Met Gly Ser Phe Ser Phe Glu Thr Pro Leu
      340              345              350
Lys Arg Gly Asp Lys Ile Val Phe Gln Asp Met Leu His Tyr Thr Ile
      355              360              365
Val Lys Asn Asn Ser Phe Asn Gly Val Pro Leu Pro Ser Leu Ala Lys
      370              375              380
Ile Asp Ser Gln Gly Phe Lys Ile Leu Lys Ser Phe Ser Tyr Glu Asp
385              390              395              400
Tyr Lys Asn Arg Asn
      405

```

(2) INFORMATION FOR SEQ ID NO:982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

```

Met Ala Asp Ser Leu Ala Gly Ile Asp Gln Val Thr Ser Leu His Lys
1              5              10              15
Asn Asn Glu Leu Gln Leu Leu Cys Phe Arg Leu Gly Lys Asn Lys Asp
      20              25              30
Leu Tyr Ala Val Asn Val Phe Lys Ile Arg Glu Val Val Lys Tyr His
      35              40              45
Gly Asn Leu Thr Ile Ile Ser His Glu Asn Asn Ser Leu Val Glu Gly
      50              55              60
Leu Ile Ile Ile Arg Glu Leu Thr Ile Pro Leu Ile Asp Met Lys Lys
65              70              75              80
Trp Phe Tyr Tyr Asp Ser Gln Asn Lys Ser Lys Asp Leu Arg Pro Tyr
      85              90              95
Arg Ile Glu Lys Glu Lys Gly Glu Asp Asp Ile Val Met Ile Cys Glu
      100              105              110
Phe Ser Arg Trp Thr Ile Gly Val Arg Ile Tyr Glu Ala Asp Arg Ile
      115              120              125
Leu Ser Lys Lys Trp Thr Glu Met Glu Gln Ser Ala Gly Leu Gly Gly
      130              135              140
Ser Ala Gly Asn Asn Lys Leu Val Ser Arg Thr Arg Tyr Phe Asp Gly
145              150              155              160
Arg Leu Val Gln Val Val Asp Ile Glu Lys Met Leu Ile Asp Val Phe

```

										165					170					175					
Pro	Trp	Ile	Glu	Asp	Glu	Lys	His	Asn	Asp	Leu	Glu	Thr	Leu	Ser	Lys										
										180					185					190					
Ile	His	Ser	Asn	Gln	Cys	Val	Leu	Leu	Ala	Asp	Asp	Ser	Pro	Ser	Val										
										195					200					205					
Leu	Lys	Thr	Met	Gln	Met	Ile	Leu	Asp	Lys	Leu	Gly	Val	Lys	His	Ile										
										210					215					220					
Asp	Phe	Ile	Asn	Gly	Lys	Thr	Leu	Leu	Glu	His	Leu	Phe	Asn	Pro	Thr										
225											230					235					240				
Thr	Asp	Val	Ser	Asn	Ile	Gly	Leu	Ile	Ile	Thr	Asp	Leu	Glu	Met	Pro										
										245					250					255					
Glu	Ala	Ser	Gly	Phe	Glu	Val	Ile	Lys	Gln	Val	Lys	Asn	Asn	Pro	Leu										
										260					265					270					
Thr	Ser	Lys	Ile	Pro	Ile	Val	Val	Asn	Ser	Ser	Met	Ser	Gly	Ser	Ser										
										275					280					285					
Asn	Glu	Asp	Met	Ala	Arg	Ser	Leu	Lys	Ala	Asp	Asp	Phe	Ile	Ser	Lys										
										290					295					300					
Ser	Asn	Pro	Lys	Asp	Ile	Gln	Arg	Val	Val	Lys	Gln	Phe	Leu	Glu	Leu										
305											310					315					320				
Ala																									

(A) LENGTH: 735 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

ATGCAATTTTC	AAAAAACCTT	ATCTTCCTTA	TCTTTATTTT	TATCTTTATC	TTTATTCTTA	60
TCTTTTAGTA	TCGCTGAAGA	AAATGGGGCG	TATGCGAGCG	TGGGTTTTGA	ATATTCCATT	120
AGTCATGCCG	TTGAGCACAA	TAATCCCTTT	TTAAATCAAG	AACGCATCCA	AACGATTTCT	180
AACGCTCAAA	ACCAAATCTA	TAAACTCAAT	CAAATTGAAA	ATGAAATCAC	AAACATGCAA	240
AACACCTTTA	ACTACACCAA	CAACGCTTTG	AAAAACAATG	CTAAATTAAC	CCCCACTGAA	300
ATGCAAGCCG	AACAATACTA	CTTCCAATCC	ACCCTTCAAA	ACATTGAAAA	AATAGTCATG	360
CTTAGCGGTG	GCGTTGCGTC	TAACCCTAAA	CTAGTCCAAG	CGTTAGAAAA	AATGCAAGAA	420
CCCATTACTA	ACCCTTTAGA	ATTGGTAGAA	AACTTAAAAA	ATTTAGAATT	ACAATTCAGC	480
CAATCTCAAA	ACAGCATGCT	TTCTTCTTTG	TCTTCTCAGA	TCGCTCAAAT	TTCAAATTCT	540
TTGAACGCGC	TTGATCCCAG	CTCTTATTCT	AAAAACGTTT	CAAGCATGTA	TGGGGTAGGT	600
TTGAGCGTAG	GGTATAAGCA	TTTCTTTACC	AAGAAAAAAA	ATCAAGGGTT	TCGTTATTAC	660
TTATTCTATG	ACTATGGTTA	CACTAATTTT	GGTTTTGTGG	GTAATGGCTT	TGATGGTTTA	720

GGCAAAATGA ATAAC

735

(2) INFORMATION FOR SEQ ID NO:984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1899 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

ATGAAACCAA	CGAACGAACC	TAAAAAACCT	TTTTTTTCAA	GTCCCATTTGT	TCTTGCGGTT	60
CTTGGAGGGA	TTTACTCAT	TTTTTTCCTA	CGCTCTTTCA	ATTCTGATGG	CAGTTTTTCG	120
GACAATTTCT	TAGCTTCTAG	CACTAAAAAT	GTGAGCTACC	ATGAAATCAA	ACAGCTCATC	180
AGCAATAATG	AAGTGGAAAA	TGTGAGTATC	GGTCAAACCT	TGATCAAAGC	CAGCCATAAA	240
GAGGGCAATA	ATCGTGTGAT	TTATATCGCT	AAACGAGTGC	CTGATCTAAC	CTTAGTGCCT	300
TTGTTAGACG	AGAAAAAAT	CAATTATCT	GGTTTTAGCG	AATCTAACTT	TTTTACCGAC	360
ATGTTAGGGT	GGCTCATGCC	TATTTTAGTG	ATTTTAGGGC	TATGGATGTT	TATGGCAAAC	420
CGCATGCAAA	AAAATATGGG	TGGGGGTATT	TTTGGCATGG	GGAGCGCGAA	AAAACTCATT	480
AACGCTGAAA	AACCCAATGT	GCGTTTAAAT	GACATGGCGG	GCAATGAAGA	AGCCAAAGAA	540
GAAGTAGTAG	AAATCGTGGA	TTCTTAAAA	TACCCCGAAC	GATACGCCAA	TTAGGGGGCT	600
AAAATCCCTA	AAGGTGTGCT	GTTAGTAGGG	CCTCCAGGAA	CCGGTAAAC	CCTTTTAGCA	660
AAGGCGGTGG	CTGGCGAAGC	GCATGTGCCG	TTTTTCTCTA	TGGGAGGGAG	CAGTTTCATT	720
GAAATGTTTG	TGGGCTTAGG	GGCAAGCAGG	GTTAGGGATT	TGTTTGAAAC	CGCTAAAAAA	780
CAAGCCCCTA	GCATCATTTT	TATTGATGAA	ATTGATGCCA	TAGGCAAGAG	CAGAGCGGCT	840
GGAGGCATGA	TAAGTGGGAA	TGATGAGAGA	GAGCAAACCC	TAAACCAGCT	CTTAGCCGAA	900
ATGGATGGTT	TTGGGAGCGA	AAACGCACCT	GTCATTGTTT	TAGCCGCAAC	GAACCGCCCT	960
GAAATCTTGG	ATCCGGCTTT	AATGCGTCCA	GGGCGCTTTG	ACAGGCAGGT	TTAGTGGAT	1020
AAGCCTGATT	TTAATGGCAG	GGTGGAAATC	TTAAAAGTGC	ATATTAAAGG	CGTGAAACTC	1080
GCTAATGATG	TGAATTTGCA	AGAAGTCGCC	AACTCACCG	CAGGGCTTGC	AGGGGCGGAT	1140
TTGGCGAATA	TCATCAATGA	AGCCGCGCTT	TTAGCGGGAC	GAAACAACCA	AAAAGAAGTC	1200
AAACAACAGC	ATTTAAAAGA	AGCGGTTGAA	AGAGGGATTG	CTGGGCTAGA	AAAGAAAAGC	1260
AGGCGTATCA	GTCTAAAAGA	AAAGAAAATC	GTGCCTTACC	ATGAAAGCGG	GCATGCCGTG	1320
ATTTCTGAAA	TGACTAAAGG	GAGCACTAGG	GTGAATAAAG	TCTCTATCAT	TCCAAGGGGC	1380
ATGGCGGCTT	TAGGCTACAC	CCTTAACACG	CCTGAAGAAA	ACAAATACTT	GATGCAAAAA	1440
CACGAACCTA	TCGCTGAAAT	TGATGTGCTT	TTAGGCGGGA	GGGCGGCTGA	AGAAGTC'TTT	1500
TTAGAAGAAA	TTTCTACCGG	TGCGAGCAAC	GATTTAGAAA	GAGCGACTGA	TATTATTAAA	1560
GGCATGGTGA	GTTACTACGG	CATGAGCAGT	GTCAGCGGGC	TTATGGTGTT	AGAAAAGCAA	1620
CGGAACGCCT	TTTTAGGAGG	CGGTTATGGG	AGCAGTAGGG	AATTTAGCGA	AAAAACCGCA	1680
GAAGAAATGG	ATCTTTTCAT	TAAAAACCTA	CTAGAAGAGC	GCTATCAGCA	TGTCAAACAA	1740
ACCTTAAGCG	ACTATAGAGA	GGCGATTGAA	ATCATGGTCA	AAGAATTGTT	TGACAAAGAA	1800
GTCATTACAG	GCGAAAGGGT	GCGTGAAATC	ATCAGCGAAT	ACGAAGCCGC	CAACAATTTA	1860
GAAAGCCGTT	TGATCCCTTT	AGAAGAGCAA	GCGAGTTAA			1899

(2) INFORMATION FOR SEQ ID NO:985:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3867 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

ATGGAAATAC	AACAAACACA	CCGCAAAATC	AATCGCCCTT	TAGTTTCTCT	CGTTTTAGCA	60
GGAGCGTTGA	TTAGCGCCAT	ACCGCAAGAG	AGTCATGCCG	CCTTTTTTCAC	GACCGTGATC	120
ATTCCAGCCA	TTGTTGGGGG	TATCGCCACA	GGCACTGCTG	TAGGAACGGT	CTCAGGGCTT	180
CTTAGTTGGG	GACTCAAACA	AGCCGAAGAA	GCGAATAAAA	CCCCAGATAA	ACCCGATAAA	240
GTTTGGCGCA	TTCAAGCAGG	AAAAGGCTTT	AATGAATTTT	CTAACAAGGA	ATACGACTTA	300
TACAAATCCC	TTTTATCCAG	TAAGATTGAT	GGAGGTTGGG	ACTGGGGGAA	CGCCGCTAGG	360
CATTATTGGG	TCAAAGGCGG	GCAATGGAAC	AAGCTTGAAG	TGGATATGAA	AGACGCTGTA	420
GGGACTTATA	AACTATCAGG	GCTTAGAAAC	TTTACTGGTG	GGGATTTAGA	CGTGAATATG	480
CAAAAAGCCA	CTTTGCGTTT	GGGCCAATTC	AATGGCAATT	CTTTCACAAG	CTATAAGGAT	540
AGCGCTGATC	GCACCACGAG	AGTGAATTTT	AACGCTAAAA	ATATTTCAAT	TGATAATTTT	600
GTAGAAATCA	ATAATCGTGT	GGGTTCTGGA	GCCGGGAGAA	AAGCCAGCTC	TACGGTTTTG	660
ACTTTGCAAG	CTTCAGAAGG	GATCACTAGC	AGTAAAAATG	CGGAAATTTT	TCTTTATGAT	720
GGCGCCACGC	TCAATTTGGC	TTCAAACAGC	GTAAATTAA	ATGGTAATGT	GTGGATGGGC	780
CGTTTGCAAT	ACGTGGGAGC	GTATTTAGCC	CCTTCATACA	GCACGATCAA	CACTTCAAAA	840
GTTCAAGGGG	AAGTGGATTT	TAACCATCTC	ACTGTGGGGG	ATCAAAACGC	CGCTCAAGCG	900
GGCATTATCG	CTAGCAATAA	GACTCATATT	GGCACACTGG	ATTTGTGGCA	AAGCGCCGGG	960
TTAAATATCA	TTGCCCTCC	AGAAGGTGGC	TACAAGGATA	AACCTAATAG	TACCACTTCT	1020
CAAAGTGGCA	CTAAAAACGA	CAAGAAAGAG	ATCAGTCAAA	ATAACAATAG	CAACACAGAG	1080
GTCATTAACC	CACCCAATAA	CACGCAAAAA	ACAGAAACTG	AACCCACGCA	AGTCATTGAT	1140
GGGCCTTTTG	CTGGCGGCAA	AGACACGGTT	GTCAATATTT	TCCACTTAAA	CACTAAAGCC	1200
GATGGCACGA	TTAAAGTGGG	AGGGTTTAAA	GCTTCTCTTA	CCACGAATGC	GGCTCATTTG	1260
AATATCGGCA	AAGGCGGTGT	CAATCTGTCC	AATCAAGCGA	GCGGGCGCAC	CCTTTTAGTG	1320
GAAAATCTAA	CCGGGAATAT	CACCGTTGAT	GGGCCTTTAA	GAGTGAATAA	TCAAGTGGGT	1380
GGCTATGCTT	TGGCAGGATC	AAGCGCGAAT	TTTGAGTTTA	AGGCTGGTGT	GGATACTAAA	1440
AACGGCACAG	CCACTTTCAA	TAACGATATT	AGTTTGGGAA	GATTTGTGAA	TTTAAAGGTG	1500
GATGCTCATA	CAGCTAATTT	TAAAGGTATT	GATACGGGTA	ATGGTGGTTT	CAACACCTTA	1560
GATTTTAGTG	GTGTTACAGA	CAAAGTCAAT	ATCAACAAGC	TCATCACAGC	TTCCACTAAT	1620
GTGGCCGTTA	AAAACCTCAA	CATTAATGAA	TTGATTGTTA	AAACCAATGG	GATAAGTGTG	1680
GGGGAATACA	CTCATTTTAG	CGAAGATATA	GGCAGTCAAT	CGCGTATCAA	TACCGTGCGT	1740
TTGGAAACTG	GCACTAGGTC	AATCTTTTCT	GGGGGTGTCA	AATTTAAAG	CGGTGAAAAA	1800
CTAGTTATCA	ATGATTTTAA	CTATAGCCCT	TGGAATTATT	TTGACGCTAG	GAATGTTAAA	1860
AATGTTGAAA	TCACCAGAAA	ATTCGCTTCT	TCAACCCAG	AAAACCCCTG	GGGCACATCA	1920
AAGCTCATGT	TTAATAATCT	AACCTTGGGT	CAAAATGCGG	TCATGGACTA	TAGTCAATTT	1980

TCAAATTTAA	CCATTCAGGG	GGATTTTATC	AACAATCAAG	GCACTATCAA	CTATCTGGTC	2040
CGAGGCGGGA	AAGTGGCAAC	CTTAAATGTA	GGCAATGCAG	CAGCTATGAT	GTTTAATAAT	2100
GATATAGACA	GCGCGACCGG	ATTTTACAAA	CCGCTCATCA	AGATTAAACAG	CGCTCAAGAT	2160
CTCATTAAAA	ATACAGAGCA	TGTTTTATTG	AAAGCGAAAA	TCATTGGTTA	TGGTAATGTT	2220
TCTACAGGTA	CCAATGGCAT	TAGTAATGTT	AATCTAGAAG	AGCAATTCAA	AGAGCGCCTA	2280
GCCCTTTATA	ACAATAATAA	CCGCATGGAT	ACTTGTGTGG	TGCGAAATAC	TGATGACATT	2340
AAAGCATGCG	GTATGGCTAT	CGGCAATCAA	AGCATGGTGA	ACAACCCTGA	CAATTACAAG	2400
TATCTTATCG	GTAAGGCATG	GAGAAATATA	GGCATCAGTA	AAACGGCTAA	CGGCTCTAAA	2460
ATTTCCGTGT	ATTATTTAGG	CAATTCTACG	CCTACTGAGA	ATGGTGGCAA	TACCACCAAC	2520
TTACCCACAA	ACACCACTAA	TAATGCGCAT	TCTGCTAACT	ACGCTCTCGT	GAAGAACGCT	2580
CCTTTTCGCTC	ACAGCGCCAC	TCCTAATTTA	GTCGCTATCA	ATCAGCATGA	TTTTGGCACT	2640
ATTGAGAGCG	TGTTTGAATT	GGCTAACCGC	TCTAAAGATA	TTGACACGCT	CTATACTCAT	2700
TCAGGCGCGC	AAGGCAGGGA	TCTCTTGCAA	ACTTTATTGA	TTGATAGCCA	TGATGCGGGT	2760
TATGCCAGAC	AAATGATTGA	TAACACAAGC	ACCGGTGAAA	TCACCAAGCA	ATTGAATGCG	2820
GCCACTGACG	CTTTAAACAA	CGTAGCCAGT	TTAGAGCATA	AACAAAGCGG	CTTACAAACC	2880
TTGAGCTTGA	GTAATGCGAT	GATTTTAAAT	TCTCGTTTAG	TCAATCTCTC	TAGGAAGCAC	2940
ACCAACCATA	TTAACTCGTT	CGCTCAACGC	TTACAAGCTT	TAAAAGGCCA	AGAATTCGCT	3000
TCTTTAGAGA	GCGCGGCAGA	AGTGTGTGAT	CAATTTGCCC	CTAAATATGA	AAAACCTACC	3060
AATGTTTGGG	CTAACGCTAT	TGGGGGAGCG	AGCTTGAATA	GCGGCTCTAA	CGCTTCATTG	3120
TATGGCACAA	GCGCCGGCGT	AGACGCTTTC	CTTAACGGGA	ATGTGGAAGC	CATTGTGGGC	3180
GGTTTTGGAA	GCTATGGTTA	TAGCTCCTTT	AGCAATCAAG	CGAACTCTCT	TAACTCTGGG	3240
GCCAATAACG	CTAATTTTGG	CGTGTATAGC	CGTTTTTTTG	CCAACCAGCA	TGAATTTGAC	3300
TTTGAAGCTC	AAGGGGCGCT	AGGGAGCGAT	CAATCAAGCT	TGAATTTCAA	AAGCACTCTA	3360
TTACAAGATT	TGAATCAAAG	CTATAATTAC	TTAGCCTATA	GCGCCACAGC	AAGAGCGAGT	3420
TATGGTTATG	ACTTCGCGTT	TTTTAGGAAC	GCTTTAGTGT	TAAAACCAAG	CGTGGGCGTG	3480
AGCTATAACC	ATTTAGGTTT	AACCAACTTT	AAAAGCAATA	GCCAATCACA	AGTGGCTTTA	3540
AAAAATGGCG	CGAGCAGTCA	GCATTTATTC	AACGCTAACG	CTAACGTGGA	AGCGCGTTAT	3600
TATTATGGGG	ACACTTCATA	CTTTTATTTG	CATGCGGGAG	TTTTACAAGA	GTTTCGCTCAC	3660
TTTGGATCGA	ATGATGTGGC	GTCTTTAAAC	ACCTTTAAAA	TCAATGCCGC	TCGCAGTCCT	3720
TTAAGCACCT	ATGCAAGAGC	GATGATGGGT	GGGGAATTGC	AATTGGCTAA	AGAAGTGTTT	3780
TTGAATTTGG	GCGTGGTTTA	TTTGCACAAT	TTGATTTCCT	ACGCAAGCCA	TTTCGCTTCC	3840
AATTTAGGAA	TGAGGTATAG	TTTCTAA				3867

(2) INFORMATION FOR SEQ ID NO:986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...4455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

GGGGCGGTCT CTTTACGAGG GCAGTTTAAT TTAAGCAATA ATTCTTCTTT AGATTTTCAA

GGCTCTAGCG	CTATCACCTC	TAACACGGCG	TTTAATTTCT	ATGATAACGC	TTTTTCTCAA	120
AGCCCCATCA	CTTTCCATCA	AGCCCTTGAC	ATTAAAGTGC	CCTTGAGTTT	GGGAGGCAAC	180
CTCTTAAACC	CTAACAACAG	TAGCGTGCTG	AATTTAAAAA	ACAGCCAGCT	TGTTTTTAGC	240
GATCAAGGGA	GCTTGAATAT	CGCTAACATT	GATTTACTAA	GCGATCTGAA	TGGTAATAAA	300
AATCGTGTGT	ATAACATCAT	TCAAGCGGAC	ATGAATGGTA	ATTGGTATGA	GCGTATCAAC	360
TTCTTTGGCA	TGCGCATTAA	TGATGGGATT	TATGACGCTA	AAAACCAAAC	TTATAGTTTC	420
ACTAACCCTC	TCAATAACGC	CCTAAAAATC	ACCGAGAGCT	TTAAAAATAA	CCAAC TGAGC	480
GTTACGCTCT	CTCAAATCCC	GGGCATTAAA	AACACGCTCT	ATAACATTGG	CTCTGAAATC	540
TTTAACTACC	AAAAGGTTTA	TAACAACGCT	AATGGCGTGT	ATTCTTATAG	CGATGACGCA	600
CAAGGCGTGT	TTTATCTCAC	GAGCAGCGTG	AAAGGCTATT	ACAACCCCAA	CCAATCCTAT	660
CAAGCCAGCG	GCAGCAATAA	CACCACGAAA	AATAACAATC	TAACCTCTGA	ATCTTCTGTC	720
ATTTTCGCAA	CCTATAACGC	GCAAGGCAAC	CCTATCAGCG	CGTTACACGT	CTATAACAAG	780
GGCTATAATT	TCAGTAATAT	CAAAGCGTTA	GGGCAAATGG	CGCTCAAAC	CTACCCTGAA	840
ATCAAAAAGA	TATTAGGGAA	TGATTTTTTCG	CTTTCAGTT	TGAGCAATTT	AAAAGGCGAT	900
GCGCTAAACC	AGCTTACCAA	GCTCATCACG	CCTAGCGATT	GGAAAAACAT	TAACGAGTTG	960
ATTGATAACG	CAAACAATTC	GGTCGTGCAA	AATTTCAATA	ACGGCACTTT	GATTATAGGA	1020
GCGACTAAAA	TAGGGCAAAC	AGACACCAAT	AGTGCGGTGG	TTTTTGGGGG	CTTGGGCTAT	1080
CAAAAGCCTT	GCGATTACAC	TGATATTGTG	TGCCAAAAAT	TTAGAGGCAC	TTATTTGGGG	1140
CAGCTTTTGG	AGTCCATCTC	GGCTGATTTG	GGCTATATTG	ACACGACTTT	TAACGCTAAA	1200
GAAATTTATC	TTACCGGCAC	TTTAGGGAGC	GGGAACGCAT	GGGGGACTGG	GGGGAGTGCG	1260
AGCGTAACCT	TTAACAGCCA	AACTTCGCTC	ATTCTCAACC	AAGCGAATAT	CGTAAGCTCG	1320
CAAACCGATG	GGATTTTTAG	CATGCTGGGT	CAAGAGGGCA	TCAATAAGGT	TTTCAATCAA	1380
GCCGGGCTCG	CTAATATTTT	GGGCGAAGTG	GCAATGCAAT	CCATTAACAA	AGCCGGGGGA	1440
TTAGGGAATT	TGATAGTAAA	TACGCTAGGG	AGTGATAGCG	TGATTGGGGG	GTATTTAACG	1500
CCTGAGCAAA	AAAATCAAAC	CCTAAGCCAG	CTTTTGGGGC	AGAATAATTT	TGATAACCTC	1560
ATGAACGATA	GCGGTTTGAA	CACGGCGATT	AAGGATTTGA	TCAGACAAAA	ATTAGGCTTT	1620
TGGACCGGGC	TAGTGGGGGG	ATTAGCCGGA	CTGGGGGGCA	TTGATTTGCA	AAACCCTGAA	1680
AAGCTTATAG	GCAGCATGTC	CATCAATGAT	TTATTGAGTA	AAAAGGGGTT	GTTCAATCAG	1740
ATCACC GGCT	TTATTTCCGC	TAACGATATA	GGGCAAGTCA	TAAGCGTGAT	GCTGCAAGAT	1800
ATTGTCAAGC	CGAGCGACGC	TTTAAAAAAC	GATGTAGCCG	CTTTGGGCAA	GCAAATGATT	1860
GGCGAATTTT	TAGGCCAAGA	CACGCTCAAT	TCTTTAGAAA	GCTTGCTGCA	AAACCAGCAG	1920
ATTAAAAGCG	TTTTAGACAA	AGTCTTAGCG	GCTAAAGGAT	TAGGGTCTAT	TTATGAACAA	1980
GGTTTGGGGG	ATTTGATCCC	TAATCTTGGT	AAAAAGGGGA	TTTTCGCTCC	CTATGGCTTG	2040
AGTCAAGTGT	GGCAAAAAGG	GGATTTTAGT	TTCAACGCGC	AAGGCAATGT	TTTTGTGCAA	2100
AATTCCACTT	TCTCTAACGC	TAATGGAGGC	ACGCTCAGTT	TTAACGCAGG	AAATTCGCTC	2160
ATTTTGTCCG	GAAACAACCA	CATCGCTTTC	ACTAACCATT	CTGGAACGCT	CAATTTGTTG	2220
TCTAATCAAG	TTTCTAACAT	TAACGTCACC	ATGCTTAACG	CTAGCAACGG	CCTTAAGATT	2280
AACGCCACTA	ATAACAATGT	TTCCGTGTCT	CAAGGCAATC	TGTTTATCAA	CGCTAGCTGC	2340
GTGCAACAAA	GCGATCCAAC	GACAGCTAGC	GCCACAAACC	CTTGCAACCAC	CGCTCAAAAT	2400
AACGCTTCTT	CTAGTAATGC	GTCAAACAAC	GCGCCAATCG	CCTTAAATAA	TAACGATGAA	2460
AGCTTGGTGG	TTACGGCGAA	TGGFTTCAAT	TTTTTCAGGCA	ATATTTACGC	TAACGGGGTG	2520
GTTGATTTTT	CAAAAATTAA	AGGCTCTGCA	AACGTTAAAA	ACCTGTATCT	TTACAATAAC	2580
GCTCAATTCC	AAGCCAACAA	CCTCACGATT	TCCAACCAAG	CGGTATTAGA	GAAAAACGCT	2640
AGCTTTGTAA	CGAATAACTT	AAACATTCAA	GGAGCGTTTA	ACAACAACGC	CACGCAAAAA	2700
ATAGAGGTGC	TTCAAAATTT	AGTGATCGCT	TCAAACGCTT	CTTTAAGCAC	CGGGATTTAT	2760
GGGTTAGAAG	TAGGGGGGGC	ATTGAATAAT	TTGGGAGCGA	TCCATTTTAA	TTTAGAAAAT	2820
TCTCAAACGC	CTGTAAATCC	GCTCATTCAA	GTAGGGGGGA	TCATTAATCT	CAACACCACC	2880
CAAACGCCTT	TTATGAATGT	CAGCGTGGCT	AATGGCGGAA	CTTACACTTT	ATTAAAAAGC	2940
AGCCGTTATA	TTGATTACAA	TATCAACCCT	AACAGCTTGC	AATCGTATTT	GAAGCTCTAT	3000
ACCTTAATCA	ATATCAACGG	AAACCACATA	GAGGAAAAAA	ACGGCGTATT	GACTTATTTG	3060
GGCCAACGGG	TTTTATTACA	AGATAAGGGG	TTATTATTGA	GTGTAGCACT	ACCTAACTCA	3120
AACAACGCCT	CTCAAAACAA	CATTTTAAGC	CTTCTGTGCC	TTCACAACCA	GATTTAAATG	3180
TCTTATGGTA	ATAAAGTGAT	GGACTTTACC	CCTCCACCT	TACAGGATTA	CATTGTGGGC	3240
ATTC AAGGAC	AAAGCGCACT	CAATCAAATT	GAAGCTGTTG	GGGGGAATAA	CGCTATCAAG	3300
TGGCTTTCAA	CATTGATGAT	GGAGACTAAA	GAAAACCCGC	TTTTTGCGCC	GATTTATTTA	3360
GAAAACCACT	CTTTAAATGA	AATCTTAGGC	GTAACAAAAG	ATCTTCAAAA	CACCGCAAGC	3420
TTGATTTCTA	ACCCTAATTT	TAGAAATAAC	GCTACCAGCC	TTTTAGAAAT	GGCGAGTTAC	3480

ACCCAACAAA	CCAGCCGTTT	GACAAACTC	TCTGATTTTA	GGGCTAGAGA	GGGAGAGTCC	3540
AATTTTTCAG	AGCGCTTGTT	AGAGCTTAAA	AACAAGCGTT	TTAGCGATCC	TAACCCTAGT	3600
GAGGTTTTTG	TCAAATACTC	TCAACTCAGC	AAACACCCCA	ATAACCTTTG	GATTCAAGGG	3660
GTGGGAGGAG	CGAGCTTTAT	TTCTGGGGGC	AATGGCACGC	TTTATGGCTT	GAATGTGGGC	3720
TATGACCGAT	TGGTTAAAAG	CGTGATCCTT	GGGGGTTATG	TGGCTTATGG	CTATAGCGGT	3780
TTTAACGGGA	ACATCATGCA	TTCTTTGGCT	AATAATGTGG	ATGTGGGGAT	GTATGCGAGG	3840
GCTTTTTTGA	AAAGAAACGA	ATTCACCTTG	AGCGCGAATG	AAACTTATGG	AGGCAATGCG	3900
AGTCATATCA	ATTCTTCTAA	TTCCTTGCTC	TCTGTGTTGA	ACCAACGCTA	CAACTACAAC	3960
ACCTGGACAA	CGAGCGTGAA	TGGGAATTAC	GGCTATGATT	TCATGTTCAA	ACAAAAAAGC	4020
GTGGTGCTAA	AACCTCAAGT	GGGCTTGAGC	TATCATTTCA	TAGGCTTGAG	CGGGATGAAA	4080
GGTAAAATGC	AAAATCCAGC	TTACCAACAA	TTCGTCATGC	ATTCAAACCC	TTCTAACGAA	4140
TCGGTTTTAA	CGCTCAACAT	GGGGTTAGAG	AGCCGTAAAT	ATTTTGGTAA	AAATTCCTAT	4200
TATTTTGTAA	CGGCGAGGTT	GGGTAGGGAT	CTTTTGATCA	AAGCTAAAGG	CGACAATGTG	4260
GTGCGTTTTG	TGGGTGAAAA	CACTTTATTG	TACCGCAAGG	GGGAAATTTT	TAACACTTTT	4320
GCGAGCGTGA	TCACAGGAGG	CGAAATGCAT	TTGTGGCGTT	TGATGTATGT	GAATGCGGGG	4380
GTGGGGCTTA	AAATGGGCTT	GCAATACCAA	GATCTTAATA	TCACTGGGAA	TGTGGGCATG	4440
CGAGTGCCGT	TTTAG					4455

(2) INFORMATION FOR SEQ ID NO:987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

ATGAGAAAAA	CGATTTTCAGC	GTTGTTTTTA	TCAGCGTGTA	TAGGGTTATC	GTCTGTTTCAT	60
GCGAGTAACG	CTTTGATTTT	ACAAACAGAT	TTTAGCCTAA	AAGATGGGGC	CGTCTCGGCG	120
ATGAAAGGCG	TCGCTTTCAG	CGTTGATTCT	AATCTTAAAA	TCTTTGATTT	AACGCACGAA	180
ATCCCCCGGT	ATAACATTTG	GGAAGGCGCT	TACCGCTTGT	ATCAGACCGC	TAGTTATTGG	240
CCAAAAGGCT	CGGTATTTGT	GAGCGTAGTG	GATCCGGGCG	TAGGCACTAA	TCGTAAATCG	300
GTGGTATTGA	AAACTAAAAA	CGGCCAGTAT	TTCGTCTCTC	CAGATAACGG	CACGCTGACT	360
TTGGTAGCGC	AAACTTTGGG	GATTGATAGC	GTGCGTGAAA	TTGATGAAAA	AGCCAACCGC	420
TTGAAAGGTT	CTGAAAAATC	CTATACTTTC	CATGGCCGTG	ATGTGTATGC	TTACTACTGGG	480
GCGCGCTTGG	CTTCTGGGGC	GATCACATTC	GAGCAGGTCG	GGCCAGAGCT	TCCTATAAAA	540
GTTGTTGAAA	TTCCTTACCA	AAAAGCGAAA	GCCACAAAAG	GGGGAGTGAA	AGGCAATATC	600
CCGATTTTGG	ATATTCAATA	TGGCAATGTT	TGGAGCAATA	TCAGCGATAA	ACTGCTCAAT	660
CAAGCAGGGA	TCAAACGAAA	CGATACAGTG	TGTGTAACATA	TTTTTAAAAA	TTCCAAGAAA	720
CAATACGAAG	GGAAAATGCC	GTATGTCGCG	AGCTTTGGCG	ATGTGCCAGA	AGGCCAGCCG	780
TTGGTCTATT	TAAACAGCTT	GTTGAATGTT	TCCGTGGCGT	TGAATATGGA	TAATTTTCGCG	840
CAAAAACATC	AAATTAAATC	TGGTGCTGAC	TGGAATATTG	ATATAAAGAA	GTGCGCTAAA	900
TAA						903

(2) INFORMATION FOR SEQ ID NO:988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

```

ATGAAACTTT TTAACCCTCG TTTAATCGTT TTTATATTCG CGCTTCCTTT AGGGGTAGGG      60
TTTTCTGTGC CTTCTTTGCT AGAACTAAA GGCCCTAAAA TCACTTTAGG TTTGGATTTA      120
AGGGGGGGGT TGAACATGCT TTTAGGGGTG CAAACCGATG AGGCTTTAAA AAACAAGTAT      180
TTAAGCCTAG CGTCTGCTTT AGAATACAAC GCTAAAAAGC AAAATATCTT GCTTAAAGAC      240
ATTAAATCCA GTTTAGAGGG GATCAGTTTT GAGCTTTTAG ATGAAGATGA GGCGAAAAAA      300
TTAGACGCGC TTTTATTGGA ATTGCAAGGT CATAGCCAGT TTGAAATCAA AAAAGAAGCG      360
GAGTTTTATA GCGTGAAACT CACCCCTTTA GAGCAAGAGG AATTGCGTAA AAACACGATC      420
TTGCAAGTGA TAGGGATCAT TCGTAACCGC TTGGATCAAT TTGGTTTGGC AGAGCCTGTA      480
GTCATTCAGC AAGGCCGAGA AGAAATTTTC GTGCAATTGC CCGGCATTAA GACTTTAGAA      540
GAAGAGCGGC GCGCTAAAGA CTTGATTTCT AAATCCGCTC ATTTGCAGAT GATGGCAGTG      600
GATGAAGAAC ACAATAAAGA TGCATGAAT ATGACGGATT TAGAGGCTCA AAAATTAGGC      660
AGCGTGTTGT TGTCTGATGC GGAAATGGGG GGTAAATCTT TACTCAAAGC GATCCCTATT      720
TTAGATGGCG AAATGCTTAC AGATGCGAAA GTGGTGTATG ATCAAATAA CCAGCCGGTG      780
GTGAGCTTCA CGCTAGATGC GCAAGGGGCT AAGATTTTTC GGGATTTTTC AGGCGCGAAT      840
GTGGGCAAAC GCATGGCGAT CGTTTATAGC AATAAGGTCT ATTCAGCCCC GGTGATTAGG      900
GAACGCATTG GTGGGGGGAG CGGGCAGATT AACGGGAATT TTAGCGTGGC TCAAGCGAGC      960
GATTTAGCGA TCGCTTTAAG GAGTGGGGCG ATGAACGCGC CCATTCAGGT TTTAGAAAAA     1020
AGGATTGTAG GTCCGAGTTT AGGGAAGAC AGCATTAAAA CTTCCATTAT CGCTCTAGTT     1080
GGAGGCTTTA TTTTAGTGAT GGGCTTTATG GCACTTTATT ACTCCATGGC TGGGGTGATC     1140
GCTTGCATGG CGTTAGTGGT CAATCTTTTT TTGATCGTGG CGGTCATGGC GATTTTTGGA     1200
GCGACGCTGA CTTTACCGGG AATGGCAGGG ATTGTTTTAA CCGTGGGGAT TGCCGTGGAT     1260
GCTAATATCA TTATCAACGA ACGCATTAGA GAAGTTTTAA GAGAAGGAGA GGGTGTTGTT     1320
AAGGCATCC ATTTAGGCTA TATCAATGCG AGCCGGGCGA TTTTGGACTC CAATATCACT     1380
TCCTTGATCG CTTCCGTGTT GCTATACGCT TATGGCACAG GAGCGATTAA AGGCTTTGCC     1440
CTCACCACAG GCATTGGGAT TTTAGCCTCT ATCATCACCG CTATTATAGG CACGCAAGGG     1500
ATTTATCAAG CCCTTTTACC TAAATTAGCC CAAACGAAAA GCCTTTACTT TTGGTTTGGC     1560
GTGAAAAATA AAAGAGCTTA G

```

(2) INFORMATION FOR SEQ ID NO:989:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2382 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

ATAATGAATG	GTTATTTGAG	GGTAAAAACC	CCGTATTTT	TAGCGTCGGT	CGTTTTGACT	60
TTTTGGACTT	TTAATTCCTT	TATGAGCGCG	AAAGATAAGC	ACCATTTTTT	AAAAAAGTT	120
ACAACCACCG	AGCAAAAATT	CAGTTCTAGT	GCCCCAATTT	CATGGCAAAG	CGAAGAGGTG	180
CGTAATTCCA	CAAGCTCTCG	CACGGTGATT	TCCAACAAAG	AACTCAAAAA	AACGGGGAAT	240
TTGAATATTG	AAAACGCCTT	GCAAAATGTG	CCAGGGATTC	AAATCAGAGA	CGCTACAGGC	300
ACGGGCGTGC	TGCCTAAAAT	TTCGGTGCGC	GGTTTGGTG	GGGGCGGTAA	CGGGCATAGC	360
AACACCAACA	TGATTTTAGT	CAATGGTATC	CCCATTTATG	GCGCGCCGTA	TTCCAATATT	420
GAAGTGGCGA	TTTTCCCTGT	AACTTTCCAG	TCAGTGGATA	GGATTGATGT	GATTAAGGGG	480
GGAACGAGCG	TCCAATACGG	CCCTAACACT	TTTGGAGGCG	TGGTGAATGT	CATCACTAAA	540
GAAATCCCCA	AAGAGTGGGA	AAATCAAGCG	GCTGAAAGGA	TCACTTTTTG	GGGGCGCTCC	600
TCTAATGGGA	ATTTTGTCTG	TCCCAAAGAA	AAAGGCAAGC	CCTTAGCCCA	AACTTTAGGA	660
AACCAAATGC	TGTTTAACAC	TTATGGGCGA	ACGGCTGGGA	TGTTGGGTAA	ATATATAGGC	720
ATTAGCGCTC	AAGGCAATTG	GATTAATGGG	CAAGGTTTCA	GGCAAATAG	CCCTACAAAG	780
GTGCAAAACT	ACTTGTTGGA	TGCGATTAT	AAGATCAATG	CGACCAATAC	TTTTAAAGCT	840
TATTACCACT	ATTATCAATA	CAACTCTTAC	CATCCAGGCA	CTTTGAGCGC	GCAAGATTAC	900
GCCTATAACC	GCTTCATCAA	TGAGCGCCCT	GACAATCAAG	ATGGAGGGCG	AGCCAAGCGC	960
TTTGGGATCG	TGTATCAAAA	CTACTTTGGC	GATCCGGATA	GGAAAGTGGG	GGGCGATTTT	1020
AAATTCACCT	ATTTACGCA	TGACATGAGT	AGGGATTTTG	GGTTTCCAA	CCAATACCAA	1080
AGCGTGTATA	TGAGCGGTCA	AAATAAGATT	TTACCCTTTA	AAGGCAAGGG	AGAAATCAGC	1140
GCAAAAAACC	CTAATTGCGG	TCTGTATTCT	TATAGCGACA	CGAATAGCCC	TTGCTGGCAA	1200
TTTTTTGACA	ATATCCGCCG	ATCCGTGGTG	AATGCCTTTG	AGCCAAAAC	CAATCTTATC	1260
GTCAATACTG	GTAAAGTCAA	ACAACTTTT	AACATGGGAA	TGCGCTTTT	AACTGAAGAT	1320
TTATACCGCC	GATCCACCAC	CAGGAAAAAC	CCTAGCATGC	CTAATAATGG	GAGTGGGTTT	1380
GATGCAGGAA	CTTCACTCAA	TAATTTCAAC	AATTATACCG	CTGTGTATGC	CAGCGATGAA	1440
ATCAATTTCA	ATAACGGCAT	GCTAACGATC	ACGCCGGGCT	TGAGATACAC	TTTTTTAAAT	1500
TACGAAAAAA	AAGACGCTCC	TCCCTTTAAG	GTGGGTCAA	CCCCAAAAAC	CACGAAAGAG	1560
CGTTATAACC	AATGGAATCC	GGCAGTCAAT	GTCGGCTATA	AACCCATTAA	AGAATTATTG	1620
TTTTATTTC	ATTACCAAAG	AAGCTACATT	CCGCCCAAT	TCAGCAATAT	CGGTAATTTT	1680
GTAGGCACAA	GCACGGATTA	TTTTCAAATC	TTTAATGTCA	TGGAAGGCGG	CTCAAGATAT	1740
TATTTTAACC	ATCAAGTGAG	TTTTAACCGG	AACATTTTGT	TGATTTTTCG	GAATCATTAT	1800
TTTACCGGGC	GCTATGGGGA	CAACAGAGAG	CCGGTCAATG	CGAGATCGCA	AGGCGTGGAG	1860
CTGGAACCT	ACTACACGCC	TATTAGGGGG	CTTAATTTCC	ATGCGGCTTA	CACTTTTATA	1920
GACGCTAATA	TCACAAGCCA	CACGATGGTT	ACTAACCTTG	CTAATCCTAA	AGGGCCTAAA	1980
AAAGATATTT	TTGGCAAAAA	GCTCCCTTTT	GTCAGCCCGC	ACCAATTCAT	TTTAGACGCG	2040
AGTTACACTT	ACGCTAAAAC	CACGATTGGG	TTAAGCTCTT	TCTTTTATAG	CCGCGCTTAT	2100
AGCGATGTGT	TAAACACCGT	GCCTTTTACA	GAATACGCGC	CCACGATTAA	AAATGGGGCT	2160
ATCGTTACCA	AAACAGCGGG	CATGACGCCG	TACTATTGGG	TGTGGAATTT	GCAAAATTTCT	2220
ACCACTTTGT	GGGAACGCAA	AAATCAAAGC	GTGAATGCGA	GCTTGCAAAT	CAATAACATT	2280
TTTAACATGA	AATATTGGTT	TAGCGGGATA	GGCACTAGCC	CTAACGGGAA	AGAAGCTGCG	2340

CCTCCCAGGA GCATCACAGC GTATGTGAGT TATAATTTTT AA

2382

(2) INFORMATION FOR SEQ ID NO:990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1002 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

ATGCTAATCG CTCGCTTTAA AAAAGCTTTA ATTCCTATT CTTTAGGGGT TCTTCTTGTT	60
TCATCGTTAT TAGGCGTGGC TAACGCTTCT AATCAAGAGA TCCAAGTCAA GGATTATTTT	120
GGGGAGCAAA CCATAAAGCT TCCTGTTTCT AAAATAATCT ACTTGGGCAG CTTTGCAGAA	180
GTGCCTGCCA TGTTCAATAC TTGGGATAGG GTCGTGGGCA TTTCGGATTA CGCTTTTAAA	240
TCTGATATTG TTAAAGCCAC TCTCAAAGAT CCTGAACGCA TTAAACCCAT GAGCAGTGAT	300
CATGTGGCGG CGTTGAATGT GGAATTATTA AAAAAGCTTA GCCCTGATCT TGTGGTAACC	360
TTTGTGGGTA ACCCTAAAGC GGTAGAGCAT GCGAAAAAAT TTGGGATTTC ATTCCTTTCT	420
TTCCAAGAAA AAACCATTGT AGAGGTCATG GAAGATATTG ACGCTCAAGC TAAGGCCTTA	480
GAAGTTGACG CTTCTAAAAA ATTGGCTAAA ATGCAAGAAA CTTTGGATTT TATCAAAGAG	540
CGTTTGAAAA ATGTCAAAAA GAAAAAGGGG GTGGAGCTTT TCCATAAAGC CAATAAAATC	600
AGCGGCCATC AAGCCCTTGA TTCAGATATT TTAGAAAAAG GGGGCATAGA CAATTTTGGC	660
TTGAAATACG TCAAGTTTGG GCGCGCTGAC ATTAGTGTGG AAAAAATCGT TAAAGAAAAC	720
CCTGAGATTA TTTTATTATTG GTGGATAAGC CCGCTTAGCC CTGAAGACGT GTTGAACAAC	780
CCTAAATTTT CCACTATCAA AGCCATTAAA AACAAGCAAG TCTATAAGCT CCCCACAATG	840
GATATTGGCG GACCTAGAGC CCCACTCATT AGTCTTTTTA TCGCTTTAAA AGCCCACCCCT	900
GAAGCGTTTA AGGGCGTGGA TATTAATGCG ATAATCAAAG ATTACTATAA AGTGGTCCTT	960
GATTTGAATG ACGCGGAAGT TGAACCCTTT TTGTGGCACT GA	1002

(2) INFORMATION FOR SEQ ID NO:991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

900

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

```
ATGTATAAAT TAGGAATATT TTTATTAGCC ACCTTACTAT CAGCTAACAC GCAAAAAGTG      60
AGCGATATTG CTAAAGACAT CCAACATAAA GAAACCCTTT TGAAAAAAAC CCATGAAGAA      120
AAAAACCAAC TGAACAGTCG TTTGAGTTCT TTAGGCGAAG CGATCCGCTC TAAAGAGCTT      180
CAAAAGGTTG AGATTGAACG CCAAATGGTC GCCTTAAAAA AGAGTCTTGA AAAAAATCGT      240
AACGAAAGTT TGGTGCAAGA AAAAGTCCTA ACCAACTACC GCAAGTCTTT AGATCATTGT      300
CAAAAACAAC GATCGTTTTT ACAAAGAGA GTGTTTGATA CGCTTTTAGA GGATTTTCTT      360
TTCTCACAAG CCCTAAAGGG GCAGAATTTA GCCTCTTCTA ATGATGTGAT TTTGCAAGTG      420
GCGTTTGAAA ACTTGCACCA AAGCACCCTG TCTAAAATGT CGCAACTGAG CCAAGAAGAA      480
AAGAAGCTCA ATGTGCAAGC TTTAGAAGTC AAAAGCAGCA TTCAAAAAAT CTCCTCTGTC      540
ATAGATGAGC AAAAACTCG TGAATCAACC TTAATATCCT TGCAAACCGA ACAAATAAG      600
CTCATTTTGA GCATGCAAAA AGATTATGCG ATCTATAACC AACGGCTATC CCTTTTAGAA      660
AAAGAACGCC AGAATTTAAA CGCTCTTTTA AAACGCTTGA ATATCATCAA ACAAATAGG      720
GAAAATGAAG AGAGGGTCAG TTTGAAAAAA TCTTCTCAAG CTTTAGAAGT CAAACAAGTG      780
GCTAGCTCTT ATCAAAATAT CAACACCACG AGCTATAACG GGCCAAAAAC GATCGCTCCC      840
TTGAACGATT ACGAAGTGGT GCAAAAATTT GGCCCTATA TTGACCCGGT TTATAATTTA      900
AAAATTTTGA GCGAGTCTAT CACGCTAGTG TCAAAAACCC CAAACGCTTT GGTGCGTAAT      960
GTTTTAGACG GGAAAATCGT GTTCGCTAAA GAAATCAACA TGCTTAAAAA AGTCGTTATC     1020
ATTGAGCATA AAAACGGGAT CCGCACGATT TATTCTCAAT TGGATAAAAT CGCCCCCACC     1080
ATTAAAAGCG GCATGCGGAT CCAAAAAGGC TATGTTTTAG GACGCATTGA TCAACGCTTG     1140
GGCTTTGAAG TTACCATGAG AGAAAAGCAC ATTAACCCCT TAGAACTCAT CGCGCGCAAT     1200
TAA                                     1203
```

(2) INFORMATION FOR SEQ ID NO:992:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1650 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

```
ATGGATAAAA ACAACAATAA TAATCTCCGC TTGATTTTAG CGATCGCTCT GTCTTTCTTG      60
TTTATCGCTC TTTATAGCTA TTTTTCCTAA GAACCAACA AAACAACAAC CGAAACCACA      120
AAGCAAGAAA CAACCAACAA CCACACAGCA ACAAGCCCCA CCGCGTCCAA TACCATCACC      180
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CAAGATTTTA	GCGTTACCCA	AACCATCCCT	CAAGAGAGTT	TGTTAAGCAC	GATTTCTTTT	240
GAACATGCCA	AAATTGAAAT	TGATTCTTTA	GGGCGCATCA	AACAGGTTTA	TCTCAAAGAT	300
AAAAAGTATC	TAACCCCTAA	AGAAAAGGGC	TTTTTAGAGC	ATGTGAGCCA	TCTTTTTTAGC	360
TCCAAAGAAA	ACTCGCAACC	CTCCCTAAAA	GAGCTCCCCC	TTTTAGCAGC	CGATAAACTC	420
AAGCCTTTAG	AAGTGCGTTT	TTTAGACCCC	ACGCTCAATA	ATAAAGCGTT	CAACACCCCT	480
TATAGCGCCT	CAAAAACCAC	CCTTGGGCCT	AACGAACAGC	TCGTTTTAAC	CCAAGATTTA	540
GGCACTCTTA	GCATCATTAA	AACCCTGACT	TTTTATGATG	ATTTGCATTA	TGATTTAAAA	600
ATCGCATTCA	AATCGCCCAA	TAACCTTATC	CCTAGCTATG	TGATCACCAA	TGGTTACAGG	660
CCGGTGGCTG	ATTTAGACAG	CTACACCTTT	TCAGGCGTGC	TTTTAGAAAA	CACCGACAAA	720
AAAATTGAAA	AAATTGAAGA	TAAAGACGCT	AAAGAAATCA	AACGCTTTTC	TAACACCCTC	780
TTTTTATCCA	GCGTGGATAG	GTATTTCACT	ACTTTGCTTT	TCACTAAAGA	TCCTCAAGGT	840
TTTGAAGCCT	TAATTGATTG	AGAAATAGGG	ACTAAAAACC	CCTTAGGGTT	CATTTCCCTT	900
AAAAACGAAG	CGAATTTGCA	TGGCTATATT	GGCCCTAAAG	ATTACCGCTC	TTTGAAAGCG	960
ATTTACCCCA	TGCTCACTGA	TGTGATAGAG	TATGGCTTGA	TCACTTTCTT	TGCCAAAGGC	1020
GTGTTTGTTT	TACTGGATTA	TTTGTATCAA	TTTGTGGGCA	ATTGGGGTTG	GGCTATCATT	1080
CTTTTAACGA	TTATCGTGCG	CATTATCCTC	TACCCCTTAA	GCTATAAGGG	CATGGTGAGC	1140
ATGCAAAAGC	TCAAAGAATT	AGCCCCTAAA	ATGAAAGAAC	TCCAAGAAAA	ATACAAGGGC	1200
GAACCCCAAA	AGTTACAAGC	CCACATGATG	CAGCTTTACA	AAAAACATGG	GGCTAACCCG	1260
CTAGGGGGTT	GTTTGCCCTT	AATCTTACAA	ATCCCAGTAT	TTTTTGCGAT	TTATAGAGTG	1320
CTTTATAACG	CTGTGGAATT	GAAAAGCTCA	GAGTGGGTTT	TATGGATCCA	TGATTTATCC	1380
ATCATGGATC	CGTATTTTAT	TTTACCGCTT	CTTATGGGAG	CGTCTATGTA	TTGGCACCAG	1440
AGCGTTACGC	CAAACACCAT	GACCGATCCC	ATGCAAGCAA	AGATTTTTAA	ACTCTTGCCC	1500
CTATTATTCA	CGATCTTTCT	AATCACTTTC	CCTGCAGGGT	TAGTCTTGTA	TTGGACCACA	1560
CACAACATCC	TTTCGGTGTT	GCAGCAACTC	ATCATTAATA	AAGTCTTAGA	GAATAAAAAA	1620
CGCGCGCAGC	CTCAAAACAT	AAAGGAATAA				1650

(2) INFORMATION FOR SEQ ID NO:993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

ATGAAAAAAT	CCCTTTGTTT	GTCTTTCTTT	CTGACCTTCT	CTAACCCCTCT	TCAAGCCCTT	60
GTCATTGAGC	TTTTAGAAGA	GATTAAAACT	TCGCCGCATA	AAGGCACTTT	TAAGGCTAAA	120
GTCCTTGATT	CTAAAGAACC	AAGACAAGTT	TTAGGCGTTT	ATAATATCTC	CCCACACAAA	180
AAACTCACGC	TCATATCAC	TCACATATCC	ACGGCAATCG	TCTATCAACC	CCTTGATGAA	240
AAACTTTCTT	TAGAAACGAC	CTTAAGCCCT	AACCGCCCTA	CTATCCCTAG	AAACACCCAA	300
ATCGTTTTTT	CTTCAAAAGA	ATTGAAAGAA	CCGCACTCAA	ACCCAATACC	TTCTTTAAAC	360
GCGCCCATGC	AAAAACCACA	AAATAAACCC	AGCTCATCGC	AACAATCTCC	TCAAAACTTT	420
TCTTACCCAG	AGTCCAAACT	AGGCTCTAAA	AACTCTAAAA	ACAGCCTTTT	ACAGCCTTTA	480

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GTAAGTCTTA GCAAAGTAAG CCCACTAAC GAAGTTAAAA CGCCAACAAA CGACGCTAAT 540
CCCCCTTTAA AGCATTCTTC ACAAGATCAA GAAAACAACC TCTTTGTAGC GCCACCCACT 600
GAAAAAACGC TCCCTAACAA CACCTCTAGT GCTGATGCGA GTGAAAACAA TGAAAGCAAC 660
GAAAATAGGG ATAATGTGGA AAAACAAGCG ATTAGAGATC CTAATATCAA AGAATTGCGA 720
TGCGGGAAGT GGGTTTATGA TGATGAAAAT TTACAAGCCT ATCGCCCAAG CATTTTAAAA 780
CGCGTTGATA AAGACAAAGA GATTACAACA GACATTACCC CTTGCGATTA CAGCACCGCT 840
GAAAATAAAA GCGGTAAAAT CATTACCCCC TATACTAAAA TCTCTGTTCA TAAAACAGAG 900
CCTTTAGAAG ACCCTCAAAC TTTTGAAGCT AAAAATAATT TCGCCATTCT CCAAGCCAGA 960
AGCTCTACAG AAAAGTGTA AAGGGCTAGA GCGAGAAAAG ACGGCACGAC CAGGCAATGC 1020
TATCTGATAG AAGAGCCTTT AAAACAAGCG TGGGAGAGCG AGTATGAAAT CACCACGCAA 1080
TTAGTGAAAG CCATATATGA ACGCCCCAAA CAAGACGATC AAGTAGAGCC GACTTTTTAT 1140
GAAACCAGCG AATTGGCTTA TTCTCCACA CGAAAAAGCG AAATAACGCG TAATGAATTG 1200
AATTTGAATG AAAAATTCAT GGAATTTGTG GAAGTGTATG AGGGGCATTA TTTAAACGAT 1260
ATAATCAAAG AGAGCAGCGA ATACAAAGAA TGGGTAAAA ACCATGTGCG CTTTAAAGAA 1320
GGGGTGTGCA TGGCCTTAGA AATAGAAGAG CAACCACGAG CCAAAAGCAC GCCTTTGAGT 1380
ATTGAAAACCT CTCGTGTTGT GTGTGTCAA AAGGGGAATT ATTTATTCAA TGAAGTTTAA 1440

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(2) INFORMATION FOR SEQ ID NO:994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

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GTGAAAGTTT ATCCGCAAGT TTTAAGCATT GCTGGTAGCG ATAGCGGTGG GGGCGCTGGG 60
ATACAGGCCG ATTTGAAAGC GTTTCAAACT TTTGGCGTGT TTGGGACAAG CGTGATCACT 120
TGCATCACCG CTCAAACAC ACAGGGCGTG CATGGGGTGT ATCCATTGAG TGTAGAGAGC 180
GTGAAAGCGC AAATCCTAGC TATTAGAGAT GATTTTTCGA TCAAGGCGTT CAAAATGGGG 240
GCGTTATGCA ACGCTCAAAT CATTGAATGC GTAGCGAACG CTTTAGAAAC TTGTGATTTT 300
GGGTGTGCG TTTTAGATCC GGTGATGGTG GCAAAGAATG GGGCTTTGCT TTTAGAAGAG 360
GAGGCGATTT TAAGCTTAAA AAAACGCCTT TTACCTAAAA CCAATTTACT AACCCTAAC 420
CTCCCTGAAG TCTATGCGCT CACAGGCGTT CAAGCGCGAG ACGATAAAG CGCTTCAAAA 480
GCGATGGGTG TTTTAAGGGA TTTAGGCGTT AAAAACGCTG TGATTAAAGG GGGGCATACA 540
GAACATTTTC AAGGGGAATT TAGCAACGAT TGGGTGTTTT TAGAAGACGC TGAATTTATC 600
TTAAGCGCCA AGCGATTCAA CACCAAAAAC ACGCATGGCA CGGGTTGTAC TTTGTCTAGC 660
TTGATTGTGG GCTTACTCGC TCAAGGGCTG GATTTAAAAA ACGCTATCAC AAAGGCTAAA 720
GAGCTTTTAA CTATCATCAT TCAAAACCCC TTAAACATTG GGCATGGGCA TGGGCCTTTG 780
AATTTGTGGA GCATCAAAA GCATGTTTGA 810

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(2) INFORMATION FOR SEQ ID NO:995:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1197 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1197
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

TTGGGGGCTA	TCATGGATAC	TTTTTTAACA	AGTATCTTGG	TCCTGCTTAT	GCGGGGACTT	60
CTCAATCAGC	GAGCTATCAT	GCAAGGCCTT	ATGTGGTGGA	TACCGCTTTT	TTACGATACG	120
ATTACCAAAG	ATGTTTTTGG	GTTTAAGGCG	GGGCGCTATG	AAGCGAATAT	TGATTTTCATG	180
AGCGGTTCGA	ATCAAGGGTG	GGAAGTGTAT	TATCAGCCCT	ATAAGACTGA	GACGCAAAGG	240
TTAAGGTTTT	GGTGGTGGAG	TTCTTTTGGG	AGAGGTTTGG	CGTTTAACTC	TTGGATTTAT	300
GAGTTTTTTG	CGACCGTGCC	TTATTTGAAA	AAGGGAGGCA	ACCCTAGTAA	CAGCAACGAT	360
TTCATCAATT	ATGGCTGGCA	TGGGATCACC	ACGACTTATT	CTTATAAAGG	TTTAGACGCT	420
CAATTTTTTT	ATTATTTTGC	ACCTAAAACT	TATAACGCTC	CCGGTTTTAA	GCTAGTCTAT	480
GACACGAATA	GGAATTTTGA	AAACGTAGGC	TTTCGCTCTC	AAAGCATGAT	CATGACGACC	540
TTCCCTTTAT	ATTATAGGGG	GTGGTATAAC	CCAGAGACAA	ACACTTATAG	CTTAGAAGAC	600
AGCACGCCTC	ATGGCTCTTT	GTTAGGGAGG	AATGGCGTTA	CTTTAAATAT	CCGCCAGGTT	660
TTTTGGTGGG	ATAATTTCAA	CTGGTCCATT	GGCTTTTATA	ACACCTTTGG	CAATTCAGAC	720
GCTTTTTTTAG	GCTCTCACAC	CATGCCAAGG	GGGAATAACA	CTTCCTATAT	CAGTAATGAA	780
ATCTCAGTAA	CGACTAGGCA	TGCCGGAATG	ATCGGCTATG	ATTTTTGGGA	TAATACGGCT	840
TATGATGGGC	TGGCTGATGC	GATCACTAAC	GCGAACACTT	TCACTTTTTA	CACTTCGGTT	900
GGAGGGATCC	ATAAGCGTTT	TGCATGGCAT	GTTTTTGGGC	GCGTCTCTCA	TGCGAATAAA	960
AATGCGTTAG	GGCAAGTGGG	GAGGGCTAAT	GAATATTCTT	TGCAATTCAA	TGCGAGCTAT	1020
GCGTTCACTG	AATCGGTTCT	CCTTAACTTT	AGGATCACTT	ATTATGGGGC	TAGGATCAAT	1080
AAAGGGTATC	AAGCAGGGTA	TTTTGGAGCG	CCCAAATTCA	ATAACCCGGA	TGGCGATTTT	1140
AGCGCTAATT	ACCAAGACAG	AAGTTACATG	ATGACCAACC	TCACGCTGAA	GTTTTTGA	1197

(2) INFORMATION FOR SEQ ID NO:996:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1335 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:

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TTGAGTAACG CTTTCTCCCA ATACCTTTAT TCGCTTTTAG GGGCGTATCC CACGAAACTC      60
AATGGTAACG ACGTGTCTGC GAACGCTCTT TTAAGTGGTG CGGTAGGCAG TGGGACTTGC      120
GCGGCTGCAG GGACGGCTGG TGGCACAACCT CTTAACACTC AAAGCGCTTG CACCGCTGCG      180
GGCTATTACT GGCTCCCTAG CTTGACTGAT AGGATTTTAA GCACGATCGG CAGCCAGACT      240
AACTACGGCA CGAACACCAA TTTCCCCAAC ATGCAACAAC AGCTCACCTA CTTGAATGCG      300
GGGAATGTGT TTTTAAATGC GATGAATAAG GCTTTAGAGA AGAATGGGAC TGCTACTGCT      360
AATAGCACTA GTAGCACTAG CGGTGCGACT GGTTGAGATG GTCAAACTTA CTCTCAACAA      420
GCTATTCAAT ACCTTCAAGG CCAACAAAAT ATCTTAAATA ACGCAGCGAA CTTGCTCAAG      480
CAAGATGAAT TGCTCCTAGA AGCTTTCAAC TCTGCCGTAG CTGCTAACAT TGGGAATAAG      540
GAATTCAATT CAGCCGCTTT TACAGGTTTG GTGCAAGGCA TTATTGATCA ATCTCAATTG      600
GTTTATAACG AGCTCACTAA AAACACCATT AGCGGGAGCG CGGTTAATAA CGCTGGGATA      660
AACTCCAACC AAGCTAACGC TGTGCAAGGG CGTGCTAGTC AGCTCCCTAA CGCTCTTTAT      720
AACGTGCAAG TAACTTTGGA TAAAATCAAC GCGCTCAACA ATCAGGTGAG AAGCATGCCT      780
TACTTGCCCC AATTCAGAGC CGGGAACAGC CGTGCAACGA ATATTTTAAA CGGGTTTTAC      840
ACTAAAGTGG GCTATAAGCA ATTCTTCGGG AAGAAAAGGA ATATCGGTTT GCGCTATTAT      900
GGTTTCTTTT CTTATAACGG AGCGAGCGTG GGCTTTAGAT CCACTCAAAA TAATGTAGGG      960
TTATACACTT ATGGGGTGGG GACTGATGTG TTGTATAACA TCTTTAGCCG CTCCTATCAA      1020
AACCGCTCTG TGGATATGGG CTTTTTTTAGC GGTATCCAAT TAGCCGGTGA GACCTTCCAA      1080
TCCACGCTCA GAGATGACCC CAATGTGAAA TTGCATGGGA AAATCAATAA CACGCACTTC      1140
CAGTTCCTCT TTGACTTCGG TATGAGAATG AACTTCGGTA AGTTGGACGG GAAATCCAAC      1200
CGCCACAACC AGCACACGGT GGAATTTGGC GTAGTAGTGC CTACGATTTA TAACACTTAT      1260
TACAAATCAG CAGGGACTAC CGTGAAGTAT TTCCGTCCTT ATAGCGTTTA TTGGTCTTAT      1320
GGGTATTCAT TCTAA                                     1335

