NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *HELICOBACTER PYLORI* FOR DIAGNOSTICS AND THERAPEUTICS

Background of the Invention

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 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 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 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 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: 1892-1895; 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* because of bacterial resistance, altered drug distribution, patient non-compliance or poor drug availabilty. (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 Suppl 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 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.

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 *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 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 or treatment of infection by *H. pylori* are 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.

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* infected mice with specific antigens dissolved in buffer containing DOC.

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: 384. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide of SEQ ID NO: 384, such nucleic acid

is contained in SEQ ID NO: 1. The *H. pylori* polypeptide sequences of the invention described herein are contained in the Sequence Listing, and the nucleic acids encoding *H. pylori* polypeptides of the invention 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: 384 through SEQ ID NO: 389, SEQ ID NO: 391 through SEQ ID NO: 400, SEQ ID NO: 402 through SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 411 through SEQ ID NO: 412, SEQ ID NO: 414 through SEQ ID NO: 430, SEQ ID NO: 432 through SEQ ID NO: 434, SEQ ID NO: 436 through SEQ ID NO: 441, and SEQ ID NO: 443. 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: 384 through SEQ ID NO: 389, SEQ ID NO: 391 through SEQ ID NO: 400, SEQ ID NO: 402 through SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 411 through SEQ ID NO: 412, SEQ ID NO: 414 through SEQ ID NO: 430, SEQ ID NO: 432 through SEQ ID NO: 434, SEQ ID NO: 436 through SEQ ID NO: 441, and SEQ ID NO: 443, 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: 444, SEQ ID NO: 446 through SEQ ID NO: 448, SEQ ID NO: 450 through SEQ ID NO: 462, SEQ ID NO: 465 through SEQ ID NO: 466, SEQ ID NO: 468 through SEQ ID NO: 469, SEQ ID NO: 471 through SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 478 through SEQ ID NO: 479, SEQ ID NO: 481 through SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488 through SEQ ID NO: 501, and SEQ ID NO: 503 through SEQ ID NO: 506. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 444, SEQ ID NO: 446 through SEQ ID NO: 448, SEQ ID NO: 450 through SEQ ID NO: 462, SEQ ID NO: 465 through SEQ ID NO: 466, SEQ ID NO: 468 through SEQ ID NO: 469, SEQ ID NO: 471 through SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 478 through SEQ ID NO: 479, SEQ ID NO: 481 through SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488 through SEQ ID NO: 501, and SEQ ID NO: 503 through SEQ ID NO: 506, 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: 509 through SEQ ID NO: 510, SEQ ID NO: 512 through SEQ ID NO: 514, SEQ ID NO: 516, SEQ ID NO: 518 through SEQ ID NO: 520, SEQ ID NO: 522 through SEQ ID NO: 525, SEQ ID NO: 527 through SEQ ID NO: 533, SEQ ID NO: 535 through SEQ ID NO: 537, SEQ ID NO: 539 through SEQ ID NO: 540, SEQ ID NO: 542 through SEQ ID NO: 544, SEQ ID NO: 546 through SEQ ID NO: 548, SEQ ID NO:

550, SEQ ID NO: 553 through SEQ ID NO: 556, SEQ ID NO: 558, SEQ ID NO: 560, SEQ ID NO: 562 through SEQ ID NO: 568, SEQ ID NO: 570, and SEQ ID NO: 572 through SEQ ID NO: 575. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 509 through SEQ ID NO: 510, SEQ ID NO: 512 through SEQ ID NO: 514, SEQ ID NO: 516, SEQ ID NO: 518 through SEQ ID NO: 520, SEQ ID NO: 522 through SEQ ID NO: 525, SEQ ID NO: 527 through SEQ ID NO: 533, SEQ ID NO: 535 through SEQ ID NO: 537, SEQ ID NO: 539 through SEQ ID NO: 540, SEQ ID NO: 542 through SEQ ID NO: 544, SEQ ID NO: 546 through SEQ ID NO: 548, SEQ ID NO: 550, SEQ ID NO: 553 through SEQ ID NO: 556, SEQ ID NO: 558, SEQ ID NO: 560, SEQ ID NO: 562 through SEQ ID NO: 568, SEQ ID NO: 570, and SEQ ID NO: 572 through SEQ ID NO: 575, 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: 576 through SEQ ID NO: 579, SEQ ID NO: 581 through SEQ ID NO: 583, SEQ ID NO: 585 through SEQ ID NO: 593, SEQ ID NO: 596 through SEQ ID NO: 614, SEQ ID NO: 617 through SEQ ID NO: 623, SEQ ID NO: 625, SEQ ID NO: 627, SEQ ID NO: 629 through SEQ ID NO: 631, SEQ ID NO: 633, and SEQ ID NO: 635 through SEQ ID NO: 636. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 576 through SEQ ID NO: 579, SEQ ID NO: 581 through SEQ ID NO: 583, SEQ ID NO: 585 through SEQ ID NO: 593, SEQ ID NO: 596 through SEQ ID NO: 614, SEQ ID NO: 617 through SEQ ID NO: 623, SEQ ID NO: 625, SEQ ID NO: 627, SEQ ID NO: 629 through SEQ ID NO: 631, SEQ ID NO: 633, and SEQ ID NO: 635 through SEQ ID NO: 636, 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: 638 through SEQ ID NO: 640, SEQ ID NO: 642 through SEQ ID NO: 643, SEQ ID NO: 647, SEQ ID NO: 649 through SEQ ID NO: 651, SEQ ID NO: 653 through SEQ ID NO: 661, SEQ ID NO: 663 through SEQ ID NO: 670, SEQ ID NO: 673 through SEQ ID NO: 674, SEQ ID NO: 676, SEQ ID NO: 678 through SEQ ID NO: 683, SEQ ID NO: 687 through SEQ ID NO: 692, and SEQ ID NO: 694 through SEQ ID NO: 702. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 638 through SEQ ID NO: 640, SEQ ID NO: 642 through SEQ ID NO: 643, SEQ ID NO: 647, SEQ ID NO: 649 through SEQ ID NO: 651, SEQ ID NO: 653 through SEQ ID NO: 661, SEQ ID NO: 663 through SEQ ID NO: 670, SEQ ID NO: 673 through SEQ ID NO: 674, SEQ ID NO: 676, SEQ ID NO: 678 through SEQ ID NO: 683, SEQ ID NO: 687