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(2) INFORMATION FOR SEQ ID NO:997:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

```

ATGGAGTTAA TTAAGAAATT GGAAAAAGAA AGCGAAGTTT TAAAGAAAGA TTTACAACAA      60
CATTCAAACG AGCTTTTTTAA AATGTTGATT ATTGATAATG AAGATTTGTT TAAAGAGCAA      120

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TTTGAGATTA	TGTTTAAAGC	ATGGGTTGAA	ATCGTAAAAA	TGATGTTTGA	ATTAACCAAA	180
AAAACCAAAAT	TTGATGGCGA	AATGATTGGC	TACACAGAAG	AACTTTTAAC	CTTTTTAGTT	240
AGAGATTTTTT	TTAATGGGAT	TTTTAAATCC	AAAGTAATAC	CTAAAATGCC	TATTTTTTGC	300
GGTGATGTTA	AATGCGAAGA	TTTTAATGCC	CTAAGAAGTT	TAGTTTATCT	TTCTGTGCTT	360
GAGTTGGAAG	AAACGATAAA	TCCTAATAAA	ATCCCATTTT	AA		402

(2) INFORMATION FOR SEQ ID NO:998:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2091 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

ATGAAAATCA	AAAAATCCCT	CTTTGCTCTC	TCTTTCTCTC	TCATGGCTTC	ATTATCAAGG	60
GCTGAAGATG	ACGGATTTTA	CATGAGTGTG	GGCTATCAAA	TCGGTGAAGC	GGTCCAAAAA	120
GTGAAAAACA	CTGGAGCATT	ACAAAATCTT	GCAGACAGAT	ACGATAACTT	GAGCAACCTT	180
TTAAACCAAT	ACAATTACTT	AAATTCCCTA	GTCAATCTAG	CCAGCACGCC	TAGCGCGATT	240
ACCGGTGCGA	TTGACAATCT	AAGCTCAAGC	GCGATCAATC	TACTAGCGC	TACCACCACT	300
TCTCCGGCCT	ATCAAGCTGT	GGCTTTAGCG	CTCAATGCGG	CTGTGGGCAT	GTGGCAAGTC	360
ATAGCCTTTG	GCATCAGCTG	TGGCCCTGGC	CCCAATCTTG	GCCCAGAACA	TTTAGAAAAT	420
GGGGGCGTTC	GATCGTTTGA	CAACACGCCA	AACTACAGCT	ACAACACCGG	TAGCGGAACG	480
ACCACCACCA	CTTGTAATGG	AGCCAGTAAT	GTAGGGCCCCA	ATGGTATCCT	ATCTAGCAGC	540
GAATACCAGG	TTCTCAATAC	CGCTTATCAA	ACTATCCAAA	CCGCTTTAAA	CCAAAACCAA	600
GGAGGCGGGA	TGCCTGCCTT	GAATAGCTCC	AAAAATATGG	TAGTCAATAT	CAATCAAACCT	660
TTACAAAAA	ACCCTACCAC	AGAATACACT	TACCCCGATG	GGAATGGCAA	TTATTATTCA	720
GGCGGTTCAT	CAATCCCAAT	CCAGCTAAAG	ATTAGTAGCG	TCAATGACGC	TGAAAACCTT	780
TTGCAACAAG	CCGCTACTAT	CATCAATGTC	CTTACCACCC	AAAACCCGCA	TGTGAATGGT	840
GGCGGTGGGG	CATGGGGGTT	TGGCGGTAAG	ACCGGGAATG	TGATGGATAT	TTTTGGCGAT	900
AGTTTTTAACG	CTATTAACGA	AATGATCAAA	AACGCTCAAG	CCGTTTTAGA	AAAAACCCAA	960
CAGCTTAACG	CTAATGAAAA	CACCCAAATC	ACGCAACCAG	ACAATTTCAA	CCCCTACACT	1020
TCTAAAGACA	CGCAGTTCGC	TCAAGAAATG	CTCAATAGAG	CTAACGCTCA	AGCAGAGATT	1080
TTGAGCTTAG	CCCAACAAGT	AGCGGACAAT	TTCCACAGCA	TTCAAGGGCC	TATCCAACAA	1140
GATCTAGAAG	AATGCACCGC	AGGATCAGCT	GGTGTGATTA	ACGACAACAC	TTATGGTTCA	1200
GGTTGCGCGT	TTGTGAAAGA	GACTCTCAAT	TCCTTAGAGC	AACACACCGC	TTATTATGGC	1260
AACCAGGTCA	ATCAGGATAG	GGCTTTGTCT	CAAACCATTT	TGAATTTTAA	AGAAGCCCTT	1320
AGCACTTTAG	GGAACGACTC	AAAAGCGATC	AATAGCGGTA	TCTCTAACTT	GCCTAACGCT	1380
AAGTCCCTTC	AAAACATGAC	GCATGCCACT	CAAAACCCTA	ATTCCCCAGA	AGGTTTGCTC	1440
ACTTATTCTT	TGGATACCAG	CAAATACAAC	CAGCTCCAAA	CTGTTGCGCA	AGAATTAGGC	1500
AAAAACCCCT	TTAGGCGCAT	CGGCGTGATT	AACTATCAAA	ACAATAACGG	GGCGATGAAC	1560
GGCATCGGCG	TGCAAGCGGG	CTATAAGCAA	TTCTTTGGCA	AAAAAAGGAA	TTGGGGGTTA	1620
AGGTATTATG	GTTTCTTTGA	TTATAACCAT	GCTTATATCA	AATCTAATTT	TTTTAACTCG	1680

GCTTCTGATG	TGTGGACTTA	TGGGGTGGGT	ATGGACGCGC	TTTATAACTT	CATCAACGAT	1740
AAAAACACCA	ACTTTTTAGG	CAAAAATAAC	AAGCTTTCTG	TGGGGCTTTT	TGGTGGCTTT	1800
GCGTTAGCCG	GGACTTCGTG	GCTTAATTCC	CAACAAGTGA	ATTGACCAT	GATGAATGGC	1860
ATTTATAACG	CTAATGTCAG	CGCTTCTAAC	TTCCAATTTT	TGTTTGATTT	AGGCTTGAGA	1920
ATGAACCTCG	CTAGGCCCAA	GAAAAAAGAC	AGCGATCATG	CCGCTCAGCA	TGGCATGGAA	1980
TTGGGCGTGA	AAATCCCCAC	CATTAAACAG	GATTATTATT	CTTTCATGGG	GGCTGAACTC	2040
AAATACAGAA	GGCTCTATAG	CGTGTATCTC	AATTATGTGT	TGCTTACTA	G	2091

(2) INFORMATION FOR SEQ ID NO:999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

ATGCAATTC	AAAAACCTT	ATCTTCCTTA	TCTTTATTTT	TATCTTTATC	TTTATTCTTA	60
TCTTTTAGTA	TCGCTGAAGA	AAATGGGGCG	TATGCGAGCG	TGGGTTTTGA	ATATTCCATC	120
AGTCATGCCG	TTGAACACAA	TAACCCTTTT	TTGAATCAAG	AACGCATCCA	AACGATTTCT	180
AACGCTCAAA	ACAAAATCTA	TAAACTCAAT	CAAGTCAAAA	ATGAAATCAC	AAACATGCCC	240
AACACCTTTA	ACTACATCAA	CAACGCTTTA	AAAAACAATG	CTAAATTAAC	CCCTACTGAA	300
AAGCAAGCCG	AAACCTACTA	CCTGCAATCT	ACCCCTCAAA	ACATTGAAAA	AATAGTCATG	360
CTTAGCGGGG	GCGTTGCGTC	TAACCCATAA	TTAGCCCAAG	CGTTAGAAAA	AATGCAAGAA	420
CCCATTACTA	ACCCTTTAGA	ATTGGTAGAA	AACTTAAAAA	ATTTAGAATT	ACAATTCAGC	480
CAATCTCAAA	ACAGCATGCT	TTCTTCTTTG	TCTTCTCAGA	TCGCTCAAAT	TTCAAATTCT	540
TTGAACGCGC	TTGATCCCAG	CTCTTATTCT	AAAAACGTTT	CAAGCATGTA	TGGGGTAGGT	600
TTGAGCGTAG	GGTATAAGCA	TTTCTTTACC	AAGAAAAAAA	ATCAAGGGTT	TCGTTATTAC	660
TTATTCTATG	ACTATGGTTA	CACTAATTTT	GGTTTGTGG	GTAATGGCTT	TGATGGTTTA	720
GGCAAAATGA	ATAACCACCT	CTATGGGCTT	GGCATAGATT	ATCTTTTCAA	TTTCATTGAT	780
AATGCGCAAA	AACATTCGAG	CGTGGGGTTT	TATGTAGGCT	TTGCTTTAGC	GGGGAGTTCG	840
TGGGTAGGGA	GTGGTTTAGG	CATGTGGGTG	AGTCAAATGG	ATTTCATCAA	CAACTATTTG	900
ACGGATTATC	GGGCTAAAAT	GCACACGAGT	TTTTTCCAAA	TCCCTTTGAA	TTTTGGGGTT	960
CGTGTGAATG	TGGATAGGCA	CAATGGCTTT	GAAATGGGCT	TAAAGATCCC	TTTAGCGGTC	1020
AATTCCTTTT	ATGAAACGCA	TGGCAAAGGG	TTAAACGCTT	CCCTCTTTTT	CAAACGCCTT	1080
GTCATGTTTA	ACGTGAGTTA	TGTTTATAGT	TTTTAG			1116

(2) INFORMATION FOR SEQ ID NO:1000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

ATGGCTAAAA	TCACAACCGT	GATTGACATA	GGCTCTAATT	CAGTGCCTTT	GGCTGTCTTT	60
AAAAAGACGA	GCCAGTTTGG	GTTTTACTTG	CTTTTTGAGA	CTAAGTCCAA	GGTTAGGATT	120
TCAGAGGGCT	GTTATGCGTT	TAAAGGGGTT	TTACAAGAAA	TCCCCATGCA	ACGAGCCGTT	180
AAAGCCTTGA	GCGAATTTAA	AGAAATCGCC	CTCAAATACA	AAAGCAAAAA	AATCCTGTGC	240
GTGGCGACCT	CAGCGGTGCG	CGATGCCCCCT	AATCGGTTAG	AGTTTGTAGC	GAGGGTGAAA	300
AAGGCTTGCG	GTTTGCAAAT	CAAAATCATT	GATGGGCAAA	AAGAAGCGCT	CTATGGTGGG	360
ATCGCGTGCG	CGAATTTGCT	GCATAAAAAAT	TCAGGGATCA	CGATAGACAT	TGGAGGGGGT	420
AGCACCGAGT	GCGCGTTGAT	TGAGAAAGGT	AAGATTAAAG	ACTTAATCTC	GCTTGATGTC	480
GGGACGATTC	GCATTAAAGA	AATGTTTCTA	GACAAAGACT	TAGATGTCAA	ATTGGCTAAA	540
GCCTTTATCC	AAAAAGAGGT	CTCTAAACTG	CCTTTTAAGC	ATAAAAACGC	CTTTGGGGTG	600
GGGGGGACGA	TCAGAGCCTT	GAGTAAGGTG	CTGATGAAAC	GCTTTGATTA	CCCTATAGAT	660
TCTTTGCATG	GCTATGAAAT	AGATGCGCAT	AAAAATTTAG	CGTTCATTGA	AAAAATCGTC	720
ATGCTCAAAG	AAGACAAATT	ACGGCTTTTA	GGGGTGAATG	AAGAGCGTTT	GGATAGCATT	780
AGGAGCGGGG	CGTTGATTTT	ATCAGTCGTG	TTAGAGCATT	TGAAAACCTC	CTTGATGATC	840
ACTAGCGGGG	TAGGGGTGAG	AGAGGGCGTG	TTTTTGAGCG	ATTTATTGCG	CCACCATTAC	900
CATAAATTCC	CCCCCAATAT	CAACCCCTCT	CTCATCTCTC	TAAAAGATCG	CTTTTTACCC	960
CATGAAAAGC	ACAGCCAAAA	GGTCAAAAAA	GAATGCGTGA	AATTGTTTGA	AGTTTTATCG	1020
CCTTTGCATA	AAATAGATGA	AAAATACCTT	TTCCATTTAA	AGATTGCGGG	GGAATTGGCG	1080
AGCATGGGTA	AGATTTTAAG	TGTATATTTA	GCCCACAAGC	ACAGCGCGTA	TTTCATTTTA	1140
AACGCTTTGA	GTTACGGCTT	TAGCCACCAG	GATAGGGCGA	TCATTTGCTT	ATTGGCGCAA	1200
TTTAGCCATA	AAAAAATCCC	TAAAGACAAC	GCTATCGCCC	ACATGAGTGC	GATGATGCCA	1260
AGCCTTTTGA	CCTTGCACTG	GCTGAGTTTT	ATCCTTTCTT	TAGCCGAAAA	TTTGTGCCTG	1320
ACAGACAGCC	ATCATTTAAA	ATACACGCTA	GAAAAAACA	AGCTTGTGAT	CCATTCTAAT	1380
GATGCGCTTT	ACTTGGCTAA	AGAAATGCTC	CCCAAACCTCA	TTAAGCCCAT	TCCTTTGACG	1440
ATAGAGTTTG	CTTGA					1455

(2) INFORMATION FOR SEQ ID NO:1001:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 762 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

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AAACAGGTTA AATCTCGCAT GAAAGAAAAG CCGTTCAATA GCGAGCAGAT GGCTTTTTTTA    60
GAAGAGCTTT TAAGCCACCA AGAAAAGCAT TTAGAGAGCA AGCTTCTGCG TTTTTCGGTG    120
AATGATTTGG ACATGCAAAG CGTGTTCGG CTAGAAAGGA ACCGCTTGAA AATCGCTTAC    180
AGGCTTTTAG GTTTGATGAG CTTTATCGCG CTTGTCTTAG CGATCGTTTT AATCAGTATC    240
CTGCCCTTAC AAAAAACCGA ACACCATTTC GTGGATTTT TAAACCAGGA CAAGCATTAC    300
GCCATTATCC AAAGAGCGGA TAAAAGCATT TCCAGTAATG AAGCGTTGGC TCGTTCGCTC    360
ATTGGGGCGT ATGTGTTAAA CCGAGAGAGC ATTAATCGCA TTGACGATAA ATCCCGCTAT    420
GAACTGGTGC GCTTGCAAAG CAGCTCTAAA GTGTGGCAAC GCTTTGAAGA TTTGATTAAA    480
GCCCAAACA GCATCTATGT GCAAAGCCAT TTAGAAAGAG AAGTCCATAT CGTCAATATT    540
GCGATCTATC AGCAAGACAA TAACCCCAT GCGAGCGTGT CCATTGCGGC TAAACTTTTG    600
AATGAAAACA AGCTCGTGTA TGAAAAGCGT TATAAAATCG TATTGAGCTA TTTGTTTGAC    660
ACCCCGGATT TTGATTACGC TTCCATGCCT AAAAACCCCTA CCGGCTTTAA AATCACTCGC    720
TACAGCATCA CTGAAATCGC GCCGACTAAT AGGAATGATT GA                    762

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(2) INFORMATION FOR SEQ ID NO:1002:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1440 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

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ATGAAAAAAT CCCTTTGTTT GTCTTCTTT CTGACCTTCT CTAACCTCT TCAAGCCCTT    60
GTCATTGAGC TTTTAGAAGA GATTAAACT TCGCCGCATA AAGGCACTTT TAAGGCTAAA    120
GTCCTTGATT CTAAAGAACC AAGACAAGTT TTAGGCGTTT ATAATATCTC CCCACACAAA    180
AAACTCACGC TCACTATCAC TCACATATCC ACGGCAATCG TCTATCAACC CCTTGATGAA    240
AAACTTTCTT TAGAAACGAC CTTAAGCCCT AACCGCCCTA CTATCCCTAG AAACACCCAA    300
ATCGTTTTTT CTTCAAAGA ATTGAAAGAA CCGCACTCAA ACCCAATACC TTCTTTAAAC    360
GCGCCCATGC AAAAACCACA AAATAAACCC AGCTCATCGC AACAATCTCC TCAAAACTTT    420
TCTTACCCAG AGTCCAAACT AGGCTCTAAA AACTCTAAAA ACAGCCTTTT ACAGCCTTTA    480
GTAACCTCCTA GCAAAGTAAG CCCCACTAAC GAAGTTAAAA CGCCAACAAA CGACGCTAAT    540
CCCCCTTTAA AGCATTCTTC ACAAGATCAA GAAAACAACC TCTTTGTAGC GCCACCCACT    600
GAAAAACGC TCCCTAACAA CACCTCTAGT GCTGATGCGA GTGAAACAA TGAAAGCAAC    660

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GAAAATAGGG	ATAATGTGGA	AAAACAAGCG	ATTAGAGATC	CTAATATCAA	AGAATTCGCA	720
TGCGGGAAGT	GGGTTTATGA	TGATGAAAAT	TTACAAGCCT	ATCGCCCAAG	CATTTTAAAA	780
CGCGTTGATA	AAGACAAAGA	GATTACAACA	GACATTACCC	CTTGCGATTA	CAGCACCGCT	840
GAAAATAAAA	GCGGTAAAT	CATTACCCCC	TATACTAAAA	TCTCTGTTCA	TAAAACAGAG	900
CCTTTAGAAG	ACCCTCAAAC	TTTTGAAGCT	AAAAATAATT	TCGCCATTCT	CCAAGCCAGA	960
AGCTCTACAG	AAAAGTGTA	AAGGGCTAGA	GCGAGAAAAG	ACGGCACGAC	CAGGCAATGC	1020
TATCTGATAG	AAGAGCCTTT	AAAACAAGCG	TGGGAGAGCG	AGTATGAAAT	CACCACGCAA	1080
TTAGTGAAAG	CCATATATGA	ACGCCCCAAA	CAAGACGATC	AAGTAGAGCC	GACTTTTTTAT	1140
GAAACCAGCG	AATTGGCTTA	TTCTTCCACA	CGAAAAAGCG	AAATAACGCG	TAATGAATTG	1200
AATTTGAATG	AAAAATTCAT	GGAATTTGTG	GAAGTGATG	AGGGGCATTA	TTTAAACGAT	1260
ATAATCAAAG	AGAGCAGCGA	ATACAAAGAA	TGGGTAAAA	ACCATGTGCG	CTTTAAAGAA	1320
GGGGTGTGCA	TGGCCTTAGA	AATAGAAGAG	CAACCACGAG	CCAAAAGCAC	GCCTTTGAGT	1380
ATTGAAACT	CTCGTGTGT	GTGTGTCAA	AAGGGGAATT	ATTTATTCAA	TGAAGTTTAA	1440

(2) INFORMATION FOR SEQ ID NO:1003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1704 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

ATGATTTTTG	GGGATTTTAA	ATATCAAAAA	AGCGTTAAAA	AACTCACAGC	CACTAACCTT	60
AACGAGCTTA	AAAACGCCCT	GGATTTTATC	TCTCAAAATA	GGGGGAAGGG	GTATTTTGTG	120
GGGTATCTTT	TGTATGAAGC	GCGCTTAGCG	TTTTTAGATG	AAAATTTTCA	AAGCCAAACC	180
CCTTTTTTGT	ATTTTGAACA	ATTTTGTAGAA	AGAAAAAAT	ACCCTTTAGA	GCCTTTAAAA	240
GAGCATGCGT	TTTACCCTAA	AATCCACAGC	TCTTTAGATC	AAAAAACTTA	TTTCAAGCAG	300
TTTAAGGCCG	TTAAAGAGCA	TCTCAAAAAC	GGCGATACCT	ATCAAGTGAA	TTTGACAATG	360
GATTTATTGT	TAAACACTAA	AGCCAAACCA	AAGCGCGTTT	TTAAGGAAGT	GATACACAAC	420
CAAAACACGC	CTTTTAAGGC	TTTTATAGAA	AATGAGTTTG	GGAGCGTTTT	AAGCTTTTCG	480
CCGGAATTGT	TTTTTGAATT	AGAGTTTTTA	GACACAGCGA	TTAAGATTAT	CACAAAACCC	540
ATGAAAGGCA	CGATCGCTCG	CTCAAACAAC	CCCTTGATAG	ATGAAAAAAA	CCGATTGTTT	600
TTGCAAAATG	ATGACAAAAA	TAGAAGCGAA	AATGTGATGA	TCGTGGATTT	ATTGCGTAAC	660
GATTTGAGCC	GCTTGGCCTT	AAAAAATAGC	GTGAAAGTCA	ATCAATTGTT	TGAAATCATC	720
AGTTTGCCGA	GCGTGTATCA	AATGATAAGC	GAGATTGAAG	CTCAATTGCC	CCTAAAAACA	780
AGCTTGTTTG	AGATTTTTAA	GGCGTTGTTC	CCTTGCGGCT	CTGTGACCGG	ATGCCCTAAA	840
ATCAAAACCA	TGCAAATCAT	TGAAAGTTTA	GAAAAACGCC	CTAGGGGGGT	GTATTGTGGG	900
GCGATAGGCA	TGGTTGGAGG	AAAAAAGGCC	CTTTTGTAGC	TGCCTATCCG	CACTTTAGAA	960
AAAAGAGCGC	ATGAAGATTT	TTTGCATTTA	GGGGTAGGGA	GTGGGGTAAC	TTATAAAAGT	1020
AAAGCTTCAA	AGGAATATGA	AGAGAGCTTT	TTAAATCCT	TTTTTGTGAT	GCCCCAAATA	1080
GAATTTGAGA	TCGTGGAAAC	GATGAGAGTT	ATCAAAAGGG	ATCAAAAATT	AGAGATTAAC	1140
AATAAAAACG	CCCATAAAGA	ACGCTTAATG	CATAGCGCCC	AATATTTTAA	CTTTAAATAC	1200

GATGAAAATC	TTTTAGACTT	TGAATTAGAA	AAAGAAGGGG	TTTAAAGGGT	TTTACTCAAT	1260
AAAAGGGGCA	AGCTCATTAA	AGAATACAGA	ACCTTAGAGC	CTTTAAAAAG	CCTAGAAAATC	1320
CGTTTGAGTG	AAGCCCCCAT	TGACAAACAC	GATGATTTTT	TATACCATAA	GACCGCTTAT	1380
GCCCCTTTTT	ATCAAAACGC	TCGAGCGCTC	ATTAAAAAAG	GCGTTATTTT	TGATGAAAATC	1440
TTTTATAACC	AGGATTTGGA	ACTCACTGAG	GGCGCTAGGA	GTAATCTTAT	TTTAGAAAATC	1500
CACAACAGGC	TTTAAACCCC	TTATTTTCAGC	GTGGGCGCAT	TAACCGGGAC	GGGCGTTGTG	1560
GGGTTGTAA	AAAAAGGTCT	TGTTGAGCAT	GCCCCTTTAA	AATTACAAGA	CTTGCAAAGA	1620
GCGGCTAAAA	TCTATTGTAT	TAACGCGCTA	TACGGCTTAG	TGGAGGTGGG	AATAATAGGT	1680
TACCCAATGG	AGCAAAAAAG	TTAA				1704

(2) INFORMATION FOR SEQ ID NO:1004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

ATGAAAATCA	GTGTTAGTAA	AAACGATTTA	GAAAACACTT	TGCGCTACTT	GCAAGCTTTT	60
TTGGATAAAA	AGGACGCTTC	CTCTATCGCT	TCACACATCC	ATTTAGAAGT	CATTAAAGAA	120
AAGCTCTTTT	TAAAAGCCAG	CGATTTCAGAT	ATTGGACTAA	AAAGCTATAT	TTCTACGCAA	180
TCTACCGATA	AAGAGGGCGT	AGGCACGATC	AACGGGAAGA	AGTTTTTAGA	TATTATCTCA	240
TGTTTGAAAG	ACTCTAATAT	TGTTTTAGAG	ACTAAAGATG	ACAGCTTGGT	GATCAAACAA	300
AATAAAAGCT	CTTTCAAACT	CCCCATGTTT	GACGCTGATG	AGTTCCCTGA	ATTCCCTGTT	360
ATTGATCCAA	AAGTGAGTTT	AGAAATCAAT	GCCCCCTTTT	TGGTGGATGC	GTTTAAAAAG	420
ATCGCTCCTG	TGATTGAGCA	AACTAGCCAT	AAAAGGGAAT	TAGCCGGTGT	TTTAATGCAA	480
TTCAATCAAA	AACACCAAAC	CCTTTCAGTG	GTAGGCACGG	ATACCAAGCG	GCTCTCTTAC	540
ACGCAGTTAG	AAAAAATCTC	TATCCATTCC	ACCGAAGAAG	ACATCTCTTG	CATTTTGCCCT	600
AAAAGGGCTT	TATTGGAAAT	CCTTAAACTT	TTTTATGAAA	ATTTTCAGTTT	TAAAAGCGAC	660
GGCATGTTAG	CGGTGGTTGA	AAACGAAACG	CACGCTTTTT	TCACCAAGCT	CATTGATGGG	720
AATTACCCTG	ATTATCAAAA	AATCCTCCCT	AAAGAATACA	CTTCTTCTTT	CACTTTAGGC	780
AAGGAAGAAT	TTAAAGAGGG	CATTAAGTTG	TGCAGTTCTT	TAAGCTCCAC	CATTAAGCTC	840
ACTTTAGAAA	AAAACAACGC	TTTGTTTGAA	TCTTTGGATT	CTGAGCATAG	CGAAACCGCC	900
AAAACCTCTG	TTGAGATTGA	AAAAGGTTTG	GATATTGAAA	AAGCCTTTCA	TTTGGGCGTG	960
AACGCAAAAT	TTTTCCTTGA	AGCCTTAAAC	GCTTTAGGGA	CAACGCAATT	TGTTTTAAAA	1020
TGCAATGAGC	CTTCTTCGCC	TTTTTTGATT	CAAGAACCTC	TTGATGAAAA	GCAAAGCCAC	1080
TTGAACGCTA	AAATTTCAC	TTTGATGATG	CCAATCACAC	TATAA		1125

(2) INFORMATION FOR SEQ ID NO:1005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 base pairs

911

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

ATGGTTGTTT	TAGGAAGCAC	CGGCTCTATC	GGGAAAAACG	CCCTTAAAAT	CGCAAAAAAA	60
TTTGGTGTA	AAATAGAAGC	CTTAAGCTGT	GGGAAAAATA	TCGCTTTAAT	CAATGAACAA	120
ATCAAAGTTT	TCAAACCCAA	AAAAGTAGCG	ATCTTAGATC	CTAACGATTT	GAATAATTTA	180
GAGCCTTTGG	GCGCGGAAGT	GTTTGTGGGG	TTAGACGGCA	TTGATGCGAT	GATAGAGGAG	240
TGCGTTTCCA	ATTTAGTCAT	TAACGCCATT	GTGGGCGTAG	CCGGATTGAA	AGCGAGCTTT	300
AAAAGCTTAC	AAAGGAACAA	AAAAC TAGCC	CTAGCGAATA	AAGAAAGTTT	AGTGAGCGCG	360
GGGCATTTAT	TAGACATTC	ACAAATCACG	CCCGTTGATA	GCGAGCATTT	TGGTTTGTGG	420
GCGTTGTTGC	AAAACAAGAC	TTTAAAGCCT	AAATCTTTAA	TCATTAGCGC	GAGTGGGGGG	480
GCTTTTAGGG	ACACGCCCTT	AGATCTTATC	GCTATTCAAA	ATGCGCAAAA	CGCGCTCAAG	540
CACCCTAATT	GGAGCATGGG	GGATAAAATC	ACCATTGATT	CAGCGAGCAT	GGTCAATAAA	600
CTTTTGTAAA	TTT TAGAAAC	CTATTGGCTT	TTTGGTGCGT	CTTTAAAGAT	TGACGCGCTG	660
ATTGAAAGAA	GTTCTATCGT	GCATGCTTTG	GTGGAGTTTG	AAGACAAC TC	TGTCATTGCG	720
CATTTAGCGA	GTGCGGACAT	GCAATTACCC	ATAAGCTATG	CCATTAACCC	TAAATTAGCT	780
TCTTTGAGTG	CTTCATTAA	ACCCTTAGAT	TTATACGCTT	TAAGCGCGAT	TAAATTCGAA	840
CCCATTAGCG	TGGAGCGCTA	CAC TTTGTGG	CGTTATAAAG	ATTTGTTGTT	GGAAAACCCA	900
AAGCTTGGCG	TGGTGCTGAA	TGCGAGCAAT	GAAGTGGCGA	TGAAGAAGTT	CTTGAATCAA	960
GAAATCGCTT	TTGGTGGCTT	TATCCAAATC	ATCTCTCAAG	CTTTAGAATT	GTATGCTAAA	1020
AAATCTTTCA	AGCTCTCTAG	TTTAGATGAA	GTGCTAGCGT	TAGATAAGGA	AGTTAGGGAG	1080
CGTTTGTGAA	GTGTAGCGAG	AGTGTAG				1107

(2) INFORMATION FOR SEQ ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1254 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

ATGAAATATT	TATGGCTTTT	TTTAATATAC	GCTATAGGGC	TTTTTGCAAC	AGATAAAACG	60
CTAGATATTA	TTAAAACCAT	TCAAAAACCT	CCTAAGATTG	AAGTGCCTA	CTCCATAGAT	120
AACGATGCCA	ATTACGCTTT	AAAATTGCAT	GAAGTCTTAG	CGAACGATTT	AAAGACTAGC	180
CAGCATTTTG	ATGTTTCTCA	AAACAAAGAG	CAAGGTGCTA	TCAATTACGC	AGAAGCTCAAG	240
GATAAAAAAG	TCCATCTTGT	AGCGCTTGTG	AGCGTGCGG	TAGAAAACGG	CAATAAAATT	300
TCACGATTAA	AACTTTATGA	TGTGGATACA	GGAACGCTCA	AAAAGACTTT	TGACTACCCC	360
ATTGTAAGTT	TAGATCTATA	CCCTTTTGCA	GCGCACAACA	TGGCCATTGT	GGTGAATGAT	420
TATTTAAAAG	CCCCTTCTAT	CGCTTGATG	AAGCGCCTGA	TTGTTTTTTC	TAAATACATT	480
GGACCAGGAA	TCACAAACAT	CGCACTAGCG	GATTATACGA	TGCGTTATCA	AAAAGAAATC	540
ATCAAAAACA	ACCGACTCAA	TATTTTCCCC	AAATGGGCGA	ACGCTGAGCA	AACGGAGTTT	600
TATTACACGC	AGTATGGCGA	AAAAACGCCC	ATGATTTTAA	AATACAACAT	TCAAAAAGCC	660
ACTCATGAGA	ATATCGCTAG	CTCTCAAGGA	ATGGCTGTGG	TCTCTAGCGT	GAGTTCTGAT	720
GGCTCTAAAA	TTTAAATGTC	TTTAGCCCCCT	GATGGCCAAC	CGGATGTTTA	TTTGTATGAC	780
ACGCATAAAA	AACTAAAAAC	CAAAATAACG	CGCTATCCGG	GGATAGATGT	TTCAGGCGTG	840
TTTTTAGAAG	ATGACAAGTC	TATGGCTTTT	GTTTCAGATA	GATCCGGTTA	TCCTAACATC	900
TATATGAAGA	AATTGGGGTT	AAAAGAGAGC	GCGGAGCAAC	TCCTTTATGA	AGGAAGAAGC	960
AATGAATCCA	TTGACGCCTA	TAAGGATAGT	ATCGTGTATG	TGAGCCGAGA	AAACCTTAAT	1020
GAATTGGCA	AAACGGTGTT	TAATTTGAAT	TTGATCGCTC	TAAACAGCAA	GTATATCCGC	1080
AGGCTTACCG	TGAATGGCTC	TAACCAGATG	CCTAGGTTTT	CTATGGATGG	GAGAAATATC	1140
ATGTATATCA	AAAAGACATC	TCAAGAATAC	GCCATGGGGC	TTATTTTGCT	AGACTATAAT	1200
CAGAGTTTTT	TATTCCTTT	AAAGAATGTG	AAAATACAAG	CCTTTGATTG	GTAA	1254

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

GTGAATAAAA	AGCACCGCTT	GGCTTTTTTA	GGGCTAATTG	TTGGGGTTCT	ATTCTTCTTT	60
AGCGCGTGCC	AACACCGCCT	GCACATGGGG	TATTATTAG	AAGTTACAGG	GGATTATTTG	120
TTCAATTATA	ATTCCACTAT	CGTGGTGGCT	TATGACAGAA	GCGATGCGAT	GACTTCTTAT	180
TATATCAATG	TGATTGTTTA	TGAATTGCAA	AAATTAGGCT	TTTATAATGT	CTTCACGCAA	240
GCGGAATTCC	CGCTAGATAA	AGCAAAAAAT	GTGATCTATG	TGCGTATTGT	CCGTAATATC	300
TCGGCTGTGC	CGTTTTATCA	ATACAATTAC	CAACTGATCG	ATCAAGTCAA	TAAGCCTTGT	360
TATTTTCTTG	GGGGGCAGTT	TTATTGCTCC	CAAACCCCTA	CGGATTACTA	CGCTATCAAT	420

GGCTTTAGCG	AGCAAATTTT	GATGAGCGCT	AATTCGCATT	TTATTTTGA	TTGGTATGAT	480
GTGGTGCTGC	AAAAACGGT	TTTATATGTG	GATGGGAGCG	TGAGCGGGAG	GACTTGTGGC	540
TATCAGATGC	TTTATAGAGA	TTTGATTAAA	AGCACGATCA	AACGCATTGA	TTTAAACCGC	600
CCTGAACGCT	ACTACTACAA	TTTAAGACTG	CCCCTTTATC	AGCCATGTTA	TAGGCAATGA	660

(2) INFORMATION FOR SEQ ID NO:1008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

ATGCAATATA	AGAAAAATAA	GAAAAGATAT	TATCATTTAG	CGTTAGGGAT	CCTTTTTTGT	60
AATGGTCTGT	CTTTGAAAGC	TTTAGAAATT	GCCGTCAAAC	CCTTTGGCTA	TCTGGGGCTA	120
TTGTATAATC	AAGGGACGCA	AAAAAACCTT	CACAGCTATG	TGGGGGCTTT	AGCGCGTCTT	180
GGGGTGGATT	TTTCTTATAG	CAATGGGTGG	TCGTTTGGTA	TTGGGGCTAT	TGGGGCTTGG	240
AATATTTATA	ACAAACAGCG	TTTGGCTAAC	CTTTACATCA	GTCTAGGGAA	TTTTTTTGGT	300
AACCCTAACA	ACGTTAAGCC	TTATTTGAGC	GCCGGCGATG	TTTCTGATGC	GTATCTTCAA	360
TACGCTAACC	AGCGTTTAA	AATCGCTTTA	GGGCGTTTTA	ATACCGATTT	TGTGGATTTT	420
GATTGGATAG	GGGGCAATAT	TCAAGGGGTC	TCTGTGGCTT	TCAAGCAAAA	TTCCATGCGT	480
TATTTTGGGA	TTTTTATGGA	TAGCATGCTT	TATAATGGGC	ATCAAATCAA	TAAAGAGCAA	540
GGGAATCGGA	TCGCCACTTC	CCTAAACGCT	CTAGCGTCTT	ATGATCCTGT	GTCTAAACGC	600
TTGTATGTAG	GGGGGGAAGT	GTTTGTTTTG	GGCGCAGAA	ACAAAAATAA	AAATTTGATA	660
TTCGTTCCTT	TTATTTTAAC	GGACACCCGC	TTGCCTTTGC	CCACCCAAAA	TGTTTTAGTG	720
CAAGTGGGGG	GTAAGTTGGA	GTATGACGCT	TCTTTAGCTA	AGGGTTTCAC	TTCGCGCACT	780
CTAGTGCATG	GCATGTATCA	ATACGGCAAC	ACCGATATTA	CTACAAGCGC	TAAAAATGCC	840
GGCTTGTTTT	TGATCGATCA	AACTTTCAA	TATAAAATTT	TTAATTTTGG	AACGGGTTTT	900
TATATCGTTC	CGGCAAGGAA	CAATAAGGGC	TATCTATGGA	CTTTTAATGA	CAGGACTAAA	960
TTCTATGGCC	GTGGGATCAA	CGCGCCCGGC	GTACCAGCGA	TTTATTTTGC	TAACCTCCAGC	1020
ATTTACAGGCT	ATGTTTTTTT	AGGGCTTAAG	ACTAAAAGGG	TGCGTTTAGA	TGCGATGGTG	1080
GCTTTTGGGG	ATTATCAAGA	ATATTCTTTG	ATGAGCAGTT	TTAGGGTTTG	GACTTATAGG	1140
GATTTGTCTT	TTGATATGGG	TGGGGGGTAT	GTGTATGCTT	ATAATTCTAA	AGCCACGAGA	1200
AAAAGCCTTG	GAGATAGCTC	TTTTGTCTTT	TTTGGAAGT	TTTTGTTTTA	A	1251

(2) INFORMATION FOR SEQ ID NO:1009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

ATGGTGAAAA	ACACCAAAGG	CATTCAACAG	CTTTCAGAGA	ATTATGAAAA	GTTGAACAAT	60
CTTTTAAATA	ATTACAACAC	CCTAAACACT	CTTGTAAGC	TGTCCTCCGA	TCCGAGTGCT	120
GTCAACGACG	CAAGGGATAA	TCTAGGCTCA	AGCACTAGGA	ATTTGCTAGA	TGTCAAAGCC	180
AATTCCCCCG	CCTATCAAGC	GGTGCTTTTA	GCATTGAACG	CTGCAGTGGG	CTTGTGGCAA	240
GTTACAAGCT	ATGCCCTTAC	CGCTTGTGGT	CCTGGTAGCA	ATGAGAACGC	GAATGGAGGT	300
ATCCAAACCT	TTAATAATGT	GCCAGGACAA	AACACGACGA	CCATCACTTG	TAATTCGTAT	360
TATGAGCCAG	GACATGGCGG	GCCAATATCC	ACTAAAAATT	ATGCGATCAT	CAACAAGGCT	420
TATCAAATCA	TTCAAAAGGC	TTTGACAGCC	AATGGAGAAG	GGATCCCAGT	TTTAAGCAAC	480
ACCACTACAA	AACCTGATTT	CACTATCAAT	GGAGACAAAA	GAACGGGTGG	CGAACCAAAT	540
AAAAAATTAG	TATACCCATG	GAGTCATGGG	AAAGCTATTT	CAACCTCGTG	GAATGCAACC	600
ATAACAGCAC	CAACAACAGA	AAATATCAAT	ACAACCAATA	GCGCTCAAGA	GCTTTTAAAA	660
CAAGCGAGCA	TCATTATCAC	TACCCTGAAT	AGTGCATGCC	CAAACCTCCA	AAATGGTGGT	720
AGCGGTTATT	GGGCAGGGAT	AAGTGGCAAT	GGGACAATGT	GTGGGATGTT	TAAGAATGAA	780
ATCAGCGCTA	TCCAAGGCAT	GATCGCTAAC	GCGCAAGAAG	CTGTGCGCGA	AGCCAAAATC	840
GTTAGTGAAA	ACACGCAAAA	TCAAAACAGC	CTAGACGCTG	GAAAACCATT	CAACCCCTAC	900
ACAGACGCTA	GTTTTGCTGA	AAGCATGCTC	AAAAACGCGC	AAGCCCAAGC	GGAGATTTTA	960
AACCAAGCCG	AACAAGTGGT	GAAAAACTTT	GAAAAAATCC	CTACAGCCTT	TGTAAATGAC	1020
TCTTTAGGGG	TGTGTTATGA	AGTGCAAGGA	GGTGAGCGTC	GTGGCACCAA	TCCGGGTCAG	1080
ACGACTTCTA	ACACTTGGGG	GGCAGGCTGT	GCGTATGTAG	GACAAACGAT	AACAAATCTT	1140
AAAAACAGCA	TCGCCCATT	TGGCACTCAA	GAGCAGCAGA	TACAGCAAGC	CGAAAACATC	1200
GCTGACACTC	TGGTGAATTT	CAAATCTAGA	TACAGCGAAT	TGGGCAACAC	TTATAACAGC	1260
ATCACCCTG	CGCTCTCTAA	TATCCCTAAC	GCGCAAAGCT	TGCAAAATGC	GGTGAGTAAA	1320
AAGAATAACC	CCTATAGCCC	GCAAGGCATA	GACACCAATT	ACTACCTCAA	TCAAAACTCT	1380
TACAACCAAA	TCCAAACCAT	CAACCAAGAA	CTCGGGCGTA	ACCCCTTTAG	GAAAGTGGGG	1440
ATTGTTAGTT	CTCAAACCAA	TAATGGCGCG	ATGAATGGGA	TCGGTATTCA	GGTGGGTTAC	1500
AAACAATTCT	TTGGCCAAAA	AAGAAAATGG	GGCGCTAGGT	ATTACGGCTT	TTTTGATTAC	1560
AACCATGCGT	TCATTAAATC	CAGCTTCTTC	AACTCGGCTT	CTGACGTGTG	GACTTATGGC	1620
TTTGGAGCGG	ACGCTCTTTA	TAATTTTCATC	AACGATAAAG	CCACCAATTT	CTTAGGCAAA	1680
AACAACAAGC	TTTCTGTGGG	GCTTTTTTGGG	GGTATTGCAT	TAGCCGGGAC	TTCATGGCTT	1740
AATTCTGAGT	ATGTGAATTT	AGCCACCATG	AATAACGTCT	ATAACGCTAA	AATGAACGTG	1800
GCGAATTTCC	AATTCTTATT	CAACATGGGA	GTGAGGATGA	ATTTAGCCAG	GCCTAAGAAA	1860
AAAGACAGCG	ATCATGCGGC	TCAGCATGGG	ATTGAGTTAG	GGCTTAAAT	CCCCACCATC	1920
AACACGAACT	ACTACTCCTT	TATGGGGGCT	GAACTCAAAT	ACCGAAGGCT	CTATAGCGTG	1980
TATTTGAATT	ACGTGTTTCG	TTACTAA				2007

(2) INFORMATION FOR SEQ ID NO:1010:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1029 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

TTGACTAAAA	AATTCATGTC	TTGGATGGTG	GTTATCGGGG	CTTTAATTTG	CGTGCTTTTA	60
GGGGTGTTTA	TCTTCTTCAC	TAGCATGTCG	GTTAAAAAAT	CTTTAACCGC	TTATCTTAAC	120
GCTTATTTAG	AGCAACGCCC	AAATATCGAG	GGCATGGGGA	TTATAGGAGT	TCCTTTTAAA	180
TGCGAAGGGT	TTTTTAAAT	CGCATGCGTT	TCTAAAGAAC	TTCGTTTTTT	AGATCCTCAA	240
AACTCCCCTA	TTATGGATTT	TAAAAATTTA	AAGATCAAGC	TCCATTCTTT	AGATAAAAGC	300
TCTCTTACCC	TTTCTATCCA	TTCTCAAATC	CAATCCCCTA	TTTTAGAACA	ATCCATTTCAG	360
CAAAAAATCA	GCCAAATCCC	CTTAAAAAAC	TTGAATGCCT	TATTGGAAAA	ATTCAAACCC	420
ACGCGCTTGA	ATTGCTCTTT	AACATTCAAC	GCTTTAGATG	AAAAAACCTT	AAACGATAAT	480
TTAAAAATGCG	ATTTGACTAA	TGCAGAGAAT	ATCCTTGCTT	ACACTTTTTT	TCAAGAAGGT	540
TTAATGGAGG	CGCAAGAAAA	TCTCTCCCTT	AAAAATATTT	TTAAACCTT	GAGTTCTAAA	600
GACGCTAAAG	CCATAGAAGA	GTTGCAAGAC	AAACTGCGTT	TTTTAGCGCC	AAAGTTGAGT	660
GTTTCTATCC	AAGCACGCCA	TTTTAAAAAC	GTTTLAGAGT	CCTTTTACCA	ACAAAATAAA	720
GAGAGTTTGG	GCTTTTTTTC	CCCTTATTTT	AGTTTGCGTT	CTCAAACCCC	TAGCGTCTCT	780
TATGAAAGCG	CGTTAGCTTC	TTTAGAAAAC	TATTTTATGG	CCTTGTTCCA	ATCCCATTTT	840
AAAGACGATA	CCGCGCTCCA	ACAGAATTTT	AAAGGATTGT	TGCAAGCCTT	TGTTTCTATG	900
GCTAAAGACA	AACGATCTCA	AATCGTTCTT	AACGCCCAAG	CTAAAGACAA	CACCAAGCTG	960
ACTTTTAACG	CCTTGTTAGA	AAGCCTAAGC	GTGAATTTCT	TTCAATCTTA	CAAAATAAGC	1020
CATGAGTGA						1029

(2) INFORMATION FOR SEQ ID NO:1011:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 882 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

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ATGAGATTGT TGTTCCTTGT ACTGAGCGCT ACTTTGATGT TACTGGCTGA AGAAAAAATA      60
CCTTTAAGCG ATGACGCCCC CATTAAATTG GTTCATTGGC AAAATGCGCT AAAAGAAGTC      120
CAACCCGATT CAAAAGCTCC GGCAACGCCA CCTATAAAGG CCGTGCAAAC CACGCTCACT      180
TTTGAAACGC CTTTAAATAA AACGCCTAAA ATCATGGAGG TTGAAGGGCA AAAAGTCATC      240
GTGTTAAAAA ACGCTCAATT GGATTCTAAA AAAACGATGG ATTTTAAAGA AGCCTCTTTG      300
AATGCCTTAG AAATGTTTTT CTACCAAAAT GACATCTACC TCTTGTCTAA AAAAGCTAAA      360
GCGGGATTAG AAATCCAAGC TTCAAGCAGC AAGGATAAAA AGCAACTCCG CTTTCTTTTT      420
TTACCCAAAG GTTTTCATTT AGCCCCACCG CCTAGCCTGA AAGAAAAATC TCAGCATGCC      480
AATCTCGCAA GCCAAGATGA AAAAGAGCGA GCCAAAAGCC CCTCAAACGC TCTAGAGTTA      540
AAACCCCCAC TGGATTTAAG CCATGCTTAC AAGGGGTTAG CGGTTATTGC TGTCTTACTC      600
TTAATATTGT ATGTAATCAA AAAAAAATT GTTCCTACAC CAGGGTCTTT TTTAAAAAAA      660
GATTTGAAGC TAGACATTAG CGTTTGGGT CGTGTGATG CGAACCATAA AATCATCTCA      720
ATAGAAACCA ATAAGGAGCG TTACTTGGTC TTACTAAGCG ACAAAATACGG CCTGCTTTTA      780
GACAAAATAA GCCCAAAAAC ATCTAAAGAA GAACTGATTA AAGAAGCTGA AAATAAGATA      840
AAGAATTCAA AATTAGGAAA TTTATATGCC GGAAAATTCT AA                        882

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(2) INFORMATION FOR SEQ ID NO:1012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:

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ATGCTTAGAA ATCAATTTTCG TATCGTGTTT GTCTCTTGTA TTGTCGCTAG CAGTTTGCAA      60
GCTCAAGAAA ATACCCACAC TTTGGGTAAG GTAACCACTA AGGGTGAAAG GACTTTTGAA      120
TACAACAATA AAATGTATAT TGACAGGAAA GAGCTCCAAC AACGCCAAAG CAACCAAATC      180
CGTGATATTT TTAGGACTAG GGC GGATGTG AATGTGGCCA GTGGGGGCTT AATGGCGCAA      240
AAAATCTATG TTAGGGGGAT TGAGAGCCGT CTCTTAAGGG TAACGATAGA TGGCGTCGCT      300
CAAAATGGTA ACATTTTCCA CCATGACGCT AACACCGTGA TCGATCCCAA CATGATTAAA      360
GAAGTGGAAG TGATTAAGGG GGCAGCGAAC GCTTCAGCAG GTCCAGGCGC GGTTCGCGGT      420
AAATTGTCTT TCACCACGAT TGACGCTAAC GACTTTTAA GAAAGAATCA AACTTATGGC      480
GCTAAAGCGG AAGCAGCCTT TTACACTAAC TTTGGATACC GCATGAACGC CACTGCAGCC      540
TATCGGGGGA AAAACTGGGA CATCCTAGCC TATTACAACC ATCAAAATAT TTTTACTAC      600
AGAGACGGGA ATAACGCTTT TAGGAGTCTC TTCCACCCTA ACTACGATTT ACAAGATCCA      660
AGCAATAGCG AAATGAGCGT AGGGACTCCT AGTGAAGTCA ATAGCGTTT AGCTAAAATT      720
AATGGCTATA TCAACGAAAC CGATAGCATT AGCGTGAGCT ACAACCTCAC ACGAGACAAT      780
TCTACAAGGC TTTTACGCCC TAACACCACT TCAGCCCTCT CCAAAGCCAA TGACCAGGAA      840
GCCAGCCAGC CCCCTTTGTG A                        861

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(2) INFORMATION FOR SEQ ID NO:1013:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

ATGAAACGGC	TTTTATTGTT	AGCCTTGGCC	CTCTTTTTTA	GCCTCTCATG	CACTAACGCT	60
CAAGAAATTA	AAGAAACTCA	AGAGACTAAA	AAACTAAAG	AAACTAAAAG	CCAAACCCGT	120
TTTAACATTT	CCACCACTAA	GGTCATAGAA	AAAGAATTTT	CTCAAAGCCG	GCGCTATTAC	180
GCGCTTTTAG	AGCCTAATGA	AGCGCTGATT	TTTTCTCAAA	CCCTGCGTTT	TGATGGCTAT	240
GTGGAAAAGC	TTTATGCGAA	TAAAACCTAT	ACCCCCATTA	AAAAGGGCGA	TAGGCTATTG	300
AGCGTGTATT	CCCCTGAATT	AGCGGGCGTT	CAAAGCGAGC	TGTTATCGTC	ATTGAAATTC	360
AACCAGCAAG	TGGGAGCGAT	TAAAGAAAAA	TTAAACTAC	TAGGGCTAGA	AAACTTTAGC	420
ATTGAAAAAA	TCATCAGCAG	CCATAAAGTC	CAAAATGAAA	TCACTATTTA	CTCTCGTTTC	480
AACGGCGTTA	TTTTTAAAAA	AAGCCCGGAT	CTCAATGAGG	GGAGTTTCAT	TAAAAAAGGG	540
CAAGAGCTTT	TCAAAATCAT	AGATTTAAGC	CGATTGTGGG	CGCTTGTTAA	AGTCAATCAA	600
GAGGATTTAG	AATTTTTAAA	AAACACGCAT	CAAGCGATTT	TGTTCTAGTA	GGGGGTTAAA	660
GGCAAGCAAG	CAATCACGCT	TGAAAACATC	AACCCCATCA	TAAATGCGCA	AGATAAAATG	720
CTAGAAGCGC	GCTTCAATGT	GCCTAATCTT	AAATTGCTTT	ATTACCCTAA	CATGTTTCGCT	780
CAAGTAGAAA	TCTTTCACAA	ACCCCAAAAA	ATGAAGATCT	TGCCTAAAGA	AGCGGTTTTG	840
ATTAAGGGGG	GGAAAGCTAT	CGTGTTTAAA	AAAGATGATT	TTGGCTTAAG	CCCGTTAGAA	900
ATTAAAGCCG	TCCGCTTGAG	CGATGGGAGT	TATGAAATTT	TAGAGGGTTT	AAAAGCGGGC	960
GAAGAAGTCG	CTAATAACGC	TTTATTCGTG	CTAGACGCTG	ACGCTCAAAA	CAATGGGGAT	1020
TATTGA						1026

(2) INFORMATION FOR SEQ ID NO:1014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

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ATGGCTTTTT GCGCTCGCCA AAAGCCTCTA AAGGAAATCA TCGGTTTTTT TATTTTATTT      60
TTTATGGGTA TGCTTGCGGT TGGTTTTTCT CAAACCGAGT TGGATTAAAA GGATTTAGAA      120
AAAAAGCCCG CCGGGATCGT TAGGGATTAT TATTTATGGC GTTATATTAG CGATAAAAAA      180
ACGAGTTTAG AAAACGCTAA AAAAGCCTAT GAATTGACTC AAAATAAAAA CAGCGCCCTA      240
CAAAAAGCCA TGCAAGAAAA AGGCGTAGAA AATTCAGATA AAAGCCCTGA TGCCAAAATG      300
CCTGAAGATA TTTATTGCAA GCAAATTACC TTAGAAAGCA TGTAGAAAC AACAGACGCT      360
TTCCAAGCGA GTTGATCGC TATCGCTTTA AAATCAAAAA TCAGAGATT TGTATAAATC      420
CCCATTCAAA CCTTTAAACC TTTACAAGAA AAAATCAAAG AGGCTTACCC CATTCCTTAT      480
GAAGAATTAG AAATCTTGCA AAGTAAGAAC GTGAGCGCTT CTTTGTTTAA GGCTAACGCG      540
CAAGTGTTTA GCGCGCTCTT TAATCATTTG AGTTATGAAA AAAAGCTCCA AATTTTTGAA      600
AAGCATATCC CGATTAAAGA GTTAAACCGC CTTTATAGATG AAGATTACCC GCGGTTTAA      660
CGCTTGATCT ATCAAGTCAT CTTAGATCCT AAATTGGATC ATTTTAAAGA CGCTCTCGCT      720
AAAAGTAACG CCACCCAAAG CAACGCGCAA ACCTTTTTTA TTCTAGGAAT CAATGAAATC      780
TTGCACAAAA AAACCTCTAA AGCGCTCAAG TATTTTGAAC GCTCAGAAGC GGTGTCAAG      840
GACGATGATT TTTCAAAAGA CAGAGCGATT TTTTGGCAGT ATTTAGCCTC TAAAAAGAAA      900
AAAACCTTGG AGCACCTTTC ACAAAGCCCA GCCCTAAACC TCTATAGTCT TTATGCGAGC      960
CGCAAACCTA AAACCACGCC CAGTTATCGC ATCATTCTCT ATATCCAAAA TTTAAGCCAA     1020
GAGAACCCTC CTTTAAACAC TTACGATCCT TTTTCGTGGC AAATTTTAA GGAAAAAACT     1080
TTGAGTTTGA AAGATGAGGG CGCGTTTAA TCGATGCTAA AAAGCCTGTA TTATGAAAAA     1140
AGCGCTCCTG AATTGACTTA CCTTTTAAGC CAACGCAATA AAGACAAGAT TTATTATTAT     1200
TTATCCCCTT ATGAGGGCAT TATTGAGTGG CAAAATACAG ATGAAAGGGC TATGGCGTAT     1260
GCGATCGCTA GGCAAGAAAG CTTTTTGCTC CCGGCTTTAA TCTCTCGCTC CTTGCTCTA     1320
GGGCTTATGC AGATCATGCC TTTTAATGTA GGGCCTTTTC CTAAAGCCTT GGCATGGATA     1380
ATGTTGATCT AA                                     1392

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(2) INFORMATION FOR SEQ ID NO:1015:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1125 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

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ATGCCAAAAA GAATGAAGTG TTTTAGTCAA AAATGGTTGG TTTTTTTTGT TACCCATTGG      60

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CTTTTGTGG	CTTCTTTAAG	TCATGCGAAG	ATGGCTTTTG	AATCCAATAT	TGACACCAAA	120
GCGTTAGAGG	CTTTTGGGGT	CAATGCGAGC	TTTTTATCCC	AAATGCCAGG	CGCTTTAAAA	180
AAGGTGAATA	AGGAAGAGGA	ATGGAAAAAG	TTAGTCAAAA	GATTTGACGT	GAATTACCAA	240
TTCATCCCTA	TCATTAAAAA	CATGCTCATA	GGAGCGAGCG	TGCCGCAAGA	ATTTTTGTTT	300
TTAGCCATGG	CCGAGTCTAA	GTTTTTCATCA	AGGGCTTATA	GCAGGAAAAA	AGCGGTAGGG	360
ATTTGGCAAT	TCATGCCAAG	CACGGCCAAA	GAGTTAGGGC	TTAAGGTCAA	TCATTACATT	420
GATGAAAGAA	GAGATCCCAT	TAAAAGCACT	CAAGCGGCGA	TCGCTTATTT	GAAACGGCTC	480
TACAAGCAAA	CCGGTGAGTG	GTATTTGGTC	GCTATGGCGT	ATAATTACGG	CTTACGCAAG	540
GTTCAAAACG	CTATTAAAGC	CGCCGGCACT	TCAGACATTA	AAGTCTTGCT	AGATGAAGAT	600
AAAAAATACC	TCCCTAAAGA	AACACGAGAG	TATATCCGCT	CCATTCTAAG	CCTGGCGTTG	660
AAATTCAACA	GCCTAGACAA	TCTCAAAGAT	AAAGAGTATT	TGCTCAATCG	TGGGGCGAGG	720
GTGAGTTTAG	TGGGCGTCCC	GTTTAAAAGA	CACACTTCTT	TAGTCCAGGT	GGCCAAAAAT	780
TTGAATTTGA	GTTTAGAAAC	CTTAAATCT	TACAACCACC	AATTCGCTA	TAACATTCTG	840
CCCTCTAAAG	ACCCACCTA	CACCATTAT	ATCCCTTATG	AAAAACTCGC	CCTTTTCAAA	900
CAACGCCAAC	TCAAACAAA	TAAAAACGCT	CAAGCTAATC	CTAAAAGCCC	TTTCATCACC	960
CATGTGGTCT	TGCCTAAAGA	AACCTTATCT	TCTATCGCTA	AACGCTATCA	AGTCAGCATT	1020
TCCAGTATCC	AATTAGCCAA	TAACCTCAAA	GATTCTAATA	TCTTTATCCA	CCAGCGCTTA	1080
ATCATCCCCA	CTAACAAAA	ATTACTCGCT	ACAAGGGAAT	TTTAA		1125

(2) INFORMATION FOR SEQ ID NO:1016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1002 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

ATGCTAATCG	CTCGCTTTAA	AAAAGCTTTA	ATTCCTATT	CTTTAGGGGT	TCTTCTTGTT	60
TCATCGTTAT	TAGGCGTGGC	TAACGCTTCT	AATCAAGAGA	TCCAAGTCAA	GGATTATTTT	120
GGGGAGCAAA	CCATAAAGCT	TCCTGTTTCT	AAAATAATCT	ACTTGGGCAG	CTTTGCAGAA	180
GTGCCTGCCA	TGTTCAATAC	TTGGGATAGG	GTCGTGGGCA	TTTCGGATTA	CGCTTTTAAA	240
TCTGATATTG	TTAAAGCCAC	TCTCAAAGAT	CCTGAACGCA	TTAAACCCAT	GAGCAGTGAT	300
CATGTGGCGG	CGTTGAATGT	GGAATTATTA	AAAAAGCTTA	GCCCTGATCT	TGTGGTAACC	360
TTTGTGGGTA	ACCCTAAAGC	GGTAGAGCAT	GCGAAAAAAT	TTGGGATTTC	ATTCCTTTCT	420
TTCCAAGAAA	AAACCATTGT	AGAGGTCATG	GAAGATATTG	ACGCTCAAGC	TAAGGCCCTTA	480
GAAGTTGACG	CTTCTAAAAA	ATTGGCTAAA	ATGCAAGAAA	CTTTGGATTT	TATCAAAGAG	540
CGTTTGAAAA	ATGTCAAAAA	GAAAAAGGGG	GTGGAGCTTT	TCCATAAAGC	CAATAAAATC	600
AGCGGCCATC	AAGCCCTTGA	TTCAGATATT	TTAGAAAAAG	GGGGCATAGA	CAATTTTGGC	660
TTGAAATACG	TCAAGTTTGG	GCGCGCTGAC	ATTAGTGTGG	AAAAAATCGT	TAAAGAAAAC	720
CCTGAGATTA	TTTTTATTTG	GTGGATAAGC	CCGCTTAGCC	CTGAAGACGT	GTTGAACAAC	780
CCTAAATTTT	CCACTATCAA	AGCCATTAAA	AACAAGCAAG	TCTATAAGCT	CCCCACAATG	840
GATATTGGCG	GACCTAGAGC	CCCACTCATT	AGTCTTTTTA	TCGCTTTAAA	AGCCCACCCT	900

GAAGCGTTTA AGGGCGTGGA TATTAATGCG ATAATCAAAG ATTACTATAA AGTGGTCTTT 960
GATTTGAATG ACGCGGAAGT TGAACECTTT TTGTGGCACT GA 1002

(2) INFORMATION FOR SEQ ID NO:1017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

ATGGAAATTA	GAAACATCAA	AGAGTTTGAA	AAAGCTTCCA	AAAAACTCCA	AAAAGACACT	60
TTAAAGATCG	CTCTCGCTCT	TTTGTTCCTC	ATTGGCGCCG	CTTTGCTCGC	TCTCATTTTT	120
GGGCAGGCTA	ATTCTAAGGG	ATTGTTGCTC	ATCTTTGCGG	CCGTGATTGG	GGGGTATATG	180
GCGATGAATA	TTGGCGCGAA	CGATGTGTCT	AATAATGTCG	GCCCTGCCGT	AGGCTCTAAA	240
GCCATTAGCA	TGGGTGGGGC	GATTTTGATC	GCTGCGGTTT	GTGAAATGCT	AGGAGCGATC	300
ATTGCTGGGG	GGGAAGTGGT	TTCTACGATT	AAGGGCCGTA	TCGTTTCGCC	TGAATTTATT	360
AACGATGCGC	ATGTTTTTCAT	TAATGTTCATG	TTGGCTAGCC	TTTTGAGTGG	GGCGTTATGG	420
TTGCATGTAG	CCACTTTAAT	AGGCGCTCCC	GTTTCCACTT	CGCACTCCGT	AGTGGGAGGG	480
ATTATGGGGG	CTGGAATGGC	AGCAGCTGGA	ATGTCGTGTA	TCAATTGGCA	TTTTTTATCC	540
GGCATTGTGG	CTAGTTGGGT	AATCTCGCCT	TTAATGGGGG	CTTTGATAGC	CATGTTTTTT	600
TTAATGCTCA	TTAAAAAGAC	TATCGCTTAT	AAAGAAGATA	AAAAGAGCGC	GGCTTTAAAG	660
GTCGTGCCTT	ATTTGGTGGC	GTTGATGAGC	TTAGCCTTTA	GCTGGTATTT	GATCGTGAAG	720
GTTTTTAAAC	GCCTCTATGC	GGTGGGTTTT	GAAATCCAGC	TCGCTTGCGG	TTGTGTCCCT	780
GCGCTTTTGA	TTTTTATCCT	TTTTTAAAGA	TTTGTGTAA	AAAAAGCCCC	GCAATTAGAA	840
AATAGCCACG	AAAGCGTCAA	TGAGCTTTTT	AATGTCCCTT	TGATTTTTGC	CGCCGCGCTT	900
TTAAGCTTTG	CGCATGGGGC	TAATGATGTA	GCTAACGCTA	TCGGTCCTTT	AGCCGCAATC	960
AGTCAAACCT	TAGAAGATGC	GAGCAGCCCT	ATGGGGAGTA	CTTTAAACTC	TGTGCCGTTG	1020
TGGATTATGG	TAGTAGGGGC	AGCTGGGATC	GCTTTAGGCT	TGAGCTTGTA	TGGGCCAAAG	1080
CTCATTAATA	CGGTGGGGTC	TGAAATCACA	GAATTAGACA	AAATGCAAGC	TTTTTGCATC	1140
GCGCTTTTCA	GCGTCATCAC	CGTGCTTTTA	GCCTCTCAAT	TAGGCTTACC	GGTAAGCTCT	1200
ACGCATATTG	TGGTGGGCGC	GGTGTTTGGG	GTGGGCTTTT	TAAGGGAGCG	TTTGAGGGAG	1260
CAATCCAGAA	GGCGTTTTGC	TAGAATCAGA	GACAACATTG	TAGCGGCGCA	CTTTGGGGAA	1320
GATTTAGAAG	AAATTGAAGG	CTTTTATAGAG	CGCTTTGATA	AAGCCAATTT	GAAAGAAAAA	1380
TCGCTCATGC	TAGAGAGCTT	GAAAAAAGC	AAGAACACCG	CTATCGCTTT	GGAATTGAAA	1440
AAGAAAGAAA	AAAAGTCGCT	TAAAAAAGTG	TATAAAGAAG	AAGTGATCAA	ACGCTCCATT	1500
TTGAAAAAGA	TTGTTACCGC	TTGGTTGGTA	ACCGTGCCGG	TTTCTGCGCT	TTTAGGGGCG	1560
CTTCTTTTTG	TAGCTCTTGG	TTTTATAGAA	AAGTATTTCT	AG		1602

(2) INFORMATION FOR SEQ ID NO:1018:

(i) SEQUENCE CHARACTERISTICS:

921

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

ATGTCAAATA	GCATGTTGGA	TAAAAATAAA	GCGATTCTTA	CAGGGGGTGG	GGCTTTATTG	60
TTAGGGCTAA	TCGTGCTTTT	TTATTTGGCT	TATCGCCCTA	AGGCTGAAAGT	GTTGCAAGGG	120
TTTTTAGAGG	CTAGGGAATA	CAGCGTGAGC	TCTAAAGTCC	CTGGCCGCAT	TGAAAAGGTG	180
TTTGTTAAAA	AAGGCGATCG	CATTAAAAAG	GGCGATTTAG	TTTTTAGCAT	TTCTAGCCCT	240
GAATTAGAAG	CCAAGCTCGC	TCAAGCTGAA	GCCGGGCATA	AAGCCGCTAA	AGCCGTTAGC	300
GATGAAGTGA	AAAGAGGCTC	AAGAGATGAA	ACGATCAATT	CTGCGAGGGA	CGTTTGGCAA	360
GCGGCAAAAT	CCCAAGCGAA	TTTGGCTAAA	GAGACTTATA	AGCGCGTTCA	AGATTTGTAT	420
GACAATGGCG	TGGCGAGTTT	GCAAAAGCGC	GATGAAGCCT	ATGCGGCTTA	TGAAAGCACC	480
AAATACAACG	AGAGCGCGGC	TTACCAAAAAG	TATAAAATGG	CTTTAGGGGG	GGCGAGTTCT	540
GAAAGCAAGA	TTGCCGCTAA	GGCTAAAGAG	AGCGCGGCTT	TAGGGCAAGT	GAATGAAGTG	600
GAATCCTACT	TAAAAGACGT	CAAAGCCCTA	GCCCCATTATG	ATGGGGAAGT	GAGTAACGTG	660
CTTTTAAGCG	GTGGCGAGCT	TAGCCCTAAG	GGCTTTCCTG	TGGTGCTCAT	GATAGATTTA	720
AAGGATAGTT	GGTTAAAAAT	CAGCGTGCCT	GAAAAGTATT	TGAACGAGTT	TAAAGTGGGT	780
AAGGAATTTG	AAGGCTATAT	CCCAGCGTTG	AAAAGAAGCG	CGAAATTCAG	GGTCAAATAT	840
TTGAGCGTGA	TGGGGGATTT	TGCGACCTGG	AAAGCGACGA	ATAATTCCAA	CACCTACGAC	900
ATGAAAAGCT	ATGAAGTGGA	GGCCATACCC	TTAGAAGAGT	TGGAAAACCT	TAGGGTGGGG	960
ATGAGCGTGT	TGTTTACCAT	TAAACCTTAA				990

(2) INFORMATION FOR SEQ ID NO:1019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

AGACTGGAAT	CACCGCTACA	CTCAGGCTTT	AGCCCTAGCG	CGGCCCTTGT	GATCAGCCCC	60
ATTGAGCCTT	TATCTCTAAA	AATCACTTAT	TCTCAAGTTA	CAAGGGGGGT	TATGCCAGGA	120
GATGGCGTGT	ACATGCGTCA	AAACGATTTA	CGATACGCTA	AAAATATCAA	GCCTGAAGTG	180
GGCTCTAACG	CTGAATTTAA	TATTGACTAT	TCAAGCCAGT	ATTTTAGCGG	GAGGGCTGCG	240
GCGTTCTATC	AAGCTTTGGA	TAATTTTCATC	TCACAATACG	CGCAACGCTT	GATCGTAACC	300
AATTTGAGTC	AAGCGATTCG	CATTTATGGC	TATGAAGTGG	GTGGGACTTT	TAGATACAAG	360
GGCGTGAGTT	TGAATGTGGG	GATCTCGCGC	ACTTGGCCCA	CCACTAGGGG	GTATTTAATG	420
GCGGACAGCT	ATGAGCTTGC	CGCAAGCACC	GGTAATGTTT	TTATCATTA	ATTGGATTAC	480
ACCATTCCAA	AAACAGGGAT	CAATCTTGCA	TGGCTTAGCC	GCTTTGTTAC	CGGTTTGGAT	540
TATTGCGGGT	TTGATATTTA	CTTGCCGTGAT	TATGGGACAG	CTGAAAACC	CAAAACCCCT	600
ACCGATTTAG	CCAAATGCGG	ATCCCAATTG	GGGTTAGTGC	ATATGCACAA	ACCGGGCTAT	660
GGCGTGAGTA	ATTTTATAT	CAATTGGAGC	CCTAAAACCA	AAAGCCACTG	GAAGGGTTTG	720
CTGCTTTCAG	CCGTGTTTAA	TAATGTTTTC	AACAAATTCT	ATGTGGATCA	AACAAGCCCC	780
TATGTCATGA	GCCCGGATAT	GCCAGGCACT	GACGCTATTA	AAAGAGCGAT	CGCAGAGCCT	840
GGGTTTAATG	CGCGTTTGA	AGTGGCTTAC	AAATGGTAG			879

(2) INFORMATION FOR SEQ ID NO:1020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

ATGGCTAAAA	TCACAACCGT	GATTGACATA	GGCTCTAATT	CAGTGCCTTT	GGCTGTCTTT	60
AAAAAGACGA	GCCAGTTTGG	GTTTTACTTG	CTTTTGTAGA	CTAAGTCCAA	GGTTAGGATT	120
TCAGAGGGCT	GTTATGCGTT	TAAAGGGGTT	TTACAAGAAA	TCCCCATGCA	ACGAGCCGTT	180
AAAGCCTTGA	GCGAATTTAA	AGAAATCGCC	CTCAAATACA	AAAGCAAAAA	AATCCTGTGC	240
GTGGCGACCT	CAGCGGTGCG	CGATGCCCCCT	AATCGGTTAG	AGTTTGTAGC	GAGGGTGAAA	300
AAGGCTTGCG	GTTTGCAAAT	CAAAATCATT	GATGGGCAAA	AAGAAGCGCT	CTATGGTGGG	360
ATCGCGTGCG	CGAATTTGCT	GCATAAAAT	TCAGGGATCA	CGATAGACAT	TGGAGGGGGT	420
AGCACCGAGT	GCGCGTTGAT	TGAGAAAGGT	AAGATTAAGG	ACTTAATCTC	GCTTGATGTC	480
GGGACGATTC	GCATTAAAGA	AATGTTTCTA	GACAAAGACT	TAGATGTCAA	ATTGGCTAAA	540
GCCTTTATCC	AAAAAGAGGT	CTCTAAACTG	CCTTTTAAAG	ATAAAAACGC	CTTTGGGGTG	600
GGGGGGACGA	TCAGAGCCTT	GAGTAAGGTG	CTGATGAAAC	GCTTTGATTA	CCCTATAGAT	660
TCTTTGCATG	GCTATGAAAT	AGATGCGCAT	AAAAATTTAG	CGTTCATTGA	AAAAATCGTC	720
ATGCTCAAAG	AAGACAAATT	ACGGCTTTTA	GGGGTGAATG	AAGAGCGTTT	GGATAGCATT	780
AGGAGCGGGG	CGTTGATTTT	ATCAGTCGTG	TTAGAGCATT	TGAAAACCTC	CTTGATGATC	840

ACTAGCGGGG	TAGGGGTGAG	AGAGGGCGTG	TTTTTGAGCG	ATTTATTGCG	CCACCATTAC	900
CATAAATTCC	CCCCCAATAT	CAACCCCTCT	CTCATCTCTC	TAAAAGATCG	CTTTTACCC	960
CATGAAAAGC	ACAGCCAAAA	GGTCAAAAAA	GAATGCGTGA	AATTGTTTGA	AGTTTATCG	1020
CCTTTGCATA	AAATAGATGA	AAAATACCTT	TTCCATTTAA	AGATTGCGGG	GGAATTGGCG	1080
AGCATGGGTA	AGATTTTAAG	TGTATATTTA	GCCCACAAGC	ACAGCGCGTA	TTTCATTTTA	1140
AACGCTTTGA	GTTACGGCTT	TAGCCACCAG	GATAGGGCGA	TCATTGCTT	ATTGGCGCAA	1200
TTTAGCCATA	AAAAAATCCC	TAAAGACAAC	GCTATCGCCC	ACATGAGTGC	GATGATGCCA	1260
AGCCTTTTGA	CCTTGCACTG	GCTGAGTTTT	ATCCTTTCTT	TAGCCGAAAA	TTTGTGCCTG	1320
ACAGACAGCC	ATCATTTAAA	ATACACGCTA	GAAAAAACA	AGCTTGTGAT	CCATTCTAAT	1380
GATGCGCTTT	ACTTGCTAA	AGAAATGCTC	CCCAAATCA	TTAAGCCCAT	TCCTTTGACG	1440
ATAGAGTTTG	CTTGA					1455

(2) INFORMATION FOR SEQ ID NO:1021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

ATGGTAGGAA	TGAAACTGA	GATGAAATCT	TTTTTAAAC	TTTTTGCACA	GCCTTTGTTG	60
GTGGTTTTAG	CGTTCATGTT	GTTGTATGCT	TTAGCGCATG	CTGTGCTTGG	TTTTTACGTG	120
AAAAAAGACA	GCGCTCCAAT	GAGTCCAAAT	GTAAGAAAAA	GCGAGACAGA	GCGCCAAAAC	180
AGCACGTTTT	CGCCTAAAGA	AGAAGCCAAC	GCAACCACAA	CCGCCACAGA	ACAAAACCCC	240
ACCAAAGAQA	CAGTGCCACC	TTTAGACACA	GCCACACAAA	AACAAGAGAT	TAAACAAGAG	300
ATTAAACAAG	AGATTAAACA	AGAGATTAAA	CAAGAGATTA	AACAAGAGAT	TAAACAAGAG	360
ATTAAACAAG	AAACTAAACA	AGAGCAAGAA	AAAGAAAATA	AGCCTAAACA	AAACAGTGTC	420
TCGCCCCGTT	AAAACGATCA	AAAAACCCCC	ACAACCCCTT	TAATGGGAAA	AAAACCTCTA	480
GAGTATAAAG	TCGCAGTCAG	TGGCGTGAAC	GTGCGCGCTT	TTCCTAGCAC	AAAAGGCAAA	540
ATCATTGGCT	CGCTTATAAA	AAATAAAGC	GTGAAGGTTT	TAGAAATCCA	AAACGATTGG	600
GCTGAAATTG	AATTTTCTCA	CGAAACAAAG	GGATATGTGT	TTTTAAAACT	TTTAAAAAAG	660
GCTGAATGA						669

(2) INFORMATION FOR SEQ ID NO:1022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

GAGCCTGATG	CAACAAGCCG	CAGAACATTG	AATCACCCCT	ATTTTGGCGT	TTTGTTTTG	60
TTGGTATTCA	CCTTTTGGGT	GTTAACTTA	ACCTTAAGGA	TTCAAAGGT	TTAAGCCGT	120
AAAATGGCTC	AAAAAAGGG	CGAAAAGCTC	AAGCTCGCTC	CCTATGAATG	TGGGCCTGTG	180
GCTCTCAAGC	AGCCTAATAG	GGTGTCCCAT	CATTTTTATA	TCATGGCCAT	GCTTTTATT	240
TTATTTGATG	TAGAAATCGT	TTTCATGTTT	CCTTGGGCGA	TTGATTTTAA	AAAGTTAGGC	300
TTGTTTGGGC	TCGTTGAAAT	GCTAGGCTTT	GTCTTCTTTT	TGGCAATCGG	TTTATTTAC	360
GCTTTAAAGC	GAAACGCTTT	GAGCTGGCAA	AAATTAGAGG	TGAAATAA		408

(2) INFORMATION FOR SEQ ID NO:1023:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1908 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

CTGTCCTCCG	ATCCGAGTGC	TGTCAACGAC	GCAAGGGATA	ATCTAGGCTC	AAGCACTAGG	60
AATTTGCTAG	ATGTCAAAGC	CAATTCCCCC	GCCTATCAAG	CGGTGCTTTT	AGCATTGAAC	120
GCTGCAGTGG	GCTTGTGGCA	AGTTACAAGC	TATGCCTTTA	CCGCTTGTGG	TCCTGGTAGC	180
AATGAGAACG	CGAATGGAGG	TATCCAAACC	TTTAATAATG	TGCCAGGACA	AAACACGACG	240
ACCATCACTT	GTAATTCGTA	TTATGAGCCA	GGACATGGCG	GGCCAATATC	CACTAAAAAT	300
TATGCGATCA	TCAACAAGGC	TTATCAAATC	ATTCAAAAGG	CTTTGACAGC	CAATGGAGAA	360
GGGATCCCAG	TTTTAAGCAA	CACCACTACA	AAACTTGATT	TCATATCAA	TGGAGACAAA	420
AGAACGGGTG	GCGAACCAAA	TAAAAAATTA	GTATACCCAT	GGAGTCATGG	GAAAGCTATT	480
TCAACCTCGT	GGAATGCAAC	CATAACAGCA	CCAACAACAG	AAAAATATCA	TACAACCAAT	540
AGCGCTCAAG	AGCTTTTAAA	ACAAGCGAGC	ATCATTATCA	CTACCCTGAA	TAGTGCATGC	600
CCAAACTTCC	AAAATGGTGG	TAGCGGTTAT	TGGGCAGGGA	TAAGTGGCAA	TGGGACAATG	660
TGTGGGATGT	TTAAGAATGA	AATCAGCGCT	ATCCAAGGCA	TGATCGCTAA	CGCGCAAGAA	720

GCTGTCGCGC	AAGCCAAAAT	CGTTAGTGAA	AACACGCAAA	ATCAAAACAG	CCTAGACGCT	780
GGAAAACCAT	TCAACCCCTA	CACAGACGCT	AGTTTTGCTG	AAAGCATGCT	CAAAAACGCG	840
CAAGCCCAAG	CGGAGATTTT	AAACCAAGCC	GAACAAGTGG	TGAAAAACTT	TGAAAAAATC	900
CCTACAGCCT	TTGTAAATGA	CTCTTTAGGG	GTGTGTTATG	AAGTGCAAGG	AGGTGAGCGT	960
CGTGGCACCA	ATCCGGGTCA	GACGACTTCT	AACACTTGGG	GGGCAGGCTG	TGCGTATGTA	1020
GGACAAACGA	TAACAAATCT	TAAAAACAGC	ATCGCCCATT	TTGGCACTCA	AGAGCAGCAG	1080
ATACAGCAAG	CCGAAAACAT	CGCTGACACT	CTGGTGAATT	TCAAATCTAG	ATACAGCGAA	1140
TTGGGCAACA	CTTATAACAG	CATCACCCT	GCGCTCTCTA	ATATCCCTAA	CGCGCAAAGC	1200
TTGCAAAATG	CGGTGAGTAA	AAAGAATAAC	CCCTATAGCC	CGCAAGGCAT	AGACACCAAT	1260
TACTACCTCA	ATCAAAACTC	TTACAACCAA	ATCCAAACCA	TCAACCAAGA	ACTCGGGCGT	1320
AACCCCTTTA	GGAAAGTGGG	GATTGTTAGT	TCTCAAACCA	ATAATGGCGC	GATGAATGGG	1380
ATCGGTATTC	AGGTGGGTTA	CAAACAATTC	TTTGGCCAAA	AAAGAAAATG	GGGCGCTAGG	1440
TATTACGGCT	TTTTTGATTA	CAACCATGCG	TTCATTAAAT	CCAGCTTCTT	CAACTCGGCT	1500
TCTGACGTGT	GGACTTATGG	CTTTGGAGCG	GACGCTCTTT	ATAATTTTAT	CAACGATAAA	1560
GCCACCAATT	TCTTAGGCAA	AAACAACAAG	CTTCTGTGG	GGCTTTTTTG	GGGTATTGCA	1620
TTAGCCGGGA	CTTCATGGCT	TAATTCTGAG	TATGTGAATT	TAGCCACCAT	GAATAACGTC	1680
TATAACGCTA	AAATGAACGT	GGCGAATTTT	CAATTCTTAT	TCAACATGGG	AGTGAGGATG	1740
AATTTAGCCA	GGCCTAAGAA	AAAAGACAGC	GATCATGCGG	CTCAGCATGG	GATTGAGTTA	1800
GGGCTTAAAA	TCCCCACCAT	CAACACGAAC	TACTACTCCT	TTATGGGGGC	TGAACTCAAA	1860
TACCGAAGGC	TCTATAGCGT	GTATTTGAAT	TACGTGTTTC	CTTACTAA		1908

(2) INFORMATION FOR SEQ ID NO:1024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

ATCAAAACGCA	TCATTAAATC	AAACGCATCA	TTAAATCAAT	TAAATACCAC	TAGATACAAT	60
ACCCCAAGTC	ATCTTTTTTT	CAAAAAGGG	GTAGGAATGG	CAACCATTCA	ACCATTCAAC	120
CATTCAACCA	TTCAACCATT	CAACCATTCA	ACCATTCAAC	CATTCAATCA	TTCAATCATT	180
CAATCATTCA	ATCATTCAAC	CATTCAAGCA	ACGCTACCTT	ATTTTATAA	CTATTTATCT	240
TTTACAAAA	ACCTATTTAA	AAATCCCCTA	TTTTTTATTA	TTCCCCCTTT	TATTAACCCT	300
TTTATTAACC	CTTTTATTAA	CCCTTTTATT	AACCCTTTTA	TTAACCCTTT	TATTAACCCT	360
TTTATTAACC	CTTTTATTAA	CCCTTTTATT	AACCCTTTTA	TTAACCCTTT	TATTAACCCT	420
TTTATTAACC	CTTTTATTAA	CCCTTTTATT	AACCCTTTTA	TTAACCCTTT	TATTTCCCCT	480
TCATTAACCC	ACGCTACAAC	ATTTTCAAAC	CATTTGATTC	CATAA		525

(2) INFORMATION FOR SEQ ID NO:1025:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

ATGGAAGACT	TTTTGTATAA	CACCTTATAT	TTCATAGAGG	ATTATAAGTT	GGTTGTTATT	60
TTTAGTTTCA	TAGGGTTAAT	AGCGTTATTT	TTCCTCTACA	AATTCATAAA	AACTCAAAAA	120
AAGGTTTTTA	AAGATAAAGC	TAACCAGCCT	CAAAAGAAAA	AAAGCTTTAA	AGAAATCATT	180
ATAGATGGGC	TGAAAGAAAAG	GGTTAAAACC	TTTGGCTTTT	GGTTGCAAGC	TATACTATTA	240
CTATCCTATT	CTTTTATCAC	ATCAGGGTTA	TTTTTCTTGA	TTCTCTTAGG	TAATTTTTTAT	300
GATGATAATA	GATTGCCTGA	GAGCGATGAT	GATCTTTTTG	ATATATGGGT	CTATGCGATA	360
CAAGATTTTC	CTGCATACTA	TTTAAAGGCA	CTCACTTTTA	GCTCGCTCAA	GATTTATGGG	420
TTCAATATAT	CCTTAGTCGT	ATATAGTTCT	ATTTTATGCT	CTTATATATT	CATTACCTTT	480
TTTGTGTGGT	TCTTAAAATA	CTTAACCTCG	ACTAGGGACA	TAGGAGCGAA	TAAAAAAGTT	540
GATGATCTCT	TTGGTAGCGC	GAGTTGGGAA	ACTGAAGAGA	AAATGATCAA	AGCCAAGCTT	600
ATCACACCCA	ACAATAAAAA	ACGCGCCTTT	GACAAACGAG	AGGTTATTGT	AGGCAGGCGT	660
GGCTTAGGGG	ATTTTATCGC	TTACGCAGGA	CAGGCGTTTA	TTGGCTTGAT	TGCTCCTACT	720
AGGAGCGGTA	AGGGTGTGGG	TTTCATCATG	CCCAATATGA	TCAATTACCC	TCAAAATATC	780
GTTGTGTTTG	ATCCTAAGGC	TGACACTATG	GAAACTTGCG	GGAAAATCAG	AGAAAAACGC	840
TTCAACCAAA	AAGTGTTTCAT	CTATGAACCT	TTCTCCTTAA	AAACACACCG	ATTTAATCCT	900
TTGCTTATG	TGGATTTTGG	TAATGATGTG	GTTTTGACTG	AAGACATACT	CTCTCAAATT	960
GACACACGCC	TAAAAGGGCA	TGGCATGGTG	GCTAGTGGAG	GGGATTTTTT	CACCTCAAATC	1020
TTTGGATTGG	CTAAGTTGGT	GTTCCCTGAA	AGACCTAATG	AAAAAGATCC	TTTTTTTTAGC	1080
AATCAGGCGC	GAAACCTTTT	TGTCATCAAT	TGCAATATTT	ATAGGGATCT	CATGTGGACT	1140
AAAAAGGGGC	TTGAGTTTGT	CAAAAGAAAA	AAAATCATCA	TGCCTGAAAC	CCCCACGATG	1200
TTTTTCATAG	GTTCTATGGC	AAGCGGTATC	AACCTGATTG	ATGAAGACAC	AAACATGGAA	1260
AAAGTCGTGT	CTTTAATGGA	ATTTTTTTGGA	GGTGAAGAAG	ATAAGAGTGG	CGACAATCTA	1320
AGAGCGCTTA	GTCCTGCCAC	TAGAAACATG	TGGAATAACT	TCAAGACAAT	GGGTGGCGCT	1380
AAAGAACTT	ACAGCTCGGT	TCAAGGGGTC	TATACATCAG	CGTTTGCGCC	TTACAATAAC	1440
GCCATGATCA	GGAATTTTAC	GAGCGCTAAT	GATTTTGATT	TCAGGCGTTT	AAGGATCGAT	1500
GCAGTGAGTA	TTGGTGTGAT	CGCTAATCCT	AAAGAAAGCA	CTATTGTTGG	ACCGATATTA	1560
GAGCTGTTTT	TCAACGTGAT	GATTTATAGC	AATTTGATTC	TGCCAATCCA	TGATCCACAA	1620
TGCAAAAGAA	GCTGCTTGAT	GCTCATGGAT	GAATTTACGC	TCTGTGGCTA	TTTAGAGACC	1680
TTTGTAAAG	CGGTAGGGAT	CATGGCAGAA	TACAACATGC	GCCCCGCTTT	TGTGTTTCAA	1740
AGTAAGGCGC	AATTAGAAAA	CGACCCCCCA	CTTGTTATG	GTAGGAATGG	CGCTAAGACT	1800
ATTTTAGACA	ACCTTTCCTT	GAATATGTAT	TATGGGATCA	ACAACGATAA	CTACTATGAA	1860
CATTTTGAAA	AGCTTTCCTA	AGTGTTAGGG	AAATACACAA	GGCAAGATGT	GAGCCGGAGC	1920
ATTGATGATA	ATACGGGTAA	GACCAACACT	TCTATCAGCA	ACAAGGAGCG	GTTTTTGTATG	1980
ACCCCTGATG	AATTGATGAC	TATGGGCGAT	GAGCTTATCA	TTTLAGAAAA	CACGCTCAAA	2040
CCCATCAAGT	GCCACAAGGC	GCTTTACTAT	GATGATCCCT	TCTTCACCGA	TGAGCTCATT	2100
AAGGTGAGTC	CAAGCTTGAG	CAAGAAATAC	AAATTGGGGA	AAGTGCCTAA	TCAAGCAACA	2160
TTTTATGATG	ACTTGCAAGC	CGCTAAAACC	AGAGGCGAAT	TGAGCTATGA	TAAATCTTTA	2220

GTGCCTGTGG GTTCAAGCGA ACTGTGA

2247

(2) INFORMATION FOR SEQ ID NO:1026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

CTGAATGCAA AATCTCAATC CTCCCTAAAA AACAAAATCA CTCTTAAGAA TAAGCTAAAT	60
CATGCTAGAA TTATACTTGA ATTTATTCCT AGTTTAATTT ATTTCTTAAT ACAAAGGTG	120
AGCGTTTTGA AACATTTAGC CCCACTCATT CATATCCCTT TTAAAGCCTT ATGGCTAGGC	180
ACAGCCTTAA GCATGTTCTT AAGTTTGAAT TTGAACGCTG AAGAAAACCC TACTAAACA	240
GAGCCTAAGC CCGCTAAAGG GGTAAAAAC AAGCCCAAT CGCCTGTTAC TAATGTCATG	300
ATGACCAATT GCGATAACCT TAAAGACTTT AACGCTAAGC AAAAAGAAGT TTTAAAAGCC	360
GCTTATCAAT TCGGATCTAA AGAAAATTTA GGCTATGAAA TGGCGGGCAT TCGTGGA	420
GAATCATGCG CAGGGACTTA TAAAATCAAT TTTTCGGATC CGAGTGCGGG CATTTACCAT	480
GCGTATATCC CTAGCGTTTT AAAAAGCTAT GGGCATAATA ATAGCCCCTT TTTGCGTAAC	540
GTGATGGGGG AATTGCTCAT TAAAGACGAT GCGTTTGCTT CTGAAGTGGC CCTAAAAGAA	600
TTGCTCTATT GGAAAACGCG CTACCATGAC AACCTAAAAG ACATGATCAA GTCTTACAAT	660
AAGGGCAGTC GTTGGGAAAA AAACGAGAAA GCTAACGCTG ATGCTGAAAA ATATTATGAA	720
GAGATACAAG ATAGAATCAG GCGTTTGAAA GAATCTAAAA TCTTTGACTC GCAGTCTAGT	780
AATGACCAAG AATTGCAAAA AAGCGCTAAT AGCAATTTGG ATCTAGACCC TATCGGCAAC	840
GCCATGCCCC AAACCTTAGC TCAAACAGAG ACCCAAAAAT CTCAAATAGA AAAATCTCAA	900
ATAGAGGAACT CTCAAACGCA AAAATCTCAA GAAATGAAAG AGGCAGCTAG CGAGCAAGCC	960
ATTAAGAAGC CGCTAGAAAA AGAAAAAGAT AAACCCATGT ATTTGGCTCA AATCAATAGT	1020
GCTGATTTTCG CGCCCGCTAA AAAAAGCCCA AAAAAACCGG CTAAAGCGAG TCCAAAACGC	1080
TCCTCTAAAA ATAATATCAG CGTTAAAGC AACACCAAAA CCGCTTCCAA AAATAAAGAA	1140
GTGTGCAAAA ATTGCTCTCC AGGGCAAAGG AATGCGATTT TAGCTAACCA TATCACCCCTC	1200
ATGCAAGAGC TTAA	1215

(2) INFORMATION FOR SEQ ID NO:1027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

ATGAAAAAGT TTGTAGTGTT TAAAACGCTC TGTTTATCGG TAGTGTTAGG TAATAGTCTT	60
GTGGCAGCAG AAGGTAGCAC AGAAGTGCAA AAGCAATTGG AAAAGCCAAA AGATTATAAA	120
GCAGTGAAAG GCGAGAAAAA CGCTTGGTAT CTGGGGATTA GCTATCAAGT CCGTCAGGCT	180
TCACAAAGCG TTA AAAAACC CCCC AAAAGC AGTGAATTTA ACTATCCTAA GTTCCCTGTG	240
GGTAAACCG ACTATCTGGC CGTTATGCAA GGCTTAGGGC TTAGTGTGGG TTATAAGCAG	300
TTTTTCGGGG AGAAAAGATG GTTGGTGCG CGCTATTACG GCTTTATGGA TTATGGGCAT	360
GCCGTGTTTG GAGCGAACGC TTTGACATCA GATAATGGTG GGGTGTGCAA ACTCAATGAG	420
CCATGCGCGA CCAAAGTAGG GACTATGGGC AATCTGTCTG ACATGTTTAC TTATGGTGTG	480
GGTATTGACA CTTTATACAA TGTCATTAAT AAGGAAGACG CGAGTTTGG TTTCTTTTTT	540
GGGGCTCAA TCGCGGGTAA CTCTTGGGGT AATACGACAG GGGCCTTTTT GGAAACTAAA	600
AGCCCTTATA AGCACACCTC CTATAGCCTT GATCCGGCGA TTTTCCAGTT CCTTTTAAAT	660
TTAGGGATTG GCACCCATAT TGGTCAGCAT CAAGAATTTG ACTTTGGCGT GAAGATTCCT	720
ACTATCAATG TTTATTATTT TAACCATGGG AACTTGAGCT TCACTTACCG CCGTCAATAC	780
AGCCTTTATG TAGGGTATCG TTACAATTT TGA	813

(2) INFORMATION FOR SEQ ID NO:1028:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 759 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

ATGAAACCTT ATTTCACTTT GGAGAAATTG GATTTATACC ATGGCGATGC GAGCGTTTTA	60
GAGACTTTTG AAAAAGGTTT TTATGATTTG TGCGTTACTT CACCGCCCTA TAATTTGAGT	120
ATTGAATACC AAGGGAGTAA TGATTTTAGG GCTTATGACG ATTATTTGAA TTGGTGTA	180
AATTGGCTTA AAAATTGTTA TTTTGGGGT AAGGAACAGG CGAGGTTGTG TTTGAATGTC	240
CCTTTGGATA CGAATAAGCA TGGCAAGCAA AGTTTGGGGG CTGATATTAC TATAGTGGCT	300
AAAGAATGCG GTTGGAATA CCAAATACG ATTATTTGGA ATGAAAGCAA TATCTCAAGA	360

CGCACCGCTT	GGGGGAGTTG	GCTGCAAGCT	AGCGCACCTT	ATGCGATCGC	TCCTGTGGAG	420
TTGATCGTTG	TTTTTTATAA	AAACGAATAC	AAACGAAAAA	AACAAACTTC	TACGATGAGT	480
AGAGAGGAAT	TTTACTCTA	CACGAACGGG	CTTTGGAATT	TTAGCGGTGA	ATCCAAAAAG	540
CGCCTAAAGC	ACCCAGCCCC	ATTCCCAAGG	GAATTACCCA	GGCGTTGCAT	CCAATTGTTT	600
TCTTTTTTGG	AAGACACGAT	TTTTGATCCC	TTTAGCGGCT	CTGGCACGAC	TATTTTAGAG	660
GCCAACGCTT	TAGGGCGTTT	TAGCGTGGGT	TTAGAGATTG	AAAAAGAATA	TTGCGAGTTG	720
TCTAAAAAGC	GTATTTTAGA	GAGTTTGTCT	TTAGTGTGA			759

(2) INFORMATION FOR SEQ ID NO:1029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

TTAGTTATAA	TATCGCTACT	AACAACACTC	AAGCTAAAAT	CCATTAAGGA	AATCAGTATT	60
AAAAAATTTA	TTCTATCTTC	TCTTGTTTTC	GCATGTATCA	ATACCGGCGT	TGAAGCTTTA	120
GAAAATGACG	GCTCTAAACC	AAACGATTTG	GCTTCTCCAA	AAGAAACCCC	AAAAGAGGCT	180
CAAAAAAATG	AAGCTCAAAA	CGAAACCTCT	CAATCCAATC	AAACGCCCTAA	AGAAATGAAA	240
GTCAAGTCCA	TTTCTTATGT	CGGGCTTTCT	TACATGTCTG	ACATGCTCGC	TAATGAAATT	300
GCAAAGATTC	GCGTGCGCGA	TATGGTGGAT	TCTAAAAAAA	TAGACACCGC	TGTTTTAGCT	360
TTGTTCAACC	AAGGGTATTT	TAAAGACGTT	TATGCCACTT	TTGAAAACGG	CATTTTAGAG	420
TTTCATTTTG	ATGAAAAAGC	CAGGATTGCC	GGGGTAGAAA	TCAAGGGTTA	TGGGACTGAA	480
AAGGAAAAAG	ACGGCTTAAA	ATCCCAAATG	GGGATCAAAA	AGGGCGACAC	CTTTGATGAG	540
CAAAAATTAG	AGCATGCTAA	AACGGCTTTA	AAAACGGCTT	TAGAGGGGCA	GGGCTATTAT	600
GGGAGCGTGG	TGGAGGTGCG	CACAGAAAAG	GTCAGTGAGG	GAGCGTTATT	GATCGTGTTT	660
GATGTGAATA	GGGGGGACAG	TATTTATATC	AAACAATCCA	TTATGAGGG	AAGCGATAAA	720
TTAAAACGCC	GTGTGATTGA	ATCTTTGAGC	GCGAACAAGC	AGCGCGATTT	CATGGGCTGG	780
ATGTGGGGCT	TGAATGACGG	GAAATTGCGC	TTAGATCAAT	TAGAATACGA	TTCTTTGCGT	840
ATCCAAGATG	TGTATATGCG	TAGGGGTTAC	TTAGACGCTC	ATATTTCTTC	GCCTTTTTTG	900
AAAACGGATT	TTTCCACCCA	TGACGCTAAG	CTCCATTATA	AGGTCAAAGA	GGGGATCCAA	960
TACAGGATTT	CAGATATTTT	AATAGAGATT	GACAACCCGG	TAGTCCCCTT	AAAAACCTTA	1020
GAAAAAGCGC	TTAAAGTTAA	AAGGAAAGAT	GTCTTTAATA	TTGAGCATTT	AAGAGCGGAT	1080
GCGCAAATTT	TAAAAACCGA	AATCGCCGAT	AAGGGCTATG	CGTTTGCGGT	GGTGAAGCCA	1140
GACTTGATA	AAGACGAAAA	AAACGGGCTT	GTGAAAGTCA	TTTATCGTAT	TGAAGTGGGC	1200
GATATGGTGC	ATATCAATGA	TGTCATCATT	TCAGGGAACC	AGCGCACGAG	CGATAGGATC	1260
ATTAGGAGGG	AATTGTTACT	AGGGCCTAAA	GATAAATACA	ACTTGACCAA	ACTGAGAAAT	1320
TCCGAAAATT	CTTTGAGGCG	TTTAGGGTTT	TTCTCTAAAG	TCAAGATTGA	AGAAAAAAGG	1380
GTCAATAGCT	CATTGATGGA	TTTGTTAGTG	AGCGTAGAAG	AGGGGCGCAC	CGGGCAGTTG	1440
CAATTCGGGT	TGGGCTATGG	CTCTTATGGA	GGGCTCATGC	TTAATGGGAG	CGTGAGCGAA	1500
AGGAATCTTT	TTGGCACAGG	GCAAAGCATG	AGCTTGTATG	CTAACATTGC	CACAGGGGGG	1560

GGTAGATCTT	ATCCGGGCAT	GCCAAAAGGG	GCGGGGCGTA	TGTTTGCCGG	GAATTTGAGC	1620
TTGACTAATC	CAAGGATTTT	TGACAGCTGG	TATAGCTCTA	CGATCAATCT	TTATGCGGAT	1680
TACAGGATAA	GCTACCAATA	CATCCAACAA	GGCGGGGGCT	TTGGGGTGAA	TGTCGGGCGC	1740
ATGCTGGGTA	ATAGAACCCA	TGTGAGCTTA	GGGTATAACT	TGAATGTTAC	CAAACCTCTT	1800
GGTTTCAGCA	GCCCCTTATA	CAACCGCTAC	TATTCCTCTG	TTAATGAAGT	GGCCTCTCCA	1860
AGGCAATGTT	CCACACCCGC	ATCGGTGATT	ATCAACCGCT	TATCAGGCGG	TAGAACTCCA	1920
TTGGTTCCTG	AAAGCTGTTC	TAGTCCTGGA	GCGATCACCA	CTTCACCAGA	AATAAAAGGT	1980
ATTTGGGATA	GGGATTACCA	CACGCCTATC	ACCAGTTCTT	TCACCCTTGA	TGTGAGCTAT	2040
GACAACACCG	ATGATTATTA	TTTCCCTAGA	AATGGGGTTA	TCTTTAGTTC	CTATGCGACA	2100
ATGTCTGGTT	TGCCAAGCTC	TGGCACGCTC	AATTCTTGGA	ACGGGTTAGG	CGGGAATGTC	2160
CGTAACACCA	AAGTTTATGG	TAAATTCGCC	GCTTACCACC	ATTTGCAAAA	ATATTTATTG	2220
ATAGATTTGA	TCGCTCGTTT	TAAACGCAA	GGGGGCTATA	TCTTTAGGTA	TAACACCGAT	2280
GATTACTTGC	CCTTAAACTC	CACTTTCCTAC	ATGGGGGGCG	TAACCACGGT	GAGAGGCTTT	2340
AGGAACGGCT	CAATCACACC	TAAAGATGAG	TTTGGCTTGT	GGCTTGAGG	CGATGGGATT	2400
TTTACCGCTT	CTACTGAATT	GAGCTATGGG	GTGTTAAAG	CGGCTAAAAT	GCGTTTAGCG	2460
TGGTTTTTTG	ACTTTGGTTT	CTTAACCTTT	AAAACCCCAA	CTAGGGGGAG	TTTCTTCTAT	2520
AACGCTCCCA	CCACGACGGC	GAATTTTAAA	GATTATGGCG	TTGTAGGGGC	TGGGTTTGAA	2580
AGGGCGACTT	GGAGGGCTTC	TACAGGCTTA	CAGATTGAAT	GGATTTCGCC	CATGGGGCCT	2640
TTGGTGTTGA	TTTTCCCTAT	AGCGTTTTTC	AACCAATGGG	GCGATGGCAA	TGGCAAAAAA	2700
TGTAAAGGGC	TGTGCTTTAA	CCCTAACATG	AACGATTACA	CGCAACATTT	TGAATTTTCT	2760
ATGGGAACAA	GGTTTTAA					2778

(2) INFORMATION FOR SEQ ID NO:1030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

ATGAAACAAC	TATTTTTGAT	TATTGGAGCC	CCAGGGAGTG	GTAAAACCAC	TGACGCAGAG	60
CTTATCGCTA	AGAATAACAG	CGAAACAATC	GCTCATTTTT	CTACTGGGGA	TTTACTCAGG	120
GCTGAGAGCG	CTAAAAAGAC	TGAGCGAGGC	TTATTGATTG	AGAAATTCAC	TTCTCAAGGC	180
GAATTAGTGC	CTTTAGAAAT	TGTGGTAGAA	ACGATCCTTT	CAGCGATTAA	AAGCTCTAGT	240
AAAGGGATCA	TTTTAATTGA	TGGCTATCCC	AGGAGCGTGG	AGCAAATGCA	AGCTTTGGAT	300
AAGGAATTGA	ACGCTCAAAA	TGAAGTGATC	TTAAAAAGCG	TGATTGAAGT	AGAAGTGAGC	360
GAAACACCG	CTAAAGAAAG	GGTTTTAGGG	CGCTCTAGGG	GGGCTGATGA	TAATGAAAGG	420
GTGTTTCATA	ACCGCATGCG	GGTGTTTTTA	GATCCGTTGG	TTGAAATCCA	AACTTCTTAC	480
AAGGCCAAGC	ATTTGCATAA	AATTATCAAT	GGTGAAAGAA	GCATTGAAGA	AATCGTGAAT	540
GAAATGCAAA	AATATATTTT	GTCTTTTGCA	AATTAA			576

(2) INFORMATION FOR SEQ ID NO:1031:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1023 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1023
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

TTGAGTTCGT	TATGGCTGAC	AAACCCCTTA	AATGCCCATG	AAAAGAATGG	CGCGTTTG TG	60
GGGATTAGCT	TGGAAGTGGG	TAGGGTCGAT	CAAAAGACCA	ACGCTTATAG	AAACGGCGAG	120
TTGTTTCAAG	TGCCTTTTGG	CGATGTTTCG	GCTAATGATG	ATGGCAAAGT	CCCTGATGGG	180
CAGACCGGTG	GCTGTCAGCC	AGCTTCAGGG	ACTCCAGGAA	CGCCAGGCTA	TACTAAAGCT	240
AATTGCGTGG	TCAATTGGAC	TTCTCGCACC	ATGCTTAGCA	CCAATAAGGA	CATTCCTGGC	300
CGTAACCAGC	CGATGTATGG	GCTAGGCGTG	ATGACAGGGT	ATAAGCATTT	TGTGGGTAAA	360
AAAAGGTGGT	TTGGGCTGCG	TTATTATGGC	TTTTTTGATT	ACGGGCATAC	CAATTTCTCT	420
AACTCTAGGG	CCGCTAACGC	CATATCGCCC	TTTTATTGTA	GCGATCAAAA	AGCGGACATG	480
TATACTTATG	GTTTTGGCAC	AGACATGCTT	TTTAACGTTA	TAGACAAGCC	TAAAGCCACG	540
GCCGGGTTTT	TTGTGGGCGT	GAATTTTGCG	GGTAACACTT	GGACTAATAA	TCGTGTGGGG	600
TATTTTAAGG	ACGGGTATGT	TTATGGCGTC	AATACGGACG	CTGACGCTTA	CATGACTAAC	660
GCTGATGGCA	CGATCACATG	CGGAGACACG	ACGCCGGCGA	GTTGTAATGT	GGGGATTAAAC	720
CCTAACAGCG	TCTATACCAC	AGGAAAATTA	AACGCTAAAG	TGAATCACAC	GATTTTCCAA	780
TTTTTAGTGA	ATGTGGGCAT	TAGAACCAAT	ATTTTGAAC	ACCATGGCAT	TGAGTTTGGT	840
ATCAAAATCC	CCACGCTCCC	TAATTACTTT	TTCAAAGGTT	CTACTACTAT	AAGAGCGAAA	900
AAACAAGGCC	CAC TAGAGAA	TGGGAACCCG	ACTACTATCA	CCGGAGCAGA	AACCAATTTC	960
AGCTTAACCC	AAACCTTACG	CCGTCAGTAT	TCTATGTATT	TGCGTTATGT	TTATACTTTT	1020
TAA						1023

(2) INFORMATION FOR SEQ ID NO:1032:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1587 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

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ATGAAATTAA AAAACGAAA AGTTGCGGCT ACATTGCTAA AGCGTTTGAC CTTGCCACTA      60
TTGTTCACTA CGGGTTCATT AGGGGCGGTT ACTTATGAAG TGCATGGGGA TTTTATCAAC      120
TTCTCCAAAG TGGGTTTTAA CCGTTCGCCT ATTAACCCCTG TTAAAGGTAT CTATCCTACA      180
GAAACTTTTTG TTAACCTTAC GGGTAAGCTA GAGGGGTCTG TGCATTTAGG TAGGGGATGG      240
ACCGTGAATG TAGGCGGTGT TTTGGGCGGA CAAGTTTATG ATAACACTAG GTATGATAGG      300
TGGGCAAAGG ATTTTACCCC CCCAAGCTAT TGGGATAAAA CTTCTTGCGG CACTGATTCT      360
TTGAGCCTTT GTATGAATGC GACTAAAATG TGGCAACAGC AAGGGCCAGG TGGTATCATT      420
GACCCTAGGG GTATTGGCTA TATGTATATG GGTGAGTGGA ACGGCTTGTT CCCTAATTAC      480
TATCCGGCTA ACGCCTACTT GCCCGGGCAT TCAAGGCGCT ATGAAGTTTA TAAAGCGAAT      540
CTTACCTATG ACAGCGACAG AGTCCATATG GTAATGGGGC GCTTTGATGT TACCAGACAG      600
GAGCAAATGG ATTGGATTTA CCAATTGTTC CAAGGTTTTT ATGGGACTTT CAAGCTTACT      660
AAGAACATGA AATTCTTGCT CTTTAGCTCT TGGGGTCGTG GTATCGCTGA TGGTCAATGG      720
TTGTTCCCTA TCTATCGTGA AAAGCCTTGG GGTATTCATA AGGCGGGTAT TATTTATCGC      780
CCTACAAAGA ATCTAATGAT CCACCCTTAT GTGTATCTCA TCCCAATGGT AGGTACATTG      840
CCCGGTGCTA AAATAGAATA CGATACCAAT CCTGAGTTTA GCGGTAGAGG TATAAGGAAT      900
AAAACGACTT TCTATGTGTT GTATGACTAT CGTTGGAATA ACGCTGAATA CGGCCGTTAC      960
GCACCCGCTC GTTATAACAC TTGGGATCCG TTCTTGATA ATGGTAAGTG GCGTGGCTTG     1020
CAAGGTCTCT GTGGTGCGAC GCTCTATTTG CACCACCACA TAGACATTAA CAACTACTTT     1080
GTGGTTGGTG GTGCTTACCT CAACATCGGT AACCCTAACA TGAACCTAGG TACTTGGGGT     1140
AACCCTGTGG CTCTTGATGG TATCGAACAA TGGGTTCGGTG GCATCTACAG CTTAGGCTTT     1200
GCGGGGATTG ACAACATTAC CGATGCTGAT GCGTTCCTG AGTATGTTAA AGGTGGAGGT     1260
AAGCATGGTA AGTTCAGTTG GAGCGTTTAT CAGCGCTTCA CTACCGCACC AAGGGCTTTG     1320
GAATATGGTA TTGGTATGTA TCTAGACTAT CAGTTCAGCA AGCATGTTAA AGCGGGTCTC     1380
AAACTCGTGT GGTAGAGTT CCAAATCCGT GCGGGTTACA ACCCTGGAAC CGGTTTCCTT     1440
GGGCCAAACG GTCAGCCGCT CAACTTGAAT AATGGTTTGT TTGAATCTTC GCGGTTTCGG     1500
CAAGGCCCTC AAAACATGGG TGGTATCGCA AAAAGCATTA CTCAAGACAG AAGCCATTG     1560
ATGACACACA TCAGTTATAG TTTCTAA

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(2) INFORMATION FOR SEQ ID NO:1033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

ATGACAAAAA	TTGCCATGGC	TAATTTCAAA	TCCGCTATGC	CTGTTTTTAA	AAGCCATGCG	60
TATTTAAAG	AATTGGAAAA	AACTTTAAAG	CCGCAGCATT	TTGATAGGGT	GTTTGTATTC	120
CCTGATTTT	TGGGGTTATT	GCCTAACGCG	TTTTTGCATT	TCACTTTAGG	AGCGCAAAAC	180
GCTTACCCTA	GAGATTGTGG	GGCTTTTACC	GGTGAAATCA	CTTCCAAACA	TTTAGAAGAA	240
CTGAAAATCC	ACACGCTTTT	AATAGGGCAT	AGCGAGAGGC	GAGTGCTTTT	AAAGGAAAGC	300
CCTAGCTTTT	TGAAAGAAAA	ATTTGATTTT	TTTAAAGGTA	AAAATTTTAA	AATTGTCTAT	360
TGTATTGGCG	AAGATTTAAC	GACCAGAGAA	AAGGGTTTTA	GGGCTGTAAA	GGAATTTTAA	420
AGCGAGCAAT	TAGAAAATAT	TGATCTTAAT	TATTCCAATT	TAATTGTGGC	TTATGAGCCT	480
ATTTGGGCGA	TTGGCACTAA	AAAAAGCGCG	TCTTTAGAAG	ATATTACCT	CACGCATGGT	540
TTTTTAAAGC	AAATCTTAA	TCAAAAACG	CCCTTATTGT	ATGGGGGGAG	CGTGAATGCG	600
CAAACGCTA	AAGAAATTTT	AGGGATTGAT	AGCGTGGATG	GCTTATTGAT	TGGGAGCGCG	660
TCTTTGGAAT	TAGAAAATTT	TAAAACAATC	ATTTTCATTT	TATAA		705

(2) INFORMATION FOR SEQ ID NO:1034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:

ATGTTTCATTT	ATGATACCAA	ATTAAAACAA	AAAGTCCCTT	TTGAGCCTTT	AGTCCACAAT	60
AAGGCGAATA	TTTATGTGTG	TGGGCCTACG	GTGTATGATG	ACGCTCATTT	AGGGCATGCC	120
AGGAGCGCGA	TTGCTTTTGA	TTTGTGTGAG	CGCACGCTTG	AATTGAGCGG	CTATGAAGTG	180
GTGCTAGTAA	GGAATTTTAC	GGATATTGAC	GATAAGATTA	TCAATAAAGC	CTTCAAAGAA	240
AACAAAAGCA	TTCAAGAATT	AAGCAGCATT	TACATTGAAT	CTTACACGAG	GGATCTAAAC	300
GCTTTGAACG	TGAAACAACC	CAGCCTAGAG	CCTAAAGCGA	GCGAGTATTT	AGACGCTATG	360
GTGCGCATGA	TTGAAACGCT	TTTAGAAAAA	AATTTTCGCTT	ATAGAGTTTC	TAATGGGGAT	420
ATTTATTTAG	ACACGAGCAA	GGACAAAGAT	TACGGCTCTT	TGAGCATGCA	TAATAGCAGC	480
GTGGAATTTA	GCCGTATCGG	TTTGGTGCAA	GAAAAACGGC	TTGAGCAGGA	TTTTGTGTTA	540
TGGAAGAGCT	ATAAGGGGGA	TAATGATGTG	GGCTTTGATA	GCCCTTTAGG	CAAAGGGCGC	600
CCTGGCTGGC	ACATAGAATG	CTCTAGCATG	GTTTTTGAAA	CTTTAGCGCT	CGCTAACGCC	660
CCTTATCAAA	TTGATATTCA	TGCTGGCGGA	ACGGATTGTG	TATTCCCCCA	CCATGAAAAT	720
GAAGCGTGCC	AAACCCGTTG	TGCCTTTGGC	GTGGAGATCG	CTAAATACTG	GATGCACAAT	780
GGCTTTGTGA	ATATCAATAA	CGAAAAAATG	TCTAAAAGTT	TAGGGAATAG	CTTTTTTCATT	840
AAAGACGCCC	TCAAAAACCTA	TGATGGCGAG	ATTTTGCCTA	ATTACTTACT	AGGGGTGCAT	900
TACCGCTCTG	TTTTGAATTT	CAATGAAGAA	GACTTGTTAA	TGAGTAAAAA	ACGCTTGGAT	960
AAAATCTATC	GTTTGAACA	GCGCGTTTTA	GGGACTTTAG	GAGGAATAAA	TCCAAACTTT	1020
AAAAAGAAA	TTTTAGAATG	CATGCAAGAT	GATTTAAACG	TTTCTAAAGC	GTTGAGCGTT	1080
TTAGAAAGCA	TGCTTTCTTC	TACGAATGAA	AAACTGGATC	AAAACCCTAA	AAACAAGGCT	1140
TTGAAAGGCG	AAATTTTAGC	GAATCTGAAA	TTCATAGAAG	AACTGCTTGG	TATTGGGTTT	1200

AAAGACCCTA	GCGCGTATTT	CCAATTAGGC	GTGAGCGAGA	GCGAAAAACA	AGAAATTGAA	1260
AACAAGATAG	AAGAAAGAAA	ACGTGCCAAA	GAACAAAAAG	ATTTTTTTAA	AGCCGATAGC	1320
ATCAGAGAAG	AGCTTTTACA	ACAAAAAATC	GCTTTGATGG	ACACCCCA	AGGCACGATT	1380
TGGGAGAAGC	TTTTTTAA					1398

(2) INFORMATION FOR SEQ ID NO:1035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

ATGAAACAAT	TTAAAAAGAA	ACCAAAAAAG	ATAAACGAT	CGCATCAAAA	TCAAAAAACA	60
ATCTTAAAGC	GTCCTTTATG	GCTTATGCCT	TTACTGATTG	GCGGGTTTGC	TAGTGGGGTG	120
TATGCGGATG	GAACAGACAT	TTTGGGGCTT	AGTTGGGGGG	AAAAAAGCCA	AAAGGTATGC	180
GTGCATCGTC	CATGGTATGC	TATATGGAGT	TGCGATAAAT	GGGAGGAAAA	AACACAACAA	240
TTTACAGGAA	ACCAACTCAT	CACAAAAACT	TGGGCAGGGG	GTAATGCGGC	TAAC TACTAC	300
CACTCTCAAA	ACAACCAAGA	CATCACAGCC	AATTTAAAAA	ATGATAACGG	CAC TTATTTT	360
TTAAGCGGTC	TGTATAACTA	CACCGGAGGG	GAATATAATG	GGGGGAATTT	AGACATTGAA	420
TTAGGCAGTA	ACGCTACTTT	TAATCTAGGT	GCGAGTAGTG	GGAATAGCTT	CAC TTCTTGG	480
TATCCTAATG	GGCATACTGA	TGTTACTTTT	AGCGCTGGGA	CTATCAATGT	GAATAACAGC	540
GTAGAAGTGG	GCAATCGTGT	GGGATCGGGA	GCTGGCACGC	ACACCGGCAC	AGCCACTTTA	600
AACTTGAACG	CTAATAAGGT	TACTATCAAT	TCCAATATCA	GCGCGTATAA	AACTTCGCAA	660
GTGAATGTAG	GCAATGCTAA	CAGCGTTATT	ACCATTAAAT	CGGTTTCTTT	AAATGGGGAT	720
ACTTGCAGTT	CTTTAGCTAG	GGTGGGCGTA	GGGGCTAATT	GCTCCACTTC	TGGGCCTAGC	780
TATTCTTTTA	AAGGGACGAC	TAACGCTACT	AACACGACTT	TTAGCAATTC	AAGCGGCAGT	840
TTCACTTTTG	AAGAGAACGC	CAC TTTTAGC	GGGGCGAAAT	TAAATGGGGG	GGCATTCACT	900
TTCAATAAAA	AGTTTAACGC	TACCAATAAT	ACCGCTTTTA	ATAGCGGTAG	TTTTACTTTT	960
AAAGGCACAA	GCTCTTTTAA	TGGTGCGAAT	TTTAGTAACG	CTTCCTATAC	TTTTAATAAT	1020
CAAGCCACTT	TCCAAAACAG	CTCCTTTAAT	GGGGGGACTT	TTACTTTTAA	TGACCAGACC	1080
AATCAAAGCA	CCCAGCACCC	CCAAATTCAA	AACAGCTCTT	TTAGCGGCAG	TGCTACCACT	1140
CTTAAGGGTT	TTGCGACTTT	TGAGCAAGCC	TTTAACAATT	CAAACCACCA	ACTAACGATA	1200
CAAAACGCTT	CCTTTAATAA	CGCTACTTTC	AACAATACCG	GTAATAATCAC	TATAGAAAAA	1260
GATGCGAGCT	TTAATAACAC	TTCGTTCAAC	ACTCCTGTTG	ATACAAACAA	CATGACTATT	1320
AGTGGTGGCG	TTACTTTAAG	CGGTAAAAAT	GACTTGAAAA	ATGGTGCAAC	CCTTGATTTT	1380
GGGAGTTCTA	AAATCACTCT	CACTCAAGGG	ACGACTTTCA	ACCTCACAAG	TTTAGGCAGT	1440
GAGAAGAGCG	TAACGATTTT	AAATTCTAGA	GGTGGGATCA	CTTACAATCA	TCTTTTAAAC	1500
CATGCGATCA	ATAGCTTGAC	AAACGCCCTA	AAAACGAACG	AAAGCTCTTC	AAAACCGCAA	1560
AGTTTCGCTC	AAGGTTTGTG	GGATATGATC	ACTTACAATG	GGGTTACCGG	GCAGCTTTTG	1620
AATGAAAACG	CTGCAACATC	TAAACCCACT	GACTCTTCGC	CCTCTAAATC	CTCTACAAAC	1680
TCTACGCAAG	TCTATCAAGT	GGGTTACAAA	ATAGGGGATA	CTATCTACAA	ACTGCAAGAA	1740

ACTTTCAGCC	ACAATTCCAT	TATTATTCAG	GCTTTAGAGA	GCGGGACTTA	CACGCCACCC	1800
CCTGTCAATTA	ACGGCTCCAA	ATTTGACTTA	TCCGCTTCAA	ATTATATCAA	TGCTGACATG	1860
CCTTGGTATA	ACCATAAATA	TTATATTCCT	AAATCCCAAA	ATTTTACAGA	GAGCGGGACT	1920
TATTACTTGC	CGAGCGTTCA	AATATGGGGG	AGCTACACTA	ACTCGTTTAA	ACAAACCTTT	1980
AGCGCAAGTA	ATAGCAATCT	GGTGATTGGG	TATAACGCAA	CATGGACTGA	TCACAATGTT	2040
TCTTCTAGCG	ACACGGTGGC	TTTGGGGGAC	ACTTCAGGGA	GCGCTCTTAA	TGGGCATTGC	2100
GGGCCTTGGC	CCTATTACCA	ATGCACAGGC	ACGACTAACG	GCACTTATAG	CGCTTATCAT	2160
GTCTATATCA	CAGCGAATCT	GCGTTCCTGG	AATCGTATAG	GCACCGGTGG	GGCAGCCAAT	2220
CTAATCTTTA	ATGGGGTAGA	TAGTATCAAT	ATCGCTAACG	CTACCATCAC	GCAACATAAC	2280
GCCGGGGCTT	ATTCAAGCTC	TATGACTTTT	TCCACGCAAA	ACATGGACAA	TTCGCAGAAT	2340
TTGAATGGCC	TAAATTCTAA	CGGCAAGCTT	TTGGTGTATG	GCACAACTTT	CACCTAACCA	2400
GCCAAAGACG	GGAAATTCAT	TTTCAATGCA	GGGCAAGCGA	CTTTTGAAAA	CACCAACTTT	2460
AATGGAGGGA	GTTACCAATT	CAGCGGCGAT	AGCTTGAATT	TTTCAAATAA	CAACCAGTTC	2520
AATAGCGGTT	CGTTTGAGAT	TGGCGCAAAA	AATACTATTT	TTAATAACGC	TAATTTTAAC	2580
AACAGCACTT	CTTTTAATTT	CAATAATTCT	AGCGCGACCA	CTTCGTTTGT	GGGGGATTTT	2640
ACTAACGCTA	ATTCAAATTT	GCAAATCGCT	GGGAACGCTG	TTTTTGGGAA	CTCTACTAAT	2700
GGCTCTCAAA	ATACCGCTAA	TTTTAATAAT	ACCGGCTCTG	TTAATATTGC	AGGGAATGCA	2760
ACCTTTGATA	ACGTGGTATT	TAACAGCCCT	ACGAACACGA	GCGTGAAAGG	GAAAGTTACT	2820
CTCAATAACA	TCACTTTAAA	AACTTGAAC	GCTCCTTTGT	CTTTTGGCGA	TGGGACGATT	2880
GTTTTTAGCG	CTCATTCGGT	GATTAATATT	GGTGAAGCTA	TCACAAATGG	CAACCCTATC	2940
ACCCTTGTA	GCTCTTCTAA	AGCAATTGAA	TACAACGACG	CTTTCAGTAA	AAATCTATGG	3000
CAGCTCATCA	ACTACCAAGG	GCATGGGGCT	AGCAGTGAAA	AGCTCGTTTC	TAGTGCGGGT	3060
AATGGCGTCT	ATGATGTGGT	GTATTCTTTC	AACAACCAAA	CCTACAATTT	CCAAGAGGTT	3120
TTTTACCCCA	ACAGCATTTT	TATCCGGCGT	TTGGGCGTTG	GCATGGTGTG	TGATTATGTG	3180
GATATGGAAA	AATCGGATCG	TTTGTATTAT	CAAAACGCTC	TCGGTTTTAT	GACCTACATG	3240
CCTAATAGCT	ATAACAATAA	TTTAGGGAAT	TTAAACAACA	CCATTTACTA	TTACGACAAC	3300
AGCATTGACT	TTTATGCGAG	CGGGAAAAC	CTATTCACCTA	AAGCGGAATT	TTCTCAAACG	3360
TTCACTGGGC	AAAACAGCGC	GATCGTTTTT	GGGGCTAAAA	ATATATGGAC	GAGCGTAAGC	3420
GATGCGCCGC	AATCTAATGT	GATCATTTCG	TTTGGGGACA	ATAAGGGAGC	AGGGAGTAAT	3480
GATGCGAGTG	GGCATTGCTG	GAATTTGCAA	TGCATAGGCT	TTATCACAGG	GCATTATGAA	3540
GCGCAAAAGA	TTTACATCAC	CGGCAGTATT	GAAAGCGGGA	ACCGCATTTT	TAGCGGTGGG	3600
GCGCGAGCCT	TAATTTTAAC	GGGCTTCAAG	GCATTCTTTT	AA		3642

(2) INFORMATION FOR SEQ ID NO:1036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

ATGGCTGAAT GGAAAACGGA CACAGAAGAA GTCAAAAAGG TTGTTGGAAG ATGCAGGGAA

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TTTAAAAGAT CCCTGCAAGA AGAAAAATGC AGTCCATTTA TCAAAGACCT TGATAGTTAC 120
GCGCTAAAAA TCATAGTGGA GCGCAGAAAA ACTGAAATGC AATTGGAAAA AGCCATAGGA 180
GAATTAAAAA AAGCCAAAAG CAATGAAGAT GACGCTAAAG TTGCTTTAAG AGTCTTGCAA 240
GGTGCTTCTG TCGTCTCGTG GATTTGGCCT CCTGCTAGAA TAGCTGCTAC GGCAGCCATT 300
GTAGCCGCTG AAGCTGTTTT GAAATTTATG AAAGAAGACA CAGAAAAATG CAAAAGGAAT 360
GTGGAGCTAT TAGAACGAAT GCTTGAAATC TACTCGAATC AAGCCAAAGC GAGCGCGAAT 420
CTTATGAATC AAGCTTGGA GGGCATTAAA AAGAGGTTGC ATTTTATAC TGATAAGCAC 480
CAGGAATTTA TCAGGCGTTT GAAACAAGCG AGCGATGCGA TAGATAACGA ATACAACTTT 540
CCAACCTCCAG GCGTTTTATT GGAATACGAT TTTGAACGGC CTGCTATCTC TTATACCCCT 600
AAAAAAGCG TTTTAAATGA GCGCTTGAAG GATTTGAGGG AAAATTTTAG CGCTTCTTTA 660
TACGCTGATT TGAAAGACAA GATCCATCAT AACGCCTTGT CTAACGATGA TTTAGAACGC 720
ATGATAGCTT TTAGAGAGCA AGAATTTGAA AAGAGTTTAG AGGATTGGAT GGGTGCATAT 780
TCTTATGATG AAAACCCTAA CGATGAATTA GATCGCATGG CAATATCTAA AGAGCAGGAG 840
TTGGAAAAGA GTTTAGAGGA TTTGATGCCA AGCGTTTTAG GCGTGCCTTC TTATAACGAA 900
AGCTTGACTT TAGCCAAAAA TCGTTGCGTT AAAAATTTA AGGAAGCTTT AGAAGGTTTT 960
ACAGAAAAAA TCAAAGAATC CCCTAACGAT TCAAACGCTA TCAATGAAGC CTTTGATAAT 1020
TTAGAAACAG AGTTAGAGCG CGCTACAGAA AATTTGAGTC AAAAAATCGA TCCCGTTTTA 1080
GAACGGAATG AAAATTATAC GCAAAAAGCG TTGGAGTATA GGGAGTTTTT AGAAAGCCGT 1140
AAAGAGAGCT TTATTGTAGA TGAAAAAAC CCCTATCCGG AAGAAGTCAG CTTTAATGAA 1200
TGGCGTTGGG CGGAATTTGA TAGCGTTTTT AGCGCCATTG TGCCTTTAGA AGATTTAAAT 1260
AAAACCGCAT GCGCTCATCA TGCCCTAAAG GCTTTACAAG CTACGCTTAA AGACAACGAT 1320
TTGGGCTTTG ATGCGACAGA GTTGGAACAG ATCGCAAAAG GATTCATCCC TAGGGGGTAT 1380
TTGTGGCATT TTGACGCGAA TGTTTATAGG AATTTAGCGC TGGTGAGAGA AGAGTTATTA 1440
TTAGGCGTGA AACACACGAA AGGATATTCA CTATGGACAG AATTTCTACA GAAACAGAAT 1500
TGA 1503

```

(2) INFORMATION FOR SEQ ID NO:1037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

```

Met Gln Phe Gln Lys Thr Leu Ser Ser Leu Ser Leu Phe Leu Ser Leu
1           5           10           15
Ser Leu Phe Leu Ser Phe Ser Ile Ala Glu Glu Asn Gly Ala Tyr Ala
20           25           30
Ser Val Gly Phe Glu Tyr Ser Ile Ser His Ala Val Glu His Asn Asn
35           40           45
Pro Phe Leu Asn Gln Glu Arg Ile Gln Thr Ile Ser Asn Ala Gln Asn
50           55           60
Gln Ile Tyr Lys Leu Asn Gln Ile Glu Asn Glu Ile Thr Asn Met Gln
65           70           75           80
Asn Thr Phe Asn Tyr Thr Asn Asn Ala Leu Lys Asn Asn Ala Lys Leu

```

937

(2) INFORMATION FOR SEQ ID NO:1038:

(A) LENGTH: 632 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) **FEATURE:**

(A) NAME/KEY: misc_feature

(B) LOCATION 1...632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

Met	Lys	Pro	Thr	Asn	Glu	Pro	Lys	Lys	Pro	Phe	Phe	Gln	Ser	Pro	Ile
1				5					10					15	
Val	Leu	Ala	Val	Leu	Gly	Gly	Ile	Leu	Leu	Ile	Phe	Phe	Leu	Arg	Ser
			20					25					30		
Phe	Asn	Ser	Asp	Gly	Ser	Phe	Ser	Asp	Asn	Phe	Leu	Ala	Ser	Ser	Thr
		35					40					45			
Lys	Asn	Val	Ser	Tyr	His	Glu	Ile	Lys	Gln	Leu	Ile	Ser	Asn	Asn	Glu
	50					55					60				
Val	Glu	Asn	Val	Ser	Ile	Gly	Gln	Thr	Leu	Ile	Lys	Ala	Ser	His	Lys
65					70					75					80
Glu	Gly	Asn	Asn	Arg	Val	Ile	Tyr	Ile	Ala	Lys	Arg	Val	Pro	Asp	Leu
				85					90					95	
Thr	Leu	Val	Pro	Leu	Leu	Asp	Glu	Lys	Lys	Ile	Asn	Tyr	Ser	Gly	Phe
			100					105					110		
Ser	Glu	Ser	Asn	Phe	Phe	Thr	Asp	Met	Leu	Gly	Trp	Leu	Met	Pro	Ile

115	120	125
Leu Val Ile Leu Gly Leu Trp Met Phe Met Ala Asn Arg Met Gln Lys		
130	135	140
Asn Met Gly Gly Gly Ile Phe Gly Met Gly Ser Ala Lys Lys Leu Ile		
145	150	155
Asn Ala Glu Lys Pro Asn Val Arg Phe Asn Asp Met Ala Gly Asn Glu		
165	170	175
Glu Ala Lys Glu Glu Val Val Glu Ile Val Asp Phe Leu Lys Tyr Pro		
180	185	190
Glu Arg Tyr Ala Asn Leu Gly Ala Lys Ile Pro Lys Gly Val Leu Leu		
195	200	205
Val Gly Pro Pro Gly Thr Gly Lys Thr Leu Leu Ala Lys Ala Val Ala		
210	215	220
Gly Glu Ala His Val Pro Phe Phe Ser Met Gly Gly Ser Ser Phe Ile		
225	230	235
Glu Met Phe Val Gly Leu Gly Ala Ser Arg Val Arg Asp Leu Phe Glu		
245	250	255
Thr Ala Lys Lys Gln Ala Pro Ser Ile Ile Phe Ile Asp Glu Ile Asp		
260	265	270
Ala Ile Gly Lys Ser Arg Ala Ala Gly Gly Met Ile Ser Gly Asn Asp		
275	280	285
Glu Arg Glu Gln Thr Leu Asn Gln Leu Leu Ala Glu Met Asp Gly Phe		
290	295	300
Gly Ser Glu Asn Ala Pro Val Ile Val Leu Ala Ala Thr Asn Arg Pro		
305	310	315
Glu Ile Leu Asp Pro Ala Leu Met Arg Pro Gly Arg Phe Asp Arg Gln		
325	330	335
Val Leu Val Asp Lys Pro Asp Phe Asn Gly Arg Val Glu Ile Leu Lys		
340	345	350
Val His Ile Lys Gly Val Lys Leu Ala Asn Asp Val Asn Leu Gln Glu		
355	360	365
Val Ala Lys Leu Thr Ala Gly Leu Ala Gly Ala Asp Leu Ala Asn Ile		
370	375	380
Ile Asn Glu Ala Ala Leu Leu Ala Gly Arg Asn Asn Gln Lys Glu Val		
385	390	395
Lys Gln Gln His Leu Lys Glu Ala Val Glu Arg Gly Ile Ala Gly Leu		
405	410	415
Glu Lys Lys Ser Arg Arg Ile Ser Pro Lys Glu Lys Lys Ile Val Ala		
420	425	430
Tyr His Glu Ser Gly His Ala Val Ile Ser Glu Met Thr Lys Gly Ser		
435	440	445
Thr Arg Val Asn Lys Val Ser Ile Ile Pro Arg Gly Met Ala Ala Leu		
450	455	460
Gly Tyr Thr Leu Asn Thr Pro Glu Glu Asn Lys Tyr Leu Met Gln Lys		
465	470	475
His Glu Leu Ile Ala Glu Ile Asp Val Leu Leu Gly Gly Arg Ala Ala		
485	490	495
Glu Glu Val Phe Leu Glu Glu Ile Ser Thr Gly Ala Ser Asn Asp Leu		
500	505	510
Glu Arg Ala Thr Asp Ile Ile Lys Gly Met Val Ser Tyr Tyr Gly Met		
515	520	525
Ser Ser Val Ser Gly Leu Met Val Leu Glu Lys Gln Arg Asn Ala Phe		
530	535	540
Leu Gly Gly Gly Tyr Gly Ser Ser Arg Glu Phe Ser Glu Lys Thr Ala		
545	550	555
Glu Glu Met Asp Leu Phe Ile Lys Asn Leu Leu Glu Glu Arg Tyr Gln		
565	570	575

```

His Val Lys Gln Thr Leu Ser Asp Tyr Arg Glu Ala Ile Glu Ile Met
      580                      585                      590
Val Lys Glu Leu Phe Asp Lys Glu Val Ile Thr Gly Glu Arg Val Arg
      595                      600                      605
Glu Ile Ile Ser Glu Tyr Glu Ala Ala Asn Asn Leu Glu Ser Arg Leu
      610                      615                      620
Ile Pro Leu Glu Glu Gln Ala Ser
625                      630

```

(2) INFORMATION FOR SEQ ID NO:1039:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1288 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

```

Met Glu Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser
1           5           10           15
Leu Val Leu Ala Gly Ala Leu Ile Ser Ala Ile Pro Gln Glu Ser His
      20           25           30
Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile
      35           40           45
Ala Thr Gly Thr Ala Val Gly Thr Val Ser Gly Leu Leu Ser Trp Gly
      50           55           60
Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys
65           70           75           80
Val Trp Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys
      85           90           95
Glu Tyr Asp Leu Tyr Lys Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly
      100          105          110
Trp Asp Trp Gly Asn Ala Ala Arg His Tyr Trp Val Lys Gly Gly Gln
      115          120          125
Trp Asn Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Lys
      130          135          140
Leu Ser Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met
145          150          155          160
Gln Lys Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr
      165          170          175
Ser Tyr Lys Asp Ser Ala Asp Arg Thr Thr Arg Val Asn Phe Asn Ala
      180          185          190
Lys Asn Ile Ser Ile Asp Asn Phe Val Glu Ile Asn Asn Arg Val Gly
      195          200          205
Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala
210          215          220

```

Ser Glu Gly Ile Thr Ser Ser Lys Asn Ala Glu Ile Ser Leu Tyr Asp
 225 230 235 240
 Gly Ala Thr Leu Asn Leu Ala Ser Asn Ser Val Lys Leu Asn Gly Asn
 245 250 255
 Val Trp Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser
 260 265 270
 Tyr Ser Thr Ile Asn Thr Ser Lys Val Gln Gly Glu Val Asp Phe Asn
 275 280 285
 His Leu Thr Val Gly Asp Gln Asn Ala Ala Gln Ala Gly Ile Ile Ala
 290 295 300
 Ser Asn Lys Thr His Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly
 305 310 315 320
 Leu Asn Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Asn
 325 330 335
 Ser Thr Thr Ser Gln Ser Gly Thr Lys Asn Asp Lys Lys Glu Ile Ser
 340 345 350
 Gln Asn Asn Asn Ser Asn Thr Glu Val Ile Asn Pro Pro Asn Asn Thr
 355 360 365
 Gln Lys Thr Glu Thr Glu Pro Thr Gln Val Ile Asp Gly Pro Phe Ala
 370 375 380
 Gly Gly Lys Asp Thr Val Val Asn Ile Phe His Leu Asn Thr Lys Ala
 385 390 395 400
 Asp Gly Thr Ile Lys Val Gly Gly Phe Lys Ala Ser Leu Thr Thr Asn
 405 410 415
 Ala Ala His Leu Asn Ile Gly Lys Gly Gly Val Asn Leu Ser Asn Gln
 420 425 430
 Ala Ser Gly Arg Thr Leu Leu Val Glu Asn Leu Thr Gly Asn Ile Thr
 435 440 445
 Val Asp Gly Pro Leu Arg Val Asn Asn Gln Val Gly Gly Tyr Ala Leu
 450 455 460
 Ala Gly Ser Ser Ala Asn Phe Glu Phe Lys Ala Gly Val Asp Thr Lys
 465 470 475 480
 Asn Gly Thr Ala Thr Phe Asn Asn Asp Ile Ser Leu Gly Arg Phe Val
 485 490 495
 Asn Leu Lys Val Asp Ala His Thr Ala Asn Phe Lys Gly Ile Asp Thr
 500 505 510
 Gly Asn Gly Gly Phe Asn Thr Leu Asp Phe Ser Gly Val Thr Asp Lys
 515 520 525
 Val Asn Ile Asn Lys Leu Ile Thr Ala Ser Thr Asn Val Ala Val Lys
 530 535 540
 Asn Phe Asn Ile Asn Glu Leu Ile Val Lys Thr Asn Gly Ile Ser Val
 545 550 555 560
 Gly Glu Tyr Thr His Phe Ser Glu Asp Ile Gly Ser Gln Ser Arg Ile
 565 570 575
 Asn Thr Val Arg Leu Glu Thr Gly Thr Arg Ser Ile Phe Ser Gly Gly
 580 585 590
 Val Lys Phe Lys Ser Gly Glu Lys Leu Val Ile Asn Asp Phe Tyr Tyr
 595 600 605
 Ser Pro Trp Asn Tyr Phe Asp Ala Arg Asn Val Lys Asn Val Glu Ile
 610 615 620
 Thr Arg Lys Phe Ala Ser Ser Thr Pro Glu Asn Pro Trp Gly Thr Ser
 625 630 635 640
 Lys Leu Met Phe Asn Asn Leu Thr Leu Gly Gln Asn Ala Val Met Asp
 645 650 655
 Tyr Ser Gln Phe Ser Asn Leu Thr Ile Gln Gly Asp Phe Ile Asn Asn
 660 665 670
 Gln Gly Thr Ile Asn Tyr Leu Val Arg Gly Gly Lys Val Ala Thr Leu

675	680	685
Asn Val Gly Asn Ala Ala Ala Met Met Phe Asn Asn Asp Ile Asp Ser		
690	695	700
Ala Thr Gly Phe Tyr Lys Pro Leu Ile Lys Ile Asn Ser Ala Gln Asp		
705	710	715
Leu Ile Lys Asn Thr Glu His Val Leu Leu Lys Ala Lys Ile Ile Gly		
725	730	735
Tyr Gly Asn Val Ser Thr Gly Thr Asn Gly Ile Ser Asn Val Asn Leu		
740	745	750
Glu Glu Gln Phe Lys Glu Arg Leu Ala Leu Tyr Asn Asn Asn Asn Arg		
755	760	765
Met Asp Thr Cys Val Val Arg Asn Thr Asp Asp Ile Lys Ala Cys Gly		
770	775	780
Met Ala Ile Gly Asn Gln Ser Met Val Asn Asn Pro Asp Asn Tyr Lys		
785	790	795
Tyr Leu Ile Gly Lys Ala Trp Arg Asn Ile Gly Ile Ser Lys Thr Ala		
805	810	815
Asn Gly Ser Lys Ile Ser Val Tyr Tyr Leu Gly Asn Ser Thr Pro Thr		
820	825	830
Glu Asn Gly Gly Asn Thr Thr Asn Leu Pro Thr Asn Thr Thr Asn Asn		
835	840	845
Ala His Ser Ala Asn Tyr Ala Leu Val Lys Asn Ala Pro Phe Ala His		
850	855	860
Ser Ala Thr Pro Asn Leu Val Ala Ile Asn Gln His Asp Phe Gly Thr		
865	870	875
Ile Glu Ser Val Phe Glu Leu Ala Asn Arg Ser Lys Asp Ile Asp Thr		
885	890	895
Leu Tyr Thr His Ser Gly Ala Gln Gly Arg Asp Leu Leu Gln Thr Leu		
900	905	910
Leu Ile Asp Ser His Asp Ala Gly Tyr Ala Arg Gln Met Ile Asp Asn		
915	920	925
Thr Ser Thr Gly Glu Ile Thr Lys Gln Leu Asn Ala Ala Thr Asp Ala		
930	935	940
Leu Asn Asn Val Ala Ser Leu Glu His Lys Gln Ser Gly Leu Gln Thr		
945	950	955
Leu Ser Leu Ser Asn Ala Met Ile Leu Asn Ser Arg Leu Val Asn Leu		
965	970	975
Ser Arg Lys His Thr Asn His Ile Asn Ser Phe Ala Gln Arg Leu Gln		
980	985	990
Ala Leu Lys Gly Gln Glu Phe Ala Ser Leu Glu Ser Ala Ala Glu Val		
995	1000	1005
Leu Tyr Gln Phe Ala Pro Lys Tyr Glu Lys Pro Thr Asn Val Trp Ala		
1010	1015	1020
Asn Ala Ile Gly Gly Ala Ser Leu Asn Ser Gly Ser Asn Ala Ser Leu		
1025	1030	1035
Tyr Gly Thr Ser Ala Gly Val Asp Ala Phe Leu Asn Gly Asn Val Glu		
1045	1050	1055
Ala Ile Val Gly Gly Phe Gly Ser Tyr Gly Tyr Ser Ser Phe Ser Asn		
1060	1065	1070
Gln Ala Asn Ser Leu Asn Ser Gly Ala Asn Asn Ala Asn Phe Gly Val		
1075	1080	1085
Tyr Ser Arg Phe Phe Ala Asn Gln His Glu Phe Asp Phe Glu Ala Gln		
1090	1095	1100
Gly Ala Leu Gly Ser Asp Gln Ser Ser Leu Asn Phe Lys Ser Thr Leu		
1105	1110	1115
Leu Gln Asp Leu Asn Gln Ser Tyr Asn Tyr Leu Ala Tyr Ser Ala Thr		
1125	1130	1135

Ala Arg Ala Ser Tyr Gly Tyr Asp Phe Ala Phe Phe Arg Asn Ala Leu
 1140 1145 1150
 Val Leu Lys Pro Ser Val Gly Val Ser Tyr Asn His Leu Gly Ser Thr
 1155 1160 1165
 Asn Phe Lys Ser Asn Ser Gln Ser Gln Val Ala Leu Lys Asn Gly Ala
 1170 1175 1180
 Ser Ser Gln His Leu Phe Asn Ala Asn Ala Asn Val Glu Ala Arg Tyr
 1185 1190 1195 1200
 Tyr Tyr Gly Asp Thr Ser Tyr Phe Tyr Leu His Ala Gly Val Leu Gln
 1205 1210 1215
 Glu Phe Ala His Phe Gly Ser Asn Asp Val Ala Ser Leu Asn Thr Phe
 1220 1225 1230
 Lys Ile Asn Ala Ala Arg Ser Pro Leu Ser Thr Tyr Ala Arg Ala Met
 1235 1240 1245
 Met Gly Gly Glu Leu Gln Leu Ala Lys Glu Val Phe Leu Asn Leu Gly
 1250 1255 1260
 Val Val Tyr Leu His Asn Leu Ile Ser Asn Ala Ser His Phe Ala Ser
 1265 1270 1275 1280
 Asn Leu Gly Met Arg Tyr Ser Phe
 1285

(2) INFORMATION FOR SEQ ID NO:1040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1484 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

Gly Ala Val Ser Leu Arg Gly Gln Phe Asn Leu Ser Asn Asn Ser Ser
 1 5 10 15
 Leu Asp Phe Gln Gly Ser Ser Ala Ile Thr Ser Asn Thr Ala Phe Asn
 20 25 30
 Phe Tyr Asp Asn Ala Phe Ser Gln Ser Pro Ile Thr Phe His Gln Ala
 35 40 45
 Leu Asp Ile Lys Val Pro Leu Ser Leu Gly Gly Asn Leu Leu Asn Pro
 50 55 60
 Asn Asn Ser Ser Val Leu Asn Leu Lys Asn Ser Gln Leu Val Phe Ser
 65 70 75 80
 Asp Gln Gly Ser Leu Asn Ile Ala Asn Ile Asp Leu Leu Ser Asp Leu
 85 90 95
 Asn Gly Asn Lys Asn Arg Val Tyr Asn Ile Ile Gln Ala Asp Met Asn
 100 105 110
 Gly Asn Trp Tyr Glu Arg Ile Asn Phe Phe Gly Met Arg Ile Asn Asp
 115 120 125

Gly Ile Tyr Asp Ala Lys Asn Gln Thr Tyr Ser Phe Thr Asn Pro Leu
 130 135 140
 Asn Asn Ala Leu Lys Ile Thr Glu Ser Phe Lys Asn Asn Gln Leu Ser
 145 150 155 160
 Val Thr Leu Ser Gln Ile Pro Gly Ile Lys Asn Thr Leu Tyr Asn Ile
 165 170 175
 Gly Ser Glu Ile Phe Asn Tyr Gln Lys Val Tyr Asn Asn Ala Asn Gly
 180 185 190
 Val Tyr Ser Tyr Ser Asp Asp Ala Gln Gly Val Phe Tyr Leu Thr Ser
 195 200 205
 Ser Val Lys Gly Tyr Tyr Asn Pro Asn Gln Ser Tyr Gln Ala Ser Gly
 210 215 220
 Ser Asn Asn Thr Thr Lys Asn Asn Asn Leu Thr Ser Glu Ser Ser Val
 225 230 235 240
 Ile Ser Gln Thr Tyr Asn Ala Gln Gly Asn Pro Ile Ser Ala Leu His
 245 250 255
 Val Tyr Asn Lys Gly Tyr Asn Phe Ser Asn Ile Lys Ala Leu Gly Gln
 260 265 270
 Met Ala Leu Lys Leu Tyr Pro Glu Ile Lys Lys Ile Leu Gly Asn Asp
 275 280 285
 Phe Ser Leu Ser Ser Leu Ser Asn Leu Lys Gly Asp Ala Leu Asn Gln
 290 295 300
 Leu Thr Lys Leu Ile Thr Pro Ser Asp Trp Lys Asn Ile Asn Glu Leu
 305 310 315 320
 Ile Asp Asn Ala Asn Asn Ser Val Val Gln Asn Phe Asn Asn Gly Thr
 325 330 335
 Leu Ile Ile Gly Ala Thr Lys Ile Gly Gln Thr Asp Thr Asn Ser Ala
 340 345 350
 Val Val Phe Gly Gly Leu Gly Tyr Gln Lys Pro Cys Asp Tyr Thr Asp
 355 360 365
 Ile Val Cys Gln Lys Phe Arg Gly Thr Tyr Leu Gly Gln Leu Leu Glu
 370 375 380
 Ser Ile Ser Ala Asp Leu Gly Tyr Ile Asp Thr Thr Phe Asn Ala Lys
 385 390 395 400
 Glu Ile Tyr Leu Thr Gly Thr Leu Gly Ser Gly Asn Ala Trp Gly Thr
 405 410 415
 Gly Gly Ser Ala Ser Val Thr Phe Asn Ser Gln Thr Ser Leu Ile Leu
 420 425 430
 Asn Gln Ala Asn Ile Val Ser Ser Gln Thr Asp Gly Ile Phe Ser Met
 435 440 445
 Leu Gly Gln Glu Gly Ile Asn Lys Val Phe Asn Gln Ala Gly Leu Ala
 450 455 460
 Asn Ile Leu Gly Glu Val Ala Met Gln Ser Ile Asn Lys Ala Gly Gly
 465 470 475 480
 Leu Gly Asn Leu Ile Val Asn Thr Leu Gly Ser Asp Ser Val Ile Gly
 485 490 495
 Gly Tyr Leu Thr Pro Glu Gln Lys Asn Gln Thr Leu Ser Gln Leu Leu
 500 505 510
 Gly Gln Asn Asn Phe Asp Asn Leu Met Asn Asp Ser Gly Leu Asn Thr
 515 520 525
 Ala Ile Lys Asp Leu Ile Arg Gln Lys Leu Gly Phe Trp Thr Gly Leu
 530 535 540
 Val Gly Gly Leu Ala Gly Leu Gly Gly Ile Asp Leu Gln Asn Pro Glu
 545 550 555 560
 Lys Leu Ile Gly Ser Met Ser Ile Asn Asp Leu Leu Ser Lys Lys Gly
 565 570 575
 Leu Phe Asn Gln Ile Thr Gly Phe Ile Ser Ala Asn Asp Ile Gly Gln

Asn Asn Ala Ser Gln Asn Asn Ile Leu Ser Leu Ser Val Leu His Asn
 1045 1050 1055
 Gln Ile Lys Met Ser Tyr Gly Asn Lys Val Met Asp Phe Thr Pro Pro
 1060 1065 1070
 Thr Leu Gln Asp Tyr Ile Val Gly Ile Gln Gly Gln Ser Ala Leu Asn
 1075 1080 1085
 Gln Ile Glu Ala Val Gly Gly Asn Asn Ala Ile Lys Trp Leu Ser Thr
 1090 1095 1100
 Leu Met Met Glu Thr Lys Glu Asn Pro Leu Phe Ala Pro Ile Tyr Leu
 1105 1110 1115 1120
 Glu Asn His Ser Leu Asn Glu Ile Leu Gly Val Thr Lys Asp Leu Gln
 1125 1130 1135
 Asn Thr Ala Ser Leu Ile Ser Asn Pro Asn Phe Arg Asn Asn Ala Thr
 1140 1145 1150
 Ser Leu Leu Glu Met Ala Ser Tyr Thr Gln Gln Thr Ser Arg Leu Thr
 1155 1160 1165
 Lys Leu Ser Asp Phe Arg Ala Arg Glu Gly Glu Ser Asn Phe Ser Glu
 1170 1175 1180
 Arg Leu Leu Glu Leu Lys Asn Lys Arg Phe Ser Asp Pro Asn Pro Ser
 1185 1190 1195 1200
 Glu Val Phe Val Lys Tyr Ser Gln Leu Ser Lys His Pro Asn Asn Leu
 1205 1210 1215
 Trp Ile Gln Gly Val Gly Gly Ala Ser Phe Ile Ser Gly Gly Asn Gly
 1220 1225 1230
 Thr Leu Tyr Gly Leu Asn Val Gly Tyr Asp Arg Leu Val Lys Ser Val
 1235 1240 1245
 Ile Leu Gly Gly Tyr Val Ala Tyr Gly Tyr Ser Gly Phe Asn Gly Asn
 1250 1255 1260
 Ile Met His Ser Leu Ala Asn Asn Val Asp Val Gly Met Tyr Ala Arg
 1265 1270 1275 1280
 Ala Phe Leu Lys Arg Asn Glu Phe Thr Leu Ser Ala Asn Glu Thr Tyr
 1285 1290 1295
 Gly Gly Asn Ala Ser His Ile Asn Ser Ser Asn Ser Leu Leu Ser Val
 1300 1305 1310
 Leu Asn Gln Arg Tyr Asn Tyr Asn Thr Trp Thr Thr Ser Val Asn Gly
 1315 1320 1325
 Asn Tyr Gly Tyr Asp Phe Met Phe Lys Gln Lys Ser Val Val Leu Lys
 1330 1335 1340
 Pro Gln Val Gly Leu Ser Tyr His Phe Ile Gly Leu Ser Gly Met Lys
 1345 1350 1355 1360
 Gly Lys Met Gln Asn Pro Ala Tyr Gln Gln Phe Val Met His Ser Asn
 1365 1370 1375
 Pro Ser Asn Glu Ser Val Leu Thr Leu Asn Met Gly Leu Glu Ser Arg
 1380 1385 1390
 Lys Tyr Phe Gly Lys Asn Ser Tyr Tyr Phe Val Thr Ala Arg Leu Gly
 1395 1400 1405
 Arg Asp Leu Leu Ile Lys Ala Lys Gly Asp Asn Val Val Arg Phe Val
 1410 1415 1420
 Gly Glu Asn Thr Leu Leu Tyr Arg Lys Gly Glu Ile Phe Asn Thr Phe
 1425 1430 1435 1440
 Ala Ser Val Ile Thr Gly Gly Glu Met His Leu Trp Arg Leu Met Tyr
 1445 1450 1455
 Val Asn Ala Gly Val Gly Leu Lys Met Gly Leu Gln Tyr Gln Asp Leu
 1460 1465 1470
 Asn Ile Thr Gly Asn Val Gly Met Arg Val Ala Phe
 1475 1480