through SEQ ID NO: 692, and SEQ ID NO: 694 through SEQ ID NO: 702, 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: 705 through SEQ ID NO: 708, SEQ ID NO: 712 through SEQ ID NO: 714, SEQ ID NO: 716 through SEQ ID NO: 722, SEQ ID NO: 725 through SEQ ID NO: 730, SEQ ID NO: 732 through SEQ ID NO: 733, SEQ ID NO: 735 through SEQ ID NO: 744, SEQ ID NO: 746 through SEQ ID NO: 752, SEQ ID NO: 755 through SEQ ID NO: 757, SEQ ID NO: 759, SEQ ID NO: 761 through SEQ ID NO: 763, and SEQ ID NO: 767 through SEQ ID NO: 770. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 705 through SEQ ID NO: 708, SEQ ID NO: 712 through SEQ ID NO: 714, SEQ ID NO: 716 through SEQ ID NO: 722, SEQ ID NO: 725 through SEQ ID NO: 730, SEQ ID NO: 732 through SEQ ID NO: 733, SEQ ID NO: 735 through SEQ ID NO: 744, SEQ ID NO: 746 through SEQ ID NO: 752, SEQ ID NO: 755 through SEQ ID NO: 757, SEQ ID NO: 759, SEQ ID NO: 761 through SEQ ID NO: 763, and SEQ ID NO: 767 through SEQ ID NO: 770, such nucleic acids are contained in SEQ ID NO: 251 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: 771 through SEQ ID NO: 773, SEQ ID NO: 775, SEQ ID NO: 777, SEQ ID NO: 779 through SEQ ID NO: 784, SEQ ID NO: 786 through SEQ ID NO: 787, SEQ ID NO: 789 through SEQ ID NO: 792, SEQ ID NO: 794, SEQ ID NO: 796, SEQ ID NO: 798 through SEQ ID NO: 805, SEQ ID NO: 807 through SEQ ID NO: 811, SEQ ID NO: 813 through SEQ ID NO: 819, SEQ ID NO: 821 through SEQ ID NO: 822, SEQ ID NO: 824 through SEQ ID NO: 826, SEQ ID NO: 828 through SEQ ID NO: 832, and SEQ ID NO: 835. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 771 through SEQ ID NO: 773, SEQ ID NO: 775, SEQ ID NO: 777, SEQ ID NO: 779 through SEQ ID NO: 784, SEQ ID NO: 786 through SEQ ID NO: 787, SEQ ID NO: 789 through SEQ ID NO: 792, SEQ ID NO: 794, SEQ ID NO: 796, SEQ ID NO: 798 through SEQ ID NO: 805, SEQ ID NO: 807 through SEQ ID NO: 811, SEQ ID NO: 813 through SEQ ID NO: 819, SEQ ID NO: 821 through SEQ ID NO: 822, SEQ ID NO: 824 through SEQ ID NO: 826, SEQ ID NO: 828 through SEQ ID NO: 832, and SEQ ID NO: 835, such nucleic acids are contained in SEQ ID NO: 301 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: 836 through SEQ ID NO: 841, SEQ ID NO: 843 through SEQ ID NO: 851, SEQ ID NO: 853, SEQ ID NO: 855 through SEQ ID NO: 857, SEQ ID NO:

859 through SEQ ID NO: 862, SEQ ID NO: 866, SEQ ID NO: 868 through SEQ ID NO: 871, SEQ ID NO: 873 through SEQ ID NO: 876, and SEQ ID NO: 879. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 836 through SEQ ID NO: 841, SEQ ID NO: 843 through SEQ ID NO: 851, SEQ ID NO: 853, SEQ ID NO: 855 through SEQ ID NO: 857, SEQ ID NO: 859 through SEQ ID NO: 862, SEQ ID NO: 866, SEQ ID NO: 868 through SEQ ID NO: 871, SEQ ID NO: 873 through SEQ ID NO: 876, and SEQ ID NO: 879, such nucleic acids are contained in SEQ ID NO: 351 through SEQ ID NO: 383.

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: 385, SEQ ID NO: 390, SEQ ID NO: 401, SEQ ID NO: 407, SEQ ID NO: 409 through SEQ ID NO: 410, SEQ ID NO: 413, SEQ ID NO: 431, SEQ ID NO: 435, SEQ ID NO: 442, SEQ ID NO: 445, SEQ ID NO: 449, SEQ ID NO: 463 through SEQ ID NO: 464, SEQ ID NO: 467, SEQ ID NO: 470, SEQ ID NO: 474, SEQ ID NO: 476 through SEQ ID NO: 477, SEQ ID NO: 480, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 502, SEQ ID NO: 507 through SEQ ID NO: 508, SEQ ID NO: 511, SEQ ID NO: 515, SEQ ID NO: 517, SEQ ID NO: 521, SEQ ID NO: 526, SEQ ID NO: 534, SEQ ID NO: 538, SEQ ID NO: 541, SEQ ID NO: 545, SEQ ID NO: 549, SEQ ID NO: 551 through SEQ ID NO: 552, SEQ ID NO: 557, SEQ ID NO: 559, SEQ ID NO: 561, SEQ ID NO: 569, SEQ ID NO: 571, SEQ ID NO: 580, SEQ ID NO: 584, SEQ ID NO: 594 through SEQ ID NO: 595, SEQ ID NO: 615 through SEQ ID NO: 616, SEQ ID NO: 624, and SEQ ID NO: 626. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 385, SEQ ID NO: 390, SEQ ID NO: 401, SEQ ID NO: 407, SEQ ID NO: 409 through SEQ ID NO: 410, SEQ ID NO: 413, SEQ ID NO: 431, SEQ ID NO: 435, SEQ ID NO: 442, SEQ ID NO: 445, SEQ ID NO: 449, SEQ ID NO: 463 through SEQ ID NO: 464, SEQ ID NO: 467, SEQ ID NO: 470, SEQ ID NO: 474, SEQ ID NO: 476 through SEQ ID NO: 477, SEQ ID NO: 480, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 502, SEQ ID NO: 507 through SEQ ID NO: 508, SEQ ID NO: 511, SEQ ID NO: 515, SEQ ID NO: 517, SEQ ID NO: 521, SEQ ID NO: 526, SEQ ID NO: 534, SEQ ID NO: 538, SEQ ID NO: 541, SEQ ID NO: 545, SEQ ID NO: 549, SEQ ID NO: 551 through SEQ ID NO: 552, SEQ ID NO: 557, SEQ ID NO: 559, SEQ ID NO: 561, SEQ ID NO: 569, SEQ ID NO: 571, SEQ ID NO: 580, SEQ ID NO: 584, SEQ ID NO: 594 through SEQ ID NO: 595, SEQ ID NO: 615 through SEQ ID NO: 616, SEQ ID NO: 624, and SEQ ID NO: 626, such nucleic acids are contained in SEQ ID NO: 881 through SEQ ID NO: 930.