(2) INFORMATION FOR SEQ ID NO:1041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

```

Met Arg Lys Thr Ile Ser Ala Leu Phe Leu Ser Ala Cys Ile Gly Leu
1           5           10           15
Ser Ser Val His Ala Ser Asn Ala Leu Ile Leu Gln Thr Asp Phe Ser
20           25           30
Leu Lys Asp Gly Ala Val Ser Ala Met Lys Gly Val Ala Phe Ser Val
35           40           45
Asp Ser Asn Leu Lys Ile Phe Asp Leu Thr His Glu Ile Pro Pro Tyr
50           55           60
Asn Ile Trp Glu Gly Ala Tyr Arg Leu Tyr Gln Thr Ala Ser Tyr Trp
65           70           75           80
Pro Lys Gly Ser Val Phe Val Ser Val Val Asp Pro Gly Val Gly Thr
85           90           95
Asn Arg Lys Ser Val Val Leu Lys Thr Lys Asn Gly Gln Tyr Phe Val
100          105          110
Ser Pro Asp Asn Gly Thr Leu Thr Leu Val Ala Gln Thr Leu Gly Ile
115          120          125
Asp Ser Val Arg Glu Ile Asp Glu Lys Ala Asn Arg Leu Lys Gly Ser
130          135          140
Glu Lys Ser Tyr Thr Phe His Gly Arg Asp Val Tyr Ala Tyr Thr Gly
145          150          155          160
Ala Arg Leu Ala Ser Gly Ala Ile Thr Phe Glu Gln Val Gly Pro Glu
165          170          175
Leu Pro Ile Lys Val Val Glu Ile Pro Tyr Gln Lys Ala Lys Ala Thr
180          185          190
Lys Gly Gly Val Lys Gly Asn Ile Pro Ile Leu Asp Ile Gln Tyr Gly
195          200          205
Asn Val Trp Ser Asn Ile Ser Asp Lys Leu Leu Asn Gln Ala Gly Ile
210          215          220
Lys Arg Asn Asp Thr Val Cys Val Thr Ile Phe Lys Asn Ser Lys Lys
225          230          235          240
Gln Tyr Glu Gly Lys Met Pro Tyr Val Ala Ser Phe Gly Asp Val Pro
245          250          255
Glu Gly Gln Pro Leu Val Tyr Leu Asn Ser Leu Leu Asn Val Ser Val
260          265          270
Ala Leu Asn Met Asp Asn Phe Ala Gln Lys His Gln Ile Lys Ser Gly
275          280          285
Ala Asp Trp Asn Ile Asp Ile Lys Lys Cys Ala Lys

```

290

295

300

(2) INFORMATION FOR SEQ ID NO:1042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

```

Met Lys Leu Phe Asn Pro Arg Leu Ile Val Phe Ile Phe Ala Leu Leu
1          5          10          15
Leu Gly Val Gly Phe Ser Val Pro Ser Leu Leu Glu Thr Lys Gly Pro
20          25          30
Lys Ile Thr Leu Gly Leu Asp Leu Arg Gly Gly Leu Asn Met Leu Leu
35          40          45
Gly Val Gln Thr Asp Glu Ala Leu Lys Asn Lys Tyr Leu Ser Leu Ala
50          55          60
Ser Ala Leu Glu Tyr Asn Ala Lys Lys Gln Asn Ile Leu Leu Lys Asp
65          70          75          80
Ile Lys Ser Ser Leu Glu Gly Ile Ser Phe Glu Leu Leu Asp Glu Asp
85          90          95
Glu Ala Lys Lys Leu Asp Ala Leu Leu Leu Glu Leu Gln Gly His Ser
100          105          110
Gln Phe Glu Ile Lys Lys Glu Ala Glu Phe Tyr Ser Val Lys Leu Thr
115          120          125
Pro Leu Glu Gln Glu Glu Leu Arg Lys Asn Thr Ile Leu Gln Val Ile
130          135          140
Gly Ile Ile Arg Asn Arg Leu Asp Gln Phe Gly Leu Ala Glu Pro Val
145          150          155          160
Val Ile Gln Gln Gly Arg Glu Glu Ile Ser Val Gln Leu Pro Gly Ile
165          170          175
Lys Thr Leu Glu Glu Arg Arg Ala Lys Asp Leu Ile Ser Lys Ser
180          185          190
Ala His Leu Gln Met Met Ala Val Asp Glu Glu His Asn Lys Asp Ala
195          200          205
Met Asn Met Thr Asp Leu Glu Ala Gln Lys Leu Gly Ser Val Leu Leu
210          215          220
Ser Asp Ala Glu Met Gly Gly Lys Ile Leu Leu Lys Ala Ile Pro Ile
225          230          235          240
Leu Asp Gly Glu Met Leu Thr Asp Ala Lys Val Val Tyr Asp Gln Asn
245          250          255
Asn Gln Pro Val Val Ser Phe Thr Leu Asp Ala Gln Gly Ala Lys Ile
260          265          270
Phe Gly Asp Phe Ser Gly Ala Asn Val Gly Lys Arg Met Ala Ile Val

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275	280	285
Leu Asp Asn Lys Val Tyr Ser Ala Pro Val Ile Arg Glu Arg Ile Gly		
290	295	300
Gly Gly Ser Gly Gln Ile Asn Gly Asn Phe Ser Val Ala Gln Ala Ser		
305	310	315
Asp Leu Ala Ile Ala Leu Arg Ser Gly Ala Met Asn Ala Pro Ile Gln		
325	330	335
Val Leu Glu Lys Arg Ile Val Gly Pro Ser Leu Gly Lys Asp Ser Ile		
340	345	350
Lys Thr Ser Ile Ile Ala Leu Val Gly Gly Phe Ile Leu Val Met Gly		
355	360	365
Phe Met Ala Leu Tyr Tyr Ser Met Ala Gly Val Ile Ala Cys Met Ala		
370	375	380
Leu Val Val Asn Leu Phe Leu Ile Val Ala Val Met Ala Ile Phe Gly		
385	390	395
Ala Thr Leu Thr Leu Pro Gly Met Ala Gly Ile Val Leu Thr Val Gly		
405	410	415
Ile Ala Val Asp Ala Asn Ile Ile Ile Asn Glu Arg Ile Arg Glu Val		
420	425	430
Leu Arg Glu Gly Glu Gly Val Val Lys Ala Ile His Leu Gly Tyr Ile		
435	440	445
Asn Ala Ser Arg Ala Ile Phe Asp Ser Asn Ile Thr Ser Leu Ile Ala		
450	455	460
Ser Val Leu Leu Tyr Ala Tyr Gly Thr Gly Ala Ile Lys Gly Phe Ala		
465	470	475
Leu Thr Thr Gly Ile Gly Ile Leu Ala Ser Ile Ile Thr Ala Ile Ile		
485	490	495
Gly Thr Gln Gly Ile Tyr Gln Ala Leu Leu Pro Lys Leu Ala Gln Thr		
500	505	510
Lys Ser Leu Tyr Phe Trp Phe Gly Val Lys Asn Lys Arg Ala		
515	520	525

(2) INFORMATION FOR SEQ ID NO:1043:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 793 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

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

35					40					45					
Ser	Ser	Ala	Pro	Ile	Ser	Trp	Gln	Ser	Glu	Glu	Val	Arg	Asn	Ser	Thr
50					55					60					
Ser	Ser	Arg	Thr	Val	Ile	Ser	Asn	Lys	Glu	Leu	Lys	Lys	Thr	Gly	Asn
65					70					75					80
Leu	Asn	Ile	Glu	Asn	Ala	Leu	Gln	Asn	Val	Pro	Gly	Ile	Gln	Ile	Arg
				85					90					95	
Asp	Ala	Thr	Gly	Thr	Gly	Val	Leu	Pro	Lys	Ile	Ser	Val	Arg	Gly	Phe
			100					105					110		
Gly	Gly	Gly	Gly	Asn	Gly	His	Ser	Asn	Thr	Asn	Met	Ile	Leu	Val	Asn
			115					120					125		
Gly	Ile	Pro	Ile	Tyr	Gly	Ala	Pro	Tyr	Ser	Asn	Ile	Glu	Leu	Ala	Ile
			130					135					140		
Phe	Pro	Val	Thr	Phe	Gln	Ser	Val	Asp	Arg	Ile	Asp	Val	Ile	Lys	Gly
145					150					155					160
Gly	Thr	Ser	Val	Gln	Tyr	Gly	Pro	Asn	Thr	Phe	Gly	Gly	Val	Val	Asn
				165					170						175
Val	Ile	Thr	Lys	Glu	Ile	Pro	Lys	Glu	Trp	Glu	Asn	Gln	Ala	Ala	Glu
			180					185					190		
Arg	Ile	Thr	Phe	Trp	Gly	Arg	Ser	Ser	Asn	Gly	Asn	Phe	Val	Asp	Pro
			195					200					205		
Lys	Glu	Lys	Gly	Lys	Pro	Leu	Ala	Gln	Thr	Leu	Gly	Asn	Gln	Met	Leu
			210					215					220		
Phe	Asn	Thr	Tyr	Gly	Arg	Thr	Ala	Gly	Met	Leu	Gly	Lys	Tyr	Ile	Gly
225					230					235					240
Ile	Ser	Ala	Gln	Gly	Asn	Trp	Ile	Asn	Gly	Gln	Gly	Phe	Arg	Gln	Asn
				245					250						255
Ser	Pro	Thr	Lys	Val	Gln	Asn	Tyr	Leu	Leu	Asp	Ala	Ile	Tyr	Lys	Ile
			260					265					270		
Asn	Ala	Thr	Asn	Thr	Phe	Lys	Ala	Tyr	Tyr	Gln	Tyr	Tyr	Gln	Tyr	Asn
			275					280					285		
Ser	Tyr	His	Pro	Gly	Thr	Leu	Ser	Ala	Gln	Asp	Tyr	Ala	Tyr	Asn	Arg
								295					300		
Phe	Ile	Asn	Glu	Arg	Pro	Asp	Asn	Gln	Asp	Gly	Gly	Arg	Ala	Lys	Arg
305					310					315					320
Phe	Gly	Ile	Val	Tyr	Gln	Asn	Tyr	Phe	Gly	Asp	Pro	Asp	Arg	Lys	Val
				325					330						335
Gly	Gly	Asp	Phe	Lys	Phe	Thr	Tyr	Phe	Thr	His	Asp	Met	Ser	Arg	Asp
			340					345					350		
Phe	Gly	Phe	Ser	Asn	Gln	Tyr	Gln	Ser	Val	Tyr	Met	Ser	Gly	Gln	Asn
			355					360					365		
Lys	Ile	Leu	Pro	Phe	Lys	Gly	Lys	Gly	Glu	Ile	Ser	Ala</			

950

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Thr Phe Leu Asn Tyr Glu Lys Lys Asp Ala Pro Pro Phe Lys Val Gly
      500                      505                      510
Gln Thr Pro Lys Thr Thr Lys Glu Arg Tyr Asn Gln Trp Asn Pro Ala
      515                      520                      525
Val Asn Val Gly Tyr Lys Pro Ile Lys Glu Leu Leu Phe Tyr Phe Asn
      530                      535                      540
Tyr Gln Arg Ser Tyr Ile Pro Pro Gln Phe Ser Asn Ile Gly Asn Phe
545                      550                      555                      560
Val Gly Thr Ser Thr Asp Tyr Phe Gln Ile Phe Asn Val Met Glu Gly
      565                      570                      575
Gly Ser Arg Tyr Tyr Phe Asn His Gln Val Ser Phe Asn Ala Asn Tyr
      580                      585                      590
Phe Val Ile Phe Ala Asn His Tyr Phe Thr Gly Arg Tyr Gly Asp Asn
      595                      600                      605
Arg Glu Pro Val Asn Ala Arg Ser Gln Gly Val Glu Leu Glu Leu Tyr
      610                      615                      620
Tyr Thr Pro Ile Arg Gly Leu Asn Phe His Ala Ala Tyr Thr Phe Ile
625                      630                      635                      640
Asp Ala Asn Ile Thr Ser His Thr Met Val Thr Asn Pro Ala Asn Pro
      645                      650                      655
Lys Gly Pro Lys Lys Asp Ile Phe Gly Lys Lys Leu Pro Phe Val Ser
      660                      665                      670
Pro His Gln Phe Ile Leu Asp Ala Ser Tyr Thr Tyr Ala Lys Thr Thr
      675                      680                      685
Ile Gly Leu Ser Ser Phe Phe Tyr Ser Arg Ala Tyr Ser Asp Val Leu
      690                      695                      700
Asn Thr Val Pro Phe Thr Glu Tyr Ala Pro Thr Ile Lys Asn Gly Ala
705                      710                      715                      720
Ile Val Thr Lys Thr Ala Gly Met Thr Pro Tyr Tyr Trp Val Trp Asn
      725                      730                      735
Leu Gln Ile Ser Thr Thr Leu Trp Glu Arg Lys Asn Gln Ser Val Asn
      740                      745                      750
Ala Ser Leu Gln Ile Asn Asn Ile Phe Asn Met Lys Tyr Trp Phe Ser
      755                      760                      765
Gly Ile Gly Thr Ser Pro Asn Gly Lys Glu Ala Ala Pro Pro Arg Ser
      770                      775                      780
Ile Thr Ala Tyr Val Ser Tyr Asn Phe
785                      790

```

(2) INFORMATION FOR SEQ ID NO:1044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

```

Met Leu Ile Ala Arg Phe Lys Lys Ala Leu Ile Ser Tyr Ser Leu Gly
1      5      10      15
Val Leu Leu Val Ser Ser Leu Leu Gly Val Ala Asn Ala Ser Asn Gln
20     25     30
Glu Ile Gln Val Lys Asp Tyr Phe Gly Glu Gln Thr Ile Lys Leu Pro
35     40     45
Val Ser Lys Ile Ile Tyr Leu Gly Ser Phe Ala Glu Val Pro Ala Met
50     55     60
Phe Asn Thr Trp Asp Arg Val Val Gly Ile Ser Asp Tyr Ala Phe Lys
65     70     75     80
Ser Asp Ile Val Lys Ala Thr Leu Lys Asp Pro Glu Arg Ile Lys Pro
85     90     95
Met Ser Ser Asp His Val Ala Ala Leu Asn Val Glu Leu Leu Lys Lys
100    105    110
Leu Ser Pro Asp Leu Val Val Thr Phe Val Gly Asn Pro Lys Ala Val
115    120    125
Glu His Ala Lys Lys Phe Gly Ile Ser Phe Leu Ser Phe Gln Glu Lys
130    135    140
Thr Ile Val Glu Val Met Glu Asp Ile Asp Ala Gln Ala Lys Ala Leu
145    150    155    160
Glu Val Asp Ala Ser Lys Lys Leu Ala Lys Met Gln Glu Thr Leu Asp
165    170    175
Phe Ile Lys Glu Arg Leu Lys Asn Val Lys Lys Lys Lys Gly Val Glu
180    185    190
Leu Phe His Lys Ala Asn Lys Ile Ser Gly His Gln Ala Leu Asp Ser
195    200    205
Asp Ile Leu Glu Lys Gly Gly Ile Asp Asn Phe Gly Leu Lys Tyr Val
210    215    220
Lys Phe Gly Arg Ala Asp Ile Ser Val Glu Lys Ile Val Lys Glu Asn
225    230    235    240
Pro Glu Ile Ile Phe Ile Trp Trp Ile Ser Pro Leu Ser Pro Glu Asp
245    250    255
Val Leu Asn Asn Pro Lys Phe Ser Thr Ile Lys Ala Ile Lys Asn Lys
260    265    270
Gln Val Tyr Lys Leu Pro Thr Met Asp Ile Gly Gly Pro Arg Ala Pro
275    280    285
Leu Ile Ser Leu Phe Ile Ala Leu Lys Ala His Pro Glu Ala Phe Lys
290    295    300
Gly Val Asp Ile Asn Ala Ile Ile Lys Asp Tyr Tyr Lys Val Val Phe
305    310    315    320
Asp Leu Asn Asp Ala Glu Val Glu Pro Phe Leu Trp His
325    330

```

(2) INFORMATION FOR SEQ ID NO:1045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

```

Met Tyr Lys Leu Gly Ile Phe Leu Leu Ala Thr Leu Leu Ser Ala Asn
1           5           10           15
Thr Gln Lys Val Ser Asp Ile Ala Lys Asp Ile Gln His Lys Glu Thr
20           25           30
Leu Leu Lys Lys Thr His Glu Glu Lys Asn Gln Leu Asn Ser Arg Leu
35           40           45
Ser Ser Leu Gly Glu Ala Ile Arg Ser Lys Glu Leu Gln Lys Val Glu
50           55           60
Ile Glu Arg Gln Met Val Ala Leu Lys Lys Ser Leu Glu Lys Asn Arg
65           70           75           80
Asn Glu Ser Leu Val Gln Glu Lys Val Leu Thr Asn Tyr Arg Lys Ser
85           90           95
Leu Asp His Leu Gln Lys Gln Arg Ser Phe Leu Gln Lys Arg Val Phe
100          105          110
Asp Thr Leu Leu Glu Asp Phe Leu Phe Ser Gln Ala Leu Lys Gly Gln
115          120          125
Asn Leu Ala Ser Ser Asn Asp Val Ile Leu Gln Val Ala Phe Glu Asn
130          135          140
Leu His Gln Ser Thr Leu Ser Lys Met Ser Gln Leu Ser Gln Glu Glu
145          150          155          160
Lys Lys Leu Asn Val Gln Ala Leu Glu Val Lys Ser Ser Ile Gln Lys
165          170          175
Ile Ser Ser Val Ile Asp Glu Gln Lys Thr Arg Glu Ser Thr Leu Lys
180          185          190
Ser Leu Gln Thr Glu Gln Asn Lys Leu Ile Leu Ser Met Gln Lys Asp
195          200          205
Tyr Ala Ile Tyr Asn Gln Arg Leu Ser Leu Leu Glu Lys Glu Arg Gln
210          215          220
Asn Leu Asn Ala Leu Leu Lys Arg Leu Asn Ile Ile Lys Gln Asn Arg
225          230          235          240
Glu Asn Glu Glu Arg Val Ser Leu Lys Lys Ser Ser Gln Ala Leu Glu
245          250          255
Val Lys Gln Val Ala Ser Ser Tyr Gln Asn Ile Asn Thr Thr Ser Tyr
260          265          270
Asn Gly Pro Lys Thr Ile Ala Pro Leu Asn Asp Tyr Glu Val Val Gln
275          280          285
Lys Phe Gly Pro Tyr Ile Asp Pro Val Tyr Asn Leu Lys Ile Phe Ser
290          295          300
Glu Ser Ile Thr Leu Val Ser Lys Thr Pro Asn Ala Leu Val Arg Asn
305          310          315          320
Val Leu Asp Gly Lys Ile Val Phe Ala Lys Glu Ile Asn Met Leu Lys
325          330          335
Lys Val Val Ile Ile Glu His Lys Asn Gly Ile Arg Thr Ile Tyr Ser
340          345          350
Gln Leu Asp Lys Ile Ala Pro Thr Ile Lys Ser Gly Met Arg Ile Gln
355          360          365
Lys Gly Tyr Val Leu Gly Arg Ile Asp Gln Arg Leu Gly Phe Glu Val
370          375          380
Thr Met Arg Glu Lys His Ile Asn Pro Leu Glu Leu Ile Ala Arg Asn

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953

385

390

395

400

(2) INFORMATION FOR SEQ ID NO:1046:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

```

Met Asp Lys Asn Asn Asn Asn Asn Leu Arg Leu Ile Leu Ala Ile Ala
1          5          10          15
Leu Ser Phe Leu Phe Ile Ala Leu Tyr Ser Tyr Phe Phe Gln Glu Pro
          20          25          30
Asn Lys Thr Thr Thr Glu Thr Thr Lys Gln Glu Thr Thr Asn Asn His
          35          40          45
Thr Ala Thr Ser Pro Thr Ala Ser Asn Thr Ile Thr Gln Asp Phe Ser
          50          55          60
Val Thr Gln Thr Ile Pro Gln Glu Ser Leu Leu Ser Thr Ile Ser Phe
65          70          75          80
Glu His Ala Lys Ile Glu Ile Asp Ser Leu Gly Arg Ile Lys Gln Val
          85          90          95
Tyr Leu Lys Asp Lys Lys Tyr Leu Thr Pro Lys Glu Lys Gly Phe Leu
          100          105          110
Glu His Val Ser His Leu Phe Ser Ser Lys Glu Asn Ser Gln Pro Ser
          115          120          125
Leu Lys Glu Leu Pro Leu Leu Ala Ala Asp Lys Leu Lys Pro Leu Glu
          130          135          140
Val Arg Phe Leu Asp Pro Thr Leu Asn Asn Lys Ala Phe Asn Thr Pro
145          150          155          160
Tyr Ser Ala Ser Lys Thr Thr Leu Gly Pro Asn Glu Gln Leu Val Leu
          165          170          175
Thr Gln Asp Leu Gly Thr Leu Ser Ile Ile Lys Thr Leu Thr Phe Tyr
          180          185          190
Asp Asp Leu His Tyr Asp Leu Lys Ile Ala Phe Lys Ser Pro Asn Asn
          195          200          205
Leu Ile Pro Ser Tyr Val Ile Thr Asn Gly Tyr Arg Pro Val Ala Asp
          210          215          220
Leu Asp Ser Tyr Thr Phe Ser Gly Val Leu Leu Glu Asn Thr Asp Lys
225          230          235          240
Lys Ile Glu Lys Ile Glu Asp Lys Asp Ala Lys Glu Ile Lys Arg Phe
          245          250          255
Ser Asn Thr Leu Phe Leu Ser Ser Val Asp Arg Tyr Phe Thr Thr Leu
          260          265          270
Leu Phe Thr Lys Asp Pro Gln Gly Phe Glu Ala Leu Ile Asp Ser Glu

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275	280	285
Ile Gly Thr Lys Asn Pro Leu Gly Phe Ile Ser Leu Lys Asn Glu Ala		
290	295	300
Asn Leu His Gly Tyr Ile Gly Pro Lys Asp Tyr Arg Ser Leu Lys Ala		
305	310	315
Ile Ser Pro Met Leu Thr Asp Val Ile Glu Tyr Gly Leu Ile Thr Phe		
325	330	335
Phe Ala Lys Gly Val Phe Val Leu Leu Asp Tyr Leu Tyr Gln Phe Val		
340	345	350
Gly Asn Trp Gly Trp Ala Ile Ile Leu Leu Thr Ile Ile Val Arg Ile		
355	360	365
Ile Leu Tyr Pro Leu Ser Tyr Lys Gly Met Val Ser Met Gln Lys Leu		
370	375	380
Lys Glu Leu Ala Pro Lys Met Lys Glu Leu Gln Glu Lys Tyr Lys Gly		
385	390	395
Glu Pro Gln Lys Leu Gln Ala His Met Met Gln Leu Tyr Lys Lys His		
405	410	415
Gly Ala Asn Pro Leu Gly Gly Cys Leu Pro Leu Ile Leu Gln Ile Pro		
420	425	430
Val Phe Phe Ala Ile Tyr Arg Val Leu Tyr Asn Ala Val Glu Leu Lys		
435	440	445
Ser Ser Glu Trp Val Leu Trp Ile His Asp Leu Ser Ile Met Asp Pro		
450	455	460
Tyr Phe Ile Leu Pro Leu Leu Met Gly Ala Ser Met Tyr Trp His Gln		
465	470	475
Ser Val Thr Pro Asn Thr Met Thr Asp Pro Met Gln Ala Lys Ile Phe		
485	490	495
Lys Leu Leu Pro Leu Leu Phe Thr Ile Phe Leu Ile Thr Phe Pro Ala		
500	505	510
Gly Leu Val Leu Tyr Trp Thr Thr His Asn Ile Leu Ser Val Leu Gln		
515	520	525
Gln Leu Ile Ile Asn Lys Val Leu Glu Asn Lys Lys Arg Ala His Ala		
530	535	540
Gln Asn Ile Lys Glu		
545		

(2) INFORMATION FOR SEQ ID NO:1047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

Met Lys Lys Ser Leu Cys Leu Ser Phe Phe Leu Thr Phe Ser Asn Pro

955

1		5		10		15									
Leu	Gln	Ala	Leu	Val	Ile	Glu	Leu	Leu	Glu	Glu	Ile	Lys	Thr	Ser	Pro
		20					25						30		
His	Lys	Gly	Thr	Phe	Lys	Ala	Lys	Val	Leu	Asp	Ser	Lys	Glu	Pro	Arg
		35					40					45			
Gln	Val	Leu	Gly	Val	Tyr	Asn	Ile	Ser	Pro	His	Lys	Lys	Leu	Thr	Leu
		50				55					60				
Thr	Ile	Thr	His	Ile	Ser	Thr	Ala	Ile	Val	Tyr	Gln	Pro	Leu	Asp	Glu
65					70					75				80	
Lys	Leu	Ser	Leu	Glu	Thr	Thr	Leu	Ser	Pro	Asn	Arg	Pro	Thr	Ile	Pro
				85					90				95		
Arg	Asn	Thr	Gln	Ile	Val	Phe	Ser	Ser	Lys	Glu	Leu	Lys	Glu	Pro	His
			100						105				110		
Ser	Asn	Pro	Ile	Pro	Ser	Leu	Asn	Ala	Pro	Met	Gln	Lys	Pro	Gln	Asn
		115					120					125			
Lys	Pro	Ser	Ser	Ser	Gln	Gln	Ser	Pro	Gln	Asn	Phe	Ser	Tyr	Pro	Glu
		130				135					140				
Ser	Lys	Leu	Gly	Ser	Lys	Asn	Ser	Lys	Asn	Ser	Leu	Leu	Gln	Pro	Leu
145					150				155					160	
Val	Thr	Pro	Ser	Lys	Val	Ser	Pro	Thr	Asn	Glu	Val	Lys	Thr	Pro	Thr
				165					170					175	
Asn	Asp	Ala	Asn	Pro	Pro	Leu	Lys	His	Ser	Ser	Gln	Asp	Gln	Glu	Asn
			180					185					190		
Asn	Leu	Phe	Val	Ala	Pro	Pro	Thr	Glu	Lys	Thr	Leu	Pro	Asn	Asn	Thr
		195					200					205			
Ser	Ser	Ala	Asp	Ala	Ser	Glu	Asn	Asn	Glu	Ser	Asn	Glu	Asn	Arg	Asp
		210				215					220				
Asn	Val	Glu	Lys	Gln	Ala	Ile	Arg	Asp	Pro	Asn	Ile	Lys	Glu	Phe	Ala
225					230					235				240	
Cys	Gly	Lys	Trp	Val	Tyr	Asp	Asp	Glu	Asn	Leu	Gln	Ala	Tyr	Arg	Pro
			245						250					255	
Ser	Ile	Leu	Lys	Arg	Val	Asp	Lys	Asp	Lys	Glu	Ile	Thr	Thr	Asp	Ile
		260						265					270		
Thr	Pro	Cys	Asp	Tyr	Ser	Thr	Ala	Glu	Asn	Lys	Ser	Gly	Lys	Ile	Ile
		275					280					285			
Thr	Pro	Tyr	Thr	Lys	Ile	Ser	Val	His	Lys	Thr	Glu	Pro	Leu	Glu	Asp
		290				295					300				
Pro	Gln	Thr	Phe	Glu	Ala	Lys	Asn	Asn	Phe	Ala	Ile	Leu	Gln	Ala	Arg
305					310					315				320	
Ser	Ser	Thr	Glu	Lys	Cys	Lys	Arg	Ala	Arg	Ala	Arg	Lys	Asp	Gly	Thr
				325					330					335	
Thr	Arg	Gln	Cys	Tyr	Leu	Ile	Glu	Glu	Pro	Leu	Lys	Gln	Ala	Trp	Glu
		340						345					350		
Ser	Glu	Tyr	Glu	Ile	Thr	Thr	Gln	Leu	Val	Lys	Ala	Ile	Tyr	Glu	Arg
		355					360					365			
Pro	Lys	Gln	Asp	Asp	Gln	Val	Glu	Pro	Thr	Phe	Tyr	Glu	Thr	Ser	Glu
		370				375					380				
Leu	Ala	Tyr	Ser	Ser	Thr	Arg	Lys	Ser	Glu	Ile	Thr	Arg	Asn	Glu	Leu
385					390					395				400	
Asn	Leu	Asn	Glu	Lys	Phe	Met	Glu	Phe	Val	Glu	Val	Tyr	Glu	Gly	His
				405					410					415	
Tyr	Leu	Asn	Asp	Ile	Ile	Lys	Glu	Ser	Ser	Glu	Tyr	Lys	Glu	Trp	Val
			420					425					430		
Lys	Asn	His	Val	Arg	Phe	Lys	Glu	Gly	Val	Cys	Met	Ala	Leu	Glu	Ile
		435					440					445			
Glu	Glu	Gln	Pro	Arg	Ala	Lys	Ser	Thr	Pro	Leu	Ser	Ile	Glu	Asn	Ser
		450				455					460				

Arg Val Val Cys Val Lys Lys Gly Asn Tyr Leu Phe Asn Glu Val
 465 470 475

(2) INFORMATION FOR SEQ ID NO:1048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

Val	Lys	Val	Tyr	Pro	Gln	Val	Leu	Ser	Ile	Ala	Gly	Ser	Asp	Ser	Gly	1	5	10	15
Gly	Gly	Ala	Gly	Ile	Gln	Ala	Asp	Leu	Lys	Ala	Phe	Gln	Thr	Phe	Gly	20	25	30	
Val	Phe	Gly	Thr	Ser	Val	Ile	Thr	Cys	Ile	Thr	Ala	Gln	Asn	Thr	Gln	35	40	45	
Gly	Val	His	Gly	Val	Tyr	Pro	Leu	Ser	Val	Glu	Ser	Val	Lys	Ala	Gln	50	55	60	
Ile	Leu	Ala	Ile	Arg	Asp	Asp	Phe	Ser	Ile	Lys	Ala	Phe	Lys	Met	Gly	65	70	75	80
Ala	Leu	Cys	Asn	Ala	Gln	Ile	Ile	Glu	Cys	Val	Ala	Asn	Ala	Leu	Glu	85	90	95	
Thr	Cys	Asp	Phe	Gly	Leu	Cys	Val	Leu	Asp	Pro	Val	Met	Val	Ala	Lys	100	105	110	
Asn	Gly	Ala	Leu	Leu	Leu	Glu	Glu	Ala	Ile	Leu	Ser	Leu	Lys	Lys		115	120	125	
Arg	Leu	Leu	Pro	Lys	Thr	Asn	Leu	Leu	Thr	Pro	Asn	Leu	Pro	Glu	Val	130	135	140	
Tyr	Ala	Leu	Thr	Gly	Val	Gln	Ala	Arg	Asp	Asp	Lys	Ser	Ala	Ser	Lys	145	150	155	160
Ala	Met	Gly	Val	Leu	Arg	Asp	Leu	Gly	Val	Lys	Asn	Ala	Val	Ile	Lys	165	170	175	
Gly	Gly	His	Thr	Glu	His	Phe	Gln	Gly	Glu	Phe	Ser	Asn	Asp	Trp	Val	180	185	190	
Phe	Leu	Glu	Asp	Ala	Glu	Phe	Ile	Leu	Ser	Ala	Lys	Arg	Phe	Asn	Thr	195	200	205	
Lys	Asn	Thr	His	Gly	Thr	Gly	Cys	Thr	Leu	Ser	Ser	Leu	Ile	Val	Gly	210	215	220	
Leu	Leu	Ala	Gln	Gly	Leu	Asp	Leu	Lys	Asn	Ala	Ile	Thr	Lys	Ala	Lys	225	230	235	240
Glu	Leu	Leu	Thr	Ile	Ile	Ile	Gln	Asn	Pro	Leu	Asn	Ile	Gly	His	Gly	245	250	255	
His	Gly	Pro	Leu	Asn	Leu	Trp	Ser	Ile	Lys	Lys	His	Val				260	265		

(2) INFORMATION FOR SEQ ID NO:1049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

```

Leu Gly Ala Ile Met Asp Thr Phe Leu Thr Ser Ile Leu Val Leu Leu
1           5           10           15
Met Arg Gly Leu Leu Asn Gln Arg Ala Ile Met Gln Gly Leu Met Trp
20           25           30
Trp Ile Pro Leu Phe Tyr Asp Thr Ile Thr Lys Asp Val Phe Gly Phe
35           40           45
Lys Ala Gly Arg Tyr Glu Ala Asn Ile Asp Phe Met Ser Gly Ser Asn
50           55           60
Gln Gly Trp Glu Val Tyr Tyr Gln Pro Tyr Lys Thr Glu Thr Gln Arg
65           70           75           80
Leu Arg Phe Trp Trp Trp Ser Ser Phe Gly Arg Gly Leu Ala Phe Asn
85           90           95
Ser Trp Ile Tyr Glu Phe Phe Ala Thr Val Pro Tyr Leu Lys Lys Gly
100          105          110
Gly Asn Pro Ser Asn Ser Asn Asp Phe Ile Asn Tyr Gly Trp His Gly
115          120          125
Ile Thr Thr Thr Tyr Ser Tyr Lys Gly Leu Asp Ala Gln Phe Phe Tyr
130          135          140
Tyr Phe Ala Pro Lys Thr Tyr Asn Ala Pro Gly Phe Lys Leu Val Tyr
145          150          155          160
Asp Thr Asn Arg Asn Phe Glu Asn Val Gly Phe Arg Ser Gln Ser Met
165          170          175
Ile Met Thr Thr Phe Pro Leu Tyr Tyr Arg Gly Trp Tyr Asn Pro Glu
180          185          190
Thr Asn Thr Tyr Ser Leu Glu Asp Ser Thr Pro His Gly Ser Leu Leu
195          200          205
Gly Arg Asn Gly Val Thr Leu Asn Ile Arg Gln Val Phe Trp Trp Asp
210          215          220
Asn Phe Asn Trp Ser Ile Gly Phe Tyr Asn Thr Phe Gly Asn Ser Asp
225          230          235          240
Ala Phe Leu Gly Ser His Thr Met Pro Arg Gly Asn Asn Thr Ser Tyr
245          250          255
Ile Ser Asn Glu Ile Ser Val Thr Thr Arg His Ala Gly Met Ile Gly
260          265          270
Tyr Asp Phe Trp Asp Asn Thr Ala Tyr Asp Gly Leu Ala Asp Ala Ile
275          280          285

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958

```

Thr Asn Ala Asn Thr Phe Thr Phe Tyr Thr Ser Val Gly Gly Ile His
 290                      295                      300
Lys Arg Phe Ala Trp His Val Phe Gly Arg Val Ser His Ala Asn Lys
305                      310                      315                      320
Asn Ala Leu Gly Gln Val Gly Arg Ala Asn Glu Tyr Ser Leu Gln Phe
                      325                      330                      335
Asn Ala Ser Tyr Ala Phe Thr Glu Ser Val Leu Leu Asn Phe Arg Ile
                      340                      345                      350
Thr Tyr Tyr Gly Ala Arg Ile Asn Lys Gly Tyr Gln Ala Gly Tyr Phe
                      355                      360                      365
Gly Ala Pro Lys Phe Asn Asn Pro Asp Gly Asp Phe Ser Ala Asn Tyr
                      370                      375                      380
Gln Asp Arg Ser Tyr Met Met Thr Asn Leu Thr Leu Lys Phe
385                      390                      395

```

(2) INFORMATION FOR SEQ ID NO:1050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

```

Leu Ser Asn Ala Phe Ser Gln Tyr Leu Tyr Ser Leu Leu Gly Ala Tyr
 1                      5                      10                      15
Pro Thr Lys Leu Asn Gly Asn Asp Val Ser Ala Asn Ala Leu Leu Ser
                      20                      25                      30
Gly Ala Val Gly Ser Gly Thr Cys Ala Ala Ala Gly Thr Ala Gly Gly
                      35                      40                      45
Thr Thr Leu Asn Thr Gln Ser Ala Cys Thr Ala Ala Gly Tyr Tyr Trp
                      50                      55                      60
Leu Pro Ser Leu Thr Asp Arg Ile Leu Ser Thr Ile Gly Ser Gln Thr
65                      70                      75                      80
Asn Tyr Gly Thr Asn Thr Asn Phe Pro Asn Met Gln Gln Gln Leu Thr
                      85                      90                      95
Tyr Leu Asn Ala Gly Asn Val Phe Phe Asn Ala Met Asn Lys Ala Leu
                      100                      105                      110
Glu Lys Asn Gly Thr Ala Thr Ala Asn Ser Thr Ser Ser Thr Ser Gly
                      115                      120                      125
Ala Thr Gly Ser Asp Gly Gln Thr Tyr Ser Gln Gln Ala Ile Gln Tyr
                      130                      135                      140
Leu Gln Gly Gln Gln Asn Ile Leu Asn Asn Ala Ala Asn Leu Leu Lys
145                      150                      155                      160
Gln Asp Glu Leu Leu Leu Glu Ala Phe Asn Ser Ala Val Ala Ala Asn
                      165                      170                      175

```

```

Ile Gly Asn Lys Glu Phe Asn Ser Ala Ala Phe Thr Gly Leu Val Gln
      180                      185                      190
Gly Ile Ile Asp Gln Ser Gln Leu Val Tyr Asn Glu Leu Thr Lys Asn
      195                      200                      205
Thr Ile Ser Gly Ser Ala Val Asn Asn Ala Gly Ile Asn Ser Asn Gln
      210                      215                      220
Ala Asn Ala Val Gln Gly Arg Ala Ser Gln Leu Pro Asn Ala Leu Tyr
      225                      230                      235                      240
Asn Val Gln Val Thr Leu Asp Lys Ile Asn Ala Leu Asn Asn Gln Val
      245                      250                      255
Arg Ser Met Pro Tyr Leu Pro Gln Phe Arg Ala Gly Asn Ser Arg Ala
      260                      265                      270
Thr Asn Ile Leu Asn Gly Phe Tyr Thr Lys Val Gly Tyr Lys Gln Phe
      275                      280                      285
Phe Gly Lys Lys Arg Asn Ile Gly Leu Arg Tyr Tyr Gly Phe Phe Ser
      290                      295                      300
Tyr Asn Gly Ala Ser Val Gly Phe Arg Ser Thr Gln Asn Asn Val Gly
      305                      310                      315                      320
Leu Tyr Thr Tyr Gly Val Gly Thr Asp Val Leu Tyr Asn Ile Phe Ser
      325                      330                      335
Arg Ser Tyr Gln Asn Arg Ser Val Asp Met Gly Phe Phe Ser Gly Ile
      340                      345                      350
Gln Leu Ala Gly Glu Thr Phe Gln Ser Thr Leu Arg Asp Asp Pro Asn
      355                      360                      365
Val Lys Leu His Gly Lys Ile Asn Asn Thr His Phe Gln Phe Leu Phe
      370                      375                      380
Asp Phe Gly Met Arg Met Asn Phe Gly Lys Leu Asp Gly Lys Ser Asn
      385                      390                      395                      400
Arg His Asn Gln His Thr Val Glu Phe Gly Val Val Val Pro Thr Ile
      405                      410                      415
Tyr Asn Thr Tyr Tyr Lys Ser Ala Gly Thr Thr Val Lys Tyr Phe Arg
      420                      425                      430
Pro Tyr Ser Val Tyr Trp Ser Tyr Gly Tyr Ser Phe
      435                      440

```

(2) INFORMATION FOR SEQ ID NO:1051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

```

Met Glu Leu Ile Lys Lys Leu Glu Lys Glu Ser Glu Val Leu Lys Lys
1              5              10              15

```

```

Asp Leu Gln Gln His Ser Asn Glu Leu Phe Lys Met Leu Ile Ile Asp
      20                      25                      30
Asn Glu Asp Leu Phe Lys Glu Gln Phe Glu Ile Met Phe Lys Ala Trp
      35                      40                      45
Val Glu Ile Val Lys Met Met Phe Glu Leu Thr Lys Lys Thr Lys Phe
      50                      55                      60
Asp Gly Glu Met Ile Gly Tyr Thr Glu Glu Leu Leu Thr Phe Leu Val
      65                      70                      75                      80
Arg Asp Phe Phe Asn Gly Ile Phe Lys Ser Lys Val Ile Pro Lys Met
      85                      90                      95
Pro Ile Phe Cys Gly Asp Val Lys Cys Glu Asp Phe Asn Ala Leu Arg
      100                     105                     110
Ser Leu Val Tyr Leu Ser Val Leu Glu Leu Glu Glu Thr Ile Asn Pro
      115                     120                     125
Asn Lys Ile Pro Phe
      130

```

(2) INFORMATION FOR SEQ ID NO:1052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

```

Met Lys Ile Lys Lys Ser Leu Phe Ala Leu Ser Phe Ser Leu Met Ala
1      5      10      15
Ser Leu Ser Arg Ala Glu Asp Asp Gly Phe Tyr Met Ser Val Gly Tyr
      20      25      30
Gln Ile Gly Glu Ala Val Gln Lys Val Lys Asn Thr Gly Ala Leu Gln
      35      40      45
Asn Leu Ala Asp Arg Tyr Asp Asn Leu Ser Asn Leu Leu Asn Gln Tyr
      50      55      60
Asn Tyr Leu Asn Ser Leu Val Asn Leu Ala Ser Thr Pro Ser Ala Ile
      65      70      75      80
Thr Gly Ala Ile Asp Asn Leu Ser Ser Ser Ala Ile Asn Leu Thr Ser
      85      90      95
Ala Thr Thr Thr Ser Pro Ala Tyr Gln Ala Val Ala Leu Ala Leu Asn
      100     105     110
Ala Ala Val Gly Met Trp Gln Val Ile Ala Phe Gly Ile Ser Cys Gly
      115     120     125
Pro Gly Pro Asn Leu Gly Pro Glu His Leu Glu Asn Gly Gly Val Arg
      130     135     140
Ser Phe Asp Asn Thr Pro Asn Tyr Ser Tyr Asn Thr Gly Ser Gly Thr
      145     150     155     160

```

961

Thr Thr Thr Thr Cys Asn Gly Ala Ser Asn Val Gly Pro Asn Gly Ile
 165 170 175
 Leu Ser Ser Ser Glu Tyr Gln Val Leu Asn Thr Ala Tyr Gln Thr Ile
 180 185 190
 Gln Thr Ala Leu Asn Gln Asn Gln Gly Gly Gly Met Pro Ala Leu Asn
 195 200 205
 Ser Ser Lys Asn Met Val Val Asn Ile Asn Gln Thr Phe Thr Lys Asn
 210 215 220
 Pro Thr Thr Glu Tyr Thr Tyr Pro Asp Gly Asn Gly Asn Tyr Tyr Ser
 225 230 235 240
 Gly Gly Ser Ser Ile Pro Ile Gln Leu Lys Ile Ser Ser Val Asn Asp
 245 250 255
 Ala Glu Asn Leu Leu Gln Gln Ala Ala Thr Ile Ile Asn Val Leu Thr
 260 265 270
 Thr Gln Asn Pro His Val Asn Gly Gly Gly Gly Ala Trp Gly Phe Gly
 275 280 285
 Gly Lys Thr Gly Asn Val Met Asp Ile Phe Gly Asp Ser Phe Asn Ala
 290 295 300
 Ile Asn Glu Met Ile Lys Asn Ala Gln Ala Val Leu Glu Lys Thr Gln
 305 310 315 320
 Gln Leu Asn Ala Asn Glu Asn Thr Gln Ile Thr Gln Pro Asp Asn Phe
 325 330 335
 Asn Pro Tyr Thr Ser Lys Asp Thr Gln Phe Ala Gln Glu Met Leu Asn
 340 345 350
 Arg Ala Asn Ala Gln Ala Glu Ile Leu Ser Leu Ala Gln Gln Val Ala
 355 360 365
 Asp Asn Phe His Ser Ile Gln Gly Pro Ile Gln Gln Asp Leu Glu Glu
 370 375 380
 Cys Thr Ala Gly Ser Ala Gly Val Ile Asn Asp Asn Thr Tyr Gly Ser
 385 390 395 400
 Gly Cys Ala Phe Val Lys Glu Thr Leu Asn Ser Leu Glu Gln His Thr
 405 410 415
 Ala Tyr Tyr Gly Asn Gln Val Asn Gln Asp Arg Ala Leu Ser Gln Thr
 420 425 430
 Ile Leu Asn Phe Lys Glu Ala Leu Ser Thr Leu Gly Asn Asp Ser Lys
 435 440 445
 Ala Ile Asn Ser Gly Ile Ser Asn Leu Pro Asn Ala Lys Ser Leu Gln
 450 455 460
 Asn Met Thr His Ala Thr Gln Asn Pro Asn Ser Pro Glu Gly Leu Leu
 465 470 475 480
 Thr Tyr Ser Leu Asp Thr Ser Lys Tyr Asn Gln Leu Gln Thr Val Ala
 485 490 495
 Gln Glu Leu Gly Lys Asn Pro Phe Arg Arg Ile Gly Val Ile Asn Tyr
 500 505 510
 Gln Asn Asn Asn Gly Ala Met Asn Gly Ile Gly Val Gln Ala Gly Tyr
 515 520 525
 Lys Gln Phe Phe Gly Lys Lys Arg Asn Trp Gly Leu Arg Tyr Tyr Gly
 530 535 540
 Phe Phe Asp Tyr Asn His Ala Tyr Ile Lys Ser Asn Phe Phe Asn Ser
 545 550 555 560
 Ala Ser Asp Val Trp Thr Tyr Gly Val Gly Met Asp Ala Leu Tyr Asn
 565 570 575
 Phe Ile Asn Asp Lys Asn Thr Asn Phe Leu Gly Lys Asn Asn Lys Leu
 580 585 590
 Ser Val Gly Leu Phe Gly Gly Phe Ala Leu Ala Gly Thr Ser Trp Leu
 595 600 605
 Asn Ser Gln Gln Val Asn Leu Thr Met Met Asn Gly Ile Tyr Asn Ala

962

610	615	620
Asn Val Ser Ala Ser	Asn Phe Gln Phe Leu Phe Asp Leu Gly Leu Arg	
625	630	635
Met Asn Leu Ala Arg	Pro Lys Lys Lys Asp Ser Asp His Ala Ala Gln	640
	645	650
His Gly Met Glu Leu Gly Val Lys Ile	Pro Thr Ile Asn Thr Asp Tyr	655
	660	665
Tyr Ser Phe Met Gly Ala Glu Leu Lys Tyr Arg Arg Leu Tyr Ser Val		670
	675	680
Tyr Leu Asn Tyr Val Phe Ala Tyr		685
690	695	

(2) INFORMATION FOR SEQ ID NO:1053:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

Met	Gln	Phe	Gln	Lys	Thr	Leu	Ser	Ser	Leu	Ser	Leu	Phe	Leu	Ser	Leu
1				5					10					15	
Ser	Leu	Phe	Leu	Ser	Phe	Ser	Ile	Ala	Glu	Glu	Asn	Gly	Ala	Tyr	Ala
			20					25					30		
Ser	Val	Gly	Phe	Glu	Tyr	Ser	Ile	Ser	His	Ala	Val	Glu	His	Asn	Asn
		35					40					45			
Pro	Phe	Leu	Asn	Gln	Glu	Arg	Ile	Gln	Thr	Ile	Ser	Asn	Ala	Gln	Asn
	50					55					60				
Lys	Ile	Tyr	Lys	Leu	Asn	Gln	Val	Lys	Asn	Glu	Ile	Thr	Asn	Met	Pro
65				70						75				80	
Asn	Thr	Phe	Asn	Tyr	Ile	Asn	Asn	Ala	Leu	Lys	Asn	Asn	Ala	Lys	Leu
			85						90					95	
Thr	Pro	Thr	Glu	Lys	Gln	Ala	Glu	Thr	Tyr	Tyr	Leu	Gln	Ser	Thr	Leu
			100					105					110		
Gln	Asn	Ile	Glu	Lys	Ile	Val	Met	Leu	Ser	Gly	Gly	Val	Ala	Ser	Asn
		115					120					125			
Pro	Lys	Leu	Ala	Gln	Ala	Leu	Glu	Lys	Met	Gln	Glu	Pro	Ile	Thr	Asn
	130					135					140				
Pro	Leu	Glu	Leu	Val	Glu	Asn	Leu	Lys	Asn	Leu	Glu	Leu	Gln	Phe	Ser
145					150					155				160	
Gln	Ser	Gln	Asn	Ser	Met	Leu	Ser	Ser	Leu	Ser	Ser	Gln	Ile	Ala	Gln
			165						170					175	
Ile	Ser	Asn	Ser	Leu	Asn	Ala	Leu	Asp	Pro	Ser	Ser	Tyr	Ser	Lys	Asn
			180					185					190		
Val	Ser	Ser	Met	Tyr	Gly	Val	Gly	Leu	Ser	Val	Gly	Tyr	Lys	His	Phe

195	200	205
Phe Thr Lys Lys Lys Asn Gln Gly Phe Arg Tyr Tyr Leu Phe Tyr Asp		
210	215	220
Tyr Gly Tyr Thr Asn Phe Gly Phe Val Gly Asn Gly Phe Asp Gly Leu		
225	230	235
Gly Lys Met Asn Asn His Leu Tyr Gly Leu Gly Ile Asp Tyr Leu Phe		240
	245	250
Asn Phe Ile Asp Asn Ala Gln Lys His Ser Ser Val Gly Phe Tyr Val		255
	260	265
Gly Phe Ala Leu Ala Gly Ser Ser Trp Val Gly Ser Gly Leu Gly Met		270
	275	280
Trp Val Ser Gln Met Asp Phe Ile Asn Asn Tyr Leu Thr Asp Tyr Arg		285
	290	295
Ala Lys Met His Thr Ser Phe Phe Gln Ile Pro Leu Asn Phe Gly Val		300
305	310	315
Arg Val Asn Val Asp Arg His Asn Gly Phe Glu Met Gly Leu Lys Ile		320
	325	330
Pro Leu Ala Val Asn Ser Phe Tyr Glu Thr His Gly Lys Gly Leu Asn		335
	340	345
Ala Ser Leu Phe Phe Lys Arg Leu Val Met Phe Asn Val Ser Tyr Val		350
	355	360
Tyr Ser Phe		365
370		

(2) INFORMATION FOR SEQ ID NO:1054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

Met	Ala	Lys	Ile	Thr	Thr	Val	Ile	Asp	Ile	Gly	Ser	Asn	Ser	Val	Arg
1			5					10						15	
Leu	Ala	Val	Phe	Lys	Lys	Thr	Ser	Gln	Phe	Gly	Phe	Tyr	Leu	Leu	Phe
		20						25					30		
Glu	Thr	Lys	Ser	Lys	Val	Arg	Ile	Ser	Glu	Gly	Cys	Tyr	Ala	Phe	Lys
		35					40					45			
Gly	Val	Leu	Gln	Glu	Ile	Pro	Met	Gln	Arg	Ala	Val	Lys	Ala	Leu	Ser
		50				55				60					
Glu	Phe	Lys	Glu	Ile	Ala	Leu	Lys	Tyr	Lys	Ser	Lys	Lys	Ile	Leu	Cys
65				70				75					80		
Val	Ala	Thr	Ser	Ala	Val	Arg	Asp	Ala	Pro	Asn	Arg	Leu	Glu	Phe	Val
			85					90					95		
Ala	Arg	Val	Lys	Lys	Ala	Cys	Gly	Leu	Gln	Ile	Lys	Ile	Ile	Asp	Gly

964

	100		105		110
Gln Lys Glu Ala Leu Tyr Gly Gly Ile Ala Cys Ala Asn Leu Leu His					
	115		120		125
Lys Asn Ser Gly Ile Thr Ile Asp Ile Gly Gly Gly Ser Thr Glu Cys					
	130		135		140
Ala Leu Ile Glu Lys Gly Lys Ile Lys Asp Leu Ile Ser Leu Asp Val					
145		150		155	160
Gly Thr Ile Arg Ile Lys Glu Met Phe Leu Asp Lys Asp Leu Asp Val					
	165		170		175
Lys Leu Ala Lys Ala Phe Ile Gln Lys Glu Val Ser Lys Leu Pro Phe					
	180		185		190
Lys His Lys Asn Ala Phe Gly Val Gly Gly Thr Ile Arg Ala Leu Ser					
	195		200		205
Lys Val Leu Met Lys Arg Phe Asp Tyr Pro Ile Asp Ser Leu His Gly					
	210		215		220
Tyr Glu Ile Asp Ala His Lys Asn Leu Ala Phe Ile Glu Lys Ile Val					
225		230		235	240
Met Leu Lys Glu Asp Lys Leu Arg Leu Leu Gly Val Asn Glu Glu Arg					
	245		250		255
Leu Asp Ser Ile Arg Ser Gly Ala Leu Ile Leu Ser Val Val Leu Glu					
	260		265		270
His Leu Lys Thr Ser Leu Met Ile Thr Ser Gly Val Gly Val Arg Glu					
	275		280		285
Gly Val Phe Leu Ser Asp Leu Leu Arg His His Tyr His Lys Phe Pro					
	290		295		300
Pro Asn Ile Asn Pro Ser Leu Ile Ser Leu Lys Asp Arg Phe Leu Pro					
305		310		315	320
His Glu Lys His Ser Gln Lys Val Lys Lys Glu Cys Val Lys Leu Phe					
	325		330		335
Glu Val Leu Ser Pro Leu His Lys Ile Asp Glu Lys Tyr Leu Phe His					
	340		345		350
Leu Lys Ile Ala Gly Glu Leu Ala Ser Met Gly Lys Ile Leu Ser Val					
	355		360		365
Tyr Leu Ala His Lys His Ser Ala Tyr Phe Ile Leu Asn Ala Leu Ser					
	370		375		380
Tyr Gly Phe Ser His Gln Asp Arg Ala Ile Ile Cys Leu Leu Ala Gln					
385		390		395	400
Phe Ser His Lys Lys Ile Pro Lys Asp Asn Ala Ile Ala His Met Ser					
	405		410		415
Ala Met Met Pro Ser Leu Leu Thr Leu Gln Trp Leu Ser Phe Ile Leu					
	420		425		430
Ser Leu Ala Glu Asn Leu Cys Leu Thr Asp Ser His His Leu Lys Tyr					
	435		440		445
Thr Leu Glu Lys Asn Lys Leu Val Ile His Ser Asn Asp Ala Leu Tyr					
	450		455		460
Leu Ala Lys Glu Met Leu Pro Lys Leu Ile Lys Pro Ile Pro Leu Thr					
465		470		475	480
Ile Glu Phe Ala					

(2) INFORMATION FOR SEQ ID NO:1055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

965

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

```

Lys Gln Val Lys Ser Arg Met Lys Glu Lys Pro Phe Asn Ser Glu Gln
1          5          10          15
Met Ala Phe Leu Glu Glu Leu Leu Ser His Gln Glu Lys His Leu Glu
20          25          30
Ser Lys Leu Ser Gly Phe Ser Val Asn Asp Leu Asp Met Gln Ser Val
35          40          45
Phe Arg Leu Glu Arg Asn Arg Leu Lys Ile Ala Tyr Arg Leu Leu Gly
50          55          60
Leu Met Ser Phe Ile Ala Leu Val Leu Ala Ile Val Leu Ile Ser Ile
65          70          75          80
Leu Pro Leu Gln Lys Thr Glu His His Phe Val Asp Phe Leu Asn Gln
85          90          95
Asp Lys His Tyr Ala Ile Ile Gln Arg Ala Asp Lys Ser Ile Ser Ser
100         105         110
Asn Glu Ala Leu Ala Arg Ser Leu Ile Gly Ala Tyr Val Leu Asn Arg
115         120         125
Glu Ser Ile Asn Arg Ile Asp Asp Lys Ser Arg Tyr Glu Leu Val Arg
130         135         140
Leu Gln Ser Ser Ser Lys Val Trp Gln Arg Phe Glu Asp Leu Ile Lys
145         150         155         160
Ala Gln Asn Ser Ile Tyr Val Gln Ser His Leu Glu Arg Glu Val His
165         170         175
Ile Val Asn Ile Ala Ile Tyr Gln Gln Asp Asn Asn Pro Ile Ala Ser
180         185         190
Val Ser Ile Ala Ala Lys Leu Leu Asn Glu Asn Lys Leu Val Tyr Glu
195         200         205
Lys Arg Tyr Lys Ile Val Leu Ser Tyr Leu Phe Asp Thr Pro Asp Phe
210         215         220
Asp Tyr Ala Ser Met Pro Lys Asn Pro Thr Gly Phe Lys Ile Thr Arg
225         230         235         240
Tyr Ser Ile Thr Glu Ile Ala Pro Thr Asn Arg Asn Asp
245         250

```

(2) INFORMATION FOR SEQ ID NO:1056:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 479 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

```

Met Lys Lys Ser Leu Cys Leu Ser Phe Phe Leu Thr Phe Ser Asn Pro
1          5          10          15
Leu Gln Ala Leu Val Ile Glu Leu Leu Glu Glu Ile Lys Thr Ser Pro
20          25          30
His Lys Gly Thr Phe Lys Ala Lys Val Leu Asp Ser Lys Glu Pro Arg
35          40          45
Gln Val Leu Gly Val Tyr Asn Ile Ser Pro His Lys Lys Leu Thr Leu
50          55          60
Thr Ile Thr His Ile Ser Thr Ala Ile Val Tyr Gln Pro Leu Asp Glu
65          70          75          80
Lys Leu Ser Leu Glu Thr Thr Leu Ser Pro Asn Arg Pro Thr Ile Pro
85          90          95
Arg Asn Thr Gln Ile Val Phe Ser Ser Lys Glu Leu Lys Glu Pro His
100         105         110
Ser Asn Pro Ile Pro Ser Leu Asn Ala Pro Met Gln Lys Pro Gln Asn
115         120         125
Lys Pro Ser Ser Ser Gln Gln Ser Pro Gln Asn Phe Ser Tyr Pro Glu
130         135         140
Ser Lys Leu Gly Ser Lys Asn Ser Lys Asn Ser Leu Leu Gln Pro Leu
145         150         155         160
Val Thr Pro Ser Lys Val Ser Pro Thr Asn Glu Val Lys Thr Pro Thr
165         170         175
Asn Asp Ala Asn Pro Pro Leu Lys His Ser Ser Gln Asp Gln Glu Asn
180         185         190
Asn Leu Phe Val Ala Pro Pro Thr Glu Lys Thr Leu Pro Asn Asn Thr
195         200         205
Ser Ser Ala Asp Ala Ser Glu Asn Asn Glu Ser Asn Glu Asn Arg Asp
210         215         220
Asn Val Glu Lys Gln Ala Ile Arg Asp Pro Asn Ile Lys Glu Phe Ala
225         230         235         240
Cys Gly Lys Trp Val Tyr Asp Asp Glu Asn Leu Gln Ala Tyr Arg Pro
245         250         255
Ser Ile Leu Lys Arg Val Asp Lys Asp Lys Glu Ile Thr Thr Asp Ile
260         265         270
Thr Pro Cys Asp Tyr Ser Thr Ala Glu Asn Lys Ser Gly Lys Ile Ile
275         280         285
Thr Pro Tyr Thr Lys Ile Ser Val His Lys Thr Glu Pro Leu Glu Asp
290         295         300
Pro Gln Thr Phe Glu Ala Lys Asn Asn Phe Ala Ile Leu Gln Ala Arg
305         310         315         320
Ser Ser Thr Glu Lys Cys Lys Arg Ala Arg Ala Arg Lys Asp Gly Thr
325         330         335
Thr Arg Gln Cys Tyr Leu Ile Glu Glu Pro Leu Lys Gln Ala Trp Glu
340         345         350
Ser Glu Tyr Glu Ile Thr Thr Gln Leu Val Lys Ala Ile Tyr Glu Arg
355         360         365
Pro Lys Gln Asp Asp Gln Val Glu Pro Thr Phe Tyr Glu Thr Ser Glu
370         375         380

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967

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Leu Ala Tyr Ser Ser Thr Arg Lys Ser Glu Ile Thr Arg Asn Glu Leu
385                      390                      395                      400
Asn Leu Asn Glu Lys Phe Met Glu Phe Val Glu Val Tyr Glu Gly His
                      405                      410                      415
Tyr Leu Asn Asp Ile Ile Lys Glu Ser Ser Glu Tyr Lys Glu Trp Val
                      420                      425                      430
Lys Asn His Val Arg Phe Lys Glu Gly Val Cys Met Ala Leu Glu Ile
                      435                      440                      445
Glu Glu Gln Pro Arg Ala Lys Ser Thr Pro Leu Ser Ile Glu Asn Ser
                      450                      455                      460
Arg Val Val Cys Val Lys Lys Gly Asn Tyr Leu Phe Asn Glu Val
465                      470                      475

```

(2) INFORMATION FOR SEQ ID NO:1057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:

```

Met Ile Phe Gly Asp Phe Lys Tyr Gln Lys Ser Val Lys Lys Leu Thr
1                      5                      10                      15
Ala Thr Asn Leu Asn Glu Leu Lys Asn Ala Leu Asp Phe Ile Ser Gln
                      20                      25                      30
Asn Arg Gly Lys Gly Tyr Phe Val Gly Tyr Leu Leu Tyr Glu Ala Arg
                      35                      40                      45
Leu Ala Phe Leu Asp Glu Asn Phe Gln Ser Gln Thr Pro Phe Leu Tyr
                      50                      55                      60
Phe Glu Gln Phe Leu Glu Arg Lys Lys Tyr Pro Leu Glu Pro Leu Lys
65                      70                      75                      80
Glu His Ala Phe Tyr Pro Lys Ile His Ser Ser Leu Asp Gln Lys Thr
                      85                      90                      95
Tyr Phe Lys Gln Phe Lys Ala Val Lys Glu His Leu Lys Asn Gly Asp
                      100                     105                     110
Thr Tyr Gln Val Asn Leu Thr Met Asp Leu Leu Leu Asn Thr Lys Ala
                      115                     120                     125
Lys Pro Lys Arg Val Phe Lys Glu Val Ile His Asn Gln Asn Thr Pro
                      130                     135                     140
Phe Lys Ala Phe Ile Glu Asn Glu Phe Gly Ser Val Leu Ser Phe Ser
145                     150                     155                     160
Pro Glu Leu Phe Phe Glu Leu Glu Phe Leu Asp Thr Ala Ile Lys Ile
                      165                     170                     175
Ile Thr Lys Pro Met Lys Gly Thr Ile Ala Arg Ser Asn Asn Pro Leu
180                     185                     190

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968

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Ile Asp Glu Lys Asn Arg Leu Phe Leu Gln Asn Asp Asp Lys Asn Arg
    195                200                205
Ser Glu Asn Val Met Ile Val Asp Leu Leu Arg Asn Asp Leu Ser Arg
    210                215                220
Leu Ala Leu Lys Asn Ser Val Lys Val Asn Gln Leu Phe Glu Ile Ile
    225                230                235                240
Ser Leu Pro Ser Val Tyr Gln Met Ile Ser Glu Ile Glu Ala Gln Leu
    245                250                255
Pro Leu Lys Thr Ser Leu Phe Glu Ile Phe Lys Ala Leu Phe Pro Cys
    260                265                270
Gly Ser Val Thr Gly Cys Pro Lys Ile Lys Thr Met Gln Ile Ile Glu
    275                280                285
Ser Leu Glu Lys Arg Pro Arg Gly Val Tyr Cys Gly Ala Ile Gly Met
    290                295                300
Val Gly Gly Lys Lys Ala Leu Phe Ser Val Pro Ile Arg Thr Leu Glu
    305                310                315                320
Lys Arg Ala His Glu Asp Phe Leu His Leu Gly Val Gly Ser Gly Val
    325                330                335
Thr Tyr Lys Ser Lys Ala Ser Lys Glu Tyr Glu Glu Ser Phe Leu Lys
    340                345                350
Ser Phe Phe Val Met Pro Lys Ile Glu Phe Glu Ile Val Glu Thr Met
    355                360                365
Arg Val Ile Lys Arg Asp Gln Lys Leu Glu Ile Asn Asn Lys Asn Ala
    370                375                380
His Lys Glu Arg Leu Met His Ser Ala Gln Tyr Phe Asn Phe Lys Tyr
    385                390                395                400
Asp Glu Asn Leu Leu Asp Phe Glu Leu Glu Lys Glu Gly Val Leu Arg
    405                410                415
Val Leu Leu Asn Lys Arg Gly Lys Leu Ile Lys Glu Tyr Arg Thr Leu
    420                425                430
Glu Pro Leu Lys Ser Leu Glu Ile Arg Leu Ser Glu Ala Pro Ile Asp
    435                440                445
Lys His Asp Asp Phe Leu Tyr His Lys Thr Ala Tyr Ala Pro Phe Tyr
    450                455                460
Gln Asn Ala Arg Ala Leu Ile Lys Lys Gly Val Ile Phe Asp Glu Ile
    465                470                475                480
Phe Tyr Asn Gln Asp Leu Glu Leu Thr Glu Gly Ala Arg Ser Asn Leu
    485                490                495
Ile Leu Glu Ile His Asn Arg Leu Leu Thr Pro Tyr Phe Ser Val Gly
    500                505                510
Ala Leu Thr Gly Thr Gly Val Val Gly Leu Leu Lys Lys Gly Leu Val
    515                520                525
Glu His Ala Pro Leu Lys Leu Gln Asp Leu Gln Arg Ala Ala Lys Ile
    530                535                540
Tyr Cys Ile Asn Ala Leu Tyr Gly Leu Val Glu Val Gly Ile Ile Gly
    545                550                555                560
Tyr Pro Met Glu Gln Lys Ser
    565

```

(2) INFORMATION FOR SEQ ID NO:1058:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

```

Met Lys Ile Ser Val Ser Lys Asn Asp Leu Glu Asn Thr Leu Arg Tyr
1      5      10      15
Leu Gln Ala Phe Leu Asp Lys Lys Asp Ala Ser Ser Ile Ala Ser His
20      25      30
Ile His Leu Glu Val Ile Lys Glu Lys Leu Phe Leu Lys Ala Ser Asp
35      40      45
Ser Asp Ile Gly Leu Lys Ser Tyr Ile Ser Thr Gln Ser Thr Asp Lys
50      55      60
Glu Gly Val Gly Thr Ile Asn Gly Lys Lys Phe Leu Asp Ile Ile Ser
65      70      75      80
Cys Leu Lys Asp Ser Asn Ile Val Leu Glu Thr Lys Asp Asp Ser Leu
85      90      95
Val Ile Lys Gln Asn Lys Ser Ser Phe Lys Leu Pro Met Phe Asp Ala
100     105     110
Asp Glu Phe Pro Glu Phe Pro Val Ile Asp Pro Lys Val Ser Leu Glu
115     120     125
Ile Asn Ala Pro Phe Leu Val Asp Ala Phe Lys Lys Ile Ala Pro Val
130     135     140
Ile Glu Gln Thr Ser His Lys Arg Glu Leu Ala Gly Val Leu Met Gln
145     150     155     160
Phe Asn Gln Lys His Gln Thr Leu Ser Val Val Gly Thr Asp Thr Lys
165     170     175
Arg Leu Ser Tyr Thr Gln Leu Glu Lys Ile Ser Ile His Ser Thr Glu
180     185     190
Glu Asp Ile Ser Cys Ile Leu Pro Lys Arg Ala Leu Leu Glu Ile Leu
195     200     205
Lys Leu Phe Tyr Glu Asn Phe Ser Phe Lys Ser Asp Gly Met Leu Ala
210     215     220
Val Val Glu Asn Glu Thr His Ala Phe Phe Thr Lys Leu Ile Asp Gly
225     230     235     240
Asn Tyr Pro Asp Tyr Gln Lys Ile Leu Pro Lys Glu Tyr Thr Ser Ser
245     250     255
Phe Thr Leu Gly Lys Glu Glu Phe Lys Glu Gly Ile Lys Leu Cys Ser
260     265     270
Ser Leu Ser Ser Thr Ile Lys Leu Thr Leu Glu Lys Asn Asn Ala Leu
275     280     285
Phe Glu Ser Leu Asp Ser Glu His Ser Glu Thr Ala Lys Thr Ser Val
290     295     300
Glu Ile Glu Lys Gly Leu Asp Ile Glu Lys Ala Phe His Leu Gly Val
305     310     315     320
Asn Ala Lys Phe Phe Leu Glu Ala Leu Asn Ala Leu Gly Thr Thr Gln
325     330     335
Phe Val Leu Lys Cys Asn Glu Pro Ser Ser Pro Phe Leu Ile Gln Glu
340     345     350
Pro Leu Asp Glu Lys Gln Ser His Leu Asn Ala Lys Ile Ser Thr Leu

```


355 360 365
Met Met Pro Ile Thr Leu
370

(2) INFORMATION FOR SEQ ID NO:1059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

```

Met Val Val Leu Gly Ser Thr Gly Ser Ile Gly Lys Asn Ala Leu Lys
1      5      10      15
Ile Ala Lys Lys Phe Gly Val Lys Ile Glu Ala Leu Ser Cys Gly Lys
      20      25      30
Asn Ile Ala Leu Ile Asn Glu Gln Ile Lys Val Phe Lys Pro Lys Lys
      35      40      45
Val Ala Ile Leu Asp Pro Asn Asp Leu Asn Asn Leu Glu Pro Leu Gly
      50      55      60
Ala Glu Val Phe Val Gly Leu Asp Gly Ile Asp Ala Met Ile Glu Glu
65      70      75      80
Cys Val Ser Asn Leu Val Ile Asn Ala Ile Val Gly Val Ala Gly Leu
      85      90      95
Lys Ala Ser Phe Lys Ser Leu Gln Arg Asn Lys Lys Leu Ala Leu Ala
      100     105     110
Asn Lys Glu Ser Leu Val Ser Ala Gly His Leu Leu Asp Ile Ser Gln
      115     120     125
Ile Thr Pro Val Asp Ser Glu His Phe Gly Leu Trp Ala Leu Leu Gln
      130     135     140
Asn Lys Thr Leu Lys Pro Lys Ser Leu Ile Ile Ser Ala Ser Gly Gly
145     150     155     160
Ala Phe Arg Asp Thr Pro Leu Asp Leu Ile Ala Ile Gln Asn Ala Gln
      165     170     175
Asn Ala Leu Lys His Pro Asn Trp Ser Met Gly Asp Lys Ile Thr Ile
      180     185     190
Asp Ser Ala Ser Met Val Asn Lys Leu Phe Glu Ile Leu Glu Thr Tyr
      195     200     205
Trp Leu Phe Gly Ala Ser Leu Lys Ile Asp Ala Leu Ile Glu Arg Ser
      210     215     220
Ser Ile Val His Ala Leu Val Glu Phe Glu Asp Asn Ser Val Ile Ala
225     230     235     240
His Leu Ala Ser Ala Asp Met Gln Leu Pro Ile Ser Tyr Ala Ile Asn
      245     250     255
Pro Lys Leu Ala Ser Leu Ser Ala Ser Ile Lys Pro Leu Asp Leu Tyr

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971

Ala	Leu	Ser	Ala	Ile	Lys	Phe	Glu	Pro	Ile	Ser	Val	Glu	Arg	Tyr	Thr
260								265					270		
275							280					285			
Leu	Trp	Arg	Tyr	Lys	Asp	Leu	Leu	Leu	Glu	Asn	Pro	Lys	Leu	Gly	Val
290						295					300				
Val	Leu	Asn	Ala	Ser	Asn	Glu	Val	Ala	Met	Lys	Lys	Phe	Leu	Asn	Gln
305					310					315					320
Glu	Ile	Ala	Phe	Gly	Gly	Phe	Ile	Gln	Ile	Ile	Ser	Gln	Ala	Leu	Glu
				325				330					335		
Leu	Tyr	Ala	Lys	Lys	Ser	Phe	Lys	Leu	Ser	Ser	Leu	Asp	Glu	Val	Leu
		340						345					350		
Ala	Leu	Asp	Lys	Glu	Val	Arg	Glu	Arg	Phe	Gly	Ser	Val	Ala	Arg	Val
		355					360					365			

(2) INFORMATION FOR SEQ ID NO:1060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

Met	Lys	Tyr	Leu	Trp	Leu	Phe	Leu	Ile	Tyr	Ala	Ile	Gly	Leu	Phe	Ala
1			5					10					15		
Thr	Asp	Lys	Thr	Leu	Asp	Ile	Ile	Lys	Thr	Ile	Gln	Lys	Leu	Pro	Lys
			20					25					30		
Ile	Glu	Val	Arg	Tyr	Ser	Ile	Asp	Asn	Asp	Ala	Asn	Tyr	Ala	Leu	Lys
		35					40					45			
Leu	His	Glu	Val	Leu	Ala	Asn	Asp	Leu	Lys	Thr	Ser	Gln	His	Phe	Asp
	50					55				60					
Val	Ser	Gln	Asn	Lys	Glu	Gln	Gly	Ala	Ile	Asn	Tyr	Ala	Glu	Leu	Lys
65				70				75					80		
Asp	Lys	Lys	Val	His	Leu	Val	Ala	Leu	Val	Ser	Val	Ala	Val	Glu	Asn
			85					90					95		
Gly	Asn	Lys	Ile	Ser	Arg	Leu	Lys	Leu	Tyr	Asp	Val	Asp	Thr	Gly	Thr
			100					105					110		
Leu	Lys	Lys	Thr	Phe	Asp	Tyr	Pro	Ile	Val	Ser	Leu	Asp	Leu	Tyr	Pro
		115					120					125			
Phe	Ala	Ala	His	Asn	Met	Ala	Ile	Val	Val	Asn	Asp	Tyr	Leu	Lys	Ala
	130					135				140					
Pro	Ser	Ile	Ala	Trp	Met	Lys	Arg	Leu	Ile	Val	Phe	Ser	Lys	Tyr	Ile
145				150				155					160		
Gly	Pro	Gly	Ile	Thr	Asn	Ile	Ala	Leu	Ala	Asp	Tyr	Thr	Met	Arg	Tyr
			165					170					175		
Gln	Lys	Glu	Ile	Ile	Lys	Asn	Asn	Arg	Leu	Asn	Ile	Phe	Pro	Lys	Trp

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

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

973

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      35              40              45
Val Ala Tyr Asp Arg Ser Asp Ala Met Thr Ser Tyr Tyr Ile Asn Val
  50              55              60
Ile Val Tyr Glu Leu Gln Lys Leu Gly Phe Tyr Asn Val Phe Thr Gln
  65              70              75              80
Ala Glu Phe Pro Leu Asp Lys Ala Lys Asn Val Ile Tyr Val Arg Ile
      85              90              95
Val Arg Asn Ile Ser Ala Val Pro Phe Tyr Gln Tyr Asn Tyr Gln Leu
      100             105             110
Ile Asp Gln Val Asn Lys Pro Cys Tyr Phe Leu Gly Gly Gln Phe Tyr
      115             120             125
Cys Ser Gln Thr Pro Thr Asp Tyr Tyr Ala Ile Asn Gly Phe Ser Glu
      130             135             140
Gln Ile Leu Met Ser Ala Asn Ser His Phe Ile Leu Asp Trp Tyr Asp
      145             150             155             160
Val Val Leu Gln Lys Arg Val Leu Tyr Val Asp Gly Ser Val Ser Gly
      165             170             175
Arg Thr Cys Gly Tyr Gln Met Leu Tyr Arg Asp Leu Ile Lys Ser Thr
      180             185             190
Ile Lys Arg Ile Asp Phe Asn Arg Pro Glu Arg Tyr Tyr Tyr Asn Leu
      195             200             205
Arg Leu Pro Leu Tyr Gln Pro Cys Tyr Arg Gln
      210             215

```

(2) INFORMATION FOR SEQ ID NO:1062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

```

Met Gln Tyr Lys Lys Asn Lys Lys Arg Tyr Tyr His Leu Ala Leu Gly
  1              5              10              15
Ile Leu Phe Cys Asn Gly Leu Ser Leu Lys Ala Leu Glu Ile Ala Val
      20              25              30
Lys Pro Phe Gly Tyr Leu Gly Leu Leu Tyr Asn Gln Gly Thr Gln Lys
      35              40              45
Asn Pro His Ser Tyr Val Gly Ala Leu Ala Arg Leu Gly Val Asp Phe
      50              55              60
Ser Tyr Ser Asn Gly Trp Ser Phe Gly Ile Gly Ala Ile Gly Ala Trp
      65              70              75              80
Asn Ile Tyr Asn Lys Gln Arg Leu Ala Asn Leu Tyr Ile Ser Leu Gly
      85              90              95
Asn Phe Phe Gly Asn Pro Asn Asn Val Lys Pro Tyr Leu Ser Ala Gly

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974

100	105	110
Asp Val Ser Asp Ala Tyr Leu Gln Tyr Ala Asn Gln Arg Phe Lys Ile		
115	120	125
Ala Leu Gly Arg Phe Asn Thr Asp Phe Val Asp Phe Asp Trp Ile Gly		
130	135	140
Gly Asn Ile Gln Gly Val Ser Val Ala Phe Lys Gln Asn Ser Met Arg		
145	150	155
Tyr Phe Gly Ile Phe Met Asp Ser Met Leu Tyr Asn Gly His Gln Ile		
165	170	175
Asn Lys Glu Gln Gly Asn Arg Ile Ala Thr Ser Leu Asn Ala Leu Ala		
180	185	190
Ser Tyr Asp Pro Val Ser Lys Arg Leu Tyr Val Gly Gly Glu Val Phe		
195	200	205
Val Leu Gly Ala Glu Tyr Lys Asn Lys Asn Leu Ile Phe Val Pro Phe		
210	215	220
Ile Leu Thr Asp Thr Arg Leu Pro Leu Pro Thr Gln Asn Val Leu Val		
225	230	235
Gln Val Gly Gly Lys Leu Glu Tyr Asp Ala Ser Leu Ala Lys Gly Phe		
245	250	255
Thr Ser Arg Thr Leu Val His Gly Met Tyr Gln Tyr Gly Asn Thr Asp		
260	265	270
Ile Thr Thr Ser Ala Lys Asn Ala Gly Leu Phe Leu Ile Asp Gln Thr		
275	280	285
Phe Lys Tyr Lys Ile Phe Asn Phe Gly Thr Gly Phe Tyr Ile Val Pro		
290	295	300
Ala Arg Asn Asn Lys Gly Tyr Leu Trp Thr Phe Asn Asp Arg Thr Lys		
305	310	315
Phe Tyr Gly Arg Gly Ile Asn Ala Pro Gly Val Pro Ala Ile Tyr Phe		
325	330	335
Ala Asn Ser Ser Ile Ser Gly Tyr Val Phe Leu Gly Leu Lys Thr Lys		
340	345	350
Arg Val Arg Leu Asp Ala Met Val Ala Phe Gly Asp Tyr Gln Glu Tyr		
355	360	365
Ser Leu Met Ser Ser Phe Arg Val Trp Thr Tyr Arg Asp Leu Ser Phe		
370	375	380
Asp Met Gly Gly Gly Tyr Val Tyr Ala Tyr Asn Ser Lys Ala Thr Arg		
385	390	395
Lys Ser Leu Gly Asp Ser Ser Phe Val Phe Phe Gly Lys Phe Leu Phe		
405	410	415

(2) INFORMATION FOR SEQ ID NO:1063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

Met	Val	Lys	Asn	Thr	Lys	Gly	Ile	Gln	Gln	Leu	Ser	Glu	Asn	Tyr	Glu	1	5	10	15
Lys	Leu	Asn	Asn	Leu	Leu	Asn	Asn	Tyr	Asn	Thr	Leu	Asn	Thr	Leu	Val	20	25	30	
Lys	Leu	Ser	Ser	Asp	Pro	Ser	Ala	Val	Asn	Asp	Ala	Arg	Asp	Asn	Leu	35	40	45	
Gly	Ser	Ser	Thr	Arg	Asn	Leu	Leu	Asp	Val	Lys	Ala	Asn	Ser	Pro	Ala	50	55	60	
Tyr	Gln	Ala	Val	Leu	Leu	Ala	Leu	Asn	Ala	Ala	Val	Gly	Leu	Trp	Gln	65	70	75	80
Val	Thr	Ser	Tyr	Ala	Phe	Thr	Ala	Cys	Gly	Pro	Gly	Ser	Asn	Glu	Asn	85	90	95	
Ala	Asn	Gly	Gly	Ile	Gln	Thr	Phe	Asn	Asn	Val	Pro	Gly	Gln	Asn	Thr	100	105	110	
Thr	Thr	Ile	Thr	Cys	Asn	Ser	Tyr	Tyr	Glu	Pro	Gly	His	Gly	Gly	Pro	115	120	125	
Ile	Ser	Thr	Lys	Asn	Tyr	Ala	Ile	Ile	Asn	Lys	Ala	Tyr	Gln	Ile	Ile	130	135	140	
Gln	Lys	Ala	Leu	Thr	Ala	Asn	Gly	Glu	Gly	Ile	Pro	Val	Leu	Ser	Asn	145	150	155	160
Thr	Thr	Thr	Lys	Leu	Asp	Phe	Thr	Ile	Asn	Gly	Asp	Lys	Arg	Thr	Gly	165	170	175	
Gly	Glu	Pro	Asn	Lys	Lys	Leu	Val	Tyr	Pro	Trp	Ser	His	Gly	Lys	Ala	180	185	190	
Ile	Ser	Thr	Ser	Trp	Asn	Ala	Thr	Ile	Thr	Ala	Pro	Thr	Thr	Glu	Asn	195	200	205	
Ile	Asn	Thr	Thr	Asn	Ser	Ala	Gln	Glu	Leu	Leu	Lys	Gln	Ala	Ser	Ile	210	215	220	
Ile	Ile	Thr	Thr	Leu	Asn	Ser	Ala	Cys	Pro	Asn	Phe	Gln	Asn	Gly	Gly	225	230	235	240
Ser	Gly	Tyr	Trp	Ala	Gly	Ile	Ser	Gly	Asn	Gly	Thr	Met	Cys	Gly	Met	245	250	255	
Phe	Lys	Asn	Glu	Ile	Ser	Ala	Ile	Gln	Gly	Met	Ile	Ala	Asn	Ala	Gln	260	265	270	
Glu	Ala	Val	Ala	Gln	Ala	Lys	Ile	Val	Ser	Glu	Asn	Thr	Gln	Asn	Gln	275	280	285	
Asn	Ser	Leu	Asp	Ala	Gly	Lys	Pro	Phe	Asn	Pro	Tyr	Thr	Asp	Ala	Ser	290	295	300	
Phe	Ala	Glu	Ser	Met	Leu	Lys	Asn	Ala	Gln	Ala	Gln	Ala	Glu	Ile	Leu	305	310	315	320
Asn	Gln	Ala	Glu	Gln	Val	Val	Lys	Asn	Phe	Glu	Lys	Ile	Pro	Thr	Ala	325	330	335	
Phe	Val	Asn	Asp	Ser	Leu	Gly	Val	Cys	Tyr	Glu	Val	Gln	Gly	Gly	Glu	340	345	350	
Arg	Arg	Gly	Thr	Asn	Pro	Gly	Gln	Thr	Thr	Ser	Asn	Thr	Trp	Gly	Ala	355	360	365	
Gly	Cys	Ala	Tyr	Val	Gly	Gln	Thr	Ile	Thr	Asn	Leu	Lys	Asn	Ser	Ile	370	375	380	
Ala	His	Phe	Gly	Thr	Gln	Glu	Gln	Gln	Ile	Gln	Gln	Ala	Glu	Asn	Ile	385	390	395	400
Ala	Asp	Thr	Leu	Val	Asn	Phe	Lys	Ser	Arg	Tyr	Ser	Glu	Leu	Gly	Asn	405	410	415	
Thr	Tyr	Asn	Ser	Ile	Thr	Thr	Ala	Leu	Ser	Asn	Ile	Pro	Asn	Ala	Gln	420	425	430	

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Ser Leu Gln Asn Ala Val Ser Lys Lys Asn Asn Pro Tyr Ser Pro Gln
    435                      440                      445
Gly Ile Asp Thr Asn Tyr Tyr Leu Asn Gln Asn Ser Tyr Asn Gln Ile
    450                      455                      460
Gln Thr Ile Asn Gln Glu Leu Gly Arg Asn Pro Phe Arg Lys Val Gly
    465                      470                      475                      480
Ile Val Ser Ser Gln Thr Asn Asn Gly Ala Met Asn Gly Ile Gly Ile
    485                      490                      495
Gln Val Gly Tyr Lys Gln Phe Phe Gly Gln Lys Arg Lys Trp Gly Ala
    500                      505                      510
Arg Tyr Tyr Gly Phe Phe Asp Tyr Asn His Ala Phe Ile Lys Ser Ser
    515                      520                      525
Phe Phe Asn Ser Ala Ser Asp Val Trp Thr Tyr Gly Phe Gly Ala Asp
    530                      535                      540
Ala Leu Tyr Asn Phe Ile Asn Asp Lys Ala Thr Asn Phe Leu Gly Lys
    545                      550                      555                      560
Asn Asn Lys Leu Ser Val Gly Leu Phe Gly Gly Ile Ala Leu Ala Gly
    565                      570                      575
Thr Ser Trp Leu Asn Ser Glu Tyr Val Asn Leu Ala Thr Met Asn Asn
    580                      585                      590
Val Tyr Asn Ala Lys Met Asn Val Ala Asn Phe Gln Phe Leu Phe Asn
    595                      600                      605
Met Gly Val Arg Met Asn Leu Ala Arg Pro Lys Lys Lys Asp Ser Asp
    610                      615                      620
His Ala Ala Gln His Gly Ile Glu Leu Gly Leu Lys Ile Pro Thr Ile
    625                      630                      635                      640
Asn Thr Asn Tyr Tyr Ser Phe Met Gly Ala Glu Leu Lys Tyr Arg Arg
    645                      650                      655
Leu Tyr Ser Val Tyr Leu Asn Tyr Val Phe Ala Tyr
    660                      665

```

(2) INFORMATION FOR SEQ ID NO:1064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

```

Leu Thr Lys Lys Phe Met Ser Trp Met Val Val Ile Gly Ala Leu Ile
1          5          10          15
Cys Val Leu Leu Gly Val Phe Ile Phe Phe Thr Ser Met Ser Val Lys
          20          25          30
Lys Ser Leu Thr Ala Tyr Leu Asn Ala Tyr Leu Glu Gln Arg Pro Asn
          35          40          45

```

977

```

Ile Glu Gly Met Gly Ile Ile Gly Val Pro Phe Lys Cys Glu Gly Phe
 50                      55                      60
Phe Lys Ile Ala Cys Val Ser Lys Glu Leu Arg Phe Leu Asp Pro Gln
65                      70                      75                      80
Asn Ser Pro Ile Met Asp Phe Lys Asn Leu Lys Ile Lys Leu His Ser
                      85                      90                      95
Leu Asp Lys Ser Ser Leu Thr Leu Ser Ile His Ser Gln Ile Gln Ser
                      100                     105                     110
Pro Ile Leu Glu Gln Ser Ile Gln Gln Lys Ile Ser Gln Ile Pro Leu
                      115                     120                     125
Lys Asn Leu Asn Ala Leu Leu Glu Lys Phe Lys Pro Thr Arg Leu Asn
                      130                     135                     140
Cys Ser Leu Thr Phe Asn Ala Leu Asp Glu Lys Thr Leu Asn Asp Asn
145                      150                      155                      160
Leu Lys Cys Asp Leu Thr Asn Ala Glu Asn Ile Leu Ala Tyr Thr Phe
                      165                      170                      175
Phe Gln Glu Gly Leu Met Glu Ala Gln Glu Asn Leu Ser Leu Lys Asn
                      180                      185                      190
Ile Phe Lys Thr Leu Ser Ser Lys Asp Ala Lys Ala Ile Glu Glu Leu
                      195                      200                      205
Gln Asp Lys Leu Arg Phe Leu Ala Pro Lys Leu Ser Val Ser Ile Gln
210                      215                      220
Ala Arg His Phe Lys Asn Val Leu Glu Ser Phe Tyr Gln Gln Asn Lys
225                      230                      235                      240
Glu Ser Leu Gly Phe Phe Ser Pro Tyr Phe Ser Leu Arg Ser Gln Thr
                      245                      250                      255
Pro Ser Val Ser Tyr Glu Ser Ala Leu Ala Ser Leu Glu Asn Tyr Phe
                      260                      265                      270
Met Ala Leu Phe Gln Ser His Phe Lys Asp Asp Thr Ala Leu Gln Gln
275                      280                      285
Asn Phe Lys Gly Leu Leu Gln Ala Phe Val Ser Met Ala Lys Asp Lys
290                      295                      300
Arg Ser Gln Ile Val Leu Asn Ala Gln Ala Lys Asp Asn Thr Lys Leu
305                      310                      315                      320
Thr Phe Asn Ala Leu Leu Glu Ser Leu Ser Val Asn Phe Phe Gln Ser
                      325                      330                      335
Tyr Lys Ile Ser His Glu
                      340

```

(2) INFORMATION FOR SEQ ID NO:1065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

```

Met Arg Leu Leu Phe Leu Leu Leu Ser Ala Thr Leu Met Leu Leu Ala
1      5      10      15
Glu Glu Lys Ile Pro Leu Ser Asp Asp Ala Pro Ile Lys Leu Val His
20      25      30
Trp Gln Asn Ala Leu Lys Glu Val Gln Pro Asp Ser Asn Ala Pro Ala
35      40      45
Thr Pro Pro Ile Lys Ala Val Gln Thr Thr Leu Thr Phe Glu Thr Pro
50      55      60
Phe Asn Lys Thr Pro Lys Ile Met Glu Val Glu Gly Gln Lys Val Ile
65      70      75      80
Val Leu Lys Asn Ala Gln Leu Asp Ser Lys Lys Thr Met Asp Phe Lys
85      90      95
Glu Ala Ser Leu Asn Ala Leu Glu Met Phe Ser Tyr Gln Asn Asp Ile
100     105     110
Tyr Leu Leu Ser Lys Lys Ala Lys Ala Gly Leu Glu Ile Gln Ala Ser
115     120     125
Ser Ser Lys Asp Lys Lys Gln Leu Arg Phe Leu Phe Leu Pro Lys Gly
130     135     140
Phe His Leu Ala Pro Pro Pro Ser Leu Lys Glu Lys Ser Gln His Ala
145     150     155     160
Asn Leu Ala Ser Gln Asp Glu Lys Glu Arg Ala Lys Ser Pro Ser Asn
165     170     175
Ala Leu Glu Leu Lys Pro Pro Leu Asp Leu Ser His Ala Tyr Lys Gly
180     185     190
Leu Ala Val Ile Ala Val Leu Leu Leu Ile Leu Tyr Val Ile Lys Lys
195     200     205
Lys Ile Val Pro Thr Pro Gly Ser Phe Leu Lys Lys Asp Leu Lys Leu
210     215     220
Asp Ile Ser Val Leu Gly Arg Val Asp Ala Asn His Lys Ile Ile Ser
225     230     235     240
Ile Glu Thr Asn Lys Glu Arg Tyr Leu Val Leu Leu Ser Asp Lys Tyr
245     250     255
Gly Leu Leu Leu Asp Lys Ile Ser Pro Lys Thr Ser Lys Glu Glu Leu
260     265     270
Ile Lys Glu Ala Glu Asn Lys Ile Lys Asn Ser Lys Leu Gly Asn Leu
275     280     285
Tyr Ala Gly Lys Phe
290

```

(2) INFORMATION FOR SEQ ID NO:1066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

```

Met Leu Arg Asn Gln Phe Arg Ile Val Phe Val Ser Cys Ile Val Ala
1           5           10           15
Ser Ser Leu Gln Ala Gln Glu Asn Thr His Thr Leu Gly Lys Val Thr
          20           25           30
Thr Lys Gly Glu Arg Thr Phe Glu Tyr Asn Asn Lys Met Tyr Ile Asp
          35           40           45
Arg Lys Glu Leu Gln Gln Arg Gln Ser Asn Gln Ile Arg Asp Ile Phe
          50           55           60
Arg Thr Arg Ala Asp Val Asn Val Ala Ser Gly Gly Leu Met Ala Gln
65          70          75          80
Lys Ile Tyr Val Arg Gly Ile Glu Ser Arg Leu Leu Arg Val Thr Ile
          85          90          95
Asp Gly Val Ala Gln Asn Gly Asn Ile Phe His His Asp Ala Asn Thr
          100         105         110
Val Ile Asp Pro Asn Met Ile Lys Glu Val Glu Val Ile Lys Gly Ala
          115         120         125
Ala Asn Ala Ser Ala Gly Pro Gly Ala Val Ala Gly Lys Leu Ser Phe
          130         135         140
Thr Thr Ile Asp Ala Asn Asp Phe Leu Arg Lys Asn Gln Thr Tyr Gly
145         150         155         160
Ala Lys Ala Glu Ala Ala Phe Tyr Thr Asn Phe Gly Tyr Arg Met Asn
          165         170         175
Ala Thr Ala Ala Tyr Arg Gly Lys Asn Trp Asp Ile Leu Ala Tyr Tyr
          180         185         190
Asn His Gln Asn Ile Phe Tyr Tyr Arg Asp Gly Asn Asn Ala Phe Arg
          195         200         205
Ser Leu Phe His Pro Asn Tyr Asp Leu Gln Asp Pro Ser Asn Ser Glu
          210         215         220
Met Ser Val Gly Thr Pro Ser Glu Val Asn Ser Val Leu Ala Lys Ile
225         230         235         240
Asn Gly Tyr Ile Asn Glu Thr Asp Ser Ile Ser Val Ser Tyr Asn Leu
          245         250         255
Thr Arg Asp Asn Ser Thr Arg Leu Leu Arg Pro Asn Thr Thr Ser Ala
          260         265         270
Leu Ser Lys Ala Asn Asp Gln Glu Ala Ser Gln Pro Pro Leu
          275         280         285

```

(2) INFORMATION FOR SEQ ID NO:1067:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

```

Met Lys Arg Leu Leu Leu Leu Ala Leu Ala Leu Phe Phe Ser Leu Ser
1      5      10      15
Cys Thr Asn Ala Gln Glu Ile Lys Glu Thr Gln Glu Thr Lys Lys Thr
      20      25      30
Lys Glu Thr Lys Ser Gln Thr Arg Phe Asn Ile Ser Thr Thr Lys Val
      35      40      45
Ile Glu Lys Glu Phe Ser Gln Ser Arg Arg Tyr Tyr Ala Leu Leu Glu
      50      55      60
Pro Asn Glu Ala Leu Ile Phe Ser Gln Thr Leu Arg Phe Asp Gly Tyr
65      70      75      80
Val Glu Lys Leu Tyr Ala Asn Lys Thr Tyr Thr Pro Ile Lys Lys Gly
      85      90      95
Asp Arg Leu Leu Ser Val Tyr Ser Pro Glu Leu Ala Gly Val Gln Ser
      100     105     110
Glu Leu Leu Ser Ser Leu Lys Phe Asn Gln Gln Val Gly Ala Ile Lys
      115     120     125
Glu Lys Leu Lys Leu Leu Gly Leu Glu Asn Phe Ser Ile Glu Lys Ile
      130     135     140
Ile Ser Ser His Lys Val Gln Asn Glu Ile Thr Ile Tyr Ser Arg Phe
145     150     155     160
Asn Gly Val Ile Phe Lys Lys Ser Pro Asp Leu Asn Glu Gly Ser Phe
      165     170     175
Ile Lys Lys Gly Gln Glu Leu Phe Lys Ile Ile Asp Leu Ser Arg Leu
      180     185     190
Trp Ala Leu Val Lys Val Asn Gln Glu Asp Leu Glu Phe Leu Lys Asn
      195     200     205
Thr His Gln Ala Ile Leu Phe Val Glu Gly Val Lys Gly Lys Gln Ala
      210     215     220
Ile Thr Leu Glu Asn Ile Asn Pro Ile Ile Asn Ala Gln Asp Lys Met
225     230     235     240
Leu Glu Ala Arg Phe Asn Val Pro Asn Leu Lys Leu Leu Tyr Tyr Pro
      245     250     255
Asn Met Phe Ala Gln Val Glu Ile Phe His Lys Pro Gln Lys Met Lys
      260     265     270
Ile Leu Pro Lys Glu Ala Val Leu Ile Lys Gly Gly Lys Ala Ile Val
      275     280     285
Phe Lys Lys Asp Asp Phe Gly Leu Ser Pro Leu Glu Ile Lys Ala Val
      290     295     300
Arg Leu Ser Asp Gly Ser Tyr Glu Ile Leu Glu Gly Leu Lys Ala Gly
305     310     315     320
Glu Glu Val Ala Asn Asn Ala Leu Phe Val Leu Asp Ala Asp Ala Gln
      325     330     335
Asn Asn Gly Asp Tyr
      340

```

(2) INFORMATION FOR SEQ ID NO:1068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

```

Met Ala Phe Cys Ala Arg Gln Lys Pro Leu Lys Glu Ile Met Arg Phe
1          5          10          15
Phe Ile Leu Phe Phe Met Gly Met Leu Gly Val Gly Phe Ser Gln Thr
          20          25          30
Glu Leu Asp Leu Lys Asp Leu Glu Lys Lys Pro Ala Gly Ile Val Arg
          35          40          45
Asp Tyr Tyr Leu Trp Arg Tyr Ile Ser Asp Lys Lys Thr Ser Leu Glu
          50          55          60
Asn Ala Lys Lys Ala Tyr Glu Leu Thr Gln Asn Lys Asn Ser Ala Leu
          65          70          75          80
Gln Lys Ala Met Gln Glu Lys Gly Val Glu Asn Ser Asp Lys Ser Pro
          85          90          95
Asp Ala Lys Met Pro Glu Asp Ile Tyr Cys Lys Gln Ile Thr Leu Glu
          100          105          110
Ser Met Leu Glu Thr Thr Asp Ala Phe Gln Ala Ser Cys Ile Ala Ile
          115          120          125
Ala Leu Lys Ser Lys Ile Arg Asp Phe Asp Lys Ile Pro Ile Gln Thr
          130          135          140
Phe Lys Pro Leu Gln Glu Lys Ile Lys Glu Ala Tyr Pro Ile Leu Tyr
          145          150          155          160
Glu Glu Leu Glu Ile Leu Gln Ser Lys Asn Val Ser Ala Ser Leu Phe
          165          170          175
Lys Ala Asn Ala Gln Val Phe Ser Ala Leu Phe Asn His Leu Ser Tyr
          180          185          190
Glu Lys Lys Leu Gln Ile Phe Glu Lys His Ile Pro Ile Lys Glu Leu
          195          200          205
Asn Arg Leu Leu Asp Glu Asp Tyr Pro Ala Phe Asn Arg Leu Ile Tyr
          210          215          220
Gln Val Ile Leu Asp Pro Lys Leu Asp His Phe Lys Asp Ala Leu Ala
          225          230          235          240
Lys Ser Asn Ala Thr Gln Ser Asn Ala Gln Thr Phe Phe Ile Leu Gly
          245          250          255
Ile Asn Glu Ile Leu His Lys Lys Thr Ser Lys Ala Leu Lys Tyr Phe
          260          265          270
Glu Arg Ser Glu Ala Val Val Lys Asp Asp Asp Phe Ser Lys Asp Arg
          275          280          285
Ala Ile Phe Trp Gln Tyr Leu Ala Ser Lys Lys Lys Lys Thr Leu Glu
          290          295          300
His Leu Ser Gln Ser Pro Ala Leu Asn Leu Tyr Ser Leu Tyr Ala Ser
          305          310          315          320
Arg Lys Leu Lys Thr Thr Pro Ser Tyr Arg Ile Ile Ser His Ile Gln
          325          330          335
Asn Leu Ser Gln Glu Asn Pro Pro Phe Asn Thr Tyr Asp Pro Phe Ser
          340          345          350
Trp Gln Ile Phe Lys Glu Lys Thr Leu Ser Leu Lys Asp Glu Gly Ala

```

```

          355          360          365
Phe Asn Ala Met Leu Lys Ser Leu Tyr Tyr Glu Lys Ser Ala Pro Glu
  370          375          380
Leu Thr Tyr Leu Leu Ser Gln Arg Asn Lys Asp Lys Ile Tyr Tyr Tyr
  385          390          395          400
Leu Ser Pro Tyr Glu Gly Ile Ile Glu Trp Gln Asn Thr Asp Glu Arg
          405          410          415
Ala Met Ala Tyr Ala Ile Ala Arg Gln Glu Ser Phe Leu Leu Pro Ala
          420          425          430
Leu Ile Ser Arg Ser Phe Ala Leu Gly Leu Met Gln Ile Met Pro Phe
          435          440          445
Asn Val Gly Pro Phe Ala Lys Ala Leu Ala Trp Ile Met Leu Ile
          450          455          460

```

(2) INFORMATION FOR SEQ ID NO:1069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

```

Met Pro Lys Arg Met Lys Cys Phe Ser Gln Lys Trp Leu Val Phe Phe
 1          5          10          15
Val Thr His Trp Leu Leu Leu Ala Ser Leu Ser His Ala Lys Met Ala
          20          25          30
Phe Glu Ser Asn Ile Asp Thr Lys Ala Leu Glu Ala Phe Gly Val Asn
          35          40          45
Ala Ser Phe Leu Ser Gln Met Pro Gly Ala Leu Lys Lys Val Asn Lys
          50          55          60
Glu Glu Glu Trp Lys Lys Leu Val Lys Arg Phe Asp Val Asn Tyr Gln
          65          70          75          80
Phe Ile Pro Ile Ile Lys Asn Met Leu Ile Gly Ala Ser Val Pro Gln
          85          90          95
Glu Phe Leu Phe Leu Ala Met Ala Glu Ser Lys Phe Ser Ser Arg Ala
          100          105          110
Tyr Ser Arg Lys Lys Ala Val Gly Ile Trp Gln Phe Met Pro Ser Thr
          115          120          125
Ala Lys Glu Leu Gly Leu Lys Val Asn His Tyr Ile Asp Glu Arg Arg
          130          135          140
Asp Pro Ile Lys Ser Thr Gln Ala Ala Ile Ala Tyr Leu Lys Arg Leu
          145          150          155          160
Tyr Lys Gln Thr Gly Glu Trp Tyr Leu Val Ala Met Ala Tyr Asn Tyr
          165          170          175
Gly Leu Arg Lys Val Gln Asn Ala Ile Lys Ala Ala Gly Thr Ser Asp

```

983

```

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

```

(2) INFORMATION FOR SEQ ID NO:1070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:

```

Met Leu Ile Ala Arg Phe Lys Lys Ala Leu Ile Ser Tyr Ser Leu Gly
1           5           10           15
Val Leu Leu Val Ser Ser Leu Leu Gly Val Ala Asn Ala Ser Asn Gln
      20      25      30
Glu Ile Gln Val Lys Asp Tyr Phe Gly Glu Gln Thr Ile Lys Leu Pro
      35      40      45
Val Ser Lys Ile Ile Tyr Leu Gly Ser Phe Ala Glu Val Pro Ala Met
      50      55      60
Phe Asn Thr Trp Asp Arg Val Val Gly Ile Ser Asp Tyr Ala Phe Lys
      65      70      75      80
Ser Asp Ile Val Lys Ala Thr Leu Lys Asp Pro Glu Arg Ile Lys Pro

```

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

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...533

(xi) SEQUENCE DESCRIPTION: SEO ID NO:1071:

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

		35					40				45				
Leu	Leu	Ile	Phe	Ala	Ala	Val	Ile	Gly	Gly	Tyr	Met	Ala	Met	Asn	Ile
	50					55					60				
Gly	Ala	Asn	Asp	Val	Ser	Asn	Asn	Val	Gly	Pro	Ala	Val	Gly	Ser	Lys
65					70					75					80
Ala	Ile	Ser	Met	Gly	Gly	Ala	Ile	Leu	Ile	Ala	Ala	Val	Cys	Glu	Met
				85					90					95	
Leu	Gly	Ala	Ile	Ile	Ala	Gly	Gly	Glu	Val	Val	Ser	Thr	Ile	Lys	Gly
			100					105					110		
Arg	Ile	Val	Ser	Pro	Glu	Phe	Ile	Asn	Asp	Ala	His	Val	Phe	Ile	Asn
		115						120				125			
Val	Met	Leu	Ala	Ser	Leu	Leu	Ser	Gly	Ala	Leu	Trp	Leu	His	Val	Ala
	130					135					140				
Thr	Leu	Ile	Gly	Ala	Pro	Val	Ser	Thr	Ser	His	Ser	Val	Val	Gly	Gly
145					150					155					160
Ile	Met	Gly	Ala	Gly	Met	Ala	Ala	Ala	Gly	Met	Ser	Ala	Ile	Asn	Trp
				165					170					175	
His	Phe	Leu	Ser	Gly	Ile	Val	Ala	Ser	Trp	Val	Ile	Ser	Pro	Leu	Met
			180					185					190		
Gly	Ala	Leu	Ile	Ala	Met	Phe	Phe	Leu	Met	Leu	Ile	Lys	Lys	Thr	Ile
		195					200					205			
Ala	Tyr	Lys	Glu	Asp	Lys	Lys	Ser	Ala	Ala	Leu	Lys	Val	Val	Pro	Tyr
	210					215					220				
Leu	Val	Ala	Leu	Met	Ser	Leu	Ala	Phe	Ser	Trp	Tyr	Leu	Ile	Val	Lys
225					230					235					240
Val	Leu	Lys	Arg	Leu	Tyr	Ala	Val	Gly	Phe	Glu	Ile	Gln	Leu	Ala	Cys
				245					250					255	
Gly	Cys	Val	Leu	Ala	Leu	Leu	Ile	Phe	Ile	Leu	Phe	Lys	Arg	Phe	Val
			260					265					270		
Leu	Lys	Lys	Ala	Pro	Gln	Leu	Glu	Asn	Ser	His	Glu	Ser	Val	Asn	Glu
		275					280					285			
Leu	Phe	Asn	Val	Pro	Leu	Ile	Phe	Ala	Ala	Ala	Leu	Leu	Ser	Phe	Ala
	290					295					300				
His	Gly	Ala	Asn	Asp	Val	Ala	Asn	Ala	Ile	Gly	Pro	Leu	Ala	Ala	Ile
305					310					315					320
Ser	Gln	Thr	Leu	Glu	Asp	Ala	Ser	Ser	Pro	Met	Gly	Ser	Thr	Leu	Asn
				325					330					335	
Ser	Val	Pro	Leu	Trp	Ile	Met	Val	Val	Gly	Ala	Ala	Gly	Ile	Ala	Leu
		340						345					350		
Gly	Leu	Ser	Leu	Tyr	Gly	Pro	Lys	Leu	Ile	Lys	Thr	Val	Gly	Ser	Glu
		355					360					365			
Ile	Thr	Glu	Leu	Asp	Lys	Met	Gln	Ala	Phe	Cys	Ile	Ala	Leu	Ser	Ala
	370					375					380				
Val	Ile	Thr	Val	Leu	Leu	Ala	Ser	Gln	Leu	G					


```

Lys Arg Ser Ile Leu Lys Lys Ile Val Thr Ala Trp Leu Val Thr Val
      500                      505                      510
Pro Val Ser Ala Leu Leu Gly Ala Leu Leu Phe Val Ala Leu Gly Phe
      515                      520                      525
Ile Glu Lys Tyr Phe
      530

```

(2) INFORMATION FOR SEQ ID NO:1072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

```

Met Ser Asn Ser Met Leu Asp Lys Asn Lys Ala Ile Leu Thr Gly Gly
1           5           10           15
Gly Ala Leu Leu Leu Gly Leu Ile Val Leu Phe Tyr Leu Ala Tyr Arg
      20           25           30
Pro Lys Ala Glu Val Leu Gln Gly Phe Leu Glu Ala Arg Glu Tyr Ser
      35           40           45
Val Ser Ser Lys Val Pro Gly Arg Ile Glu Lys Val Phe Val Lys Lys
      50           55           60
Gly Asp Arg Ile Lys Lys Gly Asp Leu Val Phe Ser Ile Ser Ser Pro
      65           70           75           80
Glu Leu Glu Ala Lys Leu Ala Gln Ala Glu Ala Gly His Lys Ala Ala
      85           90           95
Lys Ala Val Ser Asp Glu Val Lys Arg Gly Ser Arg Asp Glu Thr Ile
      100          105          110
Asn Ser Ala Arg Asp Val Trp Gln Ala Ala Lys Ser Gln Ala Asn Leu
      115          120          125
Ala Lys Glu Thr Tyr Lys Arg Val Gln Asp Leu Tyr Asp Asn Gly Val
      130          135          140
Ala Ser Leu Gln Lys Arg Asp Glu Ala Tyr Ala Ala Tyr Glu Ser Thr
      145          150          155          160
Lys Tyr Asn Glu Ser Ala Ala Tyr Gln Lys Tyr Lys Met Ala Leu Gly
      165          170          175
Gly Ala Ser Ser Glu Ser Lys Ile Ala Ala Lys Ala Lys Glu Ser Ala
      180          185          190
Ala Leu Gly Gln Val Asn Glu Val Glu Ser Tyr Leu Lys Asp Val Lys
      195          200          205
Ala Leu Ala Pro Ile Asp Gly Glu Val Ser Asn Val Leu Leu Ser Gly
      210          215          220
Gly Glu Leu Ser Pro Lys Gly Phe Pro Val Val Leu Met Ile Asp Leu
      225          230          235          240

```

987

Lys Asp Ser Trp Leu Lys Ile Ser Val Pro Glu Lys Tyr Leu Asn Glu
 245 250 255
 Phe Lys Val Gly Lys Glu Phe Glu Gly Tyr Ile Pro Ala Leu Lys Arg
 260 265 270
 Ser Ala Lys Phe Arg Val Lys Tyr Leu Ser Val Met Gly Asp Phe Ala
 275 280 285
 Thr Trp Lys Ala Thr Asn Asn Ser Asn Thr Tyr Asp Met Lys Ser Tyr
 290 295 300
 Glu Val Glu Ala Ile Pro Leu Glu Glu Leu Glu Asn Phe Arg Val Gly
 305 310 315 320
 Met Ser Val Leu Val Thr Ile Lys Pro
 325

(2) INFORMATION FOR SEQ ID NO:1073:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:

Arg Leu Glu Ser Pro Leu His Ser Gly Phe Ser Pro Ser Ala Ala Leu
 1 5 10 15
 Val Ile Ser Pro Ile Glu Pro Leu Ser Leu Lys Ile Thr Tyr Ser Gln
 20 25 30
 Val Thr Arg Gly Val Met Pro Gly Asp Gly Val Tyr Met Arg Gln Asn
 35 40 45
 Asp Leu Arg Tyr Ala Lys Asn Ile Lys Pro Glu Val Gly Ser Asn Ala
 50 55 60
 Glu Phe Asn Ile Asp Tyr Ser Ser Gln Tyr Phe Ser Gly Arg Ala Ala
 65 70 75 80
 Ala Phe Tyr Gln Ala Leu Asp Asn Phe Ile Ser Gln Tyr Ala Gln Arg
 85 90 95
 Leu Ile Val Thr Asn Leu Ser Gln Ala Ile Arg Ile Tyr Gly Tyr Glu
 100 105 110
 Val Gly Gly Thr Phe Arg Tyr Lys Gly Val Ser Leu Asn Val Gly Ile
 115 120 125
 Ser Arg Thr Trp Pro Thr Thr Arg Gly Tyr Leu Met Ala Asp Ser Tyr
 130 135 140
 Glu Leu Ala Ala Ser Thr Gly Asn Val Phe Ile Ile Lys Leu Asp Tyr
 145 150 155 160
 Thr Ile Pro Lys Thr Gly Ile Asn Leu Ala Trp Leu Ser Arg Phe Val
 165 170 175
 Thr Gly Leu Asp Tyr Cys Gly Phe Asp Ile Tyr Leu Pro Asp Tyr Gly
 180 185 190

```

Thr Ala Glu Lys Pro Lys Thr Pro Thr Asp Leu Ala Lys Cys Gly Ser
      195                200                205
Gln Leu Gly Leu Val His Met His Lys Pro Gly Tyr Gly Val Ser Asn
      210                215                220
Phe Tyr Ile Asn Trp Ser Pro Lys Thr Lys Ser His Trp Lys Gly Leu
      225                230                235                240
Leu Leu Ser Ala Val Phe Asn Asn Val Phe Asn Lys Phe Tyr Val Asp
                245                250                255
Gln Thr Ser Pro Tyr Val Met Ser Pro Asp Met Pro Gly Thr Asp Ala
                260                265                270
Ile Lys Arg Ala Ile Ala Glu Pro Gly Phe Asn Ala Arg Phe Glu Val
      275                280                285
Ala Tyr Lys Trp
      290

```

(2) INFORMATION FOR SEQ ID NO:1074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

```

Met Ala Lys Ile Thr Thr Val Ile Asp Ile Gly Ser Asn Ser Val Arg
1          5          10          15
Leu Ala Val Phe Lys Lys Thr Ser Gln Phe Gly Phe Tyr Leu Leu Phe
      20          25          30
Glu Thr Lys Ser Lys Val Arg Ile Ser Glu Gly Cys Tyr Ala Phe Lys
      35          40          45
Gly Val Leu Gln Glu Ile Pro Met Gln Arg Ala Val Lys Ala Leu Ser
      50          55          60
Glu Phe Lys Glu Ile Ala Leu Lys Tyr Lys Ser Lys Lys Ile Leu Cys
      65          70          75          80
Val Ala Thr Ser Ala Val Arg Asp Ala Pro Asn Arg Leu Glu Phe Val
      85          90          95
Ala Arg Val Lys Lys Ala Cys Gly Leu Gln Ile Lys Ile Ile Asp Gly
      100         105         110
Gln Lys Glu Ala Leu Tyr Gly Gly Ile Ala Cys Ala Asn Leu Leu His
      115         120         125
Lys Asn Ser Gly Ile Thr Ile Asp Ile Gly Gly Gly Ser Thr Glu Cys
      130         135         140
Ala Leu Ile Glu Lys Gly Lys Ile Lys Asp Leu Ile Ser Leu Asp Val
      145         150         155         160
Gly Thr Ile Arg Ile Lys Glu Met Phe Leu Asp Lys Asp Leu Asp Val
      165         170         175

```

Lys Leu Ala Lys Ala Phe Ile Gln Lys Glu Val Ser Lys Leu Pro Phe
 180 185 190
 Lys His Lys Asn Ala Phe Gly Val Gly Gly Thr Ile Arg Ala Leu Ser
 195 200 205
 Lys Val Leu Met Lys Arg Phe Asp Tyr Pro Ile Asp Ser Leu His Gly
 210 215 220
 Tyr Glu Ile Asp Ala His Lys Asn Leu Ala Phe Ile Glu Lys Ile Val
 225 230 235 240
 Met Leu Lys Glu Asp Lys Leu Arg Leu Leu Gly Val Asn Glu Glu Arg
 245 250 255
 Leu Asp Ser Ile Arg Ser Gly Ala Leu Ile Leu Ser Val Val Leu Glu
 260 265 270
 His Leu Lys Thr Ser Leu Met Ile Thr Ser Gly Val Gly Val Arg Glu
 275 280 285
 Gly Val Phe Leu Ser Asp Leu Leu Arg His His Tyr His Lys Phe Pro
 290 295 300
 Pro Asn Ile Asn Pro Ser Leu Ile Ser Leu Lys Asp Arg Phe Leu Pro
 305 310 315 320
 His Glu Lys His Ser Gln Lys Val Lys Lys Glu Cys Val Lys Leu Phe
 325 330 335
 Glu Val Leu Ser Pro Leu His Lys Ile Asp Glu Lys Tyr Leu Phe His
 340 345 350
 Leu Lys Ile Ala Gly Glu Leu Ala Ser Met Gly Lys Ile Leu Ser Val
 355 360 365
 Tyr Leu Ala His Lys His Ser Ala Tyr Phe Ile Leu Asn Ala Leu Ser
 370 375 380
 Tyr Gly Phe Ser His Gln Asp Arg Ala Ile Ile Cys Leu Leu Ala Gln
 385 390 395 400
 Phe Ser His Lys Lys Ile Pro Lys Asp Asn Ala Ile Ala His Met Ser
 405 410 415
 Ala Met Met Pro Ser Leu Leu Thr Leu Gln Trp Leu Ser Phe Ile Leu
 420 425 430
 Ser Leu Ala Glu Asn Leu Cys Leu Thr Asp Ser His His Leu Lys Tyr
 435 440 445
 Thr Leu Glu Lys Asn Lys Leu Val Ile His Ser Asn Asp Ala Leu Tyr
 450 455 460
 Leu Ala Lys Glu Met Leu Pro Lys Leu Ile Lys Pro Ile Pro Leu Thr
 465 470 475 480
 Ile Glu Phe Ala

(2) INFORMATION FOR SEQ ID NO:1075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

```

Met Val Gly Met Lys Thr Glu Met Lys Ser Phe Leu Lys Leu Phe Ala
1           5           10           15
Gln Pro Leu Leu Val Val Leu Ala Phe Met Leu Leu Tyr Ala Leu Ala
          20           25           30
His Ala Val Leu Gly Phe Tyr Val Lys Lys Asp Ser Ala Pro Met Ser
          35           40           45
Pro Asn Val Glu Lys Ser Glu Thr Glu Arg Gln Asn Ser Thr Phe Ser
          50           55           60
Pro Lys Glu Glu Ala Asn Ala Thr Thr Thr Ala Thr Glu Gln Asn Pro
65           70           75           80
Thr Lys Asp Thr Val Pro Pro Leu Asp Thr Ala Thr Gln Lys Gln Glu
          85           90           95
Ile Lys Gln Glu Ile Lys Gln Glu Ile Lys Gln Glu Ile Lys Gln Glu
          100          105          110
Ile Lys Gln Glu Ile Lys Gln Glu Ile Lys Gln Glu Thr Lys Gln Glu
          115          120          125
Gln Glu Lys Glu Asn Lys Pro Lys Gln Asn Ser Val Ser Pro Val Gln
          130          135          140
Asn Asp Gln Lys Thr Pro Thr Thr Pro Leu Met Gly Lys Lys Pro Leu
145          150          155          160
Glu Tyr Lys Val Ala Val Ser Gly Val Asn Val Arg Ala Phe Pro Ser
          165          170          175
Thr Lys Gly Lys Ile Ile Gly Ser Leu Ile Lys Asn Lys Ser Val Lys
          180          185          190
Val Leu Glu Ile Gln Asn Asp Trp Ala Glu Ile Glu Phe Ser His Glu
          195          200          205
Thr Lys Gly Tyr Val Phe Leu Lys Leu Leu Lys Lys Ala Glu
          210          215          220

```

(2) INFORMATION FOR SEQ ID NO:1076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

```

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

```

991

```

Arg Ile Gln Arg Phe Leu Ser Arg Lys Met Ala Gln Lys Lys Gly Glu
   35               40               45
Lys Leu Lys Leu Ala Pro Tyr Glu Cys Gly Pro Val Ala Leu Lys Gln
   50               55               60
Pro Asn Arg Val Ser His His Phe Tyr Ile Met Ala Met Leu Phe Ile
   65               70               75               80
Leu Phe Asp Val Glu Ile Val Phe Met Phe Pro Trp Ala Ile Asp Phe
           85               90               95
Lys Lys Leu Gly Leu Phe Gly Leu Val Glu Met Leu Gly Phe Val Phe
           100              105              110
Phe Leu Ala Ile Gly Phe Ile Tyr Ala Leu Lys Arg Asn Ala Leu Ser
           115              120              125
Trp Gln Lys Leu Glu Val Lys
           130              135

```

(2) INFORMATION FOR SEQ ID NO:1077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

```

Leu Ser Ser Asp Pro Ser Ala Val Asn Asp Ala Arg Asp Asn Leu Gly
1      5      10      15
Ser Ser Thr Arg Asn Leu Leu Asp Val Lys Ala Asn Ser Pro Ala Tyr
      20      25      30
Gln Ala Val Leu Leu Ala Leu Asn Ala Ala Val Gly Leu Trp Gln Val
      35      40      45
Thr Ser Tyr Ala Phe Thr Ala Cys Gly Pro Gly Ser Asn Glu Asn Ala
      50      55      60
Asn Gly Gly Ile Gln Thr Phe Asn Asn Val Pro Gly Gln Asn Thr Thr
      65      70      75      80
Thr Ile Thr Cys Asn Ser Tyr Tyr Glu Pro Gly His Gly Gly Pro Ile
      85      90      95
Ser Thr Lys Asn Tyr Ala Ile Ile Asn Lys Ala Tyr Gln Ile Ile Gln
      100     105     110
Lys Ala Leu Thr Ala Asn Gly Glu Gly Ile Pro Val Leu Ser Asn Thr
      115     120     125
Thr Thr Lys Leu Asp Phe Thr Ile Asn Gly Asp Lys Arg Thr Gly Gly
      130     135     140
Glu Pro Asn Lys Lys Leu Val Tyr Pro Trp Ser His Gly Lys Ala Ile
      145     150     155     160
Ser Thr Ser Trp Asn Ala Thr Ile Thr Ala Pro Thr Thr Glu Asn Ile
           165           170           175

```

Asn Thr Thr Asn Ser Ala Gln Glu Leu Leu Lys Gln Ala Ser Ile Ile
 180 185 190
 Ile Thr Thr Leu Asn Ser Ala Cys Pro Asn Phe Gln Asn Gly Gly Ser
 195 200 205
 Gly Tyr Trp Ala Gly Ile Ser Gly Asn Gly Thr Met Cys Gly Met Phe
 210 215 220
 Lys Asn Glu Ile Ser Ala Ile Gln Gly Met Ile Ala Asn Ala Gln Glu
 225 230 235 240
 Ala Val Ala Gln Ala Lys Ile Val Ser Glu Asn Thr Gln Asn Gln Asn
 245 250 255
 Ser Leu Asp Ala Gly Lys Pro Phe Asn Pro Tyr Thr Asp Ala Ser Phe
 260 265 270
 Ala Glu Ser Met Leu Lys Asn Ala Gln Ala Gln Ala Glu Ile Leu Asn
 275 280 285
 Gln Ala Glu Gln Val Val Lys Asn Phe Glu Lys Ile Pro Thr Ala Phe
 290 295 300
 Val Asn Asp Ser Leu Gly Val Cys Tyr Glu Val Gln Gly Gly Glu Arg
 305 310 315 320
 Arg Gly Thr Asn Pro Gly Gln Thr Thr Ser Asn Thr Trp Gly Ala Gly
 325 330 335
 Cys Ala Tyr Val Gly Gln Thr Ile Thr Asn Leu Lys Asn Ser Ile Ala
 340 345 350
 His Phe Gly Thr Gln Glu Gln Gln Ile Gln Gln Ala Glu Asn Ile Ala
 355 360 365
 Asp Thr Leu Val Asn Phe Lys Ser Arg Tyr Ser Glu Leu Gly Asn Thr
 370 375 380
 Tyr Asn Ser Ile Thr Thr Ala Leu Ser Asn Ile Pro Asn Ala Gln Ser
 385 390 395 400
 Leu Gln Asn Ala Val Ser Lys Lys Asn Asn Pro Tyr Ser Pro Gln Gly
 405 410 415
 Ile Asp Thr Asn Tyr Tyr Leu Asn Gln Asn Ser Tyr Asn Gln Ile Gln
 420 425 430
 Thr Ile Asn Gln Glu Leu Gly Arg Asn Pro Phe Arg Lys Val Gly Ile
 435 440 445
 Val Ser Ser Gln Thr Asn Asn Gly Ala Met Asn Gly Ile Gly Ile Gln
 450 455 460
 Val Gly Tyr Lys Gln Phe Phe Gly Gln Lys Arg Lys Trp Gly Ala Arg
 465 470 475 480
 Tyr Tyr Gly Phe Phe Asp Tyr Asn His Ala Phe Ile Lys Ser Ser Phe
 485 490 495
 Phe Asn Ser Ala Ser Asp Val Trp Thr Tyr Gly Phe Gly Ala Asp Ala
 500 505 510
 Leu Tyr Asn Phe Ile Asn Asp Lys Ala Thr Asn Phe Leu Gly Lys Asn
 515 520 525
 Asn Lys Leu Ser Val Gly Leu Phe Gly Gly Ile Ala Leu Ala Gly Thr
 530 535 540
 Ser Trp Leu Asn Ser Glu Tyr Val Asn Leu Ala Thr Met Asn Asn Val
 545 550 555 560
 Tyr Asn Ala Lys Met Asn Val Ala Asn Phe Gln Phe Leu Phe Asn Met
 565 570 575
 Gly Val Arg Met Asn Leu Ala Arg Pro Lys Lys Lys Asp Ser Asp His
 580 585 590
 Ala Ala Gln His Gly Ile Glu Leu Gly Leu Lys Ile Pro Thr Ile Asn
 595 600 605
 Thr Asn Tyr Tyr Ser Phe Met Gly Ala Glu Leu Lys Tyr Arg Arg Leu
 610 615 620
 Tyr Ser Val Tyr Leu Asn Tyr Val Phe Ala Tyr

993

625

630

635

(2) INFORMATION FOR SEQ ID NO:1078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

```

Ile Lys Arg Ile Ile Lys Ser Asn Ala Ser Leu Asn Gln Leu Asn Thr
1           5           10           15
Thr Arg Tyr Asn Thr Pro Ser His Leu Phe Phe Lys Lys Gly Val Gly
          20           25           30
Met Ala Thr Ile Gln Pro Phe Asn His Ser Thr Ile Gln Pro Phe Asn
          35           40           45
His Ser Thr Ile Gln Pro Phe Asn His Ser Ile Ile Gln Ser Phe Asn
          50           55           60
His Ser Thr Ile Gln Ala Thr Leu Pro Tyr Phe Tyr Asn Tyr Leu Ser
65           70           75           80
Phe Tyr Lys Asn Leu Phe Lys Asn Pro Leu Phe Phe Ile Ile Pro Pro
          85           90           95
Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro
          100          105          110
Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro
          115          120          125
Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro
          130          135          140
Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Ser Pro
145          150          155          160
Ser Leu Thr His Ala Thr Thr Phe Ser Asn His Leu Ile Pro
          165          170

```

(2) INFORMATION FOR SEQ ID NO:1079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

```

Met Glu Asp Phe Leu Tyr Asn Thr Leu Tyr Phe Ile Glu Asp Tyr Lys
1          5          10          15
Leu Val Val Ile Phe Ser Phe Ile Gly Leu Ile Ala Leu Phe Phe Leu
20          25          30
Tyr Lys Phe Ile Lys Thr Gln Lys Lys Val Phe Lys Asp Lys Ala Asn
35          40          45
Gln Pro Gln Lys Lys Lys Ser Phe Lys Glu Ile Ile Ile Asp Gly Leu
50          55          60
Lys Glu Arg Val Lys Thr Phe Gly Phe Trp Leu Gln Ala Ile Leu Leu
65          70          75          80
Leu Ser Tyr Ser Phe Ile Thr Ser Gly Leu Phe Phe Leu Ile Leu Leu
85          90          95
Gly Asn Phe Tyr Asp Asp Asn Arg Leu Pro Glu Ser Asp Asp Asp Leu
100         105         110
Phe Asp Ile Trp Val Tyr Ala Ile Gln Asp Phe Pro Ala Tyr Tyr Phe
115         120         125
Lys Ala Leu Thr Phe Ser Ser Leu Lys Ile Tyr Gly Phe Asn Ile Ser
130         135         140
Leu Val Val Tyr Ser Ser Ile Leu Cys Ser Tyr Ile Phe Ile Thr Phe
145         150         155         160
Phe Val Trp Phe Leu Lys Tyr Leu Thr Arg Thr Arg Asp Ile Gly Ala
165         170         175
Asn Lys Lys Val Asp Asp Leu Phe Gly Ser Ala Ser Trp Glu Thr Glu
180         185         190
Glu Lys Met Ile Lys Ala Lys Leu Ile Thr Pro Asn Asn Lys Lys Arg
195         200         205
Ala Phe Asp Lys Arg Glu Val Ile Val Gly Arg Arg Gly Leu Gly Asp
210         215         220
Phe Ile Ala Tyr Ala Gly Gln Ala Phe Ile Gly Leu Ile Ala Pro Thr
225         230         235         240
Arg Ser Gly Lys Gly Val Gly Phe Ile Met Pro Asn Met Ile Asn Tyr
245         250         255
Pro Gln Asn Ile Val Val Phe Asp Pro Lys Ala Asp Thr Met Glu Thr
260         265         270
Cys Gly Lys Ile Arg Glu Lys Arg Phe Asn Gln Lys Val Phe Ile Tyr
275         280         285
Glu Pro Phe Ser Leu Lys Thr His Arg Phe Asn Pro Phe Ala Tyr Val
290         295         300
Asp Phe Gly Asn Asp Val Val Leu Thr Glu Asp Ile Leu Ser Gln Ile
305         310         315         320
Asp Thr Arg Leu Lys Gly His Gly Met Val Ala Ser Gly Gly Asp Phe
325         330         335
Ser Thr Gln Ile Phe Gly Leu Ala Lys Leu Val Phe Pro Glu Arg Pro
340         345         350
Asn Glu Lys Asp Pro Phe Phe Ser Asn Gln Ala Arg Asn Leu Phe Val
355         360         365
Ile Asn Cys Asn Ile Tyr Arg Asp Leu Met Trp Thr Lys Lys Gly Leu
370         375         380
Glu Phe Val Lys Arg Lys Lys Ile Ile Met Pro Glu Thr Pro Thr Met

```

995

385		390		395		400
Phe Phe Ile Gly Ser Met Ala Ser Gly Ile Asn Leu Ile Asp Glu Asp						
	405		410			415
Thr Asn Met Glu Lys Val Val Ser Leu Met Glu Phe Phe Gly Gly Glu						
	420		425			430
Glu Asp Lys Ser Gly Asp Asn Leu Arg Ala Leu Ser Pro Ala Thr Arg						
	435		440			445
Asn Met Trp Asn Asn Phe Lys Thr Met Gly Gly Ala Lys Glu Thr Tyr						
	450		455			460
Ser Ser Val Gln Gly Val Tyr Thr Ser Ala Phe Ala Pro Tyr Asn Asn						
	465		470			475
Ala Met Ile Arg Asn Phe Thr Ser Ala Asn Asp Phe Asp Phe Arg Arg						
	485		490			495
Leu Arg Ile Asp Ala Val Ser Ile Gly Val Ile Ala Asn Pro Lys Glu						
	500		505			510
Ser Thr Ile Val Gly Pro Ile Leu Glu Leu Phe Phe Asn Val Met Ile						
	515		520			525
Tyr Ser Asn Leu Ile Leu Pro Ile His Asp Pro Gln Cys Lys Arg Ser						
	530		535			540
Cys Leu Met Leu Met Asp Glu Phe Thr Leu Cys Gly Tyr Leu Glu Thr						
	545		550			555
Phe Val Lys Ala Val Gly Ile Met Ala Glu Tyr Asn Met Arg Pro Ala						
	565		570			575
Phe Val Phe Gln Ser Lys Ala Gln Leu Glu Asn Asp Pro Pro Leu Gly						
	580		585			590
Tyr Gly Arg Asn Gly Ala Lys Thr Ile Leu Asp Asn Leu Ser Leu Asn						
	595		600			605
Met Tyr Tyr Gly Ile Asn Asn Asp Asn Tyr Tyr Glu His Phe Glu Lys						
	610		615			620
Leu Ser Lys Val Leu Gly Lys Tyr Thr Arg Gln Asp Val Ser Arg Ser						
	625		630			635
Ile Asp Asp Asn Thr Gly Lys Thr Asn Thr Ser Ile Ser Asn Lys Glu						
	645		650			655
Arg Phe Leu Met Thr Pro Asp Glu Leu Met Thr Met Gly Asp Glu Leu						
	660		665			670
Ile Ile Leu Glu Asn Thr Leu Lys Pro Ile Lys Cys His Lys Ala Leu						
	675		680			685
Tyr Tyr Asp Asp Pro Phe Phe Thr Asp Glu Leu Ile Lys Val Ser Pro						
	690		695			700
Ser Leu Ser Lys Lys Tyr Lys Leu Gly Lys Val Pro Asn Gln Ala Thr						
	705		710			715
Phe Tyr Asp Asp Leu Gln Ala Ala Lys Thr Arg Gly Glu Leu Ser Tyr						
	725		730			735
Asp Lys Ser Leu Val Pro Val Gly Ser Ser Glu Leu						
	740		745			

(2) INFORMATION FOR SEQ ID NO:1080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

```

Leu Asn Ala Lys Ser Gln Ser Ser Leu Lys Asn Lys Ile Thr Leu Lys
1          5          10          15
Asn Lys Leu Asn His Ala Arg Ile Ile Leu Glu Phe Ile Pro Ser Leu
20          25          30
Ile Tyr Phe Leu Ile Gln Lys Val Ser Val Leu Lys His Leu Ala Pro
35          40          45
Leu Ile His Ile Pro Phe Lys Ala Leu Trp Leu Gly Thr Ala Leu Ser
50          55          60
Met Phe Leu Ser Leu Asn Leu Asn Ala Glu Glu Asn Pro Thr Lys Thr
65          70          75          80
Glu Pro Lys Pro Ala Lys Gly Val Lys Asn Lys Pro Lys Ser Pro Val
85          90          95
Thr Asn Val Met Met Thr Asn Cys Asp Asn Leu Lys Asp Phe Asn Ala
100         105         110
Lys Gln Lys Glu Val Leu Lys Ala Ala Tyr Gln Phe Gly Ser Lys Glu
115         120         125
Asn Leu Gly Tyr Glu Met Ala Gly Ile Ala Trp Lys Glu Ser Cys Ala
130         135         140
Gly Thr Tyr Lys Ile Asn Phe Ser Asp Pro Ser Ala Gly Ile Tyr His
145         150         155         160
Ala Tyr Ile Pro Ser Val Leu Lys Ser Tyr Gly His Asn Asn Ser Pro
165         170         175
Phe Leu Arg Asn Val Met Gly Glu Leu Leu Ile Lys Asp Asp Ala Phe
180         185         190
Ala Ser Glu Val Ala Leu Lys Glu Leu Leu Tyr Trp Lys Thr Arg Tyr
195         200         205
His Asp Asn Leu Lys Asp Met Ile Lys Ser Tyr Asn Lys Gly Ser Arg
210         215         220
Trp Glu Lys Asn Glu Lys Ala Asn Ala Asp Ala Glu Lys Tyr Tyr Glu
225         230         235         240
Glu Ile Gln Asp Arg Ile Arg Arg Leu Lys Glu Ser Lys Ile Phe Asp
245         250         255
Ser Gln Ser Ser Asn Asp Gln Glu Leu Gln Lys Ser Ala Asn Ser Asn
260         265         270
Leu Asp Leu Asp Pro Ile Gly Asn Ala Met Pro Gln Thr Leu Ala Gln
275         280         285
Thr Glu Thr Gln Lys Ser Gln Ile Glu Lys Ser Gln Ile Glu Glu Ala
290         295         300
Gln Thr Gln Lys Ser Gln Glu Met Lys Glu Ala Ala Ser Glu Gln Ala
305         310         315         320
Ile Lys Lys Pro Leu Glu Lys Glu Lys Asp Lys Pro Met Tyr Leu Ala
325         330         335
Gln Ile Asn Ser Ala Asp Phe Ala Pro Ala Lys Lys Ser Pro Lys Lys
340         345         350
Pro Ala Lys Ala Ser Pro Lys Arg Ser Ser Lys Asn Asn Ile Ser Val
355         360         365
Lys Ser Asn Thr Lys Thr Ala Ser Lys Asn Lys Glu Val Cys Lys Asn
370         375         380

```

Cys Ser Pro Gly Gln Arg Asn Ala Ile Leu Ala Asn His Ile Thr Leu
 385 390 395 400
 Met Gln Glu Leu

(2) INFORMATION FOR SEQ ID NO:1081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

Met Lys Lys Phe Val Val Phe Lys Thr Leu Cys Leu Ser Val Val Leu
 1 5 10 15
 Gly Asn Ser Leu Val Ala Ala Glu Gly Ser Thr Glu Val Gln Lys Gln
 20 25 30
 Leu Glu Lys Pro Lys Asp Tyr Lys Ala Val Lys Gly Glu Lys Asn Ala
 35 40 45
 Trp Tyr Leu Gly Ile Ser Tyr Gln Val Gly Gln Ala Ser Gln Ser Val
 50 55 60
 Lys Asn Pro Pro Lys Ser Ser Glu Phe Asn Tyr Pro Lys Phe Pro Val
 65 70 75 80
 Gly Lys Thr Asp Tyr Leu Ala Val Met Gln Gly Leu Gly Leu Thr Val
 85 90 95
 Gly Tyr Lys Gln Phe Phe Gly Glu Lys Arg Trp Phe Gly Ala Arg Tyr
 100 105 110
 Tyr Gly Phe Met Asp Tyr Gly His Ala Val Phe Gly Ala Asn Ala Leu
 115 120 125
 Thr Ser Asp Asn Gly Gly Val Cys Lys Leu Asn Glu Pro Cys Ala Thr
 130 135 140
 Lys Val Gly Thr Met Gly Asn Leu Ser Asp Met Phe Thr Tyr Gly Val
 145 150 155 160
 Gly Ile Asp Thr Leu Tyr Asn Val Ile Asn Lys Glu Asp Ala Ser Phe
 165 170 175
 Gly Phe Phe Phe Gly Ala Gln Ile Ala Gly Asn Ser Trp Gly Asn Thr
 180 185 190
 Thr Gly Ala Phe Leu Glu Thr Lys Ser Pro Tyr Lys His Thr Ser Tyr
 195 200 205
 Ser Leu Asp Pro Ala Ile Phe Gln Phe Leu Phe Asn Leu Gly Ile Arg
 210 215 220
 Thr His Ile Gly Gln His Gln Glu Phe Asp Phe Gly Val Lys Ile Pro
 225 230 235 240
 Thr Ile Asn Val Tyr Tyr Phe Asn His Gly Asn Leu Ser Phe Thr Tyr
 245 250 255

Arg Arg Gln Tyr Ser Leu Tyr Val Gly Tyr Arg Tyr Asn Phe
 260 265 270

(2) INFORMATION FOR SEQ ID NO:1082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

```

Met Lys Pro Tyr Phe Ser Leu Glu Lys Leu Asp Leu Tyr His Gly Asp
1      5      10      15
Ala Ser Val Leu Glu Thr Phe Glu Lys Gly Phe Tyr Asp Leu Cys Val
      20      25      30
Thr Ser Pro Pro Tyr Asn Leu Ser Ile Glu Tyr Gln Gly Ser Asn Asp
      35      40      45
Phe Arg Ala Tyr Asp Asp Tyr Leu Asn Trp Cys Lys Asn Trp Leu Lys
      50      55      60
Asn Cys Tyr Phe Trp Gly Lys Glu Gln Ala Arg Leu Cys Leu Asn Val
65      70      75      80
Pro Leu Asp Thr Asn Lys His Gly Lys Gln Ser Leu Gly Ala Asp Ile
      85      90      95
Thr Ile Val Ala Lys Glu Cys Gly Trp Lys Tyr Gln Asn Thr Ile Ile.
      100     105     110
Trp Asn Glu Ser Asn Ile Ser Arg Arg Thr Ala Trp Gly Ser Trp Leu
      115     120     125
Gln Ala Ser Ala Pro Tyr Ala Ile Ala Pro Val Glu Leu Ile Val Val
      130     135     140
Phe Tyr Lys Asn Glu Tyr Lys Arg Lys Lys Gln Thr Ser Thr Met Ser
145     150     155     160
Arg Glu Glu Phe Leu Leu Tyr Thr Asn Gly Leu Trp Asn Phe Ser Gly
      165     170     175
Glu Ser Lys Lys Arg Leu Lys His Pro Ala Pro Phe Pro Arg Glu Leu
      180     185     190
Pro Arg Arg Cys Ile Gln Leu Phe Ser Phe Leu Glu Asp Thr Ile Phe
      195     200     205
Asp Pro Phe Ser Gly Ser Gly Thr Thr Ile Leu Glu Ala Asn Ala Leu
      210     215     220
Gly Arg Phe Ser Val Gly Leu Glu Ile Glu Lys Glu Tyr Cys Glu Leu
225     230     235     240
Ser Lys Lys Arg Ile Leu Glu Ser Leu Ser Leu Val
      245     250

```

(2) INFORMATION FOR SEQ ID NO:1083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 925 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