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: 628, SEQ ID NO: 632, SEQ ID NO: 634, SEQ ID NO: 637,

SEQ ID NO: 641, SEQ ID NO: 644 through SEQ ID NO: 646, SEQ ID NO: 648, SEQ ID NO: 652, SEQ ID NO: 662, SEQ ID NO: 671 through SEQ ID NO: 672, SEQ ID NO: 675, SEQ ID NO: 677, SEQ ID NO: 684 through SEQ ID NO: 686, SEQ ID NO: 693, SEQ ID NO: 703 through SEQ ID NO: 704, SEQ ID NO: 709 through SEQ ID NO: 711, SEQ ID NO: 715, SEQ ID NO: 723 through SEQ ID NO: 724, SEQ ID NO: 731, SEQ ID NO: 734, SEQ ID NO: 745, SEQ ID NO: 753 through SEQ ID NO: 754, SEQ ID NO: 758, SEQ ID NO: 760, SEQ ID NO: 764 through SEQ ID NO: 766, SEQ ID NO: 774, SEQ ID NO: 776, SEQ ID NO: 778, SEQ ID NO: 785, SEQ ID NO: 788, SEQ ID NO: 793, SEQ ID NO: 795, SEQ ID NO: 797, SEQ ID NO: 806, SEQ ID NO: 812, SEQ ID NO: 820, SEQ ID NO: 823, and SEQ ID NO: 827. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 628, SEQ ID NO: 632, SEQ ID NO: 634, SEQ ID NO: 637, SEQ ID NO: 641, SEQ ID NO: 644 through SEQ ID NO: 646, SEQ ID NO: 648, SEQ ID NO: 652, SEQ ID NO: 662, SEQ ID NO: 671 through SEQ ID NO: 672, SEQ ID NO: 675, SEQ ID NO: 677, SEQ ID NO: 684 through SEQ ID NO: 686, SEQ ID NO: 693, SEQ ID NO: 703 through SEQ ID NO: 704, SEQ ID NO: 709 through SEQ ID NO: 711, SEQ ID NO: 715, SEQ ID NO: 723 through SEQ ID NO: 724, SEQ ID NO: 731, SEQ ID NO: 734, SEQ ID NO: 745, SEQ ID NO: 753 through SEQ ID NO: 754, SEQ ID NO: 758, SEQ ID NO: 760, SEQ ID NO: 764 through SEQ ID NO: 766, SEQ ID NO: 774, SEQ ID NO: 776, SEQ ID NO: 778, SEQ ID NO: 785, SEQ ID NO: 788, SEQ ID NO: 793, SEQ ID NO: 795, SEQ ID NO: 797, SEQ ID NO: 806, SEQ ID NO: 812, SEQ ID NO: 820, SEQ ID NO: 823, and SEQ ID NO: 827, such nucleic acids are contained in SEQ ID NO: 931 through SEQ ID NO: 980.

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: 833 through SEQ ID NO: 834, SEQ ID NO: 842, SEQ ID NO: 852, SEQ ID NO: 854, SEQ ID NO: 858, SEQ ID NO: 863, SEQ ID NO: 864 through SEQ ID NO: 865, SEQ ID NO: 867, SEQ ID NO: 872, SEQ ID NO: 877 through SEQ ID NO: 878, and SEQ ID NO: 880. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 833 through SEQ ID NO: 834, SEQ ID NO: 842, SEQ ID NO: 852, SEQ ID NO: 854, SEQ ID NO: 858, SEQ ID NO: 863, SEQ ID NO: 864 through SEQ ID NO: 865, SEQ ID NO: 867, SEQ ID NO: 872, SEQ ID NO: 877 through SEQ ID NO: 878, and SEQ ID NO: 880, such nucleic acids are contained in SEQ ID NO: 981 through SEQ ID NO: 994.

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: 1446 through SEQ ID NO: 1461, SEQ ID NO: 1463, and SEQ ID NO: 1465 through SEQ ID NO: 1495. 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: 1446 through SEQ ID NO: 1461, SEQ ID NO: 1463, and SEQ ID NO: 1465 through SEQ ID NO: 1495, such nucleic acids are contained in SEQ ID NO: 995 through SEQ ID NO: SEQ ID NO: 1010, SEQ ID NO: 1012, and SEQ ID NO: 1014 through SEQ ID NO: 1044.

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: 1497 through SEQ ID NO: 1515, and SEQ ID NO: 1517 through SEQ ID NO: 1545. 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: 1497 through SEQ ID NO: 1515, and SEQ ID NO: 1517 through SEQ ID NO: 1545, such nucleic acids are contained in SEQ ID NO: 1046 through SEQ ID NO: 1064, and SEQ ID NO: 1066 through SEQ ID NO: 1094.

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: 1546 through SEQ ID NO: 1595. 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: 1546 through SEQ ID NO: 1595, such nucleic acids are contained in SEQ ID NO: 1095 through SEQ ID NO: 1144.

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: 1596 through SEQ ID NO: 1617, SEQ ID NO: 1620 through SEQ ID NO: 1645. 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: 1596 through SEQ ID NO: 1617, SEQ ID NO: 1620 through SEQ ID NO: 1645, such nucleic acids are contained in SEQ ID NO: 1145 through SEQ ID NO: 1166, and SEQ ID NO: 1169 through SEQ ID NO: 1194.

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: 1646 through SEQ ID NO: 1681, and SEQ ID NO: 1683 through SEQ ID NO: 1695. 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: 1646 through SEQ ID NO: 1681, and SEQ ID NO: 1683 through SEQ ID NO: 1695, such nucleic acids are contained in SEQ ID NO: 1195 through SEQ ID NO: 1230, and SEQ ID NO: 1232 through SEQ ID NO: 1244.

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: 1696 through SEQ ID NO: 1745. 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: 1696 through SEQ ID NO: 1745, such nucleic acids are contained in SEQ ID NO: 1245 through SEQ ID NO: 1294.

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: 1746 through SEQ ID NO: 1783, and SEQ ID NO: 1786 through SEQ ID NO: 1795. 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: 1746 through SEQ ID NO: 1783, and SEQ ID NO: 1786 through SEQ ID NO: 1795, such nucleic acids are contained in SEQ ID NO: 1295 through SEQ ID NO: 1332, and SEQ ID NO: 1335 through SEQ ID NO: 1344.

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: 1796 through SEQ ID NO: 1817, SEQ ID NO: 1819, SEQ ID NO: 1821, SEQ ID NO: 1823 through SEQ ID NO: 1836, and SEQ ID NO: 1838 through SEQ ID NO: 1845. 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: 1796 through SEQ ID NO: 1817, SEQ ID NO: 1819, SEQ ID NO: 1821, SEQ ID NO: 1823 through SEQ ID NO: 1836, and SEQ ID NO: 1838 through SEQ ID NO: 1845, such nucleic acids are contained in SEQ ID NO: 1345 through SEQ ID NO: 1366, SEQ ID NO: 1368, SEQ ID NO: 1370, SEQ ID NO: 1372 through SEQ ID NO: 1385, and SEQ ID NO: 1387 through SEQ ID NO: 1394.

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: 1846 through SEQ ID NO: 1896. 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: 1846 through SEQ ID NO: 1896, such nucleic acids are contained in SEQ ID NO: 1395 through SEQ ID NO: 1445.

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 the invention 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 of the invention 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: 1450. Therefore, this invention encompasses a recombinant or substantially pure preparation of an *H. pylori* polypeptide of SEQ ID NO: 1450. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide of SEQ ID NO: 1450.

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: 1546 through SEQ ID NO: 1595) or nucleic acids (e.g., SEQ ID NO: 1095-SEQ ID NO: 1144), 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: 1846 through SEQ ID NO: 1896 can be divided into one or more subgroups as follows: SEQ ID NO: 1846-SEQ ID NO: 1860; SEQ ID NO: 1861-SEQ ID NO: 1875; SEQ ID NO: 1876-SEQ ID NO: 1885; SEQ ID NO: 1886-SEQ ID NO: 1896; or any combinations thereof.

Particularly perferred 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: 1020, SEQ ID NO: 1021, SEQ ID NO: 1036, SEQ ID NO: 1050, SEQ ID NO: 1071, SEQ ID NO: 1101, SEQ ID NO: 1135, SEQ ID NO: 1276, SEQ ID NO: 1150, SEQ ID NO: 1187, SEQ ID NO: 1192, SEQ ID NO: 1361, SEQ ID NO: 1379, SEQ ID NO: 1399, SEQ ID NO: 1403, SEQ ID NO: 1400, SEQ ID NO: 1189, SEQ ID NO: 1002, SEQ ID NO: 1213, SEQ ID NO: 1214, SEQ ID NO: 1215, SEQ ID NO: 1234, SEQ ID NO: 1236, SEQ ID NO: 1237, SEQ ID NO: 1224, SEQ ID NO: 1251, SEQ ID NO: 1262, SEQ ID NO: 1149, SEQ ID NO: 1220, SEQ ID NO: 1240, SEQ ID NO: 1164, SEQ ID NO: 1165, SEQ ID NO: 1404, SEQ ID NO: 1144, SEQ ID NO: 1182, SEQ ID NO: 1157, SEQ ID NO: 1160, SEQ ID NO: 1300, SEQ ID NO: 1321, SEQ ID NO: 1323, SEQ ID NO: 1329, SEQ ID NO: 1332, SEQ ID NO: 1345, SEQ ID NO: 1358, SEQ ID NO: 1375, SEQ ID NO: 1417, SEQ ID NO: 1283, SEQ ID NO: 1335, SEQ ID NO: 1368, SEQ ID NO: 1179, SEQ ID NO: 1255, SEQ ID NO: 1258, SEQ ID NO: 1044, SEQ ID NO: 1273, SEQ ID NO: 1219, SEQ ID NO: 1274, SEQ ID NO: 1210, SEQ ID NO: 1422, SEQ ID NO: 1302, SEQ ID NO: 1308, SEQ ID NO: 1310, SEQ ID NO: 1331, SEQ ID NO: 1432, SEQ ID NO: 1052, SEQ ID NO: 1091, SEQ ID NO: 1421, SEQ ID NO: 1069, SEQ ID NO: 1005, SEQ ID NO: 1007, SEQ ID NO: 1166, SEQ ID NO: 1177, SEQ ID NO: 1193, SEQ ID NO: 1206, SEQ ID NO: 1207, SEQ ID NO: 1304, SEQ ID NO: 1305, SEQ ID NO: 1346, SEQ ID NO: 1348, SEQ ID NO: 1350, SEQ ID NO: 1032, SEQ ID NO: 1053, SEQ ID NO: 1081, SEQ ID NO: 1124, SEQ ID NO: 1382, SEQ ID NO: 1437, SEQ ID NO: 1263, SEQ ID NO: 1173, SEQ ID NO: 1405, SEQ ID NO: 1406, SEQ ID NO: 1410, SEQ ID NO: 1086, SEQ ID NO: 1322, SEQ ID NO: 1266, SEQ ID NO: 1282, SEQ ID NO: 1271, SEQ ID NO: 1208, SEQ ID NO: 1126, SEQ ID NO: 1270, SEQ ID NO: 1278, SEQ ID NO: 1419, SEQ ID NO: 1125, SEQ ID NO: 1181, SEQ ID NO: 1416, SEQ ID NO: 1096, SEQ ID NO: 1082, SEQ ID NO: 1146, SEQ ID NO: 1145, SEQ ID NO: 1108, SEQ ID NO: 1148, SEQ ID NO: 1337, SEQ ID NO: 1338, SEQ ID NO: 1424, SEQ ID NO: 1000, SEQ ID NO: 1027, SEQ ID NO: 1175, SEQ