```

Leu Val Ile Ile Ser Leu Leu Thr Thr Leu Lys Leu Lys Ser Ile Lys
1           5           10           15
Glu Ile Ser Ile Lys Lys Phe Ile Leu Ser Ser Leu Val Phe Ala Cys
20           25           30
Ile Asn Thr Gly Val Glu Ala Leu Glu Asn Asp Gly Ser Lys Pro Asn
35           40           45
Asp Leu Ala Ser Pro Lys Glu Thr Pro Lys Glu Ala Gln Lys Asn Glu
50           55           60
Ala Gln Asn Glu Thr Ser Gln Ser Asn Gln Thr Pro Lys Glu Met Lys
65           70           75           80
Val Lys Ser Ile Ser Tyr Val Gly Leu Ser Tyr Met Ser Asp Met Leu
85           90           95
Ala Asn Glu Ile Ala Lys Ile Arg Val Gly Asp Met Val Asp Ser Lys
100          105          110
Lys Ile Asp Thr Ala Val Leu Ala Leu Phe Asn Gln Gly Tyr Phe Lys
115          120          125
Asp Val Tyr Ala Thr Phe Glu Asn Gly Ile Leu Glu Phe His Phe Asp
130          135          140
Glu Lys Ala Arg Ile Ala Gly Val Glu Ile Lys Gly Tyr Gly Thr Glu
145          150          155          160
Lys Glu Lys Asp Gly Leu Lys Ser Gln Met Gly Ile Lys Lys Gly Asp
165          170          175
Thr Phe Asp Glu Gln Lys Leu Glu His Ala Lys Thr Ala Leu Lys Thr
180          185          190
Ala Leu Glu Gly Gln Gly Tyr Tyr Gly Ser Val Val Glu Val Arg Thr
195          200          205
Glu Lys Val Ser Glu Gly Ala Leu Leu Ile Val Phe Asp Val Asn Arg
210          215          220
Gly Asp Ser Ile Tyr Ile Lys Gln Ser Ile Tyr Glu Gly Ser Asp Lys
225          230          235          240
Leu Lys Arg Arg Val Ile Glu Ser Leu Ser Ala Asn Lys Gln Arg Asp
245          250          255
Phe Met Gly Trp Met Trp Gly Leu Asn Asp Gly Lys Leu Arg Leu Asp
260          265          270
Gln Leu Glu Tyr Asp Ser Leu Arg Ile Gln Asp Val Tyr Met Arg Arg
275          280          285
Gly Tyr Leu Asp Ala His Ile Ser Ser Pro Phe Leu Lys Thr Asp Phe
290          295          300

```

1000

Ser Thr His Asp Ala Lys Leu His Tyr Lys Val Lys Glu Gly Ile Gln
 305 310 315 320
 Tyr Arg Ile Ser Asp Ile Leu Ile Glu Ile Asp Asn Pro Val Val Pro
 325 330 335
 Leu Lys Thr Leu Glu Lys Ala Leu Lys Val Lys Arg Lys Asp Val Phe
 340 345 350
 Asn Ile Glu His Leu Arg Ala Asp Ala Gln Ile Leu Lys Thr Glu Ile
 355 360 365
 Ala Asp Lys Gly Tyr Ala Phe Ala Val Val Lys Pro Asp Leu Asp Lys
 370 375 380
 Asp Glu Lys Asn Gly Leu Val Lys Val Ile Tyr Arg Ile Glu Val Gly
 385 390 395 400
 Asp Met Val His Ile Asn Asp Val Ile Ile Ser Gly Asn Gln Arg Thr
 405 410 415
 Ser Asp Arg Ile Ile Arg Arg Glu Leu Leu Leu Gly Pro Lys Asp Lys
 420 425 430
 Tyr Asn Leu Thr Lys Leu Arg Asn Ser Glu Asn Ser Leu Arg Arg Leu
 435 440 445
 Gly Phe Phe Ser Lys Val Lys Ile Glu Glu Lys Arg Val Asn Ser Ser
 450 455 460
 Leu Met Asp Leu Leu Val Ser Val Glu Glu Gly Arg Thr Gly Gln Leu
 465 470 475 480
 Gln Phe Gly Leu Gly Tyr Gly Ser Tyr Gly Gly Leu Met Leu Asn Gly
 485 490 495
 Ser Val Ser Glu Arg Asn Leu Phe Gly Thr Gly Gln Ser Met Ser Leu
 500 505 510
 Tyr Ala Asn Ile Ala Thr Gly Gly Gly Arg Ser Tyr Pro Gly Met Pro
 515 520 525
 Lys Gly Ala Gly Arg Met Phe Ala Gly Asn Leu Ser Leu Thr Asn Pro
 530 535 540
 Arg Ile Phe Asp Ser Trp Tyr Ser Ser Thr Ile Asn Leu Tyr Ala Asp
 545 550 555 560
 Tyr Arg Ile Ser Tyr Gln Tyr Ile Gln Gln Gly Gly Gly Phe Gly Val
 565 570 575
 Asn Val Gly Arg Met Leu Gly Asn Arg Thr His Val Ser Leu Gly Tyr
 580 585 590
 Asn Leu Asn Val Thr Lys Leu Leu Gly Phe Ser Ser Pro Leu Tyr Asn
 595 600 605
 Arg Tyr Tyr Ser Ser Val Asn Glu Val Ala Ser Pro Arg Gln Cys Ser
 610 615 620
 Thr Pro Ala Ser Val Ile Ile Asn Arg Leu Ser Gly Gly Arg Thr Pro
 625 630 635 640
 Leu Val Pro Glu Ser Cys Ser Ser Pro Gly Ala Ile Thr Thr Ser Pro
 645 650 655
 Glu Ile Lys Gly Ile Trp Asp Arg Asp Tyr His Thr Pro Ile Thr Ser
 660 665 670
 Ser Phe Thr Leu Asp Val Ser Tyr Asp Asn Thr Asp Asp Tyr Tyr Phe
 675 680 685
 Pro Arg Asn Gly Val Ile Phe Ser Ser Tyr Ala Thr Met Ser Gly Leu
 690 695 700
 Pro Ser Ser Gly Thr Leu Asn Ser Trp Asn Gly Leu Gly Gly Asn Val
 705 710 715 720
 Arg Asn Thr Lys Val Tyr Gly Lys Phe Ala Ala Tyr His His Leu Gln
 725 730 735
 Lys Tyr Leu Leu Ile Asp Leu Ile Ala Arg Phe Lys Thr Gln Gly Gly
 740 745 750
 Tyr Ile Phe Arg Tyr Asn Thr Asp Asp Tyr Leu Pro Leu Asn Ser Thr

1001

755	760	765
Phe Tyr Met Gly Gly Val Thr Thr Val Arg Gly Phe Arg Asn Gly Ser		
770	775	780
Ile Thr Pro Lys Asp Glu Phe Gly Leu Trp Leu Gly Gly Asp Gly Ile		
785	790	795
Phe Thr Ala Ser Thr Glu Leu Ser Tyr Gly Val Leu Lys Ala Ala Lys		
	805	810
Met Arg Leu Ala Trp Phe Phe Asp Phe Gly Phe Leu Thr Phe Lys Thr		
	820	825
Pro Thr Arg Gly Ser Phe Phe Tyr Asn Ala Pro Thr Thr Thr Ala Asn		
	835	840
Phe Lys Asp Tyr Gly Val Val Gly Ala Gly Phe Glu Arg Ala Thr Trp		
850	855	860
Arg Ala Ser Thr Gly Leu Gln Ile Glu Trp Ile Ser Pro Met Gly Pro		
865	870	875
Leu Val Leu Ile Phe Pro Ile Ala Phe Phe Asn Gln Trp Gly Asp Gly		
	885	890
Asn Gly Lys Lys Cys Lys Gly Leu Cys Phe Asn Pro Asn Met Asn Asp		
	900	905
Tyr Thr Gln His Phe Glu Phe Ser Met Gly Thr Arg Phe		
915	920	925

(2) INFORMATION FOR SEQ ID NO:1084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

Met Lys Gln Leu Phe Leu Ile Ile Gly Ala Pro Gly Ser Gly Lys Thr		
1	5	10
Thr Asp Ala Glu Leu Ile Ala Lys Asn Asn Ser Glu Thr Ile Ala His		
	20	25
Phe Ser Thr Gly Asp Leu Leu Arg Ala Glu Ser Ala Lys Lys Thr Glu		
	35	40
Arg Gly Leu Leu Ile Glu Lys Phe Thr Ser Gln Gly Glu Leu Val Pro		
50	55	60
Leu Glu Ile Val Val Glu Thr Ile Leu Ser Ala Ile Lys Ser Ser Ser		
65	70	75
Lys Gly Ile Ile Leu Ile Asp Gly Tyr Pro Arg Ser Val Glu Gln Met		
	85	90
Gln Ala Leu Asp Lys Glu Leu Asn Ala Gln Asn Glu Val Ile Leu Lys		
	100	105
Ser Val Ile Glu Val Glu Val Ser Glu Asn Thr Ala Lys Glu Arg Val		

1002

115	120	125
Leu Gly Arg Ser Arg Gly Ala Asp Asp Asn Glu Arg Val Phe His Asn		
130	135	140
Arg Met Arg Val Phe Leu Asp Pro Leu Val Glu Ile Gln Asn Phe Tyr		
145	150	155
Lys Ala Lys His Leu His Lys Ile Ile Asn Gly Glu Arg Ser Ile Glu		
165	170	175
Glu Ile Val Asn Glu Met Gln Lys Tyr Ile Leu Ser Phe Ala Asn		
180	185	190

(2) INFORMATION FOR SEQ ID NO:1085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

Leu Ser Ser Leu Trp Leu Thr Asn Pro Leu Asn Ala His Glu Lys Asn		
1	5	10
Gly Ala Phe Val Gly Ile Ser Leu Glu Val Gly Arg Val Asp Gln Lys		
20	25	30
Thr Asn Ala Tyr Arg Asn Gly Glu Leu Phe Gln Val Pro Phe Gly Asp		
35	40	45
Val Ser Ala Asn Asp Asp Gly Lys Val Pro Asp Gly Gln Thr Gly Gly		
50	55	60
Cys Gln Pro Ala Ser Gly Thr Pro Gly Thr Pro Gly Tyr Thr Lys Ala		
65	70	75
Asn Cys Val Val Asn Trp Thr Ser Arg Thr Met Leu Ser Thr Asn Lys		
85	90	95
Asp Ile Pro Gly Arg Asn Gln Pro Met Tyr Gly Leu Gly Val Met Thr		
100	105	110
Gly Tyr Lys His Phe Val Gly Lys Lys Arg Trp Phe Gly Leu Arg Tyr		
115	120	125
Tyr Gly Phe Phe Asp Tyr Gly His Thr Asn Phe Ser Asn Ser Arg Ala		
130	135	140
Ala Asn Ala Ile Ser Pro Phe Tyr Leu Ser Asp Gln Lys Ala Asp Met		
145	150	155
Tyr Thr Tyr Gly Phe Gly Thr Asp Met Leu Phe Asn Val Ile Asp Lys		
165	170	175
Pro Lys Ala Thr Ala Gly Phe Phe Val Gly Val Asn Phe Ala Gly Asn		
180	185	190
Thr Trp Thr Asn Asn Arg Val Gly Tyr Phe Lys Asp Gly Tyr Val Tyr		
195	200	205
Gly Val Asn Thr Asp Ala Asp Ala Tyr Met Thr Asn Ala Asp Gly Thr		

1003

```

      210              215              220
Ile Thr Cys Gly Asp Thr Thr Pro Ala Ser Cys Asn Val Gly Ile Asn
225              230              235              240
Pro Asn Ser Val Tyr Thr Thr Gly Lys Leu Asn Ala Lys Val Asn His
      245              250              255
Thr Ile Phe Gln Phe Leu Val Asn Val Gly Ile Arg Thr Asn Ile Phe
      260              265              270
Glu His His Gly Ile Glu Phe Gly Ile Lys Ile Pro Thr Leu Pro Asn
      275              280              285
Tyr Phe Phe Lys Gly Ser Thr Thr Ile Arg Ala Lys Lys Gln Gly Pro
      290              295              300
Leu Glu Asn Gly Asn Pro Thr Thr Ile Thr Gly Ala Glu Thr Asn Phe
305              310              315              320
Ser Leu Thr Gln Thr Leu Arg Arg Gln Tyr Ser Met Tyr Leu Arg Tyr
      325              330              335
Val Tyr Thr Phe
      340

```

(2) INFORMATION FOR SEQ ID NO:1086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

```

Met Lys Leu Lys Lys Arg Lys Val Ala Ala Thr Leu Leu Lys Arg Leu
1              5              10              15
Thr Leu Pro Leu Leu Phe Thr Thr Gly Ser Leu Gly Ala Val Thr Tyr
      20              25              30
Glu Val His Gly Asp Phe Ile Asn Phe Ser Lys Val Gly Phe Asn Arg
      35              40              45
Ser Pro Ile Asn Pro Val Lys Gly Ile Tyr Pro Thr Glu Thr Phe Val
      50              55              60
Asn Leu Thr Gly Lys Leu Glu Gly Ser Val His Leu Gly Arg Gly Trp
65              70              75              80
Thr Val Asn Val Gly Gly Val Leu Gly Gly Gln Val Tyr Asp Asn Thr
      85              90              95
Arg Tyr Asp Arg Trp Ala Lys Asp Phe Thr Pro Pro Ser Tyr Trp Asp
      100              105              110
Lys Thr Ser Cys Gly Thr Asp Ser Leu Ser Leu Cys Met Asn Ala Thr
      115              120              125
Lys Met Trp Gln Gln Gln Gly Pro Gly Gly Ile Ile Asp Pro Arg Gly
      130              135              140
Ile Gly Tyr Met Tyr Met Gly Glu Trp Asn Gly Leu Phe Pro Asn Tyr

```

145	Tyr	Pro	Ala	Asn	Ala	Tyr	Leu	Pro	Gly	His	155	Ser	Arg	Arg	Tyr	Glu	160	Val
				165						170						175		
Tyr	Lys	Ala	Asn	Leu	Thr	Tyr	Asp	Ser	Asp	Arg	Val	His	Met	Val	Met			
			180					185					190					
Gly	Arg	Phe	Asp	Val	Thr	Glu	Gln	Glu	Gln	Met	Asp	Trp	Ile	Tyr	Gln			
		195					200					205						
Leu	Phe	Gln	Gly	Phe	Tyr	Gly	Thr	Phe	Lys	Leu	Thr	Lys	Asn	Met	Lys			
	210					215					220							
Phe	Leu	Leu	Phe	Ser	Ser	Trp	Gly	Arg	Gly	Ile	Ala	Asp	Gly	Gln	Trp			
225					230					235								240
Leu	Phe	Pro	Ile	Tyr	Arg	Glu	Lys	Pro	Trp	Gly	Ile	His	Lys	Ala	Gly			
				245					250									255
Ile	Ile	Tyr	Arg	Pro	Thr	Lys	Asn	Leu	Met	Ile	His	Pro	Tyr	Val	Tyr			
			260					265					270					
Leu	Ile	Pro	Met	Val	Gly	Thr	Leu	Pro	Gly	Ala	Lys	Ile	Glu	Tyr	Asp			
		275					280					285						
Thr	Asn	Pro	Glu	Phe	Ser	Gly	Arg	Gly	Ile	Arg	Asn	Lys	Thr	Thr	Phe			
	290					295					300							
Tyr	Val	Leu	Tyr	Asp	Tyr	Arg	Trp	Asn	Asn	Ala	Glu	Tyr	Gly	Arg	Tyr			
305					310					315								320
Ala	Pro	Ala	Arg	Tyr	Asn	Thr	Trp	Asp	Pro	Phe	Leu	Asp	Asn	Gly	Lys			
				325					330									
Trp	Arg	Gly	Leu	Gln	Gly	Pro	Gly	Gly	Ala	Thr	Leu	Tyr	Leu	His	His			
			340				345						350					
His	Ile	Asp	Ile	Asn	Asn	Tyr	Phe	Val	Val	Gly	Gly	Ala	Tyr	Leu	Asn			
		355				360						365						
Ile	Gly	Asn	Pro	Asn	Met	Asn	Leu	Gly	Thr	Trp	Gly	Asn	Pro	Val	Ala			
	370					375					380							
Leu	Asp	Gly	Ile	Glu	Gln	Trp	Val	Gly	Gly	Ile	Tyr	Ser	Leu	Gly	Phe			
385					390					395								400
Ala	Gly	Ile	Asp	Asn	Ile	Thr	Asp	Ala	Asp	Ala	Phe	Thr	Glu	Tyr	Val			
				405					410									
Lys	Gly	Gly	Gly	Lys	His	Gly	Lys	Phe	Ser	Trp	Ser	Val	Tyr	Gln	Arg			
			420					425					430					
Phe	Thr	Thr	Ala	Pro	Arg	Ala	Leu	Glu	Tyr	Gly	Ile	Gly	Met	Tyr	Leu			
		435					440					445						
Asp	Tyr	Gln	Phe	Ser	Lys	His	Val	Lys	Ala	Gly	Leu	Lys	Leu	Val	Trp			
	450					455												

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

1005

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

```

Met Thr Lys Ile Ala Met Ala Asn Phe Lys Ser Ala Met Pro Val Phe
1           5           10           15
Lys Ser His Ala Tyr Leu Lys Glu Leu Glu Lys Thr Leu Lys Pro Gln
20           25           30
His Phe Asp Arg Val Phe Val Phe Pro Asp Phe Leu Gly Leu Leu Pro
35           40           45
Asn Ala Phe Leu His Phe Thr Leu Gly Ala Gln Asn Ala Tyr Pro Arg
50           55           60
Asp Cys Gly Ala Phe Thr Gly Glu Ile Thr Ser Lys His Leu Glu Glu
65           70           75           80
Leu Lys Ile His Thr Leu Leu Ile Gly His Ser Glu Arg Arg Val Leu
85           90           95
Leu Lys Glu Ser Pro Ser Phe Leu Lys Glu Lys Phe Asp Phe Phe Lys
100          105          110
Gly Lys Asn Phe Lys Ile Val Tyr Cys Ile Gly Glu Asp Leu Thr Thr
115          120          125
Arg Glu Lys Gly Phe Arg Ala Val Lys Glu Phe Leu Ser Glu Gln Leu
130          135          140
Glu Asn Ile Asp Leu Asn Tyr Ser Asn Leu Ile Val Ala Tyr Glu Pro
145          150          155          160
Ile Trp Ala Ile Gly Thr Lys Lys Ser Ala Ser Leu Glu Asp Ile Tyr
165          170          175
Leu Thr His Gly Phe Leu Lys Gln Ile Leu Asn Gln Lys Thr Pro Leu
180          185          190
Leu Tyr Gly Gly Ser Val Asn Ala Gln Asn Ala Lys Glu Ile Leu Gly
195          200          205
Ile Asp Ser Val Asp Gly Leu Leu Ile Gly Ser Ala Ser Leu Glu Leu
210          215          220
Glu Asn Phe Lys Thr Ile Ile Ser Phe Leu
225          230

```

(2) INFORMATION FOR SEQ ID NO:1088:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

1006

(A) NAME/KEY: misc_feature

(B) LOCATION 1...465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

```

Met Phe Ile Tyr Asp Thr Lys Leu Lys Gln Lys Val Pro Phe Glu Pro
1      5      10      15
Leu Val His Asn Lys Ala Asn Ile Tyr Val Cys Gly Pro Thr Val Tyr
20      25      30
Asp Asp Ala His Leu Gly His Ala Arg Ser Ala Ile Ala Phe Asp Leu
35      40      45
Leu Arg Arg Thr Leu Glu Leu Ser Gly Tyr Glu Val Val Leu Val Arg
50      55      60
Asn Phe Thr Asp Ile Asp Asp Lys Ile Ile Asn Lys Ala Phe Lys Glu
65      70      75      80
Asn Lys Ser Ile Gln Glu Leu Ser Ser Ile Tyr Ile Glu Ser Tyr Thr
85      90      95
Arg Asp Leu Asn Ala Leu Asn Val Lys Gln Pro Ser Leu Glu Pro Lys
100     105     110
Ala Ser Glu Tyr Leu Asp Ala Met Val Arg Met Ile Glu Thr Leu Leu
115     120     125
Glu Lys Asn Phe Ala Tyr Arg Val Ser Asn Gly Asp Ile Tyr Leu Asp
130     135     140
Thr Ser Lys Asp Lys Asp Tyr Gly Ser Leu Ser Met His Asn Ser Ser
145     150     155     160
Val Glu Phe Ser Arg Ile Gly Leu Val Gln Glu Lys Arg Leu Glu Gln
165     170     175
Asp Phe Val Leu Trp Lys Ser Tyr Lys Gly Asp Asn Asp Val Gly Phe
180     185     190
Asp Ser Pro Leu Gly Lys Gly Arg Pro Gly Trp His Ile Glu Cys Ser
195     200     205
Ser Met Val Phe Glu Thr Leu Ala Leu Ala Asn Ala Pro Tyr Gln Ile
210     215     220
Asp Ile His Ala Gly Gly Thr Asp Leu Leu Phe Pro His His Glu Asn
225     230     235     240
Glu Ala Cys Gln Thr Arg Cys Ala Phe Gly Val Glu Ile Ala Lys Tyr
245     250     255
Trp Met His Asn Gly Phe Val Asn Ile Asn Asn Glu Lys Met Ser Lys
260     265     270
Ser Leu Gly Asn Ser Phe Phe Ile Lys Asp Ala Leu Lys Asn Tyr Asp
275     280     285
Gly Glu Ile Leu Arg Asn Tyr Leu Leu Gly Val His Tyr Arg Ser Val
290     295     300
Leu Asn Phe Asn Glu Glu Asp Leu Leu Met Ser Lys Lys Arg Leu Asp
305     310     315     320
Lys Ile Tyr Arg Leu Lys Gln Arg Val Leu Gly Thr Leu Gly Gly Ile
325     330     335
Asn Pro Asn Phe Lys Lys Glu Ile Leu Glu Cys Met Gln Asp Asp Leu
340     345     350
Asn Val Ser Lys Ala Leu Ser Val Leu Glu Ser Met Leu Ser Ser Thr
355     360     365
Asn Glu Lys Leu Asp Gln Asn Pro Lys Asn Lys Ala Leu Lys Gly Glu
370     375     380
Ile Leu Ala Asn Leu Lys Phe Ile Glu Glu Leu Leu Gly Ile Gly Phe
385     390     395     400
Lys Asp Pro Ser Ala Tyr Phe Gln Leu Gly Val Ser Glu Ser Glu Lys
405     410     415

```

1007

Gln Glu Ile Glu Asn Lys Ile Glu Glu Arg Lys Arg Ala Lys Glu Gln
 420 425 430
 Lys Asp Phe Leu Lys Ala Asp Ser Ile Arg Glu Glu Leu Leu Gln Gln
 435 440 445
 Lys Ile Ala Leu Met Asp Thr Pro Gln Gly Thr Ile Trp Glu Lys Leu
 450 455 460
 Phe
 465

(2) INFORMATION FOR SEQ ID NO:1089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

Met Lys Gln Phe Lys Lys Lys Pro Lys Lys Ile Lys Arg Ser His Gln
 1 5 10 15
 Asn Gln Lys Thr Ile Leu Lys Arg Pro Leu Trp Leu Met Pro Leu Leu
 20 25 30
 Ile Gly Gly Phe Ala Ser Gly Val Tyr Ala Asp Gly Thr Asp Ile Leu
 35 40 45
 Gly Leu Ser Trp Gly Glu Lys Ser Gln Lys Val Cys Val His Arg Pro
 50 55 60
 Trp Tyr Ala Ile Trp Ser Cys Asp Lys Trp Glu Glu Lys Thr Gln Gln
 65 70 75 80
 Phe Thr Gly Asn Gln Leu Ile Thr Lys Thr Trp Ala Gly Gly Asn Ala
 85 90 95
 Ala Asn Tyr Tyr His Ser Gln Asn Asn Gln Asp Ile Thr Ala Asn Leu
 100 105 110
 Lys Asn Asp Asn Gly Thr Tyr Phe Leu Ser Gly Leu Tyr Asn Tyr Thr
 115 120 125
 Gly Gly Glu Tyr Asn Gly Gly Asn Leu Asp Ile Glu Leu Gly Ser Asn
 130 135 140
 Ala Thr Phe Asn Leu Gly Ala Ser Ser Gly Asn Ser Phe Thr Ser Trp
 145 150 155 160
 Tyr Pro Asn Gly His Thr Asp Val Thr Phe Ser Ala Gly Thr Ile Asn
 165 170 175
 Val Asn Asn Ser Val Glu Val Gly Asn Arg Val Gly Ser Gly Ala Gly
 180 185 190
 Thr His Thr Gly Thr Ala Thr Leu Asn Leu Asn Ala Asn Lys Val Thr
 195 200 205
 Ile Asn Ser Asn Ile Ser Ala Tyr Lys Thr Ser Gln Val Asn Val Gly
 210 215 220

1008

Asn	Ala	Asn	Ser	Val	Ile	Thr	Ile	Asn	Ser	Val	Ser	Leu	Asn	Gly	Asp
225					230					235					240
Thr	Cys	Ser	Ser	Leu	Ala	Arg	Val	Gly	Val	Gly	Ala	Asn	Cys	Ser	Thr
				245					250						255
Ser	Gly	Pro	Ser	Tyr	Ser	Phe	Lys	Gly	Thr	Thr	Asn	Ala	Thr	Asn	Thr
			260					265					270		
Thr	Phe	Ser	Asn	Ser	Ser	Gly	Ser	Phe	Thr	Phe	Glu	Glu	Asn	Ala	Thr
		275					280					285			
Phe	Ser	Gly	Ala	Lys	Leu	Asn	Gly	Gly	Ala	Phe	Thr	Phe	Asn	Lys	Lys
	290					295				300					
Phe	Asn	Ala	Thr	Asn	Asn	Thr	Ala	Phe	Asn	Ser	Gly	Ser	Phe	Thr	Phe
305					310					315					320
Lys	Gly	Thr	Ser	Ser	Phe	Asn	Gly	Ala	Asn	Phe	Ser	Asn	Ala	Ser	Tyr
				325					330						335
Thr	Phe	Asn	Asn	Gln	Ala	Thr	Phe	Gln	Asn	Ser	Ser	Phe	Asn	Gly	Gly
			340					345					350		
Thr	Phe	Thr	Phe	Asn	Asp	Gln	Thr	Asn	Gln	Ser	Thr	Gln	His	Pro	Gln
		355					360					365			
Ile	Gln	Asn	Ser	Ser	Phe	Ser	Gly	Ser	Ala	Thr	Thr	Leu	Lys	Gly	Phe
	370						375					380			
Ala	Thr	Phe	Glu	Gln	Ala	Phe	Asn	Asn	Ser	Asn	His	Gln	Leu	Thr	Ile
385					390					395					400
Gln	Asn	Ala	Ser	Phe	Asn	Asn	Ala	Thr	Phe	Asn	Asn	Thr	Gly	Lys	Ile
				405					410						415
Thr	Ile	Glu	Lys	Asp	Ala	Ser	Phe	Asn	Asn	Thr	Ser	Phe	Asn	Thr	Pro
			420					425					430		
Val	Asp	Thr	Asn	Asn	Met	Thr	Ile	Ser	Gly	Gly	Val	Thr	Leu	Ser	Gly
		435					440					445			
Lys	Asn	Asp	Leu	Lys	Asn	Gly	Ala	Thr	Leu	Asp	Phe	Gly	Ser	Ser	Lys
	450					455					460				
Ile	Thr	Leu	Thr	Gln	Gly	Thr	Thr	Phe	Asn	Leu	Thr	Ser	Leu	Gly	Ser
465					470					475					480
Glu	Lys	Ser	Val	Thr	Ile	Leu	Asn	Ser	Arg	Gly	Gly	Ile	Thr	Tyr	Asn
				485					490						495
His	Leu	Leu	Asn	His	Ala	Ile	Asn	Ser	Leu	Thr	Asn	Ala	Leu	Lys	Thr
			500					505					510		
Asn	Glu	Ser	Ser	Ser	Lys	Pro	Gln	Ser	Phe	Ala	Gln	Gly	Leu	Trp	Asp
		515					520					525			
Met	Ile	Thr	Tyr	Asn	Gly	Val	Thr	Gly	Gln	Leu	Leu	Asn	Glu	Asn	Ala
	530					535					540				
Ala	Thr	Ser	Lys	Pro	Thr	Asp	Ser	Ser	Pro	Ser	Lys	Ser	Ser	Thr	Asn
545					550					555					560
Ser	Thr	Gln	Val	Tyr	Gln	Val	Gly	Tyr	Lys	Ile	Gly	Asp	Thr	Ile	Tyr
				565					570						575
Lys	Leu	Gln	Glu	Thr	Phe	Ser	His	Asn	Ser	Ile	Ile	Ile	Gln	Ala	Leu
			580					585					590		
Glu	Ser	Gly	Thr	Tyr	Thr	Pro	Pro	Pro	Val	Ile	Asn	Gly	Ser	Lys	Phe
		595					600					605			
Asp	Leu	Ser	Ala	Ser	Asn	Tyr	Ile	Asn	Ala	Asp	Met	Pro	Trp	Tyr	Asn
	610					615					620				
His	Lys	Tyr	Tyr	Ile	Pro	Lys	Ser	Gln	Asn	Phe	Thr	Glu	Ser	Gly	Thr
625					630					635					640
Tyr	Tyr	Leu	Pro	Ser	Val	Gln	Ile	Trp	Gly	Ser	Tyr	Thr	Asn	Ser	Phe
				645					650						655
Lys	Gln	Thr	Phe	Ser	Ala	Ser	Asn	Ser	Asn	Leu	Val	Ile	Gly	Tyr	Asn
		660						665					670		
Ala	Thr	Trp	Thr	Asp	His	Asn	Val	Ser	Ser	Ser	Asp	Thr	Val	Ala	Phe

1009

675				680				685							
Gly	Asp	Thr	Ser	Gly	Ser	Ala	Leu	Asn	Gly	His	Cys	Gly	Pro	Trp	Pro
690						695					700				
Tyr	Tyr	Gln	Cys	Thr	Gly	Thr	Thr	Asn	Gly	Thr	Tyr	Ser	Ala	Tyr	His
705					710					715					720
Val	Tyr	Ile	Thr	Ala	Asn	Leu	Arg	Ser	Gly	Asn	Arg	Ile	Gly	Thr	Gly
				725					730					735	
Gly	Ala	Ala	Asn	Leu	Ile	Phe	Asn	Gly	Val	Asp	Ser	Ile	Asn	Ile	Ala
			740						745				750		
Asn	Ala	Thr	Ile	Thr	Gln	His	Asn	Ala	Gly	Ala	Tyr	Ser	Ser	Ser	Met
		755					760					765			
Thr	Phe	Ser	Thr	Gln	Asn	Met	Asp	Asn	Ser	Gln	Asn	Leu	Asn	Gly	Leu
	770				775						780				
Asn	Ser	Asn	Gly	Lys	Leu	Leu	Val	Tyr	Gly	Thr	Thr	Phe	Thr	Asn	Gln
785					790					795					800
Ala	Lys	Asp	Gly	Lys	Phe	Ile	Phe	Asn	Ala	Gly	Gln	Ala	Thr	Phe	Glu
				805					810					815	
Asn	Thr	Asn	Phe	Asn	Gly	Gly	Ser	Tyr	Gln	Phe	Ser	Gly	Asp	Ser	Leu
			820						825				830		
Asn	Phe	Ser	Asn	Asn	Asn	Gln	Phe	Asn	Ser	Gly	Ser	Phe	Glu	Ile	Gly
		835				840						845			
Ala	Lys	Asn	Thr	Ile	Phe	Asn	Asn	Ala	Asn	Phe	Asn	Asn	Ser	Thr	Ser
	850					855					860				
Phe	Asn	Phe	Asn	Asn	Ser	Ser	Ala	Thr	Thr	Ser	Phe	Val	Gly	Asp	Phe
865					870					875					880
Thr	Asn	Ala	Asn	Ser	Asn	Leu	Gln	Ile	Ala	Gly	Asn	Ala	Val	Phe	Gly
				885					890					895	
Asn	Ser	Thr	Asn	Gly	Ser	Gln	Asn	Thr	Ala	Asn	Phe	Asn	Asn	Thr	Gly
		900						905					910		
Ser	Val	Asn	Ile	Ala	Gly	Asn	Ala	Thr	Phe	Asp	Asn	Val	Val	Phe	Asn
		915					920					925			
Ser	Pro	Thr	Asn	Thr	Ser	Val	Lys	Gly	Lys	Val	Thr	Leu	Asn	Asn	Ile
	930					935					940				
Thr	Leu	Lys	Asn	Leu	Asn	Ala	Pro	Leu	Ser	Phe	Gly	Asp	Gly	Thr	Ile
945					950					955					960
Val	Phe	Ser	Ala	His	Ser	Val	Ile	Asn	Ile	Gly	Glu	Ala	Ile	Thr	Asn
				965					970					975	
Gly	Asn	Pro	Ile	Thr	Leu	Val	Ser	Ser	Ser	Lys	Ala	Ile	Glu	Tyr	Asn
		980							985				990		
Asp	Ala	Phe	Ser	Lys	Asn	Leu	Trp	Gln	Leu	Ile	Asn	Tyr	Gln	Gly	His
		995					1000					1005			
Gly	Ala	Ser	Ser	Glu	Lys	Leu	Val	Ser	Ser	Ala	Gly	Asn	Gly	Val	Tyr
	1010					1015					1020				
Asp	Val	Val	Tyr	Ser	Phe	Asn	Asn	Gln	Thr	Tyr	Asn	Phe	Gln	Glu	Val
1025					1030					1035					1040
Phe	Ser	Pro	Asn	Ser	Ile	Ser	Ile	Arg	Arg	Leu	Gly	Val	Gly	Met	Val
				1045					1050					1055	
Phe	Asp	Tyr	Val	Asp	Met	Glu	Lys	Ser	Asp	Arg	Leu	Tyr	Tyr	Gln	Asn
		1060						1065					1070		
Ala	Leu	Gly	Phe	Met	Thr	Tyr	Met	Pro	Asn	Ser	Tyr	Asn	Asn	Asn	Leu
		1075					1080					1085			
Gly	Asn	Leu	Asn	Asn	Thr	Ile	Tyr	Tyr	Tyr	Asp	Asn	Ser	Ile	Asp	Phe
	1090					1095					1100				
Tyr	Ala	Ser	Gly	Lys	Thr	Leu	Phe	Thr	Lys	Ala	Glu	Phe	Ser	Gln	Thr
1105					1110					1115					1120
Phe	Thr	Gly	Gln	Asn	Ser	Ala	Ile	Val	Phe	Gly	Ala	Lys	Asn	Ile	Trp
				1125					1130					1135	

1010

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Thr Ser Val Ser Asp Ala Pro Gln Ser Asn Val Ile Ile Arg Phe Gly
      1140      1145      1150
Asp Asn Lys Gly Ala Gly Ser Asn Asp Ala Ser Gly His Cys Trp Asn
      1155      1160      1165
Leu Gln Cys Ile Gly Phe Ile Thr Gly His Tyr Glu Ala Gln Lys Ile
      1170      1175      1180
Tyr Ile Thr Gly Ser Ile Glu Ser Gly Asn Arg Ile Ser Ser Gly Gly
1185      1190      1195      1200
Ala Arg Ala Leu Ile Leu Thr Gly Phe Lys Ala Phe Phe
      1205      1210

```

(2) INFORMATION FOR SEQ ID NO:1090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...500

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

```

Met Ala Glu Trp Lys Thr Asp Thr Glu Glu Val Lys Lys Val Val Gly
1           5           10           15
Arg Cys Arg Glu Phe Lys Arg Ser Leu Gln Glu Glu Lys Cys Ser Pro
      20           25           30
Phe Ile Lys Asp Leu Asp Ser Tyr Ala Leu Lys Ile Ile Val Glu Arg
      35           40           45
Arg Lys Thr Glu Met Gln Leu Glu Lys Ala Ile Gly Glu Leu Lys Lys
      50           55           60
Ala Lys Ser Asn Glu Asp Asp Ala Lys Val Ala Leu Arg Val Leu Gln
65           70           75           80
Gly Ala Ser Val Val Ser Trp Ile Trp Pro Pro Ala Arg Ile Ala Ala
      85           90           95
Thr Ala Ala Ile Val Ala Ala Glu Ala Val Leu Lys Phe Met Lys Glu
      100          105          110
Asp Thr Glu Lys Cys Lys Arg Asn Val Glu Leu Leu Glu Arg Met Leu
      115          120          125
Glu Ile Tyr Ser Asn Gln Ala Lys Ala Ser Ala Asn Leu Met Asn Gln
      130          135          140
Ala Trp Glu Gly Ile Lys Lys Arg Leu His Phe Tyr Thr Asp Lys His
145          150          155          160
Gln Glu Phe Ile Arg Arg Leu Lys Gln Ala Ser Asp Ala Ile Asp Asn
      165          170          175
Glu Tyr Asn Phe Pro Thr Pro Gly Val Leu Leu Glu Tyr Asp Phe Glu
      180          185          190
Arg Pro Ala Ile Ser Tyr Thr Pro Lys Lys Ser Val Phe Asn Glu Arg
      195          200          205

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1011

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Leu Lys Asp Leu Arg Glu Asn Phe Ser Ala Ser Leu Tyr Ala Asp Leu
 210                      215                      220
Lys Asp Lys Ile His His Asn Ala Leu Ser Asn Asp Asp Leu Glu Arg
225                      230                      235                      240
Met Ile Ala Phe Arg Glu Gln Glu Phe Glu Lys Ser Leu Glu Asp Trp
                      245                      250                      255
Met Gly Ala Tyr Ser Tyr Asp Glu Asn Pro Asn Asp Glu Leu Asp Arg
                      260                      265                      270
Met Ala Ile Ser Lys Glu Gln Glu Leu Glu Lys Ser Leu Glu Asp Leu
                      275                      280                      285
Met Pro Ser Val Leu Gly Val Pro Ser Tyr Asn Glu Ser Leu Thr Leu
                      290                      295                      300
Ala Lys Asn Arg Cys Val Lys Asn Phe Lys Glu Ala Leu Glu Gly Phe
305                      310                      315                      320
Thr Glu Lys Ile Lys Glu Ser Pro Asn Asp Ser Asn Ala Ile Asn Glu
                      325                      330                      335
Ala Phe Asp Asn Leu Glu Thr Glu Leu Glu Arg Ala Thr Glu Asn Leu
                      340                      345                      350
Ser Gln Lys Ile Asp Pro Val Leu Glu Arg Asn Glu Asn Tyr Thr Gln
                      355                      360                      365
Lys Ala Leu Glu Tyr Arg Glu Phe Leu Glu Ser Arg Lys Glu Ser Phe
370                      375                      380
Ile Val Asp Glu Lys Asn Pro Tyr Pro Glu Glu Val Ser Phe Asn Glu
385                      390                      395                      400
Trp Arg Trp Ala Glu Phe Asp Ser Val Phe Ser Ala Ile Val Pro Leu
                      405                      410                      415
Glu Asp Leu Asn Lys Thr Ala Cys Ala His His Ala Leu Lys Ala Leu
                      420                      425                      430
Gln Ala Thr Leu Lys Asp Asn Asp Leu Gly Phe Asp Ala Thr Glu Leu
                      435                      440                      445
Glu Gln Ile Ala Lys Gly Phe Ile Pro Arg Gly Tyr Leu Trp His Phe
450                      455                      460
Asp Ala Asn Val Leu Gly Asn Leu Ala Leu Val Arg Glu Glu Leu Leu
465                      470                      475                      480
Leu Gly Val Lys His Thr Lys Gly Tyr Ser Leu Trp Thr Glu Phe Leu
                      485                      490                      495
Gln Lys Gln Asn
                      500

```

(2) INFORMATION FOR SEQ ID NO:1091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

1012

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

TTAACCATGG TGAAAAGCGA TA

22

(2) INFORMATION FOR SEQ ID NO:1092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

TAGAATTCGC ATAACGATCA ATC

23

(2) INFORMATION FOR SEQ ID NO:1093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

TTAACCATGG TGAAAAGCGA TA

22

1013

(2) INFORMATION FOR SEQ ID NO:1094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

TAGAATTCGC ATAACGATCA ATC

23

(2) INFORMATION FOR SEQ ID NO:1095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

ATATCCATGG TGAGTTTGAT GA

22

(2) INFORMATION FOR SEQ ID NO:1096:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

1014

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...25
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

ATGAATTCAA TTTTATTG TCCCA

25

(2) INFORMATION FOR SEQ ID NO:1097:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...23
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

AATTCCATGG CTATCCAAAT CCG

23

(2) INFORMATION FOR SEQ ID NO:1098:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

1015

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

ATGAATTCGC CAAAATCGTA GTATT

25

(2) INFORMATION FOR SEQ ID NO:1099:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

GATACCATGG AATTTATGAA AAAG

24

(2) INFORMATION FOR SEQ ID NO:1100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...25

1016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

TGAATTCGAA AAAGTGTAGT TATAC

25

(2) INFORMATION FOR SEQ ID NO:1101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

CCCTTCATTT TAGAAATCG

19

(2) INFORMATION FOR SEQ ID NO:1102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

ATTCAACCA ATTCAATGCG

20

(2) INFORMATION FOR SEQ ID NO:1103:

(i) SEQUENCE CHARACTERISTICS:

1017

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

GCCCCTTTTG ATTGAAGCT

20

(2) INFORMATION FOR SEQ ID NO:1104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

TCGCTCCAAG ATACCAAGAA GT

22

(2) INFORMATION FOR SEQ ID NO:1105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

1018

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

CTTGAATTAG GGGCAAAGAT CG

22

(2) INFORMATION FOR SEQ ID NO:1106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

ATGCGTTTTT ACCCAAAGAA GT

22

(2) INFORMATION FOR SEQ ID NO:1107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

1019

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:

ATAACGCCAC TTCCTTATTG GT

22

(2) INFORMATION FOR SEQ ID NO:1108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

CTTTGGGTAA AAACGCATC

19

(2) INFORMATION FOR SEQ ID NO:1109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

CGATCTTTGA TCCTAATTCA

20

1020

(2) INFORMATION FOR SEQ ID NO:1110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

ATCAAGTTGC CTATGCTGA

19

(2) INFORMATION FOR SEQ ID NO:1111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

TTGAACACTT TTGATTATGC GG

22

(2) INFORMATION FOR SEQ ID NO:1112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

1021

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...23
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

GGATTATGCG ATTGTTTTAC AAG

23

(2) INFORMATION FOR SEQ ID NO:1113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

GTCTTTAGCA AAAATGGCGT C

21

(2) INFORMATION FOR SEQ ID NO:1114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

1022

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

AATGAGCGTA AGAGAGCCTT C

21

(2) INFORMATION FOR SEQ ID NO:1115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...18
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

CTTATGGGGG TATTGTCA

18

(2) INFORMATION FOR SEQ ID NO:1116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...18

1023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:

AGCATGTGGG TATCCAGC

18

(2) INFORMATION FOR SEQ ID NO:1117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

AGGTTGTTGC CTAAAGACT

19

(2) INFORMATION FOR SEQ ID NO:1118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

CTGCCTCCAC CTTTGATC

18

(2) INFORMATION FOR SEQ ID NO:1119:

1024

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...19
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

ACCAATATCA ATTGGCACT

19

(2) INFORMATION FOR SEQ ID NO:1120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...18
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

ACTTGGA AAA GCTCTGCA

18

(2) INFORMATION FOR SEQ ID NO:1121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

1025

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...19
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

CTTGCTTGTC ATATCTAGC

19

(2) INFORMATION FOR SEQ ID NO:1122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...18
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

GTTGAAGTGT TGGTGCTA

18

(2) INFORMATION FOR SEQ ID NO:1123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

1026

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

CAAGCAAGTG GTTTGGTTTT AG

22

(2) INFORMATION FOR SEQ ID NO:1124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

TGGAAAGAGC AAATCATTGA AG

22

(2) INFORMATION FOR SEQ ID NO:1125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

1027

GCCCATATC AAAAAGCCCA T

21

(2) INFORMATION FOR SEQ ID NO:1126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

CTAAAACCAA ACCACTTGCT TGTC

24

(2) INFORMATION FOR SEQ ID NO:1127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

GTAAAACGAC GGCCAG

16

(2) INFORMATION FOR SEQ ID NO:1128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid

1028

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...17
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

CAGGAAACAG CTATGAC

17

(2) INFORMATION FOR SEQ ID NO:1129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

TTGCCCCATC GTATTGATAG A

21

(2) INFORMATION FOR SEQ ID NO:1130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

1029

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

AGAGCGTATT TCACCCGAAA G

21

(2) INFORMATION FOR SEQ ID NO:1131:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

TCTTGCATCT TAATCCACTC C

21

(2) INFORMATION FOR SEQ ID NO:1132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

1030

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

CGGGTCAAAA CGACCACTTA A

21

(2) INFORMATION FOR SEQ ID NO:1133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

AATCCGTTTC GCTAATTAG T

21

(2) INFORMATION FOR SEQ ID NO:1134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

AACACTTCAA TTCCTCTAT A

21

(2) INFORMATION FOR SEQ ID NO:1135:

1031

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

TGGTATAAGG ATTTGAATGG A

21

(2) INFORMATION FOR SEQ ID NO:1136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:

TTGACTAAAC ACATGCGAGA A

21

(2) INFORMATION FOR SEQ ID NO:1137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

1032

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

ATAGAGAGCG TTGTGTTTAG C

21

(2) INFORMATION FOR SEQ ID NO:1138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

CCTTTATTGG TTTTGATCGT G

21

(2) INFORMATION FOR SEQ ID NO:1139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

1033

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

ATGTCCGTTG TCTGTATGGA A

21

(2) INFORMATION FOR SEQ ID NO:1140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:

TAGGGTGTCT AGGGATTGGA T

21

(2) INFORMATION FOR SEQ ID NO:1141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:

1034

GCGTTTGGCT TCTTCGTTGT C

-21

(2) INFORMATION FOR SEQ ID NO:1142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

GAAATGGAAA ATAGCGGTCA A

21

(2) INFORMATION FOR SEQ ID NO:1143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

GCAAATCCCC AGCCACTTCC

20

(2) INFORMATION FOR SEQ ID NO:1144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

1035

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

GTGGCTAAAA ATGAGGGCTT

20

(2) INFORMATION FOR SEQ ID NO:1145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

GTTAGGAAAT TAGAAATCAT TG

22

(2) INFORMATION FOR SEQ ID NO:1146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

1036

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

GCTAAAACTT CATCGCTCAA T

21

(2) INFORMATION FOR SEQ ID NO:1147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

GTTGGGCAGA AAATAAGGTG A

21

(2) INFORMATION FOR SEQ ID NO:1148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:

1037

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

CAAACAAACC TGACAAGAAA C

21

(2) INFORMATION FOR SEQ ID NO:1149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

CATTGATGCC TAAAACTTCG

20

(2) INFORMATION FOR SEQ ID NO:1150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

CGTGGTGGTT TTCCCGTTAG

20

1038

(2) INFORMATION FOR SEQ ID NO:1151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

GGGGCATTGT GTTTGTTTTT

20

(2) INFORMATION FOR SEQ ID NO:1152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

TGGTCTATCA TGCGAATTAT

20

(2) INFORMATION FOR SEQ ID NO:1153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

1039

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:

GCCCTGATCC ATTCCCCCT

20

(2) INFORMATION FOR SEQ ID NO:1154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:

CGCGCTAGAG GCTTGTA AAA

20

(2) INFORMATION FOR SEQ ID NO:1155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

1040

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:

GCCCTGATCC ATTCCCCCCT

20

(2) INFORMATION FOR SEQ ID NO:1156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:

CTGTTTTTAG CGTCCCTGTA

20

(2) INFORMATION FOR SEQ ID NO:1157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...20

1041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:

GGCGTTATTA AGCGACATCG

20

(2) INFORMATION FOR SEQ ID NO:1158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:

TTTCACCGGC AATTTTAGGC

20

(2) INFORMATION FOR SEQ ID NO:1159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:

GCGTTTTGAT TCTGTCTGTT A

21

(2) INFORMATION FOR SEQ ID NO:1160:

(i) SEQUENCE CHARACTERISTICS:

1042

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:

GTAAAAACAC CGCTAACGCA T

21

(2) INFORMATION FOR SEQ ID NO:1161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:

GCGTGTTTC TAAGGGTTCA

20

(2) INFORMATION FOR SEQ ID NO:1162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

1043

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:

GGAATTTTAA CGCTCTTTT

20

(2) INFORMATION FOR SEQ ID NO:1163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

AAATCTCTGT GGGCTTAGTG

20

(2) INFORMATION FOR SEQ ID NO:1164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

1044

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:

AATCAAAAAC AAGAGCGTGG

20

(2) INFORMATION FOR SEQ ID NO:1165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:

GCCCCAGCCC CATAATACAA A

21

(2) INFORMATION FOR SEQ ID NO:1166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:

GGAGGGCGCA ATTAAACATC G

21

1045

(2) INFORMATION FOR SEQ ID NO:1167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:

TCACGCTTTC TAAATCATCA

20

(2) INFORMATION FOR SEQ ID NO:1168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

CGCTAATCAC ATCCTTTCTT

20

(2) INFORMATION FOR SEQ ID NO:1169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

1046

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:

TGCCCAAAAA TCCACTAACG

20

(2) INFORMATION FOR SEQ ID NO:1170:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:

AACGGGTTTG ACACTGATGA

20

(2) INFORMATION FOR SEQ ID NO:1171:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

1047

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:

GAATGCGGTG GTTTTAGAGA G

21

(2) INFORMATION FOR SEQ ID NO:1172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:

GCGTTTTTAA GACTGAATAC A

21

(2) INFORMATION FOR SEQ ID NO:1173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...20

1048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:

GGGCGATGTG ATTGGCGATT

20

(2) INFORMATION FOR SEQ ID NO:1174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:

GGATAGCCTG CCAAAACGCC

20

(2) INFORMATION FOR SEQ ID NO:1175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

AAGTTTATGC GGGCGAGATT

20

(2) INFORMATION FOR SEQ ID NO:1176:

1049

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

GGAGCAATCA GCCATTTTTC

20

(2) INFORMATION FOR SEQ ID NO:1177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:

CTAGCGATTC AAGGCGATGG

20

(2) INFORMATION FOR SEQ ID NO:1178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

1050

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

CGGCCTCCTT CAAACACATT

20

(2) INFORMATION FOR SEQ ID NO:1179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:

AGCGGGCAGT TTAGGACCAC

20

(2) INFORMATION FOR SEQ ID NO:1180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

1051

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:

GCATTGATCG CATTTTTAGC C

21

(2) INFORMATION FOR SEQ ID NO:1181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:

ACGGGTTAGC AGGGCAGAAT

20

(2) INFORMATION FOR SEQ ID NO:1182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:

1052

CAAAAGAGGC GGGTTCATGC

20 /

(2) INFORMATION FOR SEQ ID NO:1183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:

TTAGAAGTC GTTGATGAGA

20

(2) INFORMATION FOR SEQ ID NO:1184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:

CATACACGCT CACTTCATCG

20

(2) INFORMATION FOR SEQ ID NO:1185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid

1053

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:

AGTGTGGTCG CCTGTGGTGG AG

22

(2) INFORMATION FOR SEQ ID NO:1186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:

CCCCTAATAG TCTGTCAATC AT

22

(2) INFORMATION FOR SEQ ID NO:1187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

1054

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:

CAAAAGATTG AAGCAGAAGA GT

22

(2) INFORMATION FOR SEQ ID NO:1188:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:

AATGGTTTTC CTATACCCTT GA

22

(2) INFORMATION FOR SEQ ID NO:1189:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

1055

(B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:

GAGAGCAAAT CCTTATCCAG

20

(2) INFORMATION FOR SEQ ID NO:1190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:

CATACACGCT CACTTCATCG

20

(2) INFORMATION FOR SEQ ID NO:1191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:

AGTGTGGTCG CCTGTGGTGG AG

22

(2) INFORMATION FOR SEQ ID NO:1192:

1056

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:

CCCCTAATAG TCTGTCAATC AT

22

(2) INFORMATION FOR SEQ ID NO:1193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:

CAAAAGATTG AAGCAGAAGA GT

22

(2) INFORMATION FOR SEQ ID NO:1194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

1057

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:

AATGGTTTTTCTATACCCTT GA

22

(2) INFORMATION FOR SEQ ID NO:1195:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

TTGAAACCCC AAAAGTTTTA C

21

(2) INFORMATION FOR SEQ ID NO:1196:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

1058

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

TCAACTGATA GGTAATATCC C

21

(2) INFORMATION FOR SEQ ID NO:1197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

GCTAGGATTT ATGCCAATTT A

21

(2) INFORMATION FOR SEQ ID NO:1198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:

1059

TACGAGACAA AATAGGGATT T

21

(2) INFORMATION FOR SEQ ID NO:1199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:

ATAGGCATGC AGAATTTTTC C

21

(2) INFORMATION FOR SEQ ID NO:1200:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...17
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:

CCATTACATT TCGCCTC

17

(2) INFORMATION FOR SEQ ID NO:1201:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs

1060

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201:

CGATAGATAT TGTAAGTC A

21

(2) INFORMATION FOR SEQ ID NO:1202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202:

GGGCTTGAT TCATTTGTA A

21

(2) INFORMATION FOR SEQ ID NO:1203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

1061

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:

GTTTTAAAA CGCCATAGCC A

21

(2) INFORMATION FOR SEQ ID NO:1204:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:

TTCTAAAAGG TGGTAATCTT C

21

(2) INFORMATION FOR SEQ ID NO:1205:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

1062

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:

TAAGTCAAGC CATAAAACCA AA

22

(2) INFORMATION FOR SEQ ID NO:1206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:

TTTTGGGGTA AAAAGGCTGA A

21

(2) INFORMATION FOR SEQ ID NO:1207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:

ATCTTTTGC CCTTGCTCAT A

21

1063

(2) INFORMATION FOR SEQ ID NO:1208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:

AGACAGCACC AGTTTGATAA A

21

(2) INFORMATION FOR SEQ ID NO:1209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:

CAGCCACACT TCAATGTCTA T

21

(2) INFORMATION FOR SEQ ID NO:1210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

1064

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

GTAAGGCGTT AGAAAAATAC C

21

(2) INFORMATION FOR SEQ ID NO:1211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211:

GCCCCATTAA AATCCTTTTC T

21

(2) INFORMATION FOR SEQ ID NO:1212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

1065

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212:

AAAGGATACA AGGGGGA

17

(2) INFORMATION FOR SEQ ID NO:1213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:

CTCGCTCCAT TTTATCTTTT A

21

(2) INFORMATION FOR SEQ ID NO:1214:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...21

1066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

TTTTTTAGGG AGGATTGAGA T

21

(2) INFORMATION FOR SEQ ID NO:1215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

TGTTTGAAA TGCTGGTGAT C

21

(2) INFORMATION FOR SEQ ID NO:1216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:

CTTTTGGGGG AGTTTGACAA G

21

(2) INFORMATION FOR SEQ ID NO:1217:

(i) SEQUENCE CHARACTERISTICS:

1067

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:

TTTGATAAAC GCCCACTTTT T

21

(2) INFORMATION FOR SEQ ID NO:1218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:

TTTCAAAACG CTCACCTTTT G

21

(2) INFORMATION FOR SEQ ID NO:1219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

1068

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:

TCTATTCTTT TGATGCTCTC T

21

(2) INFORMATION FOR SEQ ID NO:1220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

ATAATGAGTT TGATCGTTAC G

21

(2) INFORMATION FOR SEQ ID NO:1221:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

1069

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:

ACAATAATAG GCTTTGTCTT C

21

(2) INFORMATION FOR SEQ ID NO:1222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

AATTAGCCCT TAAAATAGAT G

21

(2) INFORMATION FOR SEQ ID NO:1223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223:

AACAACCGCT AAAATCAAAC

20

1070

(2) INFORMATION FOR SEQ ID NO:1224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:

CTTCAGCGAT ACTAAAAGAT

20

(2) INFORMATION FOR SEQ ID NO:1225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:

TAGGGGCGAT TGAAAACAGC

20

(2) INFORMATION FOR SEQ ID NO:1226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

1071

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:

GCTGGATAAG GATTGCTCT

20

(2) INFORMATION FOR SEQ ID NO:1227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:

TTTTTGGGGG TATGCTAAAA

20

(2) INFORMATION FOR SEQ ID NO:1228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

1072

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:

GGCTGGTAAA TACTGGATAG

20

(2) INFORMATION FOR SEQ ID NO:1229:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:

AGGCTATTCA AGGTGGCTAA A

21

(2) INFORMATION FOR SEQ ID NO:1230:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...22

1073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:

ATTCTCATCA ACGACTTCTA AA

22

(2) INFORMATION FOR SEQ ID NO:1231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:

GCAGTTGGCG GTATTTGGTG

20

(2) INFORMATION FOR SEQ ID NO:1232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:

GAGAGCGAAG TTTATGAGAA

20

(2) INFORMATION FOR SEQ ID NO:1233:

1074

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:

TGATTGTTGG GTAGCTCTCA

20

(2) INFORMATION FOR SEQ ID NO:1234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:

AAAATCGGTC TGATGCTCTT A

21

(2) INFORMATION FOR SEQ ID NO:1235:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

1075

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:

CTTTTCCTTT CGCTTGAAGA

20

(2) INFORMATION FOR SEQ ID NO:1236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:

AAAACAAACG CATCAAAAT

20

(2) INFORMATION FOR SEQ ID NO:1237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

1076

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237:

TTTCAAGGCG AGGAGGCAGA T

21

(2) INFORMATION FOR SEQ ID NO:1238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:

GCACAAAGAC CCCACCACGA T

21

(2) INFORMATION FOR SEQ ID NO:1239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:

1077

CGCCCGAATG GATGAGTAGG

20

(2) INFORMATION FOR SEQ ID NO:1240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:

TGCAACAAAA ATACGCCCTT

20

(2) INFORMATION FOR SEQ ID NO:1241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:

TTTTTAAGGG CGTATTTTG T

21

(2) INFORMATION FOR SEQ ID NO:1242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid

1078

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

TGGGTTTAA GGAATGTGAT G

21

(2) INFORMATION FOR SEQ ID NO:1243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

CGCGCTCAAA ATCCCTAAAT

20

(2) INFORMATION FOR SEQ ID NO:1244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

1079

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:

GGCCCATCTCT TTCGGATATT

20

(2) INFORMATION FOR SEQ ID NO:1245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:

GCCCCATTCC TGTTTTTCAGC

20

(2) INFORMATION FOR SEQ ID NO:1246:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

1080

(B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

CGCTTTAACG CTCCTTTCAC

20

(2) INFORMATION FOR SEQ ID NO:1247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

AGCGTTTTTG TAAGGGGGTA T

21

(2) INFORMATION FOR SEQ ID NO:1248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:

TCCCTATCAT AGCGTTAGTG C

21

(2) INFORMATION FOR SEQ ID NO:1249:

1081

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:

CTTAGGGGTT TTTAGCATGA A

21

(2) INFORMATION FOR SEQ ID NO:1250:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:

GCACAATTCC CACACGCTGC

20

(2) INFORMATION FOR SEQ ID NO:1251:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

1082

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:

CCAAAGCTAA AGCGGTGTTT T

21

(2) INFORMATION FOR SEQ ID NO:1252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...23
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

GCTCATGGAT ATAAAGGGGT ATT

23

(2) INFORMATION FOR SEQ ID NO:1253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

1083

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

CTTAGCCCCCT TTAGTGTTTA

20

(2) INFORMATION FOR SEQ ID NO:1254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

CGCAAAAGGG TAGGGGATAA

20

(2) INFORMATION FOR SEQ ID NO:1255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:

1084

TTTTATTTT AGAAACGAAT C

21

(2) INFORMATION FOR SEQ ID NO:1256:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

CAAACCTATC GCCCTCTCTA

20

(2) INFORMATION FOR SEQ ID NO:1257:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...23
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:

AAAGATAACG CTAGGATTTC TAC

23

(2) INFORMATION FOR SEQ ID NO:1258:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs

1085

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...23
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:

TAATTCTACA GAGTGGTTAA TGG

23

(2) INFORMATION FOR SEQ ID NO:1259:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:

GCGGTCATGG AATTTT TAGA

20

(2) INFORMATION FOR SEQ ID NO:1260:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

1086

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:

ATTCAAAGAA AGCTGGCTGT CT

22

(2) INFORMATION FOR SEQ ID NO:1261:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:

GCTTGTGGGG GTTGTTTTAT

20

(2) INFORMATION FOR SEQ ID NO:1262:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:

1087

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:

GAACCCCCTA AAATGACAAT

20

(2) INFORMATION FOR SEQ ID NO:1263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

ACCATGCTCA TTAACGCTAG G

21

(2) INFORMATION FOR SEQ ID NO:1264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:

GTAAGTTTGA GCGGCTAATT C

21

1088

(2) INFORMATION FOR SEQ ID NO:1265:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

AAAAAGAAAG AAGAACTCGT G

21

(2) INFORMATION FOR SEQ ID NO:1266:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

AAAGATACTC CCCTGTGATT A

21

(2) INFORMATION FOR SEQ ID NO:1267:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

1089

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

CAAAGAAACG CAAAATACAG

20

(2) INFORMATION FOR SEQ ID NO:1268:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

GCATGGTATT CAGCGTTTTC

20

(2) INFORMATION FOR SEQ ID NO:1269:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

1090

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:

GCAGCGGCAC AGCGACTTTA G

21

(2) INFORMATION FOR SEQ ID NO:1270:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:

CGCCCCCAAA AAGTCGCAGT A

21

(2) INFORMATION FOR SEQ ID NO:1271:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...22

1091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:

AAAGGTTTGA AACAAGAAAT CT

22

(2) INFORMATION FOR SEQ ID NO:1272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272:

CACTTGAGCG TTAGCAACAA T

21

(2) INFORMATION FOR SEQ ID NO:1273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:

GGGGTGTTTG AAATTGATAG A

21

(2) INFORMATION FOR SEQ ID NO:1274:

(i) SEQUENCE CHARACTERISTICS:

1092

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:

CGCTAGGAGA AAGGAAGGAA A

21

(2) INFORMATION FOR SEQ ID NO:1275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:

CAAGGGCGTT TTTTGGGGTA T

21

(2) INFORMATION FOR SEQ ID NO:1276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

1093

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:

GGGATTGTTA CAGGAAAAGA T

21

(2) INFORMATION FOR SEQ ID NO:1277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:

GGAATACAAT AACGCATAAA T

21

(2) INFORMATION FOR SEQ ID NO:1278:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

1094

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:

GCCTTTTGTAG ACAACCCTAC T

21

(2) INFORMATION FOR SEQ ID NO:1279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

CCCCTAAACT CAAATCTCAA T

21

(2) INFORMATION FOR SEQ ID NO:1280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

GCTAGAAATG CCATGAGAAA G

21

1095

(2) INFORMATION FOR SEQ ID NO:1281:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:

GCGATTATGG GGTATTTATT G

21

(2) INFORMATION FOR SEQ ID NO:1282:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:

TTATTGTGGA GTTGCTTGTC A

21

(2) INFORMATION FOR SEQ ID NO:1283:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

1096

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:

TATGCGGCTC ATCCTATTAA A

21

(2) INFORMATION FOR SEQ ID NO:1284:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:

CCCTAAATCC AAATCAAGCA G

21

(2) INFORMATION FOR SEQ ID NO:1285:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

1097

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:

ATCTTACCTA TCACCTCAAA T

21

(2) INFORMATION FOR SEQ ID NO:1286:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:

AGACAGCAAC ATCTTTGTGA A

21

(2) INFORMATION FOR SEQ ID NO:1287:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...25

1098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:

TTATGGATCC AAACCAATTA AAAC

25

(2) INFORMATION FOR SEQ ID NO:1288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:

TATCTCGAGT TATAGAGAAG GGC

23

(2) INFORMATION FOR SEQ ID NO:1289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...29

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:

AAATAGTCAT ATGAAAATAG GCGTTTTTG

29

(2) INFORMATION FOR SEQ ID NO:1290:

1099

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...28
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:

AGAATTCTAT TACAATTGA GCCATTCT

28

(2) INFORMATION FOR SEQ ID NO:1291:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...26
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:

GCGAATTCGA TCAGAATTTT TTTTCT

26

(2) INFORMATION FOR SEQ ID NO:1292:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

1100

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...26
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:

ATAAGTACTT GTGAATCTTA TACTAG

26

(2) INFORMATION FOR SEQ ID NO:1293:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2694 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2694
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:

ATGGAGCAGC	CAGTCATTAA	AGAAGGGACT	TTAGCTTTAA	TTGATACCTT	TGCGTATTTG	60
TTTAGAAGCT	ATTACATGAG	CGCTAAAAAT	AAGCCTTTAA	CCAACGATAA	GGGCTTTCCT	120
ACAGGGCTTT	TAACGGGGCT	TGTGGGCATG	GTAAAAAAT	TTTATAAAGA	CAGAAAAAAC	180
ATGCCTTTTA	TCGTGTTTCG	CCTAGAAAGC	CAGACTAAAA	CTAAAAGAGC	TGAAAAACTG	240
GGCGAATACA	AACAAAATCG	TAAAGACGCC	CCTAAAGAGA	TGCTTTTACA	AATCCCTATC	300
GCCTTAGAAT	GGTTGCAAAA	AATGGGTTTT	ACTTGCGTGG	AGGTGGGAGG	GTTTGAAGCC	360
GATGATGTGA	TCGCAAGTTT	AGCCACGCTA	AGCCCTTATA	AAACCCGCAT	TTATTCTAAA	420
GATAAGGATT	TTAACCAGCT	TTTGAGCGAT	AAAATCGCGC	TTTTTGATGG	CAAAACGGAG	480
TTTTTGCGCA	AAGATTGCGT	GGAAAAATAC	GGGATTTTGC	CGAGTCAATT	CACGGATTAT	540
CAGGGCATTG	TGGGGGATAG	CAGCGATAAT	TACAAGGGGG	TTAAAGGCAT	TGGGAGCAAG	600
AACGCTAAGG	AATTGTTGCA	GCGATTAGGG	AGCTTGGAAG	AAATCTATGA	AAATTTAGAC	660
TTGGCGAAAA	ATTTACTCAG	CCCTAAAATG	TATCAAGCCT	TGATACAAGA	CAAAGGAAGC	720
GCCTTTTAA	GCAAAGAATT	AGCCACTTTA	GAAAGAGGAT	GCATTAAAGA	ATTTGATTTT	780
TTAAGTTGCG	CTTTTCCGAG	CGAAAACCCC	TTGTTGAAAA	TCAAAGATGA	ATTGAAAGAA	840
TATGGTTTCA	TTTCTACCTT	AAGGGATTTA	GAAAATTCCT	CTTTCATTGT	AGAAAACGTG	900
CCCATATTAA	ACAGCACGCC	TATATTAGAC	AATACCCCCG	CCTTAGACAA	CGCCCCTAAA	960
AAATCGCGCA	TGATTGTTTT	AGAAAGCGCT	GAGCCTTTGA	GCATGTTTTT	AGAAAAATTA	1020
GAAAACCCTA	ACGCTAGGGT	TTTTATGCGT	TTGGTTTTTG	ATAAAGACAA	AAAAATTCTA	1080

1101

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GCCCTAGCGT TTTTATTACA AGATCAAGGC TATTTTTTAC CTTTAGAAGA GCGGTTGTTT 1140
TCGCCCTTTT CTTTGGAATT TTTACAAAAC GCTTTTTTCTC AAATGTTACA GCATGCGTGT 1200
ATCATTGGGC ATGATTTAAA GCCTTTATTA AGCTTTTTTAA AAGCCAAATA TCAGGTGCCT 1260
TTGGAAAATA TCCGCATCCA AGACACTCAG ATTTTAGCGT TTTTAAAGAA TCCGGAAAAA 1320
GTGGGGTTTG ATGAGGTTT AAAGGAATAT TTAAGAAG AGTTAATCCC GCATGAAAAG 1380
ATCAAAGATT TTAAGACAAA AAGTAAGGCG GAAAAATCAG AACTTTTAAG CATGGAATTA 1440
AACGCCTTAA AGCGTTTGTG CGAATACTTT GAAAAAGGGG GGCTAGAAGA GGATTTGCTC 1500
ACTTTAGCTA GAGACATTGA AACGCCGTTT GTGAAAGTTT TAATGGGCAT GGAATTTCAA 1560
GGCTTTAAGA TTGATGCGCC TTATTTCAAG CGCTTAGAGC AGGAGTTTAA GAATGAATTA 1620
AACGTTTTAG AGCGCCAAAT TTTGGATCTA ATCGGCGTGG ATTTCAACCT CAATTCGCCC 1680
AAGCAACTTG GCGAAGTCTT GTATGATAAA TTAGGGCTTC CTAAAAATAA AAGCCACTCT 1740
ACCGATGAAA AAAACTTGTT AAAAATCCTA GACAAGCACC CAAGCATCCC TTTGATTTTA 1800
GAATACAGGG AATTGAATAA GCTTTTTAAC ACTTACACGA CCCCCTTATT GCGCTTAAAA 1860
GACAAAGACG ATAAATCCA TACCACTTT ATCCAAACCG GCACAGCTAC CGGGCGTTTA 1920
AGCTCGCATT CGCCTAATTT GCAAAATATC CCGGTGCGAT CGCCTAAAGG CTTACTCATT 1980
CGTAAGGGTT TTATCGCTAG CTCTAAAGAA TATTGTTTAT TAGGGGTGGA TTATTCGCAG 2040
ATTGAATTAC GCTTGTTGGC CCATTTTCAGC CAGGATAAGG ATTTAATGGA AGCGTTTTTA 2100
AAGGGGCGAG ACATCCATTT AGAACTTCT AAGGCGTTGT TTGGAGAAGA TTTAGCCAAA 2160
GAAAAACGAT CCATCGCTAA AAGCATTAAT TTTGGGCTGG TGTATGGCAT GGGGAGTAAG 2220
AAATTGAGCG AAACTTTAAG CATCCCTTTA AGTGAGGCTA AAAGTTACAT AGAAGCGTAT 2280
TTCAAGCGAT TCCCTAGCAT TAAAGATTAT TTGAATGGCA TGCGAGAAGA GATTTTAAAA 2340
ACTTCTAAAG CTTTACTTTT GCTGGGGCGT TACCGGGTGT TTGATTTTAC CGGCGTGAAT 2400
GATTATGTCA AGGGCAATTA TTTGCGAGAG GCGGTGAATG CGATTTTTC AAGGAGTGCC 2460
AGCGATTTAT TGAAATTAGG CATGCTTAAA GTGAGCGAGC GTTTCAAAAA CAACCCTTCG 2520
GTGAGGCTGC TTTTGCAAGT GCATGACGAA TTGATTTTGT AAATTGAAGA AAAAAACGCC 2580
CCAGAGTTGC AGCAAGAAAT CCAACGCATT CTTAATGATG AAGTCTATCC TTTGAGGGTG 2640
CCGTTAGAAA CAAGCGCGT TATCGCTAAG CGTTGGAATG AATTAAGG TTAG 2694

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(2) INFORMATION FOR SEQ ID NO:1294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:

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ATGAAAAAAC CCTTTACTC TCTCTCTCTC GCTTCATCGC TTTTAAACGC TGAAGACAAC 60
GGCTTTTTTA TCAGCGCGGG CTATCAAATC GGTGAAGCCG CTCAAATGGT GAAAAACACC 120
GGCGAATTGA AAAAATTTT AGACACTTAT GAGAATTTGA GCAACCTTTT AACCAATTTT 180
AACAACCTCA ATCAGGCGGT AACGAACGCG AGCAGCCCTT CAGAAATCAA TGCTGCGATC 240
GATAATTTAA AAGCAAACAC GCAAGGGCTA ATTGGCGAAA AAACCAATTC CCCGGCGTAT 300
CAAGCGGTGT ATTTGGCGCT CAATGCGGCG GTAGGGCTGT GGAATGTCAT CGCCTATAAT 360

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1102

GTCCAATGCG	GTCCTGGTAA	CAGTGGACAA	CAAAGCGTAA	CCTTTGAGGG	CCAACCAGGA	420
CATAATTCAA	GTTCCATTAA	TTGCAATTTA	ACCGGTTATA	ACAACGGGGT	TAGCGGCCCT	480
TTATCCATTG	AGAATTTTAA	AAAGCTTAAT	CAGGCTTATC	AAACTATCCA	ACAAGCTTTA	540
AAACAAGATA	GCGGATTTCC	TGTTTTGGAT	AGTGCAGGAA	AACAAGTAAC	TATAACAATA	600
ACAACGCAAA	CTAATGGAGC	TAATAAAAGT	GAAACTACTA	CTACTACTAC	TACTACTAAT	660
GACGCTCAAA	CCCTTTTGCA	AGAAGCCAGT	AAAATGATAA	GCGTCCTCAC	TACAAACTGC	720
CCATGGGTCA	ATCACAATCA	AGGACAAAAC	GGGGGCGCGC	CGTGGGGTTT	AGATACGGCA	780
GGGAATGTGT	GTCAGGTTTT	TGCCACGGAA	TTTAGCGCCG	TTACTAGCAT	GATCAAAAAC	840
GCCCAAGAAA	TCGTAACGCA	AGCTCAAAGC	CTTAACCAGC	AAAACAATCA	AAACGCGCCG	900
CAAGATTTCA	ATCCTTACAC	CTCTGCTGAT	AGGGCTTTCG	CTCAAAACAT	GCTCAATCAC	960
GCGCAAGCGC	AAGCCAAGAT	ACTTGAGCTA	GCCGATCAAA	TGAAAAAAGA	CCTTAACACT	1020
ATCCCAAGCC	AATTTATCAC	AAATTACTTG	GCAGCTTGCC	ACAATGGGGG	TGGGACATTA	1080
CCTGATGCGG	GGGTACTAA	CAACACTTGG	GGGGCCGGTT	GCGCGTATGT	GGAAGAGACG	1140
ATAACGGCTT	TAAACAACAG	CCTTGCGCAT	TTTGGCACTC	AAGCTGAGCA	AATCAAGCAA	1200
TCTGAGTTGT	TGGCGCGCAC	CATACTTGAT	TTTAGAGGCA	GCCTTAGTAA	TTTAAACAAC	1260
ACTTATAACA	GCATCACCAC	GACCGCTTCA	AACACGCCTA	ATTCCCCATT	CCTTAAAAAT	1320
TTGATAAGCC	AATCCACTAA	CCCTAATAAC	CCCCGGGGCT	TACAGGCCGT	TTATCAAGTC	1380
AACCAAAGCG	CTTATTCGCA	ATTATTAAGC	GCCACGCAAG	AATTAGGGCA	TAACCCTTTC	1440
AGACGCGTTG	GATTAATCAG	CTCTCAAACC	AACAATGGTG	CCATGAATGG	GATCGGTGTG	1500
CAAGTGGGCT	ACAAACAATT	TTTTGGTGAA	AAGAGAAGGT	GGGGGTAAAG	GTATTACGGC	1560
TTTTTTGACT	ATAACCATGC	TTATATCAAA	TCTAGCTTTT	TCAATTCGGC	TTCTGATGTG	1620
TTCACTTATG	GGGTAGGGAC	AGATGTCCTC	TATAACTTTA	TCAATGATAA	AACCACCAAA	1680
AACAGCAAGA	TTTCTTTTGG	GGTGTFTGGG	GGGATTGCGT	TAGCTGGCAC	TTCATGGCTG	1740
AATTCCCAGT	ATGTGAATTT	AGCGACCTTC	AATAATTTCT	ATAGCGCTAA	AATGAATGTG	1800
GCGAATTTCC	AATTCTTGTT	CAATTTAGGC	TTGAGAATGA	ACCTCGCTAA	GAATAAGAAA	1860
AAAGCGAGCG	ATCATGCGGC	TCAGCATGGC	GTGGAATTAG	GCGTGAAGAT	CCCCACGATC	1920
AACACGAATT	ACTATTCTTT	GCTAGGCACT	CAACTCCAAT	ACCGAAGATT	GTATAGCGTG	1980
TATTTGAATT	ATGTGTTGCG	TTACTAA				2007