ID NO: 1330, SEQ ID NO: 217, SEQ ID NO: 217, SEQ ID NO: 367, SEQ ID NO: 911,SEQ ID NO: 944, SEQ ID NO: 18, SEQ ID NO: 107, SEQ ID NO: 894, SEQ ID NO: 943, SEQ ID NO: 203, SEQ ID NO: 85, SEQ ID NO: 290, SEQ ID NO: 5, SEQ ID NO: 199, SEQ ID NO: 992, SEQ ID NO: 934, SEQ ID NO: 899, SEQ ID NO: 302, SEQ ID NO: 215, SEQ ID NO: 893, SEQ ID NO: 984, SEQ ID NO: 97,SEQ ID NO: 22, SEQ ID NO: 49, SEQ ID NO: 309, SEQ ID NO: 150, SEQ ID NO: 240, SEQ ID NO: 957, SEQ ID NO: 57, SEQ ID NO: 2, SEQ ID NO: 92, SEQ ID NO: 255, SEQ ID NO: 164, SEQ ID NO: 201, SEQ ID NO: 278, SEQ ID NO: 245, SEQ ID NO: 921, SEQ ID NO: 896, SEQ ID NO: 248, SEQ ID NO: 159, SEQ ID NO: 979, SEQ ID NO: 194, SEQ ID NO: 194, SEQ ID NO: 946, SEQ ID NO: 916, SEQ ID NO: 76, SEQ ID NO: 905, SEQ ID NO: 914, SEQ ID NO: 931, SEQ ID NO: 50, SEQ ID NO: 250, SEQ ID NO: 969, SEQ ID NO: 66,SEQ ID NO: 275, SEQ ID NO: 330, SEQ ID NO: 204, SEQ ID NO: 383, SEQ ID NO: 303, SEQ ID NO: 70, SEQ ID NO: 983, SEQ ID NO: 972, SEQ ID NO: 929, SEQ ID NO: 972, SEQ ID NO: 936, SEQ ID NO: 267, SEQ ID NO: 197, SEQ ID NO: 55, SEQ ID NO: 54, SEQ ID NO: 210, SEQ ID NO: 90, SEQ ID NO: 15, SEQ ID NO: 913, SEQ ID NO: 227, SEQ ID NO: 79, SEQ ID NO: 191, SEQ ID NO: 238, SEQ ID NO: 274, SEQ ID NO: 27, SEQ ID NO: 258, SEQ ID NO: 295, SEQ ID NO: 10, SEQ ID NO: 160, SEQ ID NO: 225, SEQ ID NO: 964, SEQ ID NO: 166, SEQ ID NO: 56, SEQ ID NO: 980,SEQ ID NO: 903, SEQ ID NO: 261, SEQ ID NO: 71, SEQ ID NO: 955, SEQ ID NO: 361, SEQ ID NO: 58, SEQ ID NO: 114, SEQ ID NO: 940, SEQ ID NO: 960, SEQ ID NO: 144, SEQ ID NO: 362, SEQ ID NO: 40, SEQ ID NO: 285, SEQ ID NO: 11, SEQ ID NO: 161, SEQ ID NO: 974, SEQ ID NO: 111, SEQ ID NO: 316, SEQ ID NO: 257, SEQ ID NO: 78, SEQ ID NO: 966, SEQ ID NO: 352, SEQ ID NO: 981, SEQ ID NO: 158, SEQ ID NO: 989, SEQ ID NO: 963, SEQ ID NO: 48, SEQ ID NO: 68, SEQ ID NO: 135, SEQ ID NO: 910, SEQ ID NO: 236, SEQ ID NO: 241, SEQ ID NO: 949, SEQ ID NO: 945, SEQ ID NO: 207, SEQ ID NO: 977, SEQ ID NO: 978, SEQ ID NO: 994, SEQ ID NO: 163, SEQ ID NO: 256, SEQ ID NO: 287, SEQ ID NO: 184, SEQ ID NO: 45, SEQ ID NO: 136, SEQ ID NO: 214, SEQ ID NO: 16, SEQ ID NO: 192, SEQ ID NO: 373, SEQ ID NO: 892, SEQ ID NO: 239, SEQ ID NO: 34, SEQ ID NO: 340, SEQ ID NO: 41, SEQ ID NO: 332, SEQ ID NO: 134, and SEQ ID NO: 330.

In one embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* flagella-associated polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1020, SEQ ID NO: 1021, SEQ ID NO: 1036, SEQ ID NO: 1050, SEQ ID NO: 1071, SEQ ID NO: 1101, SEQ ID NO: 1135, SEQ ID NO: 1276, SEQ ID NO: 1150, SEQ ID NO: 1187, SEQ ID NO: 1192, SEQ ID NO: 1361, SEQ ID NO: 1379, SEQ ID NO: 1399, SEQ ID NO: 1403, SEQ ID NO: 1400, SEQ ID NO: 1189, SEQ ID NO: 217, SEQ ID NO: 367, SEQ ID NO: 911,SEQ ID NO: 944, SEQ ID NO: 18, SEQ ID NO: 107, SEQ ID NO: 894, SEQ ID NO: 943, SEQ ID NO:

203, SEQ ID NO: 85, SEQ ID NO: 290, SEQ ID NO: 5, SEQ ID NO: 199, SEQ ID NO: 992, SEQ ID NO: 934, SEQ ID NO: 899, SEQ ID NO: 302, and SEQ ID NO: 215.

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: 1002, SEQ ID NO: 1213, SEQ ID NO: 1214, SEQ ID NO: 1215, SEQ ID NO: 1234, SEQ ID NO: 1236, SEQ ID NO: 1237, SEQ ID NO: 1224, SEQ ID NO: 1251, SEQ ID NO: 1262, SEQ ID NO: 1149, SEQ ID NO: 1220, SEQ ID NO: 1240, SEQ ID NO: 1164, SEQ ID NO: 1165, SEQ ID NO: 1404, SEQ ID NO: 1144, SEQ ID NO: 1182, SEQ ID NO: 1157, SEQ ID NO: 1160, SEQ ID NO: 1300, SEQ ID NO: 1321, SEQ ID NO: 1323, SEQ ID NO: 1329, SEQ ID NO: 1332, SEQ ID NO: 1345, SEQ ID NO: 1358, SEQ ID NO: 1375, SEQ ID NO: 1417, SEQ ID NO: 1283, SEQ ID NO: 1335, SEQ ID NO: 1368, SEQ ID NO: 1179, SEQ ID NO: 1255, SEQ ID NO: 1258, SEQ ID NO: 1044, SEQ ID NO: 1273, SEQ ID NO: 893, SEQ ID NO: 984, SEQ ID NO: 97.SEQ ID NO: 22, SEQ ID NO: 49, SEQ ID NO: 309, SEQ ID NO: 150, SEQ ID NO: 240, SEQ ID NO: 957, SEQ ID NO: 57, SEQ ID NO: 2, SEQ ID NO: 92, SEQ ID NO: 255, SEQ ID NO: 164, SEQ ID NO: 201, SEQ ID NO: 278, SEQ ID NO: 245, SEQ ID NO: 921, SEQ ID NO: 896, SEQ ID NO: 248, SEQ ID NO: 159, SEQ ID NO: 979, SEQ ID NO: 194, SEQ ID NO: 194, SEQ ID NO: 946, SEQ ID NO: 916, SEQ ID NO: 76, SEQ ID NO: 905, SEQ ID NO: 914, SEQ ID NO: 931, SEQ ID NO: 50, SEQ ID NO: 250, SEQ ID NO: 969, SEQ ID NO: 66,SEQ ID NO: 275, SEQ ID NO: 330, SEQ ID NO: 204, SEQ ID NO: 383, SEQ ID NO: 303, SEQ ID NO: 70, SEQ ID NO: 983, SEQ ID NO: 972, SEQ ID NO: 929, SEQ ID NO: 972, SEQ ID NO: 936, SEQ ID NO: 267, SEQ ID NO: 197, SEQ ID NO: 55, SEQ ID NO: 54, and SEQ ID NO: 210.

In yet another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* transporter polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1219, SEQ ID NO: 1274, SEQ ID NO: 1210, SEQ ID NO: 1422, SEQ ID NO: 1302, SEQ ID NO: 1308, SEQ ID NO: 1310, SEQ ID NO: 1331, SEQ ID NO: 1432, SEQ ID NO: 1052, SEQ ID NO: 1091, SEQ ID NO: 1421, SEQ ID NO: 1069, SEQ ID NO: 1005, SEQ ID NO: 1007, SEQ ID NO: 1166, SEQ ID NO: 1177, SEQ ID NO: 1193, SEQ ID NO: 1206, SEQ ID NO: 1207, SEQ ID NO: 1304, SEQ ID NO: 1305, SEQ ID NO: 1346, SEQ ID NO: 1348, SEQ ID NO: 1350, SEQ ID NO: 1032, SEQ ID NO: 1053, SEQ ID NO: 1081, SEQ ID NO: 1124, SEQ ID NO: 1382, SEQ ID NO: 1437, SEQ ID NO: 1263, SEQ ID NO: 90, SEQ ID NO: 15, SEQ ID NO: 913, SEQ ID NO: 227, SEQ ID NO: 79, SEQ ID NO: 191, SEQ ID NO: 238, SEQ ID NO: 274, SEQ ID NO: 27, SEQ ID NO: 258, SEQ ID NO: 295, SEQ ID NO: 10, SEQ ID NO: 160, SEQ ID NO: 225, SEQ ID NO: 964, SEQ ID NO: 166, SEQ ID NO: 56, SEQ ID NO: 980,SEQ ID NO: 903, SEQ ID NO: 261, SEQ ID NO: 71, SEQ ID NO: 955, SEQ ID NO: 361, SEQ ID NO: 58, SEQ ID NO: 114, SEQ ID NO: 940, SEQ ID NO: 960, SEQ ID NO: 144, SEQ ID NO: 362, SEQ ID NO: 40, SEQ ID NO: 285, SEQ ID NO: 11, SEQ

ID NO: 161, SEQ ID NO: 974, SEQ ID NO: 111, SEQ ID NO: 316, SEQ ID NO: 257, SEQ ID NO: 78, and SEQ ID NO: 966.

In yet a further 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: 1173, SEQ ID NO: 1405, SEQ ID NO: 1406, SEQ ID NO: 1410, SEQ ID NO: 1086, SEQ ID NO: 1322, SEQ ID NO: 1266, SEQ ID NO: 1282, SEQ ID NO: 1271, SEQ ID NO: 1208, SEQ ID NO: 1126, SEQ ID NO: 1270, SEQ ID NO: 1278, SEQ ID NO: 1419, SEQ ID NO: 1125, SEQ ID NO: 1181, SEQ ID NO: 1416, SEQ ID NO: 1096, SEQ ID NO: 1082, SEQ ID NO: 1146, SEQ ID NO: 1145, SEQ ID NO: 1108, SEQ ID NO: 1148, SEQ ID NO: 1337, SEQ ID NO: 1338, SEQ ID NO: 1424, SEQ ID NO: 1000, SEQ ID NO: 1027, SEQ ID NO: 1175, SEQ ID NO: 1330, SEQ ID NO: 352, SEQ ID NO: 981, SEQ ID NO: 158, SEQ ID NO: 989, SEQ ID NO: 963, SEQ ID NO: 48, SEQ ID NO: 68, SEQ ID NO: 135, SEQ ID NO: 910, SEQ ID NO: 236, SEQ ID NO: 241, SEQ ID NO: 949, SEQ ID NO: 945, SEQ ID NO: 207, and SEQ ID NO: 977.

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: 1147, SEQ ID NO: 1288, SEQ ID NO: 1324, SEQ ID NO: 1363, SEQ ID NO: 997, SEQ ID NO: 1015, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1099, SEQ ID NO: 1229, SEQ ID NO: 1250, SEQ ID NO: 1268, SEQ ID NO: 1293, SEQ ID NO: 1339, SEQ ID NO: 1408, SEQ ID NO: 1429, SEQ ID NO: 1434, SEQ ID NO: 1228, SEQ ID NO: 1031, SEQ ID NO: 1034, SEQ ID NO: 1008, SEQ ID NO: 1061, SEQ ID NO: 1064, SEQ ID NO: 1191, SEQ ID NO: 1217, SEQ ID NO: 1365, SEQ ID NO: 1394, SEQ ID NO: 1414, SEQ ID NO: 1415, SEQ ID NO: 1435, SEQ ID NO: 1058, SEQ ID NO: 1059, SEQ ID NO: 1080, SEQ ID NO: 1128, SEQ ID NO: 1133, SEQ ID NO: 1211, SEQ ID NO: 1252, SEQ ID NO: 1253, SEQ ID NO: 1286, SEQ ID NO: 1289, SEQ ID NO: 1291, SEQ ID NO: 1303, SEQ ID NO: 1396, SEQ ID NO: 996, SEQ ID NO: 1095, SEQ ID NO: 1156, SEQ ID NO: 1158, SEQ ID NO: 1159, SEQ ID NO: 1277, SEQ ID NO: 1038, SEQ ID NO: 1257, SEQ ID NO: 1357, SEQ ID NO: 1436, SEQ ID NO: 1047, SEQ ID NO: 1055, SEQ ID NO: SEQ ID NO: 1141, SEQ ID NO: 1227, SEQ ID NO: 1327, SEQ ID NO: 1412, SEQ ID NO: 1003, SEQ ID NO: 1087, SEQ ID NO: 1116, SEQ ID NO: 1130, SEQ ID NO: 1132, SEQ ID NO: 1185, SEQ ID NO: 1188, SEQ ID NO: 1198, SEQ ID NO: 1218, SEQ ID NO: 1244, SEQ ID NO: 1306, SEQ ID NO: 1325, SEQ ID NO: 1397, SEQ ID NO: 1398, SEQ ID NO: 1407, SEQ ID NO: 1433, SEQ ID NO: 1216, SEQ ID NO: 1239, SEQ ID NO: 1362, SEQ ID NO: 1017, SEQ ID NO: 1019, SEQ ID NO: 1360, SEQ ID NO: 1423, SEQ ID NO: 1425, SEQ ID NO: 1374, SEQ ID NO: 1028, SEQ ID NO: 1037, SEQ ID NO: 1077, SEQ ID NO: 1115, SEQ ID NO: 1232, SEQ ID NO: 1241, SEQ ID NO: 1267, SEQ ID NO: 1163, SEQ ID NO: 1068, SEQ ID NO: 1025, SEQ ID NO: 1042, SEQ ID NO: 1046, SEQ ID NO:

1056, SEQ ID NO: 1039, SEQ ID NO: 1072, SEQ ID NO: 1073, SEQ ID NO: 1092, SEQ ID NO: 1100, SEQ ID NO: 1102, SEQ ID NO: 1103, SEQ ID NO: 1104, SEQ ID NO: 1111, SEQ ID NO: 1119, SEQ ID NO: 1136, SEQ ID NO: 1137, SEQ ID NO: 1140, SEQ ID NO: 1142, SEQ ID NO: 1233, SEQ ID NO: 1238, SEQ ID NO: 1243, SEQ ID NO: 1245, SEQ ID NO: 1247, SEQ ID NO: 1249, SEQ ID NO: 1261, SEQ ID NO: 1269, SEQ ID NO: 1279, SEQ ID NO: 1284, SEQ ID NO: 1290, SEQ ID NO: 1297, SEQ ID NO: 1328, SEQ ID NO: 1370, SEQ ID NO: 1372, SEQ ID NO: 1377, SEQ ID NO: 1383, SEQ ID NO: 1384, SEQ ID NO: 1385, SEQ ID NO: 1388, SEQ ID NO: 1401, SEQ ID NO: 1402, SEQ ID NO: 1418, SEQ ID NO: 1420, SEQ ID NO: 1427, SEQ ID NO: 1070, SEQ ID NO: 1151, SEQ ID NO: 1176, SEQ ID NO: 999, SEQ ID NO: 1006, SEQ ID NO: 1012, SEQ ID NO: 1018, SEQ ID NO: 1030, SEQ ID NO: 1033, SEQ ID NO: 1041, SEQ ID NO: 1049, SEQ ID NO: 1054, SEQ ID NO: 1057, SEQ ID NO: 1090, SEQ ID NO: 1097, SEQ ID NO: 1129, SEQ ID NO: 1139, SEQ ID NO: 1143, SEQ ID NO: 1152, SEQ ID NO: 1153, SEQ ID NO: 1155, SEQ ID NO: 1161, SEQ ID NO: 1162, SEQ ID NO: 1169, SEQ ID NO: 1170, SEQ ID NO: 1171, SEQ ID NO: 1180, SEQ ID NO: 1194, SEQ ID NO: 1195, SEQ ID NO: 1199, SEQ ID NO: 1200, SEQ ID NO: 1201, SEQ ID NO: 1202, SEQ ID NO: 1205, SEQ ID NO: 1312, SEQ ID NO: 1336, SEQ ID NO: 1349, SEQ ID NO: 1355, SEQ ID NO: 1359, SEQ ID NO: 1413, SEQ ID NO: 1426, SEQ ID NO: 1430, SEQ ID NO: 882, SEQ ID NO: 382, SEQ ID NO: 130, SEQ ID NO: 230, SEQ ID NO: 269, SEQ ID NO: 312, SEQ ID NO: 211, SEQ ID NO: 959, SEQ ID NO: 938, SEQ ID NO: 110, SEQ ID NO: 244, SEQ ID NO: 328, SEQ ID NO: 235, SEQ ID NO: 315, SEQ ID NO: 296, SEQ ID NO: 976, SEQ ID NO: 321, SEQ ID NO: 43, SEQ ID NO: 281, SEQ ID NO: 326, SEQ ID NO: 272, SEQ ID NO: 344, SEQ ID NO: 139, SEQ ID NO: 30, SEQ ID NO: 220, SEQ ID NO: 364, SEQ ID NO: 369, SEQ ID NO: 372, SEQ ID NO: 991, SEQ ID NO: 128, SEQ ID NO: 347, SEQ ID NO: 52, SEQ ID NO: 12, SEQ ID NO: 247, SEQ ID NO: 64, SEQ ID NO: 101, SEQ ID NO: 338, SEQ ID NO: 83, SEQ ID NO: 46, SEQ ID NO: 348, SEQ ID NO: 223, SEQ ID NO: 39, SEQ ID NO: 232, SEQ ID NO: 168, SEQ ID NO: 65, SEQ ID NO: 952, SEQ ID NO: 341, SEQ ID NO: 69, SEQ ID NO: 924, SEQ ID NO: 4, SEQ ID NO: 197, SEQ ID NO: 313, SEQ ID NO: 119, SEQ ID NO: 188, SEQ ID NO: 956, SEQ ID NO: 935, SEQ ID NO: 246, SEQ ID NO: 196, SEQ ID NO: 376, SEQ ID NO: 172, SEQ ID NO: 25, SEQ ID NO: 126, SEQ ID NO: 951, SEQ ID NO: 147, SEQ ID NO: 895, SEQ ID NO: 14, SEQ ID NO: 154, SEQ ID NO: 277, SEQ ID NO: 363, SEQ ID NO: 342, SEQ ID NO: 378, SEQ ID NO: 130, SEQ ID NO: 198, SEQ ID NO: 243, SEQ ID NO: 19, SEQ ID NO: 9, SEQ ID NO: 149, SEQ ID NO: 167, SEQ ID NO: 349, SEQ ID NO: 209, SEQ ID NO: 990, SEQ ID NO: 185, SEQ ID NO: 883, SEQ ID NO: 8, SEQ ID NO: 887, SEQ ID NO: 350, SEQ ID NO: 987, SEQ ID NO: 63, SEQ ID NO: 249, SEQ ID NO: 118, SEQ ID NO: 132, SEQ ID NO: 47, SEQ ID NO: 106, SEQ ID NO: 324, SEQ ID NO: 155, SEQ ID NO: 121, SEQ ID NO: 153, SEQ ID NO: 87, SEQ ID NO: 986, SEQ ID NO: 262, SEQ ID NO: 333, SEQ ID NO: 36, SEQ ID NO: 982, SEQ ID