(2) INFORMATION FOR SEQ ID NO:1295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1914 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:

ATGAAAAGAC	AATTCTACTC	TCTCTCTCTC	TCTCTCGCTT	CATCGCTCTT	GCATGCTGAA	60
GACAACGGCT	TTTTTGTGAG	CGCGGGCTAT	CAAATCGGCG	AAGCGGTGCA	AATGGTCAAA	120
AACACCGGCG	AATTGAAAAA	CTTGAACGAC	AAATACGAGC	AGTTAAGCCA	ATCTTTAGCC	180
CAACTGGCTT	CGTTAAAAAA	AAGCATTCAA	ACGGCGAACA	ACATTCAGGC	TGTCAACAAT	240
GCTTTAAGCG	ATTTAAAAAG	CTTTGCGAGT	AACAACCACA	CAAACAAAGA	AACATCGCCC	300

ATCTACAACA	CCGCGCAAGC	TGTTATCACT	TCAGTATTGG	CTTTTTGGAG	TCTTTATGCA	360
GGGAACGCTC	TCAGTTTTCA	TGTGACCGGT	TTGAATGATG	GATCTAATTC	TCCTTTAGGA	420
AGAATCCATA	GAGATGGGAA	CTGCACAGGA	TTACAACAAT	GTTTTATGAG	CAAAGAAACT	480
TATGATAAAA	TGAAGACACT	TGCCGAAAAC	CTCCAAAAAG	CTCAAGGCAA	TCTCTGTGCC	540
TTATCAGAAT	GCTCTAGCAA	TCAATCAAAT	GGAGGCCAAA	CTTCCATGAC	TACAGCTCTT	600
CAAACCGCGC	AACAGCTCAT	GGACTTAATC	GAACAGACCA	AGGTTTCTAT	GGTGTGGAAA	660
AATATCGTCA	TCGCAGGTGT	TACAAACAAA	CCCAATGGTG	CTGGCGCTAT	CACATCCACT	720
GGTCATGTAA	CCGACTATGC	GGTGTTTAAC	AACATCAAGG	CGATGCTACC	TATCTTGCAA	780
CAAGCGCTTA	CGCTTTCTCA	AAGTAACCAC	ACCCTATCCA	CTCAGTTGCA	AGCTCGAGCT	840
ATGGGATCTC	AAACAAATCG	TGAATTCGCT	AAAGACATCT	ACGCTTTAGC	TCAAAACCAA	900
AAGCAAATCC	TTTCTAACGC	TTCAAGTATC	TTCAATCTCT	TTAATTCCAT	TCCTAAAGAC	960
CAACTTAAGT	ATTTGGAGAA	CGCTTACTTG	AAAGTGCCAC	ATTTGGGTAA	AACCCCTACT	1020
AACCCTTACA	GACAGAATGT	GAATTTGAAT	AAAGAAATTA	ATGCGGTTCA	AGACAATGTA	1080
GCTAATTATG	GTAATCGTTT	GGATTCGGCT	TTAAGCGTGG	CTAAAGATGT	TTATAACCTA	1140
AAATCCAATC	AAACAGAGAT	CGTAACCACT	TATAACGATG	CTAAGAATTT	GAGCGAAGAG	1200
ATTTCTAAAC	TTCCCTATAA	CCAAGTCAAT	GTAACAAACA	TCGTTATGTC	GCCTAAAGAT	1260
TCTACAGCGG	GCCAATACCA	AATCAACCCA	GAGCAGCAAT	CCAATCTTAA	CCAAGCTTTA	1320
GCGGCGATGA	GCAATAACCC	CTTTAAAAAA	GTGGGCATGA	TCAGCTCTCA	AAACAATAAC	1380
GGCGCTTTGA	ACGGGCTTGG	CGTGCAAGTG	GGTTATAAAC	AATTCTTTGG	CGAAAGCAAA	1440
AGATGGGGGT	TAAGGTATTA	TGGTTTCTTT	GATTACAACC	ACGGCTATAT	CAAATCCAGC	1500
TTTTTTAATT	CTTCTTCTGA	TATATGGACT	TATGGCGGTG	GGAGCGATTT	GTTAGTGAAT	1560
TTTATCAACG	ATAGCATCAC	AAGAAAGAAC	AACAAGCTTT	CTGTGGGTCT	TTTTGGTGGT	1620
ATCCAAC TAG	CAGGGACTAC	ATGGCTTAAT	TCTCAATACA	TGAATTTAAC	AGCGTTCAAT	1680
AACCCTTACA	GCGCGAAAGT	CAATGCTTCC	AATTTCCAAT	TTTTGTTCAA	TCTCGGCTTG	1740
AGGACGAATC	TCGCTACAGC	TAAGAAAAAA	GACAGCGAAC	GTTCCGCGCA	ACATGGCGTT	1800
GAACTGGGCA	TTAAATCCC	TACCATTAAC	ACCAATTATT	ATTCTTTTCT	AGGCACTAAG	1860
CTAGAATACC	GAAGGCTTTA	TAGCGTGTAT	CTCAATTATG	TGTTTGCTTA	TTAA	1914

(2) INFORMATION FOR SEQ ID NO:1296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:

Met	Glu	Gln	Pro	Val	Ile	Lys	Glu	Gly	Thr	Leu	Ala	Leu	Ile	Asp	Thr
1				5					10					15	
Phe	Ala	Tyr	Leu	Phe	Arg	Ser	Tyr	Tyr	Met	Ser	Ala	Lys	Asn	Lys	Pro
			20						25					30	
Leu	Thr	Asn	Asp	Lys	Gly	Phe	Pro	Thr	Gly	Leu	Leu	Thr	Gly	Leu	Val
			35						40					45	
Gly	Met	Val	Lys	Lys	Phe	Tyr	Lys	Asp	Arg	Lys	Asn	Met	Pro	Phe	Ile
			50						55					60	
Val	Phe	Ala	Leu	Glu	Ser	Gln	Thr	Lys	Thr	Lys	Arg	Ala	Glu	Lys	Leu

1104

65					70					75				80	
Gly	Glu	Tyr	Lys	Gln	Asn	Arg	Lys	Asp	Ala	Pro	Lys	Glu	Met	Leu	Leu
				85					90					95	
Gln	Ile	Pro	Ile	Ala	Leu	Glu	Trp	Leu	Gln	Lys	Met	Gly	Phe	Thr	Cys
			100					105					110		
Val	Glu	Val	Gly	Gly	Phe	Glu	Ala	Asp	Asp	Val	Ile	Ala	Ser	Leu	Ala
			115				120					125			
Thr	Leu	Ser	Pro	Tyr	Lys	Thr	Arg	Ile	Tyr	Ser	Lys	Asp	Lys	Asp	Phe
	130					135					140				
Asn	Gln	Leu	Leu	Ser	Asp	Lys	Ile	Ala	Leu	Phe	Asp	Gly	Lys	Thr	Glu
145					150					155					160
Phe	Leu	Ala	Lys	Asp	Cys	Val	Glu	Lys	Tyr	Gly	Ile	Leu	Pro	Ser	Gln
			165						170						175
Phe	Thr	Asp	Tyr	Gln	Gly	Ile	Val	Gly	Asp	Ser	Ser	Asp	Asn	Tyr	Lys
			180					185					190		
Gly	Val	Lys	Gly	Ile	Gly	Ser	Lys	Asn	Ala	Lys	Glu	Leu	Leu	Gln	Arg
	195						200					205			
Leu	Gly	Ser	Leu	Glu	Lys	Ile	Tyr	Glu	Asn	Leu	Asp	Leu	Ala	Lys	Asn
	210					215					220				
Leu	Leu	Ser	Pro	Lys	Met	Tyr	Gln	Ala	Leu	Ile	Gln	Asp	Lys	Gly	Ser
225					230					235					240
Ala	Phe	Leu	Ser	Lys	Glu	Leu	Ala	Thr	Leu	Glu	Arg	Gly	Cys	Ile	Lys
			245						250					255	
Glu	Phe	Asp	Phe	Leu	Ser	Cys	Ala	Phe	Pro	Ser	Glu	Asn	Pro	Leu	Leu
			260					265					270		
Lys	Ile	Lys	Asp	Glu	Leu	Lys	Glu	Tyr	Gly	Phe	Ile	Ser	Thr	Leu	Arg
	275						280					285			
Asp	Leu	Glu	Asn	Ser	Pro	Phe	Ile	Val	Glu	Asn	Val	Pro	Ile	Leu	Asn
	290					295					300				
Ser	Thr	Pro	Ile	Leu	Asp	Asn	Thr	Pro	Ala	Leu	Asp	Asn	Ala	Pro	Lys
305					310					315					320
Lys	Ser	Arg	Met	Ile	Val	Leu	Glu	Ser	Ala	Glu	Pro	Leu	Ser	Met	Phe
			325						330					335	
Leu	Glu	Lys	Leu	Glu	Asn	Pro	Asn	Ala	Arg	Val	Phe	Met	Arg	Leu	Val
			340					345					350		
Leu	Asp	Lys	Asp	Lys	Lys	Ile	Leu	Ala	Leu	Ala	Phe	Leu	Leu	Gln	Asp
	355						360					365			
Gln	Gly	Tyr	Phe	Leu	Pro	Leu	Glu	Glu	Ala	Leu	Phe	Ser	Pro	Phe	Ser
	370					375					380				
Leu	Glu	Phe	Leu	Gln	Asn	Ala	Phe	Ser	Gln	Met	Leu	Gln	His	Ala	Cys
385					390					395					400
Ile	Ile	Gly	His	Asp	Leu	Lys	Pro	Leu	Leu	Ser	Phe	Leu	Lys	Ala	Lys
			405						410					415	
Tyr	Gln	Val	Pro	Leu	Glu	Asn	Ile	Arg	Ile	Gln	Asp	Thr	Gln	Ile	Leu
			420					425					430		
Ala	Phe	Leu	Lys	Asn	Pro	Glu	Lys	Val	Gly	Phe	Asp	Glu	Val	Leu	Lys
			435				440					445			
Glu	Tyr	Leu	Lys	Glu	Asp	Leu	Ile	Pro	His	Glu	Lys	Ile	Lys	Asp	Phe
	450					455					460				
Lys	Thr	Lys	Ser	Lys	Ala	Glu	Lys	Ser	Glu	Leu	Leu	Ser	Met	Glu	Leu
465					470					475					480
Asn	Ala	Leu	Lys	Arg	Leu	Cys	Glu	Tyr	Phe	Glu	Lys	Gly	Gly	Leu	Glu
			485						490					495	
Glu	Asp	Leu	Leu	Thr	Leu	Ala	Arg	Asp	Ile	Glu	Thr	Pro	Phe	Val	Lys
			500					505					510		
Val	Leu	Met	Gly	Met	Glu	Phe	Gln	Gly	Phe	Lys	Ile	Asp	Ala	Pro	Tyr
			515				520						525		

1105

Phe Lys Arg Leu Glu Gln Glu Phe Lys Asn Glu Leu Asn Val Leu Glu
 530 535 540
 Arg Gln Ile Leu Asp Leu Ile Gly Val Asp Phe Asn Leu Asn Ser Pro
 545 550 555 560
 Lys Gln Leu Gly Glu Val Leu Tyr Asp Lys Leu Gly Leu Pro Lys Asn
 565 570 575
 Lys Ser His Ser Thr Asp Glu Lys Asn Leu Leu Lys Ile Leu Asp Lys
 580 585 590
 His Pro Ser Ile Pro Leu Ile Leu Glu Tyr Arg Glu Leu Asn Lys Leu
 595 600 605
 Phe Asn Thr Tyr Thr Thr Pro Leu Leu Arg Leu Lys Asp Lys Asp Asp
 610 615 620
 Lys Ile His Thr Thr Phe Ile Gln Thr Gly Thr Ala Thr Gly Arg Leu
 625 630 635 640
 Ser Ser His Ser Pro Asn Leu Gln Asn Ile Pro Val Arg Ser Pro Lys
 645 650 655
 Gly Leu Leu Ile Arg Lys Gly Phe Ile Ala Ser Ser Lys Glu Tyr Cys
 660 665 670
 Leu Leu Gly Val Asp Tyr Ser Gln Ile Glu Leu Arg Leu Leu Ala His
 675 680 685
 Phe Ser Gln Asp Lys Asp Leu Met Glu Ala Phe Leu Lys Gly Arg Asp
 690 695 700
 Ile His Leu Glu Thr Ser Lys Ala Leu Phe Gly Glu Asp Leu Ala Lys
 705 710 715 720
 Glu Lys Arg Ser Ile Ala Lys Ser Ile Asn Phe Gly Leu Val Tyr Gly
 725 730 735
 Met Gly Ser Lys Lys Leu Ser Glu Thr Leu Ser Ile Pro Leu Ser Glu
 740 745 750
 Ala Lys Ser Tyr Ile Glu Ala Tyr Phe Lys Arg Phe Pro Ser Ile Lys
 755 760 765
 Asp Tyr Leu Asn Gly Met Arg Glu Glu Ile Leu Lys Thr Ser Lys Ala
 770 775 780
 Phe Thr Leu Leu Gly Arg Tyr Arg Val Phe Asp Phe Thr Gly Val Asn
 785 790 795 800
 Asp Tyr Val Lys Gly Asn Tyr Leu Arg Glu Gly Val Asn Ala Ile Phe
 805 810 815
 Gln Gly Ser Ala Ser Asp Leu Leu Lys Leu Gly Met Leu Lys Val Ser
 820 825 830
 Glu Arg Phe Lys Asn Asn Pro Ser Val Arg Leu Leu Leu Gln Val His
 835 840 845
 Asp Glu Leu Ile Phe Glu Ile Glu Glu Lys Asn Ala Pro Glu Leu Gln
 850 855 860
 Gln Glu Ile Gln Arg Ile Leu Asn Asp Glu Val Tyr Pro Leu Arg Val
 865 870 875 880
 Pro Leu Glu Thr Ser Ala Phe Ile Ala Lys Arg Trp Asn Glu Leu Lys
 885 890 895
 Gly

(2) INFORMATION FOR SEQ ID NO:1297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

1106

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:

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Met Lys Lys Pro Phe Tyr Ser Leu Ser Leu Ala Ser Ser Leu Leu Asn
1      5      10      15
Ala Glu Asp Asn Gly Phe Phe Ile Ser Ala Gly Tyr Gln Ile Gly Glu
20      25      30
Ala Ala Gln Met Val Lys Asn Thr Gly Glu Leu Lys Lys Leu Ser Asp
35      40      45
Thr Tyr Glu Asn Leu Ser Asn Leu Leu Thr Asn Phe Asn Asn Leu Asn
50      55      60
Gln Ala Val Thr Asn Ala Ser Ser Pro Ser Glu Ile Asn Ala Ala Ile
65      70      75      80
Asp Asn Leu Lys Ala Asn Thr Gln Gly Leu Ile Gly Glu Lys Thr Asn
85      90      95
Ser Pro Ala Tyr Gln Ala Val Tyr Leu Ala Leu Asn Ala Ala Val Gly
100     105     110
Leu Trp Asn Val Ile Ala Tyr Asn Val Gln Cys Gly Pro Gly Asn Ser
115     120     125
Gly Gln Gln Ser Val Thr Phe Glu Gly Gln Pro Gly His Asn Ser Ser
130     135     140
Ser Ile Asn Cys Asn Leu Thr Gly Tyr Asn Asn Gly Val Ser Gly Pro
145     150     155     160
Leu Ser Ile Glu Asn Phe Lys Lys Leu Asn Gln Ala Tyr Gln Thr Ile
165     170     175
Gln Gln Ala Leu Lys Gln Asp Ser Gly Phe Pro Val Leu Asp Ser Ala
180     185     190
Gly Lys Gln Val Thr Ile Thr Ile Thr Thr Gln Thr Asn Gly Ala Asn
195     200     205
Lys Ser Glu Thr Thr Thr Thr Thr Thr Thr Thr Asn Asp Ala Gln Thr
210     215     220
Leu Leu Gln Glu Ala Ser Lys Met Ile Ser Val Leu Thr Thr Asn Cys
225     230     235     240
Pro Trp Val Asn His Asn Gln Gly Gln Asn Gly Gly Ala Pro Trp Gly
245     250     255
Leu Asp Thr Ala Gly Asn Val Cys Gln Val Phe Ala Thr Glu Phe Ser
260     265     270
Ala Val Thr Ser Met Ile Lys Asn Ala Gln Glu Ile Val Thr Gln Ala
275     280     285
Gln Ser Leu Asn Gln Gln Asn Asn Gln Asn Ala Pro Gln Asp Phe Asn
290     295     300
Pro Tyr Thr Ser Ala Asp Arg Ala Phe Ala Gln Asn Met Leu Asn His
305     310     315     320
Ala Gln Ala Gln Ala Lys Ile Leu Glu Leu Ala Asp Gln Met Lys Lys
325     330     335
Asp Leu Asn Thr Ile Pro Ser Gln Phe Ile Thr Asn Tyr Leu Ala Ala
340     345     350
Cys His Asn Gly Gly Gly Thr Leu Pro Asp Ala Gly Val Thr Asn Asn

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1107

355	360	365
Thr Trp Gly Ala Gly Cys	Ala Tyr Val Glu Glu Thr Ile Thr Ala Leu	
370	375	380
Asn Asn Ser Leu Ala His	Phe Gly Thr Gln Ala Glu Gln Ile Lys Gln	
385	390	395
Ser Glu Leu Leu Ala Arg	Thr Ile Leu Asp Phe Arg Gly Ser Leu Ser	400
405	410	415
Asn Leu Asn Asn Thr Tyr	Asn Ser Ile Thr Thr Thr Ala Ser Asn Thr	
420	425	430
Pro Asn Ser Pro Phe Leu Lys	Asn Leu Ile Ser Gln Ser Thr Asn Pro	
435	440	445
Asn Asn Pro Gly Gly Leu Gln	Ala Val Tyr Gln Val Asn Gln Ser Ala	
450	455	460
Tyr Ser Gln Leu Leu Ser Ala	Thr Gln Glu Leu Gly His Asn Pro Phe	
465	470	475
Arg Arg Val Gly Leu Ile Ser	Ser Gln Thr Asn Asn Gly Ala Met Asn	
485	490	495
Gly Ile Gly Val Gln Val Gly	Tyr Lys Gln Phe Phe Gly Glu Lys Arg	
500	505	510
Arg Trp Gly Leu Arg Tyr Tyr	Gly Phe Phe Asp Tyr Asn His Ala Tyr	
515	520	525
Ile Lys Ser Ser Phe Phe Asn	Ser Ala Ser Asp Val Phe Thr Tyr Gly	
530	535	540
Val Gly Thr Asp Val Leu Tyr	Asn Phe Ile Asn Asp Lys Thr Thr Lys	
545	550	555
Asn Ser Lys Ile Ser Phe Gly	Val Phe Gly Ile Ala Leu Ala Gly	
565	570	575
Thr Ser Trp Leu Asn Ser Gln	Tyr Val Asn Leu Ala Thr Phe Asn Asn	
580	585	590
Phe Tyr Ser Ala Lys Met Asn	Val Ala Asn Phe Gln Phe Leu Phe Asn	
595	600	605
Leu Gly Leu Arg Met Asn Leu	Ala Lys Asn Lys Lys Lys Ala Ser Asp	
610	615	620
His Ala Ala Gln His Gly Val	Glu Leu Gly Val Lys Ile Pro Thr Ile	
625	630	635
Asn Thr Asn Tyr Tyr Ser Leu	Leu Gly Thr Gln Leu Gln Tyr Arg Arg	
645	650	655
Leu Tyr Ser Val Tyr Leu Asn	Tyr Val Phe Ala Tyr	
660	665	

(2) INFORMATION FOR SEQ ID NO:1298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:

Met	Lys	Arg	Gln	Phe	Tyr	Ser	Leu	Ser	Leu	Ala	Ser	Ser	Leu		
1				5				10					15		
Leu	His	Ala	Glu	Asp	Asn	Gly	Phe	Phe	Val	Ser	Ala	Gly	Tyr	Gln	Ile
			20					25					30		
Gly	Glu	Ala	Val	Gln	Met	Val	Lys	Asn	Thr	Gly	Glu	Leu	Lys	Asn	Leu
		35					40					45			
Asn	Asp	Lys	Tyr	Glu	Gln	Leu	Ser	Gln	Ser	Leu	Ala	Gln	Leu	Ala	Ser
	50					55					60				
Leu	Lys	Lys	Ser	Ile	Gln	Thr	Ala	Asn	Asn	Ile	Gln	Ala	Val	Asn	Asn
65					70					75					80
Ala	Leu	Ser	Asp	Leu	Lys	Ser	Phe	Ala	Ser	Asn	Asn	His	Thr	Asn	Lys
			85						90					95	
Glu	Thr	Ser	Pro	Ile	Tyr	Asn	Thr	Ala	Gln	Ala	Val	Ile	Thr	Ser	Val
			100					105					110		
Leu	Ala	Phe	Trp	Ser	Leu	Tyr	Ala	Gly	Asn	Ala	Leu	Ser	Phe	His	Val
		115					120					125			
Thr	Gly	Leu	Asn	Asp	Gly	Ser	Asn	Ser	Pro	Leu	Gly	Arg	Ile	His	Arg
	130				135						140				
Asp	Gly	Asn	Cys	Thr	Gly	Leu	Gln	Gln	Cys	Phe	Met	Ser	Lys	Glu	Thr
145					150					155					160
Tyr	Asp	Lys	Met	Lys	Thr	Leu	Ala	Glu	Asn	Leu	Gln	Lys	Ala	Gln	Gly
			165						170					175	
Asn	Leu	Cys	Ala	Leu	Ser	Glu	Cys	Ser	Ser	Asn	Gln	Ser	Asn	Gly	Gly
		180						185					190		
Lys	Thr	Ser	Met	Thr	Thr	Ala	Leu	Gln	Thr	Ala	Gln	Gln	Leu	Met	Asp
		195					200					205			
Leu	Ile	Glu	Gln	Thr	Lys	Val	Ser	Met	Val	Trp	Lys	Asn	Ile	Val	Ile
	210					215					220				
Ala	Gly	Val	Thr	Asn	Lys	Pro	Asn	Gly	Ala	Gly	Ala	Ile	Thr	Ser	Thr
225					230					235					240
Gly	His	Val	Thr	Asp	Tyr	Ala	Val	Phe	Asn	Asn	Ile	Lys	Ala	Met	Leu
			245						250					255	
Pro	Ile	Leu	Gln	Gln	Ala	Leu	Thr	Leu	Ser	Gln	Ser	Asn	His	Thr	Leu
		260						265					270		
Ser	Thr	Gln	Leu	Gln	Ala	Arg	Ala	Met	Gly	Ser	Gln	Thr	Asn	Arg	Glu
		275					280					285			
Phe	Ala	Lys	Asp	Ile	Tyr	Ala	Leu	Ala	Gln	Asn	Gln	Lys	Gln	Ile	Leu
	290					295					300				
Ser	Asn	Ala	Ser	Ser	Ile	Phe	Asn	Leu	Phe	Asn	Ser	Ile	Pro	Lys	Asp
305					310					315					320
Gln	Leu	Lys	Tyr	Leu	Glu	Asn	Ala	Tyr	Leu	Lys	Val	Pro	His	Leu	Gly
			325						330					335	
Lys	Thr	Pro	Thr	Asn	Pro	Tyr	Arg	Gln	Asn	Val	Asn	Leu	Asn	Lys	Glu
			340					345							

1109

Gln Ser Asn Leu Asn Gln Ala Leu Ala Ala Met Ser Asn Asn Pro Phe
 435 440 445
 Lys Lys Val Gly Met Ile Ser Ser Gln Asn Asn Asn Gly Ala Leu Asn
 450 455 460
 Gly Leu Gly Val Gln Val Gly Tyr Lys Gln Phe Phe Gly Glu Ser Lys
 465 470 475 480
 Arg Trp Gly Leu Arg Tyr Tyr Gly Phe Phe Asp Tyr Asn His Gly Tyr
 485 490 495
 Ile Lys Ser Ser Phe Phe Asn Ser Ser Ser Asp Ile Trp Thr Tyr Gly
 500 505 510
 Gly Gly Ser Asp Leu Leu Val Asn Phe Ile Asn Asp Ser Ile Thr Arg
 515 520 525
 Lys Asn Asn Lys Leu Ser Val Gly Leu Phe Gly Gly Ile Gln Leu Ala
 530 535 540
 Gly Thr Thr Trp Leu Asn Ser Gln Tyr Met Asn Leu Thr Ala Phe Asn
 545 550 555 560
 Asn Pro Tyr Ser Ala Lys Val Asn Ala Ser Asn Phe Gln Phe Leu Phe
 565 570 575
 Asn Leu Gly Leu Arg Thr Asn Leu Ala Thr Ala Lys Lys Lys Asp Ser
 580 585 590
 Glu Arg Ser Ala Gln His Gly Val Glu Leu Gly Ile Lys Ile Pro Thr
 595 600 605
 Ile Asn Thr Asn Tyr Tyr Ser Phe Leu Gly Thr Lys Leu Glu Tyr Arg
 610 615 620
 Arg Leu Tyr Ser Val Tyr Leu Asn Tyr Val Phe Ala Tyr
 625 630 635

1110

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CLAIMS

1. An isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* polypeptide selected from the group consisting of SEQ ID NO: 492-SEQ ID NO: 759, SEQ ID NO: 761, SEQ ID NO: 763, SEQ ID NO: 765-SEQ ID NO: 818, SEQ ID NO: 820-SEQ ID NO: 846, SEQ ID NO: 848-SEQ ID NO: 896, SEQ ID NO: 898-SEQ ID NO: 963, SEQ ID NO: 966-SEQ ID NO: 982, SEQ ID NO: 1037, SEQ ID NO: 1038, SEQ ID NO: 1041-SEQ ID NO: 1087, SEQ ID NO: 1090 and SEQ ID NO: 1296-SEQ ID NO: 1298.
2. A recombinant expression vector comprising the nucleic acid of claim 1 operably linked to a transcription regulatory element.
3. A cell comprising a recombinant expression vector of claim 2.
4. A method for producing an *H. pylori* polypeptide comprising culturing a cell of claim 3 under conditions that permit expression of the polypeptide.
5. A probe comprising a nucleotide sequence consisting of at least 8 nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274-SEQ ID NO: 327, SEQ ID NO: 329-SEQ ID NO: 364, SEQ ID NO: 366-SEQ ID NO: 405, SEQ ID NO: 407-SEQ ID NO: 472, SEQ ID NO: 475-SEQ ID NO: 491, SEQ ID NO: 983, SEQ ID NO: 984, SEQ ID NO: 987-SEQ ID NO: 1033, SEQ ID NO: 1036 and SEQ ID NO: 1293-SEQ ID NO: 1295 or the complement thereof.
6. An isolated nucleic acid comprising a nucleotide sequence of at least 8 nucleotides in length, wherein the sequence is hybridizable to a nucleic acid having a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274-SEQ ID NO: 327, SEQ ID NO: 329-SEQ ID NO: 364, SEQ ID NO: 366-SEQ ID NO: 405, SEQ ID NO: 407-SEQ ID NO: 472, SEQ ID NO: 475-SEQ ID NO: 491, SEQ ID NO: 983, SEQ ID NO: 984, SEQ ID NO: 987-SEQ ID NO: 1033, SEQ ID NO: 1036 and SEQ ID NO: 1293-SEQ ID NO: 1295 or the complement thereof.



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REPLACED SHEETS SG

- | | | |
|-------------------------------------|-------------|----------------------------|
| ☐ | Description | : paged 1110 to paged 1130 |
| ☒ | Claim(s) | : paged 1110 to paged 1130 |
| ☐ | Drawing(s) | : paged 1110 to paged 1130 |
| ☐ | Abstract | : paged 1110 to paged 1130 |



1111

7. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* polypeptide or a fragment thereof, said nucleic acid comprising a nucleotide sequence selected from the group consisting of
5 SEQ ID NO: 1-SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274-SEQ ID NO: 327, SEQ ID NO: 329-SEQ ID NO: 364, SEQ ID NO: 366-SEQ ID NO: 405, SEQ ID NO: 407-SEQ ID NO: 472, SEQ ID NO: 475-SEQ ID NO: 491, SEQ ID NO: 983, SEQ ID NO: 984, SEQ ID NO: 987-SEQ ID NO: 1033, SEQ ID NO: 1036 and SEQ ID NO: 1293-SEQ ID NO: 1295.

10

8. A vaccine composition of claim 7, further comprising a pharmaceutically acceptable carrier.

9. A vaccine composition of claim 8, wherein the pharmaceutically
15 acceptable carrier is an adjuvant.

10. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 7, such that treatment of *H. pylori* infection occurs.
20

11. A method of claim 10, wherein the treatment is a prophylactic treatment.

12. A method of claim 10, wherein the treatment is a therapeutic treatment.

13. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising:
25

- (a) contacting a sample with a probe of claim 5 under conditions in which a hybrid can form between the probe and a *Helicobacter* nucleic acid in the sample; and
30 (b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *Helicobacter* nucleic acid in the sample.

14. A recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of SEQ ID NO: 492-SEQ ID NO: 759,
35 SEQ ID NO: 761, SEQ ID NO: 763, SEQ ID NO: 765-SEQ ID NO: 818, SEQ ID NO: 820-SEQ ID NO: 846, SEQ ID NO: 848-SEQ ID NO: 896, SEQ ID NO: 898-SEQ ID



* C L H S *



1112

NO: 963, SEQ ID NO: 966-SEQ ID NO: 982, SEQ ID NO: 1037, SEQ ID NO: 1038, SEQ ID NO: 1041-SEQ ID NO: 1087, SEQ ID NO: 1090 and SEQ ID NO: 1296-SEQ ID NO: 1298.

5 15. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a purified *H. pylori* polypeptide or a fragment thereof, wherein said *H. pylori* polypeptide is selected from the group consisting of SEQ ID NO: 492-SEQ ID NO: 759, SEQ ID NO: 761, SEQ ID NO: 763, SEQ ID NO: 765-SEQ ID NO: 818, SEQ ID NO: 820-SEQ ID NO: 846, SEQ ID NO: 848-SEQ ID NO: 896, SEQ ID NO: 898-SEQ ID NO: 963, SEQ ID NO: 966-SEQ ID NO: 982, SEQ ID NO: 1037, SEQ ID NO: 1038, SEQ ID NO: 1041-SEQ ID NO: 1087, SEQ ID NO: 1090 and SEQ ID NO: 1296-SEQ ID NO: 1298.

15 16. A vaccine composition of claim 15, further comprising a pharmaceutically acceptable carrier.

 17. A vaccine composition of claim 16, wherein the pharmaceutically acceptable carrier is an adjuvant.

20 18. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 15, such that treatment of *H. pylori* infection occurs.

25 19. A method of claim 18, wherein the treatment is a prophylactic treatment.

 20. A method of claim 18, wherein the treatment is a therapeutic treatment.

30 21. An isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* cell envelope polypeptide or a fragment thereof, said nucleic acid selected from the group consisting of SEQ ID NO: 255, SEQ ID NO: 263, SEQ ID NO: 266, SEQ ID NO: 277, SEQ ID NO: 280, SEQ ID NO: 285, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 299, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 321, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 353, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 375, SEQ ID NO: 384, 35 SEQ ID NO: 391, SEQ ID NO: 392, SEQ ID NO: 397, SEQ ID NO: 398, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 409, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID





1113

NO: 427, SEQ ID NO: 433, SEQ ID NO: 434, SEQ ID NO: 441, SEQ ID NO: 444, SEQ
ID NO: 445, SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 453,
SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 983, SEQ ID NO:
989, SEQ ID NO: 1008, SEQ ID NO: 1011, SEQ ID NO: 1014, SEQ ID NO: 1015, SEQ
5 ID NO: 1029, SEQ ID NO: 1032, SEQ ID NO: 259, SEQ ID NO: 286, SEQ ID NO:
326, SEQ ID NO: 374, SEQ ID NO: 399, SEQ ID NO: 422, SEQ ID NO: 454, SEQ ID
NO: 465, SEQ ID NO: 998, SEQ ID NO: 1009, SEQ ID NO: 1023, SEQ ID NO: 1294,
SEQ ID NO: 1295, SEQ ID NO: 319, SEQ ID NO: 325, SEQ ID NO: 425, SEQ ID NO:
437, SEQ ID NO: 438, SEQ ID NO: 447, SEQ ID NO: 448, SEQ ID NO: 467, SEQ ID
10 NO: 996, SEQ ID NO: 1027, SEQ ID NO: 1031, SEQ ID NO: 254, SEQ ID NO: 352,
SEQ ID NO: 415, SEQ ID NO: 1019, SEQ ID NO: 381, SEQ ID NO: 389, SEQ ID NO:
1010, SEQ ID NO: 1012, SEQ ID NO: 354, SEQ ID NO: 372, SEQ ID NO: 400, SEQ
ID NO: 421, SEQ ID NO: 1022, SEQ ID NO: 463, SEQ ID NO: 281, SEQ ID NO: 988,
SEQ ID NO: 411, SEQ ID NO: 407, SEQ ID NO: 1017, SEQ ID NO: 290, SEQ ID NO:
15 417, SEQ ID NO: 430, SEQ ID NO: 992, SEQ ID NO: 1025, SEQ ID NO: 477, SEQ ID
NO: 414, SEQ ID NO: 253, SEQ ID NO: 293, SEQ ID NO: 334, SEQ ID NO: 343, SEQ
ID NO: 418, SEQ ID NO: 424, and SEQ ID NO: 443.

22. The purified nucleic acid of claim 21, wherein said *H. pylori* cell
20 envelope polypeptide or a fragment thereof is an *H. pylori* outer membrane polypeptide
or a fragment thereof encoded by the nucleic acid selected from the group consisting of
SEQ ID NO: 255, SEQ ID NO: 263, SEQ ID NO: 266, SEQ ID NO: 277, SEQ ID NO:
280, SEQ ID NO: 285, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 299, SEQ ID
NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 321, SEQ ID NO: 327, SEQ
25 ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 353, SEQ ID NO: 364, SEQ ID NO: 366,
SEQ ID NO: 368, SEQ ID NO: 375, SEQ ID NO: 384, SEQ ID NO: 391, SEQ ID NO:
392, SEQ ID NO: 397, SEQ ID NO: 398, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID
NO: 409, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 427, SEQ ID NO: 433, SEQ
ID NO: 434, SEQ ID NO: 441, SEQ ID NO: 444, SEQ ID NO: 445, SEQ ID NO: 449,
30 SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 453, SEQ ID NO: 466, SEQ ID NO:
468, SEQ ID NO: 469, SEQ ID NO: 983, SEQ ID NO: 989, SEQ ID NO: 1008, SEQ ID
NO: 1011, SEQ ID NO: 1014, SEQ ID NO: 1015, SEQ ID NO: 1029, SEQ ID NO:
1032, SEQ ID NO: 259, SEQ ID NO: 286, SEQ ID NO: 326, SEQ ID NO: 374, SEQ ID
NO: 399, SEQ ID NO: 422, SEQ ID NO: 454, SEQ ID NO: 465, SEQ ID NO: 998, SEQ
35 ID NO: 1009, SEQ ID NO: 1023, SEQ ID NO: 1294, SEQ ID NO: 1295, SEQ ID NO:
319, SEQ ID NO: 325, SEQ ID NO: 425, SEQ ID NO: 437, SEQ ID NO: 438, SEQ ID





1114

NO: 447, SEQ ID NO: 448, SEQ ID NO: 467, SEQ ID NO: 996, SEQ ID NO: 1027, SEQ ID NO: 1031, SEQ ID NO: 254, SEQ ID NO: 352, SEQ ID NO: 415, SEQ ID NO: 1019, SEQ ID NO: 381, SEQ ID NO: 389, SEQ ID NO: 1010, and SEQ ID NO: 1012.

5 23. he purified nucleic acid of claim 22, wherein said *H. pylori* outer
membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a
terminal phenylalanine residue or a fragment thereof encoded by the nucleic acid
selected from the group consisting of SEQ ID NO: 255, SEQ ID NO: 263, SEQ ID NO:
266, SEQ ID NO: 277, SEQ ID NO: 280, SEQ ID NO: 285, SEQ ID NO: 292, SEQ ID
10 NO: 294, SEQ ID NO: 299, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ
ID NO: 321, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 353,
SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 375, SEQ ID NO:
384, SEQ ID NO: 391, SEQ ID NO: 392, SEQ ID NO: 397, SEQ ID NO: 398, SEQ ID
NO: 402, SEQ ID NO: 404, SEQ ID NO: 409, SEQ ID NO: 410, SEQ ID NO: 412, SEQ
15 ID NO: 427, SEQ ID NO: 433, SEQ ID NO: 434, SEQ ID NO: 441, SEQ ID NO: 444,
SEQ ID NO: 445, SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO:
453, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 983, SEQ ID
NO: 989, SEQ ID NO: 1008, SEQ ID NO: 1011, SEQ ID NO: 1014, SEQ ID NO: 1015,
SEQ ID NO: 1029, and SEQ ID NO: 1032.

20

24. The purified nucleic acid of claim 22, wherein said *H. pylori* outer
membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a C-
terminal tyrosine cluster or a fragment thereof encoded by the nucleic acid selected from
the group consisting of SEQ ID NO: 286, SEQ ID NO: 326, SEQ ID NO: 374, SEQ ID
25 NO: 399, SEQ ID NO: 422, SEQ ID NO: 454, SEQ ID NO: 465, SEQ ID NO: 998, SEQ
ID NO: 1009, SEQ ID NO: 1023, SEQ ID NO: 1294, and SEQ ID NO: 1295.

25. The purified nucleic acid of claim 22, wherein said *H. pylori* outer
membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a
30 terminal phenylalanine residue and a C-terminal tyrosine cluster or a fragment thereof
encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 319,
SEQ ID NO: 325, SEQ ID NO: 425, SEQ ID NO: 437, SEQ ID NO: 438, SEQ ID NO:
447, SEQ ID NO: 448, SEQ ID NO: 467, SEQ ID NO: 996, SEQ ID NO: 1027, and
SEQ ID NO: 1031.

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1115

26. The purified nucleic acid of claim 21, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* inner membrane polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 354, SEQ ID NO: 372, SEQ ID NO: 400, SEQ ID NO: 421, SEQ ID NO: 1022, SEQ ID NO: 463, SEQ ID NO: 281, SEQ ID NO: 988, SEQ ID NO: 411, SEQ ID NO: 407, SEQ ID NO: 1017, SEQ ID NO: 290, SEQ ID NO: 417, SEQ ID NO: 430, SEQ ID NO: 992, and SEQ ID NO: 1025.

27. The purified nucleic acid of claim 26, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in outer membrane and cell wall synthesis or a fragment thereof encoded by the nucleic acid comprising a nucleotide sequence of SEQ ID NO: 354.

28. The purified nucleic acid of claim 26, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in energy conversion or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 372, SEQ ID NO: 400, SEQ ID NO: 421, and SEQ ID NO: 1022.

29. The purified nucleic acid of claim 26, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in cofactor metabolism or a fragment thereof encoded by the nucleic acid comprising a nucleotide sequence of SEQ ID NO: 463.

30. The purified nucleic acid of claim 26, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in secretion and adhesion or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 281 and SEQ ID NO: 988.

31. The purified nucleic acid of claim 26, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in transport or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 407 and SEQ ID NO: 1017.

32. The purified nucleic acid of claim 21, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* flagellar polypeptide or a





fragment thereof encoded by the nucleic acid comprising a nucleotide sequence of SEQ ID NO: 477.

33. The purified nucleic acid of claim 21, wherein said *H. pylori* cell
5 envelope polypeptide or a fragment thereof is an *H. pylori* transport polypeptide or a fragment thereof encoded by the nucleic acid comprising a nucleotide sequence of SEQ ID NO: 414.

34. A recombinant expression vector comprising the nucleic acid of claim 21
10 operably linked to a transcription regulatory element.

35. A cell comprising a recombinant expression vector of claim 34.

36. A method for producing an *H. pylori* polypeptide comprising culturing a
15 cell of claim 35 under conditions that permit expression of the polypeptide.

37. An isolated nucleic acid comprising a nucleotide sequence encoding an
H. pylori secreted polypeptide or a fragment thereof, said nucleic acid selected from the group consisting of SEQ ID NO: 355, SEQ ID NO: 1006, SEQ ID NO: 257, SEQ ID
20 NO: 258, SEQ ID NO: 260, SEQ ID NO: 261, SEQ ID NO: 264, SEQ ID NO: 265, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 275, SEQ ID NO: 276, SEQ ID NO: 279, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 301, SEQ
25 ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 323, SEQ ID NO: 338, SEQ ID NO: 342, SEQ ID NO: 348, SEQ ID NO: 349, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 359, SEQ ID NO: 360, SEQ ID NO: 361, SEQ ID NO: 362, SEQ ID NO: 363, SEQ ID NO: 367, SEQ ID NO: 370, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 377, SEQ ID NO: 378, SEQ ID NO: 379, SEQ ID NO: 380, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 394, SEQ ID NO: 395, SEQ ID NO: 396, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 408, SEQ ID NO: 420, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 429, SEQ ID NO: 432, SEQ ID NO: 439, SEQ ID NO: 442, SEQ ID NO: 451, SEQ ID NO: 471, SEQ ID NO: 478, SEQ ID NO: 488, SEQ ID NO: 987, SEQ ID NO: 990, SEQ ID NO: 991, SEQ ID NO: 993, SEQ ID NO: 1001, SEQ ID NO: 1002, SEQ
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1117

ID NO: 1007, SEQ ID NO: 1013, SEQ ID NO: 1016, SEQ ID NO: 1018, SEQ ID NO: 1021, and SEQ ID NO: 1026.

38. The purified nucleic acid of claim 37, wherein said *H. pylori* secreted polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in secretion and adhesion or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 355 and SEQ ID NO: 1006.

39. A recombinant expression vector comprising the nucleic acid of claim 38 operably linked to a transcription regulatory element.

40. A cell comprising a recombinant expression vector of claim 39.

41. A method for producing an *H. pylori* polypeptide comprising culturing a cell of claim 40 under conditions that permit expression of the polypeptide.

42. An isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* cytoplasmic polypeptide or a fragment thereof, said nucleic acid selected from the group consisting of SEQ ID NO: 470, SEQ ID NO: 1033, SEQ ID NO: 357, SEQ ID NO: 457, SEQ ID NO: 461, SEQ ID NO: 1030, SEQ ID NO: 345, SEQ ID NO: 383, SEQ ID NO: 387, SEQ ID NO: 455, SEQ ID NO: 1003, SEQ ID NO: 351, SEQ ID NO: 416, SEQ ID NO: 278, SEQ ID NO: 335, SEQ ID NO: 346, SEQ ID NO: 350, SEQ ID NO: 419, SEQ ID NO: 460, SEQ ID NO: 472, SEQ ID NO: 1000, SEQ ID NO: 1004, SEQ ID NO: 1020, SEQ ID NO: 1293, SEQ ID NO: 318, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 330, SEQ ID NO: 347, SEQ ID NO: 440, SEQ ID NO: 446, SEQ ID NO: 464, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 995, SEQ ID NO: 997, SEQ ID NO: 1005, SEQ ID NO: 1028.

43. The purified nucleic acid of claim 42, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in energy conversion or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 470 and SEQ ID NO: 1033.

44. The purified nucleic acid of claim 42, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in amino acid

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metabolism and transport or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 357 and SEQ ID NO: 457.

5 45. The purified nucleic acid of claim 42, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in nucleotide metabolism and transport or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 461 and SEQ ID NO: 1030.

10 46. The purified nucleic acid of claim 42, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in cofactor metabolism or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 345, SEQ ID NO: 383, SEQ ID NO: 387, SEQ ID NO: 455, and SEQ ID NO: 1003.

15 47. The purified nucleic acid of claim 42, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in lipid metabolism or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 351 and SEQ ID NO: 416.

20 48. The purified nucleic acid of claim 42, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in genome replication, transcription, recombination and repair or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 278, SEQ ID NO: 335, SEQ ID NO: 346, SEQ ID NO: 350, SEQ ID NO: 419, SEQ ID NO: 460, SEQ ID NO:
25 472, SEQ ID NO: 1000, SEQ ID NO: 1004, SEQ ID NO: 1020, and SEQ ID NO: 1293.

 49. A recombinant expression vector comprising the nucleic acid of claim 42 operably linked to a transcription regulatory element.

30 50. A cell comprising a recombinant expression vector of claim 49.

 51. A method for producing an *H. pylori* polypeptide comprising culturing a cell of claim 50 under conditions that permit expression of the polypeptide.

35 52. An isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* cellular polypeptide or a fragment thereof, said nucleic acid selected from the





group consisting of SEQ ID NO: 256, SEQ ID NO: 267, SEQ ID NO: 282, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 332, SEQ ID NO: 333, SEQ ID NO: 336, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 340, SEQ ID NO: 341, SEQ ID NO: 344,
5 SEQ ID NO: 369, SEQ ID NO: 376, SEQ ID NO: 382, SEQ ID NO: 386, SEQ ID NO: 423, SEQ ID NO: 431, SEQ ID NO: 435, SEQ ID NO: 436, SEQ ID NO: 458, SEQ ID NO: 462, SEQ ID NO: 475, SEQ ID NO: 476, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 984, SEQ ID NO: 994, SEQ ID NO: 1024, and SEQ ID NO: 1036.

53. A recombinant expression vector comprising the nucleic acid of claim 52 operably linked to a transcription regulatory element.

15 54. A cell comprising a recombinant expression vector of claim 53.

55. A method for producing an *H. pylori* polypeptide comprising culturing a cell of claim 54 under conditions that permit expression of the polypeptide.

20 56. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a nucleic acid of claim 21.

57. A vaccine composition of claim 56, further comprising a pharmaceutically acceptable carrier.

25 58. A vaccine composition of claim 57, wherein the pharmaceutically acceptable carrier is an adjuvant.

30 59. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 56, such that treatment of *H. pylori* infection occurs.

60. A method of claim 59, wherein the treatment is a prophylactic treatment.

35 61. A method of claim 59, wherein the treatment is a therapeutic treatment.





62. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a nucleic acid of claim 37.

5 63. A vaccine composition of claim 62, further comprising a pharmaceutically acceptable carrier.

64. A vaccine composition of claim 63, wherein the pharmaceutically acceptable carrier is an adjuvant.

10 65. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 62, such that treatment of *H. pylori* infection occurs.

15 66. A method of claim 65, wherein the treatment is a prophylactic treatment.

67. A method of claim 65, wherein the treatment is a therapeutic treatment.

20 68. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a nucleic acid of claim 42.

69. A vaccine composition of claim 68, further comprising a pharmaceutically acceptable carrier.

25 70. A vaccine composition of claim 69, wherein the pharmaceutically acceptable carrier is an adjuvant.

30 71. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 68, such that treatment of *H. pylori* infection occurs.

72. A method of claim 71, wherein the treatment is a prophylactic treatment.

73. A method of claim 71, wherein the treatment is a therapeutic treatment.

35 74. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a nucleic acid of claim 52.





1121

75. A vaccine composition of claim 74, further comprising a pharmaceutically acceptable carrier.

5 76. A vaccine composition of claim 75, wherein the pharmaceutically acceptable carrier is an adjuvant.

77. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 74, such that treatment of *H.*
10 *pylori* infection occurs.

78. A method of claim 77, wherein the treatment is a prophylactic treatment.

79. A method of claim 77, wherein the treatment is a therapeutic treatment.
15

80. A purified *H. pylori* cell envelope polypeptide or a fragment thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 746, SEQ ID NO: 754, SEQ ID NO: 757, SEQ ID NO: 768, SEQ ID NO: 771, SEQ ID NO: 776, SEQ ID NO: 783, SEQ ID NO: 785, SEQ ID NO: 790, SEQ ID NO: 802, SEQ ID
20 NO: 803, SEQ ID NO: 804, SEQ ID NO: 812, SEQ ID NO: 818, SEQ ID NO: 820, SEQ ID NO: 882, SEQ ID NO: 844, SEQ ID NO: 855, SEQ ID NO: 857, SEQ ID NO: 859, SEQ ID NO: 866, SEQ ID NO: 875, SEQ ID NO: 882, SEQ ID NO: 883, SEQ ID NO: 888, SEQ ID NO: 889, SEQ ID NO: 893, SEQ ID NO: 895, SEQ ID NO: 900, SEQ ID NO: 901, SEQ ID NO: 903, SEQ ID NO: 918, SEQ ID NO: 924, SEQ ID NO: 925, SEQ
25 ID NO: 932, SEQ ID NO: 935, SEQ ID NO: 936, SEQ ID NO: 940, SEQ ID NO: 941, SEQ ID NO: 943, SEQ ID NO: 944, SEQ ID NO: 957, SEQ ID NO: 959, SEQ ID NO: 960, SEQ ID NO: 1037, SEQ ID NO: 1043, SEQ ID NO: 1062, SEQ ID NO: 1065, SEQ ID NO: 1068, SEQ ID NO: 1069, SEQ ID NO: 1083, SEQ ID NO: 1086, SEQ ID NO: 750, SEQ ID NO: 777, SEQ ID NO: 817, SEQ ID NO: 865, SEQ ID NO: 890, SEQ ID
30 NO: 913, SEQ ID NO: 945, SEQ ID NO: 956, SEQ ID NO: 1052, SEQ ID NO: 1063, SEQ ID NO: 1077, SEQ ID NO: 1297, SEQ ID NO: 1298, SEQ ID NO: 810, SEQ ID NO: 816, SEQ ID NO: 916, SEQ ID NO: 928, SEQ ID NO: 929, SEQ ID NO: 938, SEQ ID NO: 939, SEQ ID NO: 958, SEQ ID NO: 1050, SEQ ID NO: 1081, SEQ ID NO: 1085, SEQ ID NO: 745, SEQ ID NO: 843, SEQ ID NO: 906, SEQ ID NO: 1073, SEQ
35 ID NO: 872, SEQ ID NO: 880, SEQ ID NO: 1064, SEQ ID NO: 1066, SEQ ID NO: 845, SEQ ID NO: 863, SEQ ID NO: 891, SEQ ID NO: 912, SEQ ID NO: 1076, SEQ ID



* C L M S *



NO: 954, SEQ ID NO: 772, SEQ ID NO: 1042, SEQ ID NO: 902, SEQ ID NO: 898,
SEQ ID NO: 1071, SEQ ID NO: 781, SEQ ID NO: 908, SEQ ID NO: 921, SEQ ID NO:
1046, SEQ ID NO: 1079, SEQ ID NO: 968, SEQ ID NO: 905, SEQ ID NO: 744, SEQ
ID NO: 784, SEQ ID NO: 825, SEQ ID NO: 834, SEQ ID NO: 909, SEQ ID NO: 915,
5 and SEQ ID NO: 934.

81. The purified polypeptide of claim 80, wherein said *H. pylori* cell
envelope polypeptide or a fragment thereof is an *H. pylori* outer membrane polypeptide
or a fragment thereof selected from the group consisting of SEQ ID NO: 746, SEQ ID
10 NO: 754, SEQ ID NO: 757, SEQ ID NO: 768, SEQ ID NO: 771, SEQ ID NO: 776, SEQ
ID NO: 783, SEQ ID NO: 785, SEQ ID NO: 790, SEQ ID NO: 802, SEQ ID NO: 803,
SEQ ID NO: 804, SEQ ID NO: 812, SEQ ID NO: 818, SEQ ID NO: 820, SEQ ID NO:
882, SEQ ID NO: 844, SEQ ID NO: 855, SEQ ID NO: 857, SEQ ID NO: 859, SEQ ID
NO: 866, SEQ ID NO: 875, SEQ ID NO: 882, SEQ ID NO: 883, SEQ ID NO: 888, SEQ
15 ID NO: 889, SEQ ID NO: 893, SEQ ID NO: 895, SEQ ID NO: 900, SEQ ID NO: 901,
SEQ ID NO: 903, SEQ ID NO: 918, SEQ ID NO: 924, SEQ ID NO: 925, SEQ ID NO:
932, SEQ ID NO: 935, SEQ ID NO: 936, SEQ ID NO: 940, SEQ ID NO: 941, SEQ ID
NO: 943, SEQ ID NO: 944, SEQ ID NO: 957, SEQ ID NO: 959, SEQ ID NO: 960, SEQ
ID NO: 1037, SEQ ID NO: 1043, SEQ ID NO: 1062, SEQ ID NO: 1065, SEQ ID NO:
20 1068, SEQ ID NO: 1069, SEQ ID NO: 1083, SEQ ID NO: 1086, SEQ ID NO: 750, SEQ
ID NO: 777, SEQ ID NO: 817, SEQ ID NO: 865, SEQ ID NO: 890, SEQ ID NO: 913,
SEQ ID NO: 945, SEQ ID NO: 956, SEQ ID NO: 1052, SEQ ID NO: 1063, SEQ ID
NO: 1077, SEQ ID NO: 1297, SEQ ID NO: 1298, SEQ ID NO: 810, SEQ ID NO: 816,
SEQ ID NO: 916, SEQ ID NO: 928, SEQ ID NO: 929, SEQ ID NO: 938, SEQ ID NO:
25 939, SEQ ID NO: 958, SEQ ID NO: 1050, SEQ ID NO: 1081, SEQ ID NO: 1085, SEQ
ID NO: 745, SEQ ID NO: 843, SEQ ID NO: 906, SEQ ID NO: 1073, SEQ ID NO: 872,
SEQ ID NO: 880, SEQ ID NO: 1064, and SEQ ID NO: 1066.

82. The purified polypeptide of claim 81, wherein said *H. pylori* outer
30 membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a
terminal phenylalanine residue or a fragment thereof selected from the group consisting
of SEQ ID NO: 746, SEQ ID NO: 754, SEQ ID NO: 757, SEQ ID NO: 768, SEQ ID
NO: 771, SEQ ID NO: 776, SEQ ID NO: 783, SEQ ID NO: 785, SEQ ID NO: 790, SEQ
ID NO: 802, SEQ ID NO: 803, SEQ ID NO: 804, SEQ ID NO: 812, SEQ ID NO: 818,
35 SEQ ID NO: 820, SEQ ID NO: 882, SEQ ID NO: 844, SEQ ID NO: 855, SEQ ID NO:
857, SEQ ID NO: 859, SEQ ID NO: 866, SEQ ID NO: 875, SEQ ID NO: 882, SEQ ID





NO: 883, SEQ ID NO: 888, SEQ ID NO: 889, SEQ ID NO: 893, SEQ ID NO: 895, SEQ ID NO: 900, SEQ ID NO: 901, SEQ ID NO: 903, SEQ ID NO: 918, SEQ ID NO: 924, SEQ ID NO: 925, SEQ ID NO: 932, SEQ ID NO: 935, SEQ ID NO: 936, SEQ ID NO: 940, SEQ ID NO: 941, SEQ ID NO: 943, SEQ ID NO: 944, SEQ ID NO: 957, SEQ ID NO: 959, SEQ ID NO: 960, SEQ ID NO: 1037, SEQ ID NO: 1043, SEQ ID NO: 1062, SEQ ID NO: 1065, SEQ ID NO: 1068, SEQ ID NO: 1069, SEQ ID NO: 1083, and SEQ ID NO: 1086.

83. The purified polypeptide of claim 81, wherein said *H. pylori* outer membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide a C-terminal tyrosine cluster or a fragment thereof selected from the group consisting of SEQ ID NO: 746, SEQ ID NO: 754, SEQ ID NO: 757, SEQ ID NO: 768, SEQ ID NO: 771, SEQ ID NO: 776, SEQ ID NO: 783, SEQ ID NO: 785, SEQ ID NO: 790, SEQ ID NO: 802, SEQ ID NO: 803, SEQ ID NO: 804, SEQ ID NO: 812, SEQ ID NO: 818, SEQ ID NO: 820, SEQ ID NO: 882, SEQ ID NO: 844, SEQ ID NO: 855, SEQ ID NO: 857, SEQ ID NO: 859, SEQ ID NO: 866, SEQ ID NO: 875, SEQ ID NO: 882, SEQ ID NO: 883, SEQ ID NO: 888, SEQ ID NO: 889, SEQ ID NO: 893, SEQ ID NO: 895, SEQ ID NO: 900, SEQ ID NO: 901, SEQ ID NO: 903, SEQ ID NO: 918, SEQ ID NO: 924, SEQ ID NO: 925, SEQ ID NO: 932, SEQ ID NO: 935, SEQ ID NO: 936, SEQ ID NO: 940, SEQ ID NO: 941, SEQ ID NO: 943, SEQ ID NO: 944, SEQ ID NO: 957, SEQ ID NO: 959, SEQ ID NO: 960, SEQ ID NO: 1037, SEQ ID NO: 1043, SEQ ID NO: 1062, SEQ ID NO: 1065, SEQ ID NO: 1068, SEQ ID NO: 1069, SEQ ID NO: 1083, and SEQ ID NO: 1086.

84. The purified polypeptide of claim 81, wherein said *H. pylori* outer membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a terminal phenylalanine residue and a C-terminal tyrosine cluster or a fragment thereof selected from the group consisting of SEQ ID NO: 810, SEQ ID NO: 816, SEQ ID NO: 916, SEQ ID NO: 928, SEQ ID NO: 929, SEQ ID NO: 938, SEQ ID NO: 939, SEQ ID NO: 958, SEQ ID NO: 1050, SEQ ID NO: 1081, and SEQ ID NO: 1085.

85. The purified polypeptide of claim 80, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* inner membrane polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 845, SEQ ID NO: 863, SEQ ID NO: 891, SEQ ID NO: 912, SEQ ID NO: 1076, SEQ ID NO: 954, SEQ ID NO: 772, SEQ ID NO: 1042, SEQ ID NO: 902, SEQ ID NO: 898, SEQ ID NO:





1071, SEQ ID NO: 781, SEQ ID NO: 908, SEQ ID NO: 921, SEQ ID NO: 1046, SEQ ID NO: 1079.

86. The purified polypeptide of claim 85, wherein said *H. pylori* inner
5 membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in outer membrane and cell wall synthesis or a fragment thereof comprising an amino acid sequence of SEQ ID NO: 845.

87. The purified polypeptide of claim 85, wherein said *H. pylori* inner
10 membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in energy conversion or a fragment thereof selected from the group consisting of SEQ ID NO: 863, SEQ ID NO: 891, SEQ ID NO: 912, and SEQ ID NO: 1076.

88. The purified polypeptide of claim 85, wherein said *H. pylori* inner
15 membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in cofactor metabolism or a fragment thereof comprising an amino acid sequence of SEQ ID NO: 954.

89. The purified polypeptide of claim 85, wherein said *H. pylori* inner
20 membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in secretion and adhesion or a fragment thereof selected from the group consisting of SEQ ID NO: 772 and SEQ ID NO: 1042.

90. The purified polypeptide of claim 85, wherein said *H. pylori* inner
25 membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in transport or a fragment thereof selected from the group consisting of SEQ ID NO: 898 and SEQ ID NO: 1071.

91. The purified polypeptide of claim 80, wherein said *H. pylori* cell
30 envelope polypeptide or a fragment thereof is an *H. pylori* flagellar polypeptide or a fragment thereof comprising an amino acid sequence of SEQ ID NO: 968.

92. The purified polypeptide of claim 80, wherein said *H. pylori* cell
35 envelope polypeptide or a fragment thereof is an *H. pylori* transport polypeptide or a fragment thereof comprising an amino acid sequence of SEQ ID NO: 905.





93. A purified *H. pylori* cellular polypeptide or a fragment thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 747, SEQ ID NO: 758, SEQ ID NO: 773, SEQ ID NO: 797, SEQ ID NO: 798, SEQ ID NO: 799, SEQ ID NO: 800, SEQ ID NO: 801, SEQ ID NO: 807, SEQ ID NO: 808, SEQ ID NO: 823, SEQ ID NO: 824, SEQ ID NO: 827, SEQ ID NO: 828, SEQ ID NO: 830, SEQ ID NO: 831, SEQ ID NO: 832, SEQ ID NO: 835, SEQ ID NO: 860, SEQ ID NO: 867, SEQ ID NO: 873, SEQ ID NO: 877, SEQ ID NO: 914, SEQ ID NO: 922, SEQ ID NO: 926, SEQ ID NO: 927, SEQ ID NO: 949, SEQ ID NO: 953, SEQ ID NO: 966, SEQ ID NO: 967, SEQ ID NO: 970, SEQ ID NO: 971, SEQ ID NO: 972, SEQ ID NO: 973, SEQ ID NO: 974, SEQ ID NO: 975, SEQ ID NO: 976, SEQ ID NO: 977, SEQ ID NO: 978, SEQ ID NO: 980, SEQ ID NO: 1038, SEQ ID NO: 1048, SEQ ID NO: 1078, and SEQ ID NO: 1090.

94. A purified *H. pylori* secreted polypeptide or a fragment thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 846, SEQ ID NO: 1060, SEQ ID NO: 748, SEQ ID NO: 749, SEQ ID NO: 751, SEQ ID NO: 752, SEQ ID NO: 755, SEQ ID NO: 756, SEQ ID NO: 759, SEQ ID NO: 761, SEQ ID NO: 763, SEQ ID NO: 765, SEQ ID NO: 766, SEQ ID NO: 767, SEQ ID NO: 770, SEQ ID NO: 774, SEQ ID NO: 775, SEQ ID NO: 778, SEQ ID NO: 779, SEQ ID NO: 780, SEQ ID NO: 782, SEQ ID NO: 786, SEQ ID NO: 787, SEQ ID NO: 788, SEQ ID NO: 789, SEQ ID NO: 791, SEQ ID NO: 792, SEQ ID NO: 793, SEQ ID NO: 794, SEQ ID NO: 795, SEQ ID NO: 796, SEQ ID NO: 805, SEQ ID NO: 806, SEQ ID NO: 814, SEQ ID NO: 829, SEQ ID NO: 833, SEQ ID NO: 839, SEQ ID NO: 840, SEQ ID NO: 849, SEQ ID NO: 850, SEQ ID NO: 851, SEQ ID NO: 852, SEQ ID NO: 853, SEQ ID NO: 854, SEQ ID NO: 858, SEQ ID NO: 861, SEQ ID NO: 862, SEQ ID NO: 864, SEQ ID NO: 868, SEQ ID NO: 869, SEQ ID NO: 870, SEQ ID NO: 871, SEQ ID NO: 879, SEQ ID NO: 881, SEQ ID NO: 885, SEQ ID NO: 886, SEQ ID NO: 887, SEQ ID NO: 892, SEQ ID NO: 894, SEQ ID NO: 896, SEQ ID NO: 899, SEQ ID NO: 911, SEQ ID NO: 917, SEQ ID NO: 919, SEQ ID NO: 920, SEQ ID NO: 923, SEQ ID NO: 930, SEQ ID NO: 933, SEQ ID NO: 942, SEQ ID NO: 962, SEQ ID NO: 969, SEQ ID NO: 979, SEQ ID NO: 1041, SEQ ID NO: 1044, SEQ ID NO: 1045, SEQ ID NO: 1047, SEQ ID NO: 1055, SEQ ID NO: 1056, SEQ ID NO: 1061, SEQ ID NO: 1067, SEQ ID NO: 1070, SEQ ID NO: 1072, SEQ ID NO: 1075, and SEQ ID NO: 1080.

95. The purified polypeptide of claim 94, wherein said *H. pylori* secreted polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in secretion and





adhesion or a fragment thereof selected from the group consisting of SEQ ID NO: 846 and SEQ ID NO: 1060.

- 5 96. A purified *H. pylori* cytoplasmic polypeptide or a fragment thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 961, SEQ ID NO: 1087, SEQ ID NO: 848, SEQ ID NO: 948, SEQ ID NO: 952, SEQ ID NO: 1084, SEQ ID NO: 836, SEQ ID NO: 874, SEQ ID NO: 878, SEQ ID NO: 946, SEQ ID NO: 1057, SEQ ID NO: 842, SEQ ID NO: 907, SEQ ID NO: 769, SEQ ID NO: 826, SEQ ID NO: 837, SEQ ID NO: 841, SEQ ID NO: 910, SEQ ID NO: 951, SEQ ID NO: 10 963, SEQ ID NO: 1054, SEQ ID NO: 1058, SEQ ID NO: 1074, SEQ ID NO: 1296, SEQ ID NO: 809, SEQ ID NO: 813, SEQ ID NO: 815, SEQ ID NO: 821, SEQ ID NO: 838, SEQ ID NO: 931, SEQ ID NO: 937, SEQ ID NO: 955, SEQ ID NO: 981, SEQ ID NO: 982, SEQ ID NO: 1049, SEQ ID NO: 1051, SEQ ID NO: 1059, and SEQ ID NO: 1082.
- 15 97. The purified polypeptide of claim 96, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in energy conversion or a fragment thereof selected from the group consisting of SEQ ID NO: 961 and SEQ ID NO: 1087.
- 20 98. The purified polypeptide of claim 96, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in amino acid metabolism and transport or a fragment thereof selected from the group consisting of SEQ ID NO: 848 and SEQ ID NO: 948.
- 25 99. The purified polypeptide of claim 96, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in nucleotide metabolism and transport or a fragment thereof selected from the group consisting of SEQ ID NO: 952 and SEQ ID NO: 1084.
- 30 100. The purified polypeptide of claim 96, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in cofactor metabolism or a fragment thereof selected from the group consisting of SEQ ID NO: 836, SEQ ID NO: 874, SEQ ID NO: 878, SEQ ID NO: 946, and SEQ ID NO: 1057.
- 35 101. The purified polypeptide of claim 96, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in lipid





metabolism or a fragment thereof selected from the group consisting of SEQ ID NO: 842 and SEQ ID NO: 907.

102. The purified polypeptide of claim 96, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in genome replication, transcription, recombination and repair or a fragment thereof selected from the group consisting of SEQ ID NO: 769, SEQ ID NO: 826, SEQ ID NO: 837, SEQ ID NO: 841, SEQ ID NO: 910, SEQ ID NO: 951, SEQ ID NO: 963, SEQ ID NO: 1054, SEQ ID NO: 1058, SEQ ID NO: 1074, and SEQ ID NO: 1296.

10

103. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 80.

104. A vaccine composition of claim 103, further comprising a pharmaceutically acceptable carrier.

15

105. A vaccine composition of claim 104, wherein the pharmaceutically acceptable carrier is an adjuvant.

106. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 103, such that treatment of *H. pylori* infection occurs.

20

107. A method of claim 106, wherein the treatment is a prophylactic treatment.

25

108. A method of claim 106, wherein the treatment is a therapeutic treatment.

109. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 93.

30

110. A vaccine composition of claim 109, further comprising a pharmaceutically acceptable carrier.

111. A vaccine composition of claim 110, wherein the pharmaceutically acceptable carrier is an adjuvant.

35





112. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 109, such that treatment of *H. pylori* infection occurs.

5

113. A method of claim 112, wherein the treatment is a prophylactic treatment.

114. A method of claim 112, wherein the treatment is a therapeutic treatment.

10

115. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 94.

116. A vaccine composition of claim 115, further comprising a pharmaceutically acceptable carrier.

15

117. A vaccine composition of claim 116, wherein the pharmaceutically acceptable carrier is an adjuvant.

118. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 115, such that treatment of *H. pylori* infection occurs.

20

119. A method of claim 118, wherein the treatment is a prophylactic treatment.

25

120. A method of claim 118, wherein the treatment is a therapeutic treatment.

121. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 96.

30

122. A vaccine composition of claim 121, further comprising a pharmaceutically acceptable carrier.

123. A vaccine composition of claim 122, wherein the pharmaceutically acceptable carrier is an adjuvant.

35

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124. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 121, such that treatment of *H. pylori* infection occurs.

5

125. A method of claim 124, wherein the treatment is a prophylactic treatment.

126. A method of claim 124, wherein the treatment is a therapeutic treatment.

10

127. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising:

(a) contacting a sample with a nucleic acid of claim 21 under conditions in which a hybrid can form between the probe and a *Helicobacter* nucleic acid in the sample; and

15

(b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *Helicobacter* nucleic acid in the sample.

128. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising:

20

(a) contacting a sample with a nucleic acid of claim 37 under conditions in which a hybrid can form between the probe and a *Helicobacter* nucleic acid in the sample; and

(b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *Helicobacter* nucleic acid in the sample.

25

129. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising:

(a) contacting a sample with a nucleic acid of claim 42 under conditions in which a hybrid can form between the probe and a *Helicobacter* nucleic acid in the sample; and

30

(b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *Helicobacter* nucleic acid in the sample.



130. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising:

- (a) contacting a sample with a nucleic acid of claim 52 under conditions in which a hybrid can form between the probe and a *Helicobacter* nucleic acid in the sample; and
- (b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *Helicobacter* nucleic acid in the sample.

1/10

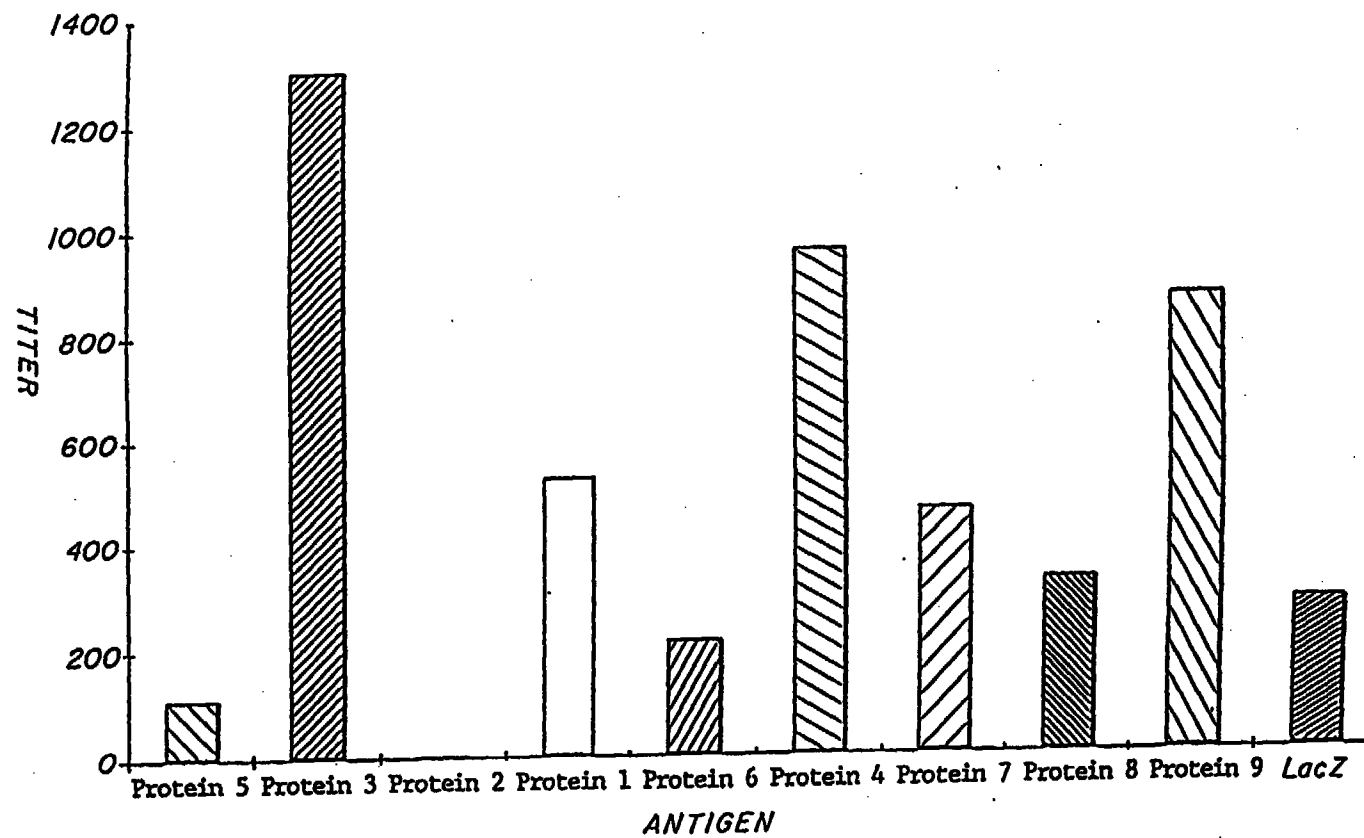


FIGURE 1

2/10

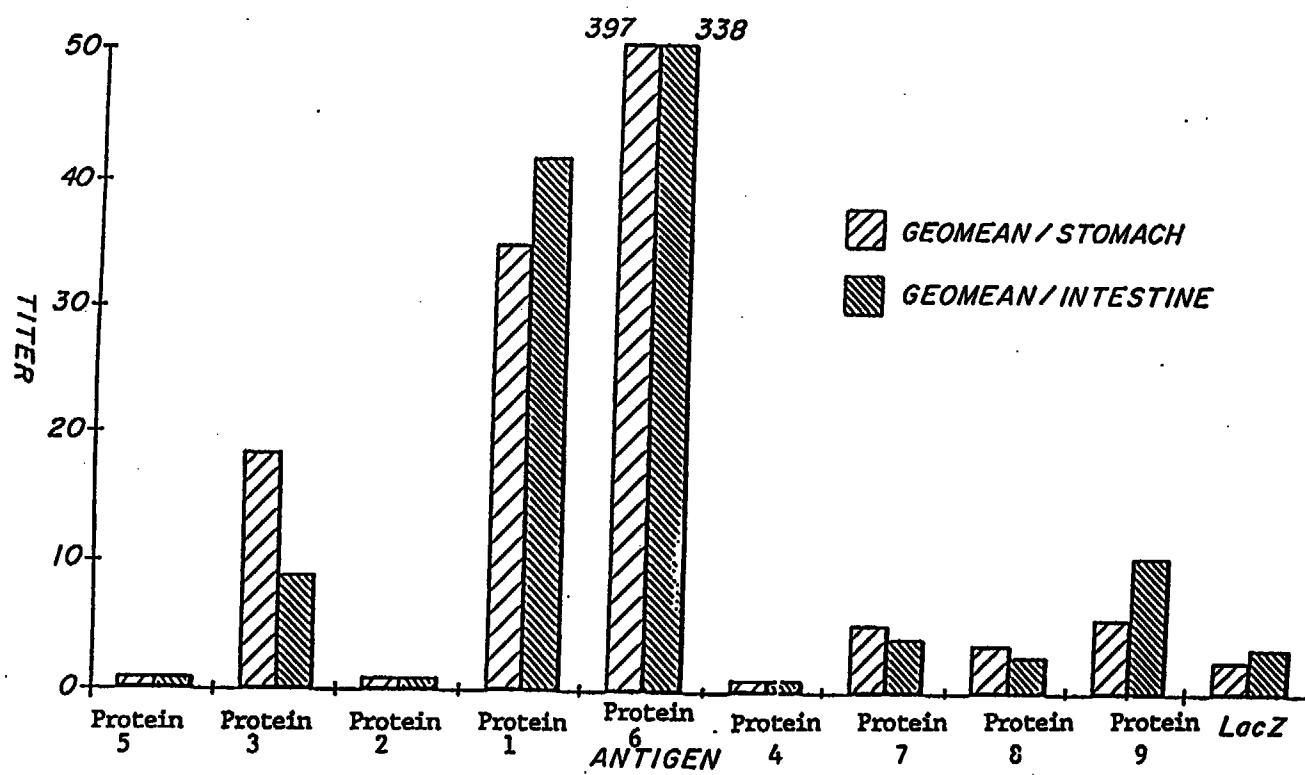


FIGURE 2

3/10

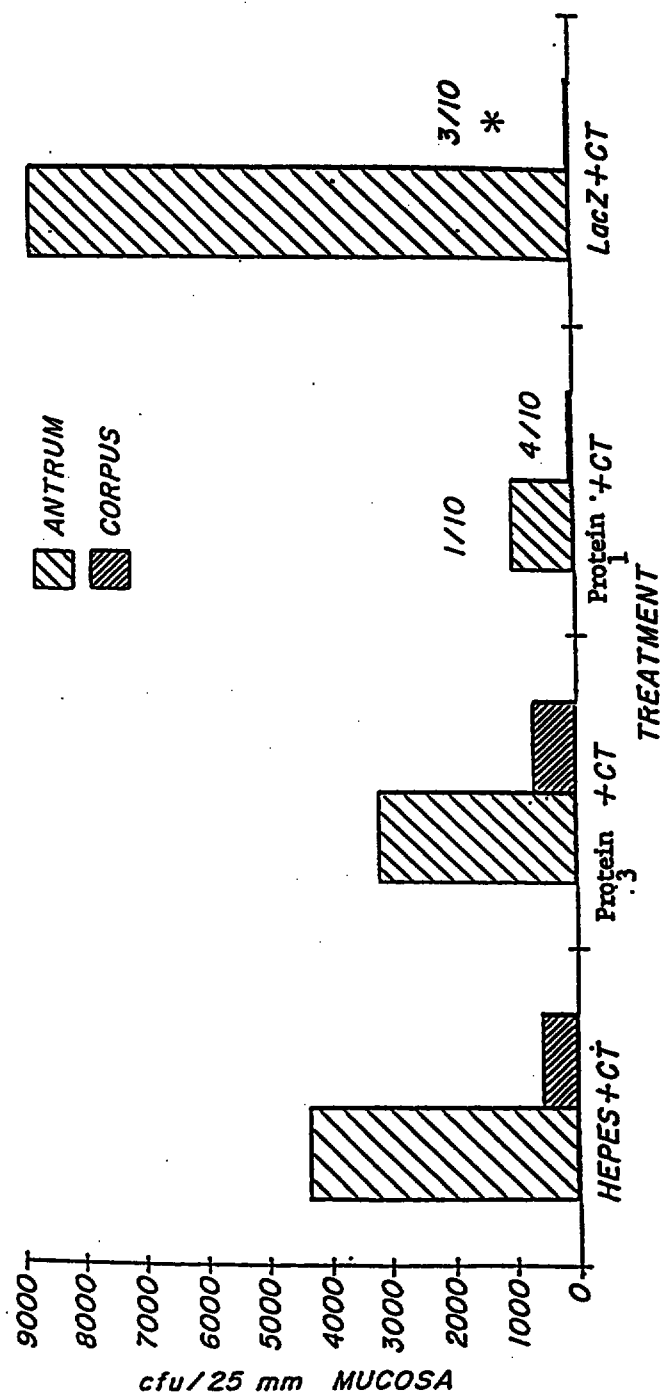


FIGURE 3

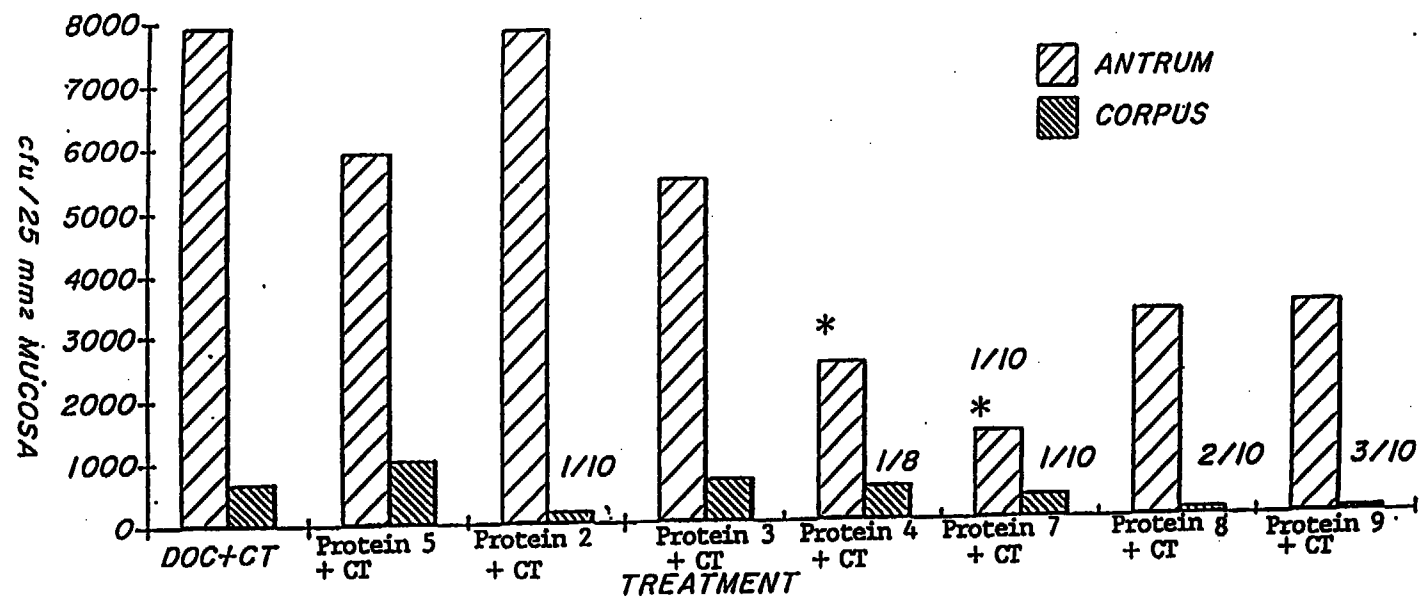


FIGURE 4

4/10

5/10

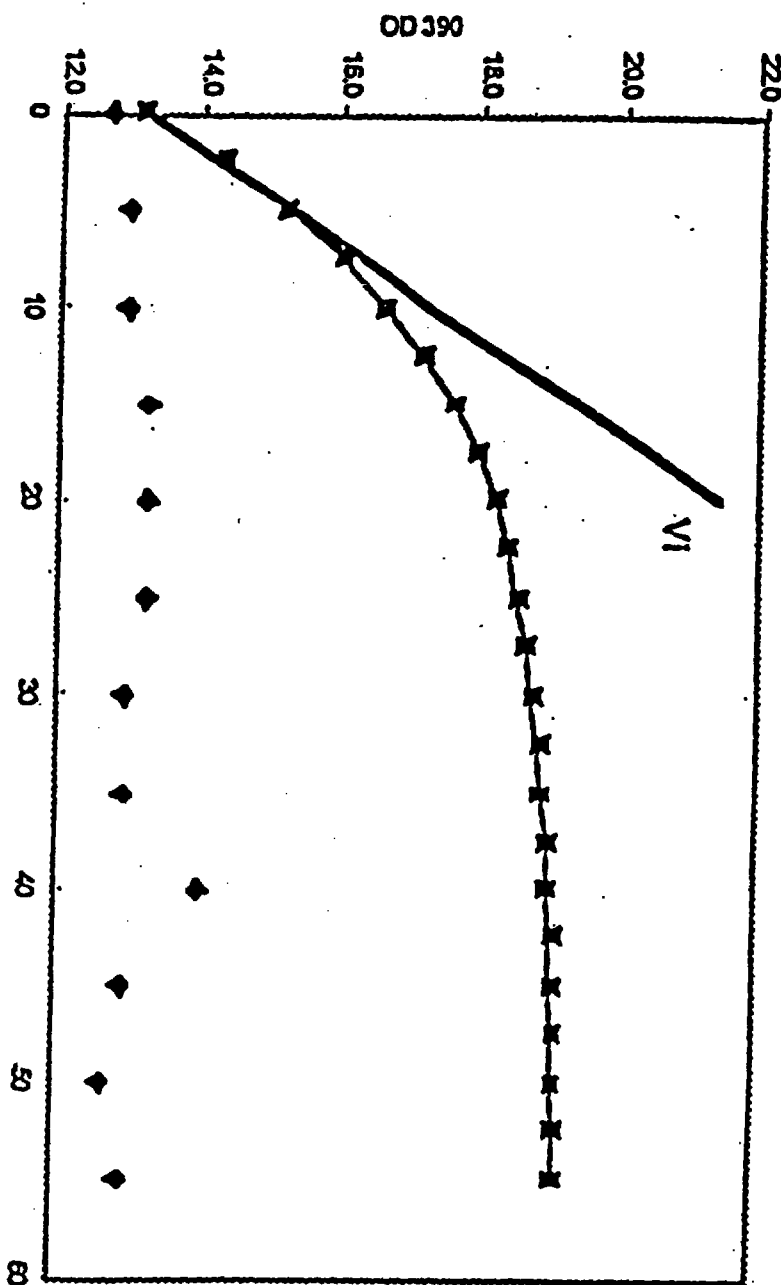
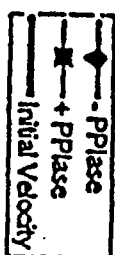


FIGURE 5



SUBSTITUTE SHEET (RULE 26)

6/10

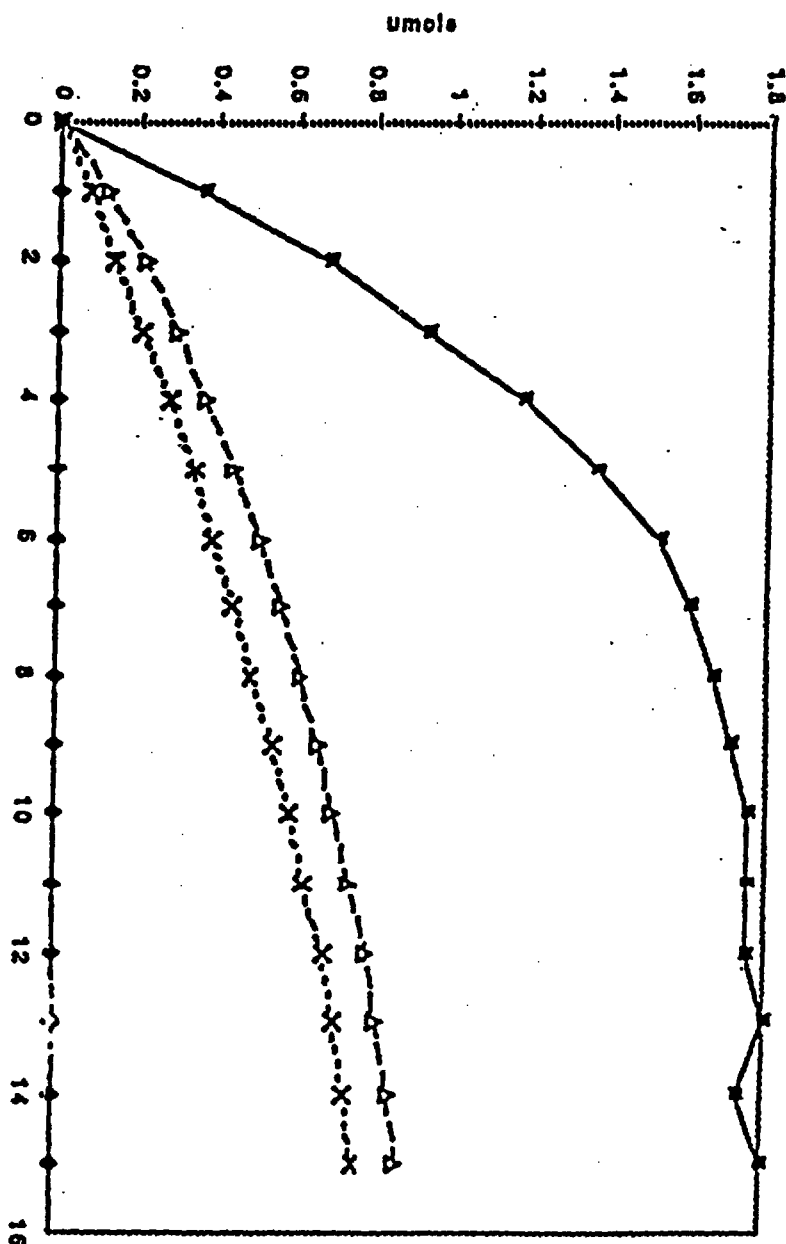
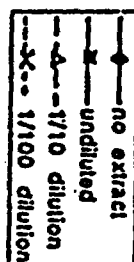


FIGURE 6



7/10

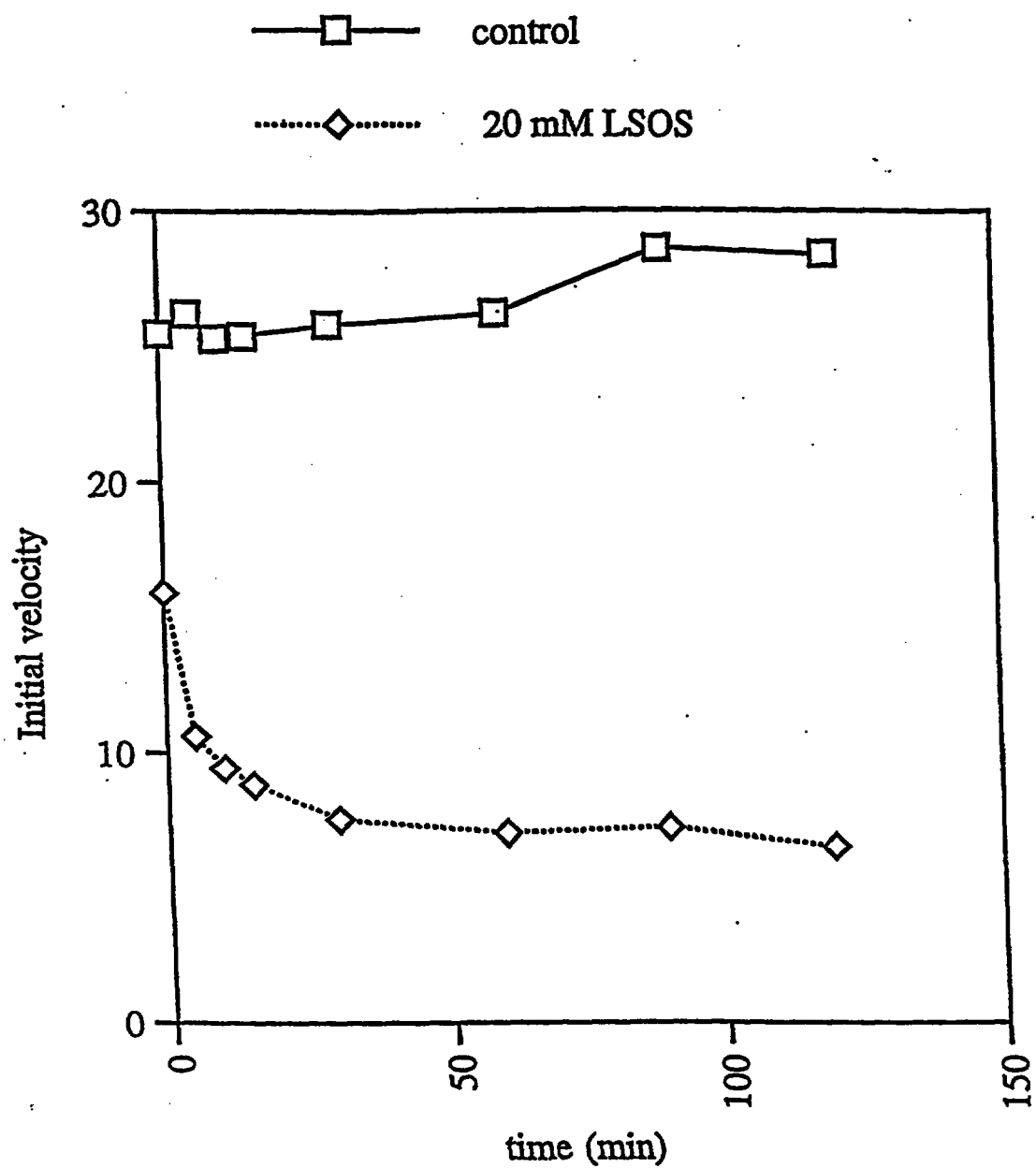


FIGURE 7

aaSeqID#:		BLOCK A										BLOCK B									
929	MNGFGAKM	GYKQFFTH	..K	KNIGLRYYGFLDY	GYANF..		.GD.....	...TNLKVGA	NLVT	YGVGTDFLYN	VYERS										
938	MNGFGVKM	GYKQFFGK	..K	RMFGLRYYGFYDF	GYAQF..		.GT.....	...ESSLVKA	TLSS	YGAGTDFLYN	VFTRK.										
810	LNGPYTKV	GYKQFFGK	..K	RNIGLRYYGFFSY	NGASV..		.GF.....	...RSTQNNV	GLYT	YGVGTDVLYN	IFSRS.										
940	SNGLGVGI	GYKYFFGK	..A	RKLGLRHYFFFDY	GFSEI..		.GL.....	...ANQSVKA	NIFA	YGVGTDFLWN	LFRRT.										
945	LNLGVQV	GYKQFFGE	..S	KRWGLRYYGFFDY	NH.....		.GYIK.SSF.	.FNS..SSDI	..WT	YGGGSDLLVN	FINDSI										
956	MNGIGVQV	GYKQFFGE	..K	RRWGLRYYGFFDY	NH.....		.AYIK.SSF.	.FNS..ASDV	..FT	YGVGTDVLYN	FINDKT										
433	MYGVGLSV	GYKHFFTK	..K	KNQGFRYYLFYDY	GYTNF..		.GFVG.NGF.	..DG..LGKM	NNHL	YGLGIDYLFN	FIDN..										
777	MYGVDAMA	GYKWFFGK	..T	KRFGFRYYGYYSY	NHANL..		.SFVG.SKLG	IMDG..ASQV	NNFT	YGVGFDALYN	FYES..										
916	INGPGFVV	GYKHFFKK	..A	PQFGMRYYGFFDF	ASSYY..		.KYTTYNDYG	MRDARKGSQS	FMFG	YGAGTDVLFN	PA										
816	SNGLGVQV	GYK.WVGK	HEET	KWFGFRWGLFYDL	SASLY..		.G.....	...SQESQSI	IIST	YGTYMOLLN	AY....										
890	FNELS..L	GYKYFLGK	..K	RIIGFRHSLFFGY	QLGGV..		.GSVPGSGL.	I	AFLP	YGFNTDLLIN	WTNDKR										
959	FAEVSLIY	GYKQFFPK	..K	EHYGFRFYVSLDY	AYGFFLK	NKGALGDSLR	ASSQIPKSYR	EKLQRKETFI	NAIF	YGVGADFLYK											

aaSeqID#:

929	.RRR.....	ERTTI.....	
938	.RGT.....	EAIDI.....	
810	.YQN.....	RSVDM.....	
940	.YNT.....	KALNF.....	
945	TRKN.....	NKLSV.....	
956	T.KN.....	SKISF.....	
433	..AQ.....	KHSSV.....	
777	..KE.....	GYNTA.....	
916	IFNR.....	ENLHL.....	
816	..NG.....	DKFFA.....	
890	ASQEYVERRV	KGLSIFYKDM	TGRTLDADTL KRASRHIIRK
959			RA

FIGURE 8

aaSeqID#: BLOCK C

BLOCK D

929	..	GLFFGAQIAGQTW	STNVT NLLSGQ....	RPD VKSSS	FQFLFDLGVR
938	..	GFFAGIQLAGQTW	KTNFL DQVDGN....	HLK PKDTS	FQFLFDLGIR
810	..	GFFSGIQLAGETF	QSTLR DDPNVKL...	HGK INNTH	FQFLDFGMR
940	..	GLFAGVQLGGATW	LSSLR QQIIDNW...	GNAND IHSTN	FQVALNFGVR
945	..	GLFGGIQLAGTTW	LNSQY M....NLTA	NNP...YSAK VNASN	FQFLFNLGLR
956	..	GVFGGIALAGTSW	LNSQY V....NLAT	NNF...YSAK MNVAN	FQFLFNLGLR
433	..	GFYVGFALAGSSW	VGSL GMWVSQMDFI	NNYLTDIRAK MHTSF	FQIPLNFGVR
777	..	GLFVGFLGGDSF	IVQGE SYLKSQMQIC	NN.TAGCSAS MNTSY	FQMPVEFGFR
916	..	GFFLGVAIGGTSW	GPTNYYF	KDLAEYRGS FHPSN	FQVLVNGGIR
816	..	GFNLGIAFAG...	...VY DRLSDALLYQ	TLLQNTFGGK VNLNG	FQFLVDLGVR
890	SS	GLVIGMELGASTW	FAS..	.NNLTPFNQV KSRTI	FQLQKFGVR
959	FG	TLILGVNFVGETW	F....	YETKIF KQWAKDSLNT YRPNM	FQVMLNVGYR

aaSeqID#:

BLOCK E

BLOCK F

929	TNFAK TNFNKH.RLD	QG.....I	EFGVKIP	VIA.HKYFATQGSS AS.....	YMRNFSFYVGYSVGF	*....
938	TNFSK IAHQKRSRFS	QG.....I	EGLKIPV	LY. HTYYQSEGV AK.....	YRRAPSFYVGYNIGF	*....
810	MNFGK LDGKSNRHNQ	HT.....V	EFGVVVP	TIY.NTYYSAGTT VK.....	YFRPYSVYWSYGYSF	*....
940	TNFAE FKRFAKKFHN	QGVISQKSV	EFGIKVP	LIN.QAYLNSAGAD VS.....	YRRLYTFYINYIMGF	*....
945	TNLAT AKKKDSERSA	QH.....GV	ELGIKIP	TIN.TNYYSFLGTK LE.....	YRRLYSVYLNIVFAY	*....
956	MNLAK NKKKASDHAA	QH.....GV	ELGVKIP	TIN.TNYYSLLGTQ LQ.....	YRRLYSVYLNIVFAY	*....
433	VNVDR	HN.....GF	EMGLKIP	LAV.NSPYETHGKG LNA.....	FKRLVMFNVSVYVSF	*....
777	SNFSK	HS.....GI	EVGFKLP	LFT.NQFYKERGV GSV.....	YKRNFYFYNYMINL	*....
916	LG...	TK HQ.....GF	EIGLKIQ	TIR.NNYTASADN VPE.....	FHRPYAFYWRYIVSF	*....
816	LGNEH NQ.....	F	GFGIKIP	TYFNYHYSMNNIS NSENVLKVL	FRRNYSVYFNYTYSF	*....
890	..FSS DEYDIDRYGD	ENYLGSSV	ELGVKVP	AFKVNYYSDDYGDK LD.....	YKRVS SVYLNITYNF	KNKH*
959	YRFSR YKN.....	WAI	EFGARIP	FL.INDYFKTP...	SVYLTSTYDF	*....

FIGURE 8 (CONTINUED)

9/10

10/10

aaSeqID#:

810	MQQQLTYLNAGNVFFNAMNKA	LEKNGTA	TANSTSSTSGATGSDG
925	MQFQKTLTSLSLLFLSYCI	AEENGAY	ASVGFEYSISHAVEHN
929	LKNHSFKKTIALSLLASMSLCN	AEEDGAF	FVIDYQTSLARQELKN
938	LQNFVFNKKWLIYSSLLPLFFLNPLM	AEDDGFF	MGVSYQTSLAVQRVDN
956	KKPFYSLSLASSLLN	AEDNGFF	ISAGYQIGEAAQMVKN
945	LH	AEDNGFF	VSAGYQIGEAVQMVKN
940	MIKKAKKFIPLFLIGSLL	AEDNGWY	MSVGYQIGGTQQFINN
890	MKKVLLTSLSLSLFWLH	AERNGFY	LGLNFAEGSYIQGQGS
777	MKKIFLGMALAFSVSM	AEKSGAF	LGGGFOYSNLENQNTT

FIGURE 9

REPLACEMENT SHEET

- ☐ Description : paged to paged
☒ Claim(s) : paged 1110 to paged 1077
☐ Drawing(s) : paged to paged
☐ Abstract : paged to paged

DATE OF RECEIPT 15/09/99

REPLACEMENT SHEET

CLAIMS

1. An isolated nucleic acid comprising a nucleotide sequence encoding an amino acid sequence that is at least 60% homologous to an amino acid sequence selected from SEQ ID NO: 795, SEQ ID NO: 745, SEQ ID NO: 929, SEQ ID NO: 890, SEQ ID NO: 956, SEQ ID NO: 904, SEQ ID NO: 777, SEQ ID NO: 938, SEQ ID NO: 940, SEQ ID NO: 945, SEQ ID NO: 925, SEQ ID NO: 844, SEQ ID NO: 754, SEQ ID NO: 960, SEQ ID NO: 810, SEQ ID NO: 817, SEQ ID NO: 809, SEQ ID NO: 816, SEQ ID NO: 855, SEQ ID NO: 802 and SEQ ID NO: 943.
2. An isolated nucleic acid comprising a nucleotide sequence encoding an amino acid sequence that is at least 60% homologous to an amino acid sequence selected from SEQ ID NO: 492-SEQ ID NO: 759, SEQ ID NO: 761, SEQ ID NO: 763, SEQ ID NO: 765-SEQ ID NO: 818, SEQ ID NO: 820-SEQ ID NO: 846, SEQ ID NO: 848-SEQ ID NO: 896, SEQ ID NO: 898-SEQ ID NO: 963, SEQ ID NO: 966-SEQ ID NO: 982, SEQ ID NO: 1037, SEQ ID NO: 1038, SEQ ID NO: 1041-SEQ ID NO: 1087, SEQ ID NO: 1090 and SEQ ID NO: 1296-SEQ ID NO: 1298.
3. An isolated nucleic acid comprising a nucleotide sequence that is at least 60% homologous to a nucleotide sequence selected from SEQ ID NO: 304, SEQ ID NO: 254, SEQ ID NO: 438, SEQ ID NO: 399, SEQ ID NO: 465, SEQ ID NO: 413, SEQ ID NO: 286, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 454, SEQ ID NO: 434, SEQ ID NO: 353, SEQ ID NO: 263, SEQ ID NO: 469, SEQ ID NO: 319, SEQ ID NO: 326, SEQ ID NO: 318, SEQ ID NO: 325, SEQ ID NO: 364, SEQ ID NO: 311 and SEQ ID NO: 452.
4. An isolated nucleic acid comprising a nucleotide sequence that is at least 60% homologous to a nucleotide sequence selected from SEQ ID NO: 1-SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274-SEQ ID NO: 327, SEQ ID NO: 329-SEQ ID NO: 364, SEQ ID NO: 366-SEQ ID NO: 405, SEQ ID NO: 407-SEQ ID NO: 472, SEQ ID NO: 475-SEQ ID NO: 491, SEQ ID NO: 983, SEQ ID NO: 984, SEQ ID NO: 987-SEQ ID NO: 1033, SEQ ID NO: 1036 and SEQ ID NO: 1293-SEQ ID NO: 1295.
5. An isolated nucleic acid comprising a nucleotide sequence of at least 8 nucleotides in length, wherein the nucleotide sequence is hybridizable to a nucleic acid



This is the replacement sheet

Date: 15 SEP 1999

having a nucleotide sequence selected from SEQ ID NO: 1-SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274-SEQ ID NO: 327, SEQ ID NO: 329-SEQ ID NO: 364, SEQ ID NO: 366-SEQ ID NO: 405, SEQ ID NO: 407-SEQ ID NO: 472, SEQ ID NO: 475-SEQ ID NO: 491, SEQ ID NO: 983, SEQ ID NO: 984, SEQ ID NO: 987-SEQ ID NO: 1033, SEQ ID NO: 1036 and SEQ ID NO: 1293-SEQ ID NO: 1295 or the complement thereof.

6. The isolated nucleic acid of claim 4 or 5, wherein said nucleotide sequence thereof encodes the amino acid sequence of an *H. pylori* cell envelope polypeptide or a fragment thereof, said selected nucleotide sequence being selected from SEQ ID NO: 255, SEQ ID NO: 263, SEQ ID NO: 266, SEQ ID NO: 277, SEQ ID NO: 280, SEQ ID NO: 285, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 299, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 321, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 353, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 375, SEQ ID NO: 384, SEQ ID NO: 391, SEQ ID NO: 392, SEQ ID NO: 397, SEQ ID NO: 398, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 409, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 427, SEQ ID NO: 433, SEQ ID NO: 434, SEQ ID NO: 441, SEQ ID NO: 444, SEQ ID NO: 445, SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 453, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 983, SEQ ID NO: 989, SEQ ID NO: 1008, SEQ ID NO: 1011, SEQ ID NO: 1014, SEQ ID NO: 1015, SEQ ID NO: 1029, SEQ ID NO: 1032, SEQ ID NO: 259, SEQ ID NO: 286, SEQ ID NO: 326, SEQ ID NO: 374, SEQ ID NO: 399, SEQ ID NO: 422, SEQ ID NO: 454, SEQ ID NO: 465, SEQ ID NO: 998, SEQ ID NO: 1009, SEQ ID NO: 1023, SEQ ID NO: 1294, SEQ ID NO: 1295, SEQ ID NO: 319, SEQ ID NO: 325, SEQ ID NO: 425, SEQ ID NO: 437, SEQ ID NO: 438, SEQ ID NO: 447, SEQ ID NO: 448, SEQ ID NO: 467, SEQ ID NO: 996, SEQ ID NO: 1027, SEQ ID NO: 1031, SEQ ID NO: 254, SEQ ID NO: 352, SEQ ID NO: 415, SEQ ID NO: 1019, SEQ ID NO: 381, SEQ ID NO: 389, SEQ ID NO: 1010, SEQ ID NO: 1012, SEQ ID NO: 354, SEQ ID NO: 372, SEQ ID NO: 400, SEQ ID NO: 421, SEQ ID NO: 1022, SEQ ID NO: 463, SEQ ID NO: 281, SEQ ID NO: 988, SEQ ID NO: 411, SEQ ID NO: 407, SEQ ID NO: 1017, SEQ ID NO: 290, SEQ ID NO: 417, SEQ ID NO: 430, SEQ ID NO: 992, SEQ ID NO: 1025, SEQ ID NO: 477, SEQ ID NO: 414, SEQ ID NO: 253, SEQ ID NO: 293, SEQ ID NO: 334, SEQ ID NO: 343, SEQ ID NO: 418, SEQ ID NO: 424, and SEQ ID NO: 443.

7. The isolated nucleic acid of claim 6, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* outer membrane polypeptide or a

This is the replacement sheet



Date: 15 SEP 2009

fragment thereof and said selected nucleotide sequence is selected from SEQ ID NO: 255, SEQ ID NO: 263, SEQ ID NO: 266, SEQ ID NO: 277, SEQ ID NO: 280, SEQ ID NO: 285, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 299, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 321, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 353, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 375, SEQ ID NO: 384, SEQ ID NO: 391, SEQ ID NO: 392, SEQ ID NO: 397, SEQ ID NO: 398, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 409, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 427, SEQ ID NO: 433, SEQ ID NO: 434, SEQ ID NO: 441, SEQ ID NO: 444, SEQ ID NO: 445, SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 453, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 983, SEQ ID NO: 989, SEQ ID NO: 1008, SEQ ID NO: 1011, SEQ ID NO: 1014, SEQ ID NO: 1015, SEQ ID NO: 1029, SEQ ID NO: 1032, SEQ ID NO: 259, SEQ ID NO: 286, SEQ ID NO: 326, SEQ ID NO: 374, SEQ ID NO: 399, SEQ ID NO: 422, SEQ ID NO: 454, SEQ ID NO: 465, SEQ ID NO: 998, SEQ ID NO: 1009, SEQ ID NO: 1023, SEQ ID NO: 1294, SEQ ID NO: 1295, SEQ ID NO: 319, SEQ ID NO: 325, SEQ ID NO: 425, SEQ ID NO: 437, SEQ ID NO: 438, SEQ ID NO: 447, SEQ ID NO: 448, SEQ ID NO: 467, SEQ ID NO: 996, SEQ ID NO: 1027, SEQ ID NO: 1031, SEQ ID NO: 254, SEQ ID NO: 352, SEQ ID NO: 415, SEQ ID NO: 1019, SEQ ID NO: 381, SEQ ID NO: 389, SEQ ID NO: 1010, and SEQ ID NO: 1012.

20

8. The isolated nucleic acid of claim 7, wherein said *H. pylori* outer membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a terminal phenylalanine residue or a fragment thereof and said selected nucleotide sequence is selected from SEQ ID NO: 255, SEQ ID NO: 263, SEQ ID NO: 266, SEQ ID NO: 277, SEQ ID NO: 280, SEQ ID NO: 285, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 299, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 321, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 353, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 375, SEQ ID NO: 384, SEQ ID NO: 391, SEQ ID NO: 392, SEQ ID NO: 397, SEQ ID NO: 398, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 409, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 427, SEQ ID NO: 433, SEQ ID NO: 434, SEQ ID NO: 441, SEQ ID NO: 444, SEQ ID NO: 445, SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 453, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 983, SEQ ID NO: 989, SEQ ID NO: 1008, SEQ ID NO: 1011, SEQ ID NO: 1014, SEQ ID NO: 1015, SEQ ID NO: 1029, and SEQ ID NO: 1032.

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This is the replacement sheet



Date:

15 SEP 1999

9. The isolated nucleic acid of claim 7, wherein said *H. pylori* outer membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a C-terminal tyrosine cluster or a fragment thereof and said selected nucleotide sequence is selected from SEQ ID NO: 286, SEQ ID NO: 326, SEQ ID NO: 374, SEQ ID NO: 399, SEQ ID NO: 422, SEQ ID NO: 454, SEQ ID NO: 465, SEQ ID NO: 998, SEQ ID NO: 1009, SEQ ID NO: 1023, SEQ ID NO: 1294, and SEQ ID NO: 1295.

10. The isolated nucleic acid of claim 7, wherein said *H. pylori* outer membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a terminal phenylalanine residue and a C-terminal tyrosine cluster or a fragment thereof and said selected nucleotide sequence is selected from SEQ ID NO: 319, SEQ ID NO: 325, SEQ ID NO: 425, SEQ ID NO: 437, SEQ ID NO: 438, SEQ ID NO: 447, SEQ ID NO: 448, SEQ ID NO: 467, SEQ ID NO: 996, SEQ ID NO: 1027, and SEQ ID NO: 1031.

11. The isolated nucleic acid of claim 6, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* inner membrane polypeptide or a fragment thereof and said selected nucleotide sequence is selected from SEQ ID NO: 354, SEQ ID NO: 372, SEQ ID NO: 400, SEQ ID NO: 421, SEQ ID NO: 1022, SEQ ID NO: 463, SEQ ID NO: 281, SEQ ID NO: 988, SEQ ID NO: 411, SEQ ID NO: 407, SEQ ID NO: 1017, SEQ ID NO: 290, SEQ ID NO: 417, SEQ ID NO: 430, SEQ ID NO: 992, and SEQ ID NO: 1025.

12. The isolated nucleic acid of claim 11, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in outer membrane and cell wall synthesis or a fragment thereof and the selected nucleotide sequence is SEQ ID NO: 354.

13. The isolated nucleic acid of claim 11, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in energy conversion or a fragment thereof and said selected nucleotide sequence is selected from SEQ ID NO: 372, SEQ ID NO: 400, SEQ ID NO: 421, and SEQ ID NO: 1022.

14. The isolated nucleic acid of claim 11, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in cofactor metabolism or a fragment thereof and the selected nucleotide sequence is SEQ ID NO: 463.

This is the replacement sheet



Date: 15 SEP 1999

15 15. The isolated nucleic acid of claim 11, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in secretion and adhesion or a fragment thereof and said selected nucleotide sequence is selected from SEQ ID NO: 281 and SEQ ID NO: 988.

10 16. The isolated nucleic acid of claim 11, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in transport or a fragment thereof and said selected nucleotide sequence is selected from SEQ ID NO: 407 and SEQ ID NO: 1017.

15 17. The isolated nucleic acid of claim 6, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* flagellar polypeptide or a fragment thereof and said selected nucleotide sequence is SEQ ID NO: 477.

18. The isolated nucleic acid of claim 6, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* transport polypeptide or a fragment thereof and said selected nucleotide sequence is SEQ ID NO: 414.

20 19. The isolated nucleic acid of claim 4 or 5, wherein said nucleotide sequence thereof encodes the amino acid sequence of an *H. pylori* secreted polypeptide or a fragment thereof, said selected nucleotide sequence being selected from SEQ ID NO: 355, SEQ ID NO: 1006, SEQ ID NO: 257, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 261, SEQ ID NO: 264, SEQ ID NO: 265, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 275, SEQ ID NO: 276, SEQ ID NO: 279, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 323, SEQ ID NO: 338, SEQ ID NO: 342, SEQ ID NO: 348, SEQ ID NO: 349, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 359, SEQ ID NO: 360, SEQ ID NO: 361, SEQ ID NO: 362, SEQ ID NO: 363, SEQ ID NO: 367, SEQ ID NO: 370, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 377, SEQ ID NO: 378, SEQ ID NO: 379, SEQ ID NO: 380, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 394, SEQ ID NO: 395, SEQ ID NO: 396, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 408, SEQ ID NO: 420, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 429, SEQ ID NO: 432, SEQ ID

This is the replacement sheet



Date: 15 SEP 1999

REPLACEMENT SHEET

NO: 439, SEQ ID NO: 442, SEQ ID NO: 451, SEQ ID NO: 471, SEQ ID NO: 478, SEQ ID NO: 488, SEQ ID NO: 987, SEQ ID NO: 990, SEQ ID NO: 991, SEQ ID NO: 993, SEQ ID NO: 1001, SEQ ID NO: 1002, SEQ ID NO: 1007, SEQ ID NO: 1013, SEQ ID NO: 1016, SEQ ID NO: 1018, SEQ ID NO: 1021, and SEQ ID NO: 1026.

5

20. The isolated nucleic acid of claim 19, wherein said *H. pylori* secreted polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in secretion and adhesion or a fragment thereof and said selected nucleotide sequence is selected from SEQ ID NO: 355 and SEQ ID NO: 1006.

10

21. The isolated nucleic acid of claim 4 or 5, wherein said nucleotide sequence thereof encodes the amino acid sequence of an *H. pylori* cytoplasmic polypeptide or a fragment thereof, said selected nucleotide sequence being selected from SEQ ID NO: 470, SEQ ID NO: 1033, SEQ ID NO: 357, SEQ ID NO: 457, SEQ ID NO: 461, SEQ ID NO: 1030, SEQ ID NO: 345, SEQ ID NO: 383, SEQ ID NO: 387, SEQ ID NO: 455, SEQ ID NO: 1003, SEQ ID NO: 351, SEQ ID NO: 416, SEQ ID NO: 278, SEQ ID NO: 335, SEQ ID NO: 346, SEQ ID NO: 350, SEQ ID NO: 419, SEQ ID NO: 460, SEQ ID NO: 472, SEQ ID NO: 1000, SEQ ID NO: 1004, SEQ ID NO: 1020, SEQ ID NO: 1293, SEQ ID NO: 318, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 330, SEQ ID NO: 347, SEQ ID NO: 440, SEQ ID NO: 446, SEQ ID NO: 464, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 995, SEQ ID NO: 997, SEQ ID NO: 1005, SEQ ID NO: 1028.

15

20

22. The isolated nucleic acid of claim 21, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in energy conversion or a fragment thereof and said selected nucleotide sequence is selected from SEQ ID NO: 470 and SEQ ID NO: 1033.

25

23. The isolated nucleic acid of claim 21, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in amino acid metabolism and transport or a fragment thereof and said selected nucleotide sequence is selected from SEQ ID NO: 357 and SEQ ID NO: 457.

30

24. The isolated nucleic acid of claim 21, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in nucleotide metabolism and transport or a fragment thereof and said selected nucleotide sequence is selected from SEQ ID NO: 461 and SEQ ID NO: 1030.

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This is the replacement sheet



Date: 15 SEP 1999

25. The isolated nucleic acid of claim 21, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in cofactor metabolism or a fragment thereof and said selected nucleotide sequence is selected from
5 SEQ ID NO: 345, SEQ ID NO: 383, SEQ ID NO: 387, SEQ ID NO: 455, and SEQ ID NO: 1003.

26. The isolated nucleic acid of claim 21, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in lipid metabolism
10 or a fragment thereof and said selected nucleotide sequence is selected from SEQ ID NO: 351 and SEQ ID NO: 416.

27. The isolated nucleic acid of claim 21, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in genome
15 replication, transcription, recombination and repair or a fragment thereof and said selected nucleotide sequence is selected from SEQ ID NO: 278, SEQ ID NO: 335, SEQ ID NO: 346, SEQ ID NO: 350, SEQ ID NO: 419, SEQ ID NO: 460, SEQ ID NO: 472, SEQ ID NO: 1000, SEQ ID NO: 1004, SEQ ID NO: 1020, and SEQ ID NO: 1293.

20 28. The isolated nucleic acid of claim 4 or 5, wherein said nucleotide sequence thereof encodes the amino acid sequence of an *H. pylori* cellular polypeptide or a fragment thereof, said selected nucleotide sequence being selected from SEQ ID NO: 256, SEQ ID NO: 267, SEQ ID NO: 282, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 332,
25 SEQ ID NO: 333, SEQ ID NO: 336, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 340, SEQ ID NO: 341, SEQ ID NO: 344, SEQ ID NO: 369, SEQ ID NO: 376, SEQ ID NO: 382, SEQ ID NO: 386, SEQ ID NO: 423, SEQ ID NO: 431, SEQ ID NO: 435, SEQ ID NO: 436, SEQ ID NO: 458, SEQ ID NO: 462, SEQ ID NO: 475, SEQ ID NO: 476, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO:
30 483, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 984, SEQ ID NO: 994, SEQ ID NO: 1024, and SEQ ID NO: 1036.

29. The isolated nucleic acid of any preceding claim, wherein the nucleotide sequence comprised by the nucleic acid is at least 70% homologous to the selected
35 nucleotide sequence.

This is the replacement sheet



Date:

15 SEP 1999

30. The isolated nucleic acid of any one of claims 1 to 28, wherein the nucleotide sequence comprised by the nucleic acid is at least 80% homologous to the selected nucleotide sequence.

5 31. The isolated nucleic acid of any one of claims 1 to 28, wherein the nucleotide sequence comprised by the nucleic acid is at least 90% homologous to the selected nucleotide sequence.

10 32. The isolated nucleic acid of any one of claims 1 to 28, wherein the nucleotide sequence comprised by the nucleic acid is at least 95% homologous to the selected nucleotide sequence.

15 33. The isolated nucleic acid of any one of claims 1 to 28, wherein the nucleotide sequence comprised by the nucleic acid is at least 98% homologous to the selected nucleotide sequence.

20 34. The isolated nucleic acid of any one of claims 1 to 28, wherein the nucleotide sequence comprised by the nucleic acid is at least 99% homologous to the selected nucleotide sequence.

35. The isolated nucleic acid of any one of claims 1 to 28, wherein the nucleotide sequence comprised by the nucleic acid is identical to the selected nucleotide sequence.

25 36. A recombinant expression vector comprising the nucleic acid of any preceding claim operably linked to a transcription regulatory element.

37. A cell comprising a recombinant expression vector of claim 36.

30 38. A method for producing a polypeptide comprising culturing a cell of claim 37 under conditions that permit expression of the polypeptide.

35 39. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an isolated nucleic acid according to any one of claims 1 to 35.



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This is the replacement sheet

Date: 15 SEP 1999

REPLACEMENT SHEET

40. The vaccine composition of claim 39, further comprising a pharmaceutically acceptable carrier.

5 41. The vaccine composition of claim 40, wherein the pharmaceutically acceptable carrier is an adjuvant.

42. The vaccine composition of claim 39, including a genetically engineered attenuated live virus or bacteria, or a recombinant virus-like particle.

10 43. Use of the nucleic acid of any one of claims 1 to 35, in the manufacture of a vaccine composition, for treating a subject for *Helicobacter pylori* infection.

44. The use according to claim 43, wherein the treatment is a prophylactic treatment.

15

45. The use according to claim 43, wherein the treatment is a therapeutic treatment.

20 46. A probe comprising a nucleotide sequence consisting of at least 8 nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274-SEQ ID NO: 327, SEQ ID NO: 329-SEQ ID NO: 364, SEQ ID NO: 366-SEQ ID NO: 405, SEQ ID NO: 407-SEQ ID NO: 472, SEQ ID NO: 475-SEQ ID NO: 491, SEQ ID NO: 983, SEQ ID NO: 984, SEQ ID NO: 987-SEQ ID NO: 1033, SEQ ID NO: 1036 and SEQ ID NO: 1293-SEQ
25 ID NO: 1295 or the complement thereof.

47. A purified polypeptide comprising an amino acid sequence that is at least 60% homologous to an amino acid sequence selected from SEQ ID NO: 795, SEQ ID NO: 745, SEQ ID NO: 929, SEQ ID NO: 890, SEQ ID NO: 956, SEQ ID NO: 904, SEQ ID
30 NO: 777, SEQ ID NO: 938, SEQ ID NO: 940, SEQ ID NO: 945, SEQ ID NO: 925, SEQ ID NO: 844, SEQ ID NO: 754, SEQ ID NO: 960, SEQ ID NO: 810, SEQ ID NO: 817, SEQ ID NO: 809, SEQ ID NO: 816, SEQ ID NO: 855, SEQ ID NO: 802 and SEQ ID NO: 943.

35 48. A purified polypeptide comprising an amino acid sequence that is at least 60% homologous to an amino acid sequence selected from SEQ ID NO: 492-SEQ ID NO: 759, SEQ ID NO: 761, SEQ ID NO: 763, SEQ ID NO: 765-SEQ ID NO: 818, SEQ ID NO: 820-SEQ ID NO: 846, SEQ ID NO: 848-SEQ ID NO: 896, SEQ ID NO: 898-SEQ ID

This is the replacement sheet



* C L N S *

Date: 15 SEP 1999

REPLACEMENT SHEET

NO: 963, SEQ ID NO: 966-SEQ ID NO: 982, SEQ ID NO: 1037, SEQ ID NO: 1038, SEQ ID NO: 1041-SEQ ID NO: 1087, SEQ ID NO: 1090 and SEQ ID NO: 1296-SEQ ID NO: 1298.

5 49. The polypeptide of claim 48, wherein said amino acid sequence comprised
by the purified polypeptide is the amino acid sequence of an *H. pylori* cell envelope
polypeptide or a fragment thereof, said selected amino acid sequence being selected from
SEQ ID NO: 746, SEQ ID NO: 754, SEQ ID NO: 757, SEQ ID NO: 768, SEQ ID NO:
771, SEQ ID NO: 776, SEQ ID NO: 783, SEQ ID NO: 785, SEQ ID NO: 790, SEQ ID
10 NO: 802, SEQ ID NO: 803, SEQ ID NO: 804, SEQ ID NO: 812, SEQ ID NO: 818, SEQ
ID NO: 820, SEQ ID NO: 882, SEQ ID NO: 844, SEQ ID NO: 855, SEQ ID NO: 857,
SEQ ID NO: 859, SEQ ID NO: 866, SEQ ID NO: 875, SEQ ID NO: 882, SEQ ID NO:
883, SEQ ID NO: 888, SEQ ID NO: 889, SEQ ID NO: 893, SEQ ID NO: 895, SEQ ID
NO: 900, SEQ ID NO: 901, SEQ ID NO: 903, SEQ ID NO: 918, SEQ ID NO: 924, SEQ
15 ID NO: 925, SEQ ID NO: 932, SEQ ID NO: 935, SEQ ID NO: 936, SEQ ID NO: 940,
SEQ ID NO: 941, SEQ ID NO: 943, SEQ ID NO: 944, SEQ ID NO: 957, SEQ ID NO:
959, SEQ ID NO: 960, SEQ ID NO: 1037, SEQ ID NO: 1043, SEQ ID NO: 1062, SEQ ID
NO: 1065, SEQ ID NO: 1068, SEQ ID NO: 1069, SEQ ID NO: 1083, SEQ ID NO: 1086,
SEQ ID NO: 750, SEQ ID NO: 777, SEQ ID NO: 817, SEQ ID NO: 865, SEQ ID NO:
20 890, SEQ ID NO: 913, SEQ ID NO: 945, SEQ ID NO: 956, SEQ ID NO: 1052, SEQ ID
NO: 1063, SEQ ID NO: 1077, SEQ ID NO: 1297, SEQ ID NO: 1298, SEQ ID NO: 810,
SEQ ID NO: 816, SEQ ID NO: 916, SEQ ID NO: 928, SEQ ID NO: 929, SEQ ID NO:
938, SEQ ID NO: 939, SEQ ID NO: 958, SEQ ID NO: 1050, SEQ ID NO: 1081, SEQ ID
NO: 1085, SEQ ID NO: 745, SEQ ID NO: 843, SEQ ID NO: 906, SEQ ID NO: 1073, SEQ
25 ID NO: 872, SEQ ID NO: 880, SEQ ID NO: 1064, SEQ ID NO: 1066, SEQ ID NO: 845,
SEQ ID NO: 863, SEQ ID NO: 891, SEQ ID NO: 912, SEQ ID NO: 1076, SEQ ID NO:
954, SEQ ID NO: 772, SEQ ID NO: 1042, SEQ ID NO: 902, SEQ ID NO: 898, SEQ ID
NO: 1071, SEQ ID NO: 781, SEQ ID NO: 908, SEQ ID NO: 921, SEQ ID NO: 1046, SEQ
ID NO: 1079, SEQ ID NO: 968, SEQ ID NO: 905, SEQ ID NO: 744, SEQ ID NO: 784,
30 SEQ ID NO: 825, SEQ ID NO: 834, SEQ ID NO: 909, SEQ ID NO: 915, and SEQ ID NO:
934.

50. The purified polypeptide of claim 49, wherein said *H. pylori* cell envelope
polypeptide or a fragment thereof is an *H. pylori* outer membrane polypeptide or a
35 fragment thereof and said selected amino acid sequence is selected from SEQ ID NO: 746,
SEQ ID NO: 754, SEQ ID NO: 757, SEQ ID NO: 768, SEQ ID NO: 771, SEQ ID NO:



This is the replacement sheet

Date: 15 SEP 1999

REPLACEMENT SHEET

776, SEQ ID NO: 783, SEQ ID NO: 785, SEQ ID NO: 790, SEQ ID NO: 802, SEQ ID NO: 803, SEQ ID NO: 804, SEQ ID NO: 812, SEQ ID NO: 818, SEQ ID NO: 820, SEQ ID NO: 882, SEQ ID NO: 844, SEQ ID NO: 855, SEQ ID NO: 857, SEQ ID NO: 859, SEQ ID NO: 866, SEQ ID NO: 875, SEQ ID NO: 882, SEQ ID NO: 883, SEQ ID NO: 888, SEQ ID NO: 889, SEQ ID NO: 893, SEQ ID NO: 895, SEQ ID NO: 900, SEQ ID NO: 901, SEQ ID NO: 903, SEQ ID NO: 918, SEQ ID NO: 924, SEQ ID NO: 925, SEQ ID NO: 932, SEQ ID NO: 935, SEQ ID NO: 936, SEQ ID NO: 940, SEQ ID NO: 941, SEQ ID NO: 943, SEQ ID NO: 944, SEQ ID NO: 957, SEQ ID NO: 959, SEQ ID NO: 960, SEQ ID NO: 1037, SEQ ID NO: 1043, SEQ ID NO: 1062, SEQ ID NO: 1065, SEQ ID NO: 1068, SEQ ID NO: 1069, SEQ ID NO: 1083, SEQ ID NO: 1086, SEQ ID NO: 750, SEQ ID NO: 777, SEQ ID NO: 817, SEQ ID NO: 865, SEQ ID NO: 890, SEQ ID NO: 913, SEQ ID NO: 945, SEQ ID NO: 956, SEQ ID NO: 1052, SEQ ID NO: 1063, SEQ ID NO: 1077, SEQ ID NO: 1297, SEQ ID NO: 1298, SEQ ID NO: 810, SEQ ID NO: 816, SEQ ID NO: 916, SEQ ID NO: 928, SEQ ID NO: 929, SEQ ID NO: 938, SEQ ID NO: 939, SEQ ID NO: 958, SEQ ID NO: 1050, SEQ ID NO: 1081, SEQ ID NO: 1085, SEQ ID NO: 745, SEQ ID NO: 843, SEQ ID NO: 906, SEQ ID NO: 1073, SEQ ID NO: 872, SEQ ID NO: 880, SEQ ID NO: 1064, and SEQ ID NO: 1066.

51. The purified polypeptide of claim 50, wherein said *H. pylori* outer membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a terminal phenylalanine residue or a fragment thereof and said selected amino acid sequence is selected from SEQ ID NO: 746, SEQ ID NO: 754, SEQ ID NO: 757, SEQ ID NO: 768, SEQ ID NO: 771, SEQ ID NO: 776, SEQ ID NO: 783, SEQ ID NO: 785, SEQ ID NO: 790, SEQ ID NO: 802, SEQ ID NO: 803, SEQ ID NO: 804, SEQ ID NO: 812, SEQ ID NO: 818, SEQ ID NO: 820, SEQ ID NO: 882, SEQ ID NO: 844, SEQ ID NO: 855, SEQ ID NO: 857, SEQ ID NO: 859, SEQ ID NO: 866, SEQ ID NO: 875, SEQ ID NO: 882, SEQ ID NO: 883, SEQ ID NO: 888, SEQ ID NO: 889, SEQ ID NO: 893, SEQ ID NO: 895, SEQ ID NO: 900, SEQ ID NO: 901, SEQ ID NO: 903, SEQ ID NO: 918, SEQ ID NO: 924, SEQ ID NO: 925, SEQ ID NO: 932, SEQ ID NO: 935, SEQ ID NO: 936, SEQ ID NO: 940, SEQ ID NO: 941, SEQ ID NO: 943, SEQ ID NO: 944, SEQ ID NO: 957, SEQ ID NO: 959, SEQ ID NO: 960, SEQ ID NO: 1037, SEQ ID NO: 1043, SEQ ID NO: 1062, SEQ ID NO: 1065, SEQ ID NO: 1068, SEQ ID NO: 1069, SEQ ID NO: 1083, and SEQ ID NO: 1086.

52. The purified polypeptide of claim 50, wherein said *H. pylori* outer membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a C-

This is the replacement sheet



Date: 15 SEP 1999

REPLACEMENT SHEET

terminal tyrosine cluster or a fragment thereof, said selected amino acid sequence being selected from SEQ ID NO: 777, SEQ ID NO: 817, SEQ ID NO: 865, SEQ ID NO: 890, SEQ ID NO: 913, SEQ ID NO: 945, SEQ ID NO: 956, SEQ ID NO: 1052, SEQ ID NO: 1063, SEQ ID NO: 1077, SEQ ID NO: 1297, SEQ ID NO: 1298.

5

53. The purified polypeptide of claim 50, wherein said *H. pylori* outer membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a terminal phenylalanine residue and a C-terminal tyrosine cluster or a fragment thereof and said selected amino acid sequence is selected from SEQ ID NO: 810, SEQ ID NO: 816, SEQ ID NO: 916, SEQ ID NO: 928, SEQ ID NO: 929, SEQ ID NO: 938, SEQ ID NO: 939, SEQ ID NO: 958, SEQ ID NO: 1050, SEQ ID NO: 1081, and SEQ ID NO: 1085.

10

54. The purified polypeptide of claim 49, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* inner membrane polypeptide or a fragment thereof and said selected amino acid sequence is selected from SEQ ID NO: 845, SEQ ID NO: 863, SEQ ID NO: 891, SEQ ID NO: 912, SEQ ID NO: 1076, SEQ ID NO: 954, SEQ ID NO: 772, SEQ ID NO: 1042, SEQ ID NO: 902, SEQ ID NO: 898, SEQ ID NO: 1071, SEQ ID NO: 781, SEQ ID NO: 908, SEQ ID NO: 921, SEQ ID NO: 1046, SEQ ID NO: 1079.

15

20

55. The purified polypeptide of claim 54, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in outer membrane and cell wall synthesis or a fragment thereof and said selected amino acid sequence is SEQ ID NO: 845.

25

56. The purified polypeptide of claim 54, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in energy conversion or a fragment thereof, said selected amino acid sequence being selected from SEQ ID NO: 863, SEQ ID NO: 891, SEQ ID NO: 912, and SEQ ID NO: 1076.

30

57. The purified polypeptide of claim 54, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in cofactor metabolism or a fragment thereof and said selected amino acid sequence is SEQ ID NO: 954.

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This is the replacement sheet

Date: 15 SEP 1999

REPLACEMENT SHEET

58. The purified polypeptide of claim 54, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in secretion and adhesion or a fragment thereof and said selected amino acid sequence is selected from SEQ ID NO: 772 and SEQ ID NO: 1042.

5

59. The purified polypeptide of claim 54, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in transport or a fragment thereof and said selected amino acid sequence is selected from SEQ ID NO: 898 and SEQ ID NO: 1071.

10

60. The purified polypeptide of claim 49, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* flagellar polypeptide or a fragment thereof and said selected amino acid sequence is SEQ ID NO: 968.

15

61. The purified polypeptide of claim 49, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* transport polypeptide or a fragment thereof and said selected amino acid sequence is SEQ ID NO: 905.

62. The purified polypeptide of claim 48, wherein said amino acid sequence comprised by the purified polypeptide is the amino acid sequence of an *H. pylori* cellular polypeptide or a fragment thereof, said selected amino acid sequence being selected from SEQ ID NO: 747, SEQ ID NO: 758, SEQ ID NO: 773, SEQ ID NO: 797, SEQ ID NO: 798, SEQ ID NO: 799, SEQ ID NO: 800, SEQ ID NO: 801, SEQ ID NO: 807, SEQ ID NO: 808, SEQ ID NO: 823, SEQ ID NO: 824, SEQ ID NO: 827, SEQ ID NO: 828, SEQ ID NO: 830, SEQ ID NO: 831, SEQ ID NO: 832, SEQ ID NO: 835, SEQ ID NO: 860, SEQ ID NO: 867, SEQ ID NO: 873, SEQ ID NO: 877, SEQ ID NO: 914, SEQ ID NO: 922, SEQ ID NO: 926, SEQ ID NO: 927, SEQ ID NO: 949, SEQ ID NO: 953, SEQ ID NO: 966, SEQ ID NO: 967, SEQ ID NO: 970, SEQ ID NO: 971, SEQ ID NO: 972, SEQ ID NO: 973, SEQ ID NO: 974, SEQ ID NO: 975, SEQ ID NO: 976, SEQ ID NO: 977, SEQ ID NO: 978, SEQ ID NO: 980, SEQ ID NO: 1038, SEQ ID NO: 1048, SEQ ID NO: 1078, and SEQ ID NO: 1090.

63. The purified polypeptide of claim 48, wherein said amino acid sequence comprised by the purified polypeptide is the amino acid sequence of an *H. pylori* secreted polypeptide or a fragment thereof, said selected amino acid sequence being selected from SEQ ID NO: 846, SEQ ID NO: 1060, SEQ ID NO: 748, SEQ ID NO: 749, SEQ ID NO:

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This is the replacement sheet



Date: 15 SEP 1999

751, SEQ ID NO: 752, SEQ ID NO: 755, SEQ ID NO: 756, SEQ ID NO: 759, SEQ ID
 NO: 761, SEQ ID NO: 763, SEQ ID NO: 765, SEQ ID NO: 766, SEQ ID NO: 767, SEQ
 ID NO: 770, SEQ ID NO: 774, SEQ ID NO: 775, SEQ ID NO: 778, SEQ ID NO: 779,
 SEQ ID NO: 780, SEQ ID NO: 782, SEQ ID NO: 786, SEQ ID NO: 787, SEQ ID NO:
 5 788, SEQ ID NO: 789, SEQ ID NO: 791, SEQ ID NO: 792, SEQ ID NO: 793, SEQ ID
 NO: 794, SEQ ID NO: 795, SEQ ID NO: 796, SEQ ID NO: 805, SEQ ID NO: 806, SEQ
 ID NO: 814, SEQ ID NO: 829, SEQ ID NO: 833, SEQ ID NO: 839, SEQ ID NO: 840,
 SEQ ID NO: 849, SEQ ID NO: 850, SEQ ID NO: 851, SEQ ID NO: 852, SEQ ID NO:
 853, SEQ ID NO: 854, SEQ ID NO: 858, SEQ ID NO: 861, SEQ ID NO: 862, SEQ ID
 10 NO: 864, SEQ ID NO: 868, SEQ ID NO: 869, SEQ ID NO: 870, SEQ ID NO: 871, SEQ
 ID NO: 879, SEQ ID NO: 881, SEQ ID NO: 885, SEQ ID NO: 886, SEQ ID NO: 887,
 SEQ ID NO: 892, SEQ ID NO: 894, SEQ ID NO: 896, SEQ ID NO: 899, SEQ ID NO:
 911, SEQ ID NO: 917, SEQ ID NO: 919, SEQ ID NO: 920, SEQ ID NO: 923, SEQ ID
 NO: 930, SEQ ID NO: 933, SEQ ID NO: 942, SEQ ID NO: 962, SEQ ID NO: 969, SEQ
 15 ID NO: 979, SEQ ID NO: 1041, SEQ ID NO: 1044, SEQ ID NO: 1045, SEQ ID NO:
 1047, SEQ ID NO: 1055, SEQ ID NO: 1056, SEQ ID NO: 1061, SEQ ID NO: 1067, SEQ
 ID NO: 1070, SEQ ID NO: 1072, SEQ ID NO: 1075, and SEQ ID NO: 1080.

64. The purified polypeptide of claim 63, wherein said *H. pylori* secreted
 20 polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in secretion and
 adhesion or a fragment thereof and said selected amino acid sequence is selected from SEQ
 ID NO: 846 and SEQ ID NO: 1060.

65. The purified polypeptide of claim 48, wherein said amino acid sequence
 25 comprised by the purified polypeptide is the amino acid sequence of an *H. pylori*
 cytoplasmic polypeptide or a fragment thereof, said selected amino acid sequence being
 selected from SEQ ID NO: 961, SEQ ID NO: 1087, SEQ ID NO: 848, SEQ ID NO: 948,
 SEQ ID NO: 952, SEQ ID NO: 1084, SEQ ID NO: 836, SEQ ID NO: 874, SEQ ID NO:
 878, SEQ ID NO: 946, SEQ ID NO: 1057, SEQ ID NO: 842, SEQ ID NO: 907, SEQ ID
 30 NO: 769, SEQ ID NO: 826, SEQ ID NO: 837, SEQ ID NO: 841, SEQ ID NO: 910, SEQ
 ID NO: 951, SEQ ID NO: 963, SEQ ID NO: 1054, SEQ ID NO: 1058, SEQ ID NO: 1074,
 SEQ ID NO: 1296, SEQ ID NO: 809, SEQ ID NO: 813, SEQ ID NO: 815, SEQ ID NO:
 821, SEQ ID NO: 838, SEQ ID NO: 931, SEQ ID NO: 937, SEQ ID NO: 955, SEQ ID
 NO: 981, SEQ ID NO: 982, SEQ ID NO: 1049, SEQ ID NO: 1051, SEQ ID NO: 1059, and
 35 SEQ ID NO: 1082.

This is the replacement sheet



Date: 15 SEP 1999

REPLACEMENT SHEET

66. The purified polypeptide of claim 65, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in energy conversion or a fragment thereof and said selected amino acid sequence is selected from SEQ ID NO: 961 and SEQ ID NO: 1087.

5

67. The purified polypeptide of claim 65, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in amino acid metabolism and transport or a fragment thereof and said selected amino acid sequence is selected from SEQ ID NO: 848 and SEQ ID NO: 948.

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68. The purified polypeptide of claim 65, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in nucleotide metabolism and transport or a fragment thereof and said selected amino acid sequence is selected from SEQ ID NO: 952 and SEQ ID NO: 1084.

15

69. The purified polypeptide of claim 65, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in cofactor metabolism or a fragment thereof and said selected amino acid sequence is selected from SEQ ID NO: 836, SEQ ID NO: 874, SEQ ID NO: 878, SEQ ID NO: 946, and SEQ ID NO: 1057.

20

70. The purified polypeptide of claim 65, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in lipid metabolism or a fragment thereof and said selected amino acid sequence is selected from SEQ ID NO: 842 and SEQ ID NO: 907.

25

71. The purified polypeptide of claim 65, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in genome replication, transcription, recombination and repair or a fragment thereof and said selected amino acid sequence is selected from SEQ ID NO: 769, SEQ ID NO: 826, SEQ ID NO: 837, SEQ ID NO: 841, SEQ ID NO: 910, SEQ ID NO: 951, SEQ ID NO: 963, SEQ ID NO: 1054, SEQ ID NO: 1058, SEQ ID NO: 1074, and SEQ ID NO: 1296.

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72. The purified polypeptide of any one of claims 47 to 71, wherein the amino acid sequence comprised by the purified polypeptide is at least 70% homologous to the selected amino acid sequence.

35

This is the replacement sheet



Date: 15 SEP 1999

REPLACEMENT SHEET

73. The purified polypeptide of any one of claims 47 to 71, wherein the amino acid sequence comprised by the purified polypeptide is at least 80% homologous to the selected amino acid sequence.

5

74. The purified polypeptide of any one of claims 47 to 71, wherein the amino acid sequence comprised by the purified polypeptide is at least 90% homologous to the selected amino acid sequence.

10

75. The purified polypeptide of any one of claims 47 to 71, wherein the amino acid sequence comprised by the purified polypeptide is at least 95% homologous to the selected amino acid sequence.

15

76. The purified polypeptide of any one of claims 47 to 71, wherein the amino acid sequence comprised by the purified polypeptide is at least 98% homologous to the selected amino acid sequence.

20

77. The purified polypeptide of any one of claims 47 to 71, wherein the amino acid sequence comprised by the purified polypeptide is at least 99% homologous to the selected amino acid sequence.

25

78. The purified polypeptide of any one of claims 47 to 71, wherein the amino acid sequence comprised by the purified polypeptide is identical to the selected amino acid sequence.

79. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a purified polypeptide according to any one of claims 47 to 78.

30

80. The vaccine composition of claim 79, further comprising a pharmaceutically acceptable carrier.

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81. The vaccine composition of claim 80, wherein the pharmaceutically acceptable carrier is an adjuvant.



This is the replacement sheet

Date: 15 SEP 1999

REPLACEMENT SHEET

82. The vaccine composition of claim 79, including a substance selected from cholera toxin, a non-toxic derivative of cholera toxin, procholeraenoid, a fungal polysaccharide, muramyl dipeptide, a muramyl dipeptide derivative, a phorbol ester, *E. coli* labile toxin, a non-*H. pylori* bacterial lysate, a block polymer, a saponin, biodegradable microcapsules, ISCOMs, cochleates, liposomes, a genetically engineered attenuated live virus or bacteria, and a recombinant virus-like particle.
83. Use of a purified polypeptide according to any one of claims 47 to 78, in the manufacture of a vaccine composition, for treating a subject for *Helicobacter pylori* infection.
84. The use according to claim 83, wherein the treatment is a prophylactic treatment.
85. The use according to claim 83, wherein the treatment is a therapeutic treatment.
86. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising:
- (a) contacting the sample with a nucleic acid according to any one of claims 1 to 35 under conditions in which a hybrid can form between the probe and a *Helicobacter* nucleic acid in the sample; and
- (b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *Helicobacter* nucleic acid in the sample.
87. A drug screening assay comprising the step of contacting a test compound with a purified polypeptide comprising an amino acid sequence that is at least 60% homologous to an amino acid sequence shown in the sequence listing.
88. The assay of claim 87, comprising determining if the compound binds to said amino acid sequence of the purified polypeptide.
89. The assay of claim 87 or 88, comprising determining if the test compound alters the binding affinity of said amino acid sequence of the purified polypeptide for a ligand thereof.



This is the replacement sheet

Date: 15 SEP 1999

REPLACEMENT SHEET

90. The assay of claim 89, wherein the ability of the test compound to inhibit the binding ability of said amino acid sequence to the ligand is determined.
- 5 91. The assay of claim 87 or 88, wherein the polypeptide has enzymatic activity, and the assay comprises detecting if the test compound changes the enzymatic activity.
- 10 92. The assay of claim 91, wherein the enzymatic activity produces a detectable reaction product with distinctive absorption, fluorescence or chemi-luminescence properties.
93. The assay of any one of claims 87 to 92, wherein the assay is a cell-free assay.
- 15 94. The assay of any one of claims 87 to 93, wherein the amino acid sequence comprised by the purified polypeptide is at least 70%, 80%, 90%, 95%, 98% or 99% homologous to an amino acid sequence shown in the sequence listing, or identical to an amino acid sequence shown in the sequence listing.
- 20 95. A drug screening assay comprising the step of contacting a test compound with an isolated nucleic acid comprising a nucleotide sequence that is at least 60% homologous to a nucleotide sequence shown in the sequence listing.
- 25 96. The assay of claim 95, comprising determining if the compound binds to, or interacts with, said nucleotide sequence of the nucleic acid.
97. The assay of claim 95, wherein the assay is an *in vitro* assay.
- 30 98. The assay of any one of claims 95 to 97, wherein the nucleotide sequence comprised by the nucleic acid is at least 70%, 80%, 90%, 95%, 98% or 99% homologous to a nucleotide sequence shown in the sequence listing, or identical to a nucleotide sequence shown in the sequence listing.



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(54) Title: **NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI AND VACCINE COMPOSITIONS THEREOF**

(57) Abstract

Recombinant or substantially pure preparations of *H. pylori* polypeptides are described. The nucleic acids encoding the polypeptides also are described. The *H. pylori* polypeptides are useful in diagnostic and vaccine compositions.

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