NO: 180, SEQ ID NO: 84, SEQ ID NO: 900, SEQ ID NO: 20, SEQ ID NO: 7, SEQ ID NO: 61, SEQ ID NO: 253, SEQ ID NO: 120, SEQ ID NO: 268, SEQ ID NO: 299, SEQ ID NO: 942, SEQ ID NO: 173, SEQ ID NO: 187, SEQ ID NO: 187, SEQ ID NO: 234, SEQ ID NO: 112, SEQ ID NO: 324, SEQ ID NO: 971, SEQ ID NO: 62, SEQ ID NO: 308, SEQ ID NO: 74, SEQ ID NO: 1, SEQ ID NO: 266, SEQ ID NO: 337, SEQ ID NO: 93, SEQ ID NO: 44, SEQ ID NO: 335, SEQ ID NO: 368, SEQ ID NO: 208, SEQ ID NO: 358, SEQ ID NO: 923, SEQ ID NO: 310, SEQ ID NO: 26, SEQ ID NO: 279, SEQ ID NO: 890, SEQ ID NO: 325, SEQ ID NO: 109, SEQ ID NO: 143, SEQ ID NO: 918, SEQ ID NO: 252, SEQ ID NO: 953, SEQ ID NO: 902, SEQ ID NO: 174, SEQ ID NO: 73, SEQ ID NO: 898, SEQ ID NO: 300, SEQ ID NO: 356, SEQ ID NO: 298, SEQ ID NO: 354, SEQ ID NO: 138, SEQ ID NO: 319, SEQ ID NO: 80, SEQ ID NO: 933, SEQ ID NO: 891, SEQ ID NO: 366, SEQ ID NO: 113, SEQ ID NO: 320, SEQ ID NO: 915, SEQ ID NO: 351, SEQ ID NO: 162, SEQ ID NO: 965, SEQ ID NO: 67, SEQ ID NO: 314, SEQ ID NO: 904, SEQ ID NO: 345, SEQ ID NO: 374, SEQ ID NO: 962, SEQ ID NO: 270, SEQ ID NO: 186, SEQ ID NO: 60, SEQ ID NO: 379, SEQ ID NO: 889, SEQ ID NO: 967, SEQ ID NO: 973, SEQ ID NO: 280, SEQ ID NO: 170, SEQ ID NO: 985, and SEQ ID NO: 932.

In one embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in energy conversion encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1147, SEQ ID NO: 1288, SEQ ID NO: 1324, SEQ ID NO: 1363, SEQ ID NO: 882, SEQ ID NO: 382, SEQ ID NO: 130, and SEQ ID NO: 230.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in amino acid metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 997, SEQ ID NO: 1015, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1099, SEQ ID NO: 1229, SEQ ID NO: 1250, SEQ ID NO: 1268, SEQ ID NO: 1293, SEQ ID NO: 1339, SEQ ID NO: 1408, SEQ ID NO: 1429, SEQ ID NO: 1434, SEQ ID NO: 1228, SEQ ID NO: 1031, SEQ ID NO: 1034, SEQ ID NO: 1008, SEQ ID NO: 269, SEQ ID NO: 312, SEQ ID NO: 211, SEQ ID NO: 959, SEQ ID NO: 938, SEQ ID NO: 110, SEQ ID NO: 244, SEQ ID NO: 328, SEQ ID NO: 235, SEQ ID NO: 315, SEQ ID NO: 296, SEQ ID NO: 976, SEQ ID NO: 321, SEQ ID NO: 43, SEQ ID NO: 281, SEQ ID NO: 326, and SEQ ID NO: 272.

In yet another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in nucleotide metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1061, SEQ ID NO: 1064, SEQ ID NO: 1191, SEQ ID NO: 1217, SEQ ID NO: 1365, SEQ ID NO: 1394, SEQ ID NO: 1414, SEQ ID NO: 1415, SEQ ID NO: 1435, SEQ ID NO: 1058, SEQ ID NO: 1059, SEQ ID NO: 344, SEQ ID NO: 139, SEQ ID NO: 30, SEQ ID NO: 220,

SEQ ID NO: 364, SEQ ID NO: 369, SEQ ID NO: 372, SEQ ID NO: 991, SEQ ID NO: 128, SEQ ID NO: 347, and SEQ ID NO: 52.

In yet a further embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in carbohydrate metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1080, SEQ ID NO: 1128, SEQ ID NO: 1133, SEQ ID NO: 1211, SEQ ID NO: 1252, SEQ ID NO: 1253, SEQ ID NO: 1286, SEQ ID NO: 1289, SEQ ID NO: 1291, SEQ ID NO: 1303, SEQ ID NO: 1396, SEQ ID NO: 996, SEQ ID NO: 12, SEQ ID NO: 247, SEQ ID NO: 64, SEQ ID NO: 101, SEQ ID NO: 338, SEQ ID NO: 83, SEQ ID NO: 46, SEQ ID NO: 348, SEQ ID NO: 223, SEQ ID NO: 39, SEQ ID NO: 232, and SEQ ID NO: 168.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in cofactor metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1095, SEQ ID NO: 1156, SEQ ID NO: 1158, SEQ ID NO: 1159, SEQ ID NO: 1277, SEQ ID NO: 1038, SEQ ID NO: 65, SEQ ID NO: 952, SEQ ID NO: 341, SEQ ID NO: 69, SEQ ID NO: 924, and SEQ ID NO: 4.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in lipid metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1257, SEQ ID NO: 1357, SEQ ID NO: 1436, SEQ ID NO: 197, SEQ ID NO: 313, and SEQ ID NO: 119.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in mRNA translation and ribosome biogenesis encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1047, SEQ ID NO: 1055, SEQ ID NO: SEQ ID NO: 1141, SEQ ID NO: 1227, SEQ ID NO: 1327, SEQ ID NO: 1412, SEQ ID NO: 188, SEQ ID NO: 956, SEQ ID NO: 935, SEQ ID NO: 246, SEQ ID NO: 196, and SEQ ID NO: 376.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in genome replication, transcription, recombination and repair encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1003, SEQ ID NO: 1087, SEQ ID NO: 1116, SEQ ID NO: 1130, SEQ ID NO: 1132, SEQ ID NO: 1185, SEQ ID NO: 1188, SEQ ID NO: 1198, SEQ ID NO: 1218, SEQ ID NO: 1244, SEQ ID NO: 1306, SEQ ID NO: 1325, SEQ ID NO: 1397, SEQ ID NO: 1398, SEQ ID NO: 1407, SEQ ID NO: 1433, SEQ ID NO: 172, SEQ ID NO: 25, SEQ ID NO: 126, SEQ ID NO: 951, SEQ ID NO: 147, SEQ ID NO: 895, SEQ ID NO: 14, SEQ ID NO: 154, SEQ ID NO: 277, SEQ ID NO: 363, SEQ ID NO: 342, SEQ ID NO: 378, SEQ ID NO: 130, SEQ ID NO: 198, SEQ ID NO: 243, SEQ ID NO: 19, and SEQ ID NO: 9.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in outer membrane or cell wall

biosynthesis encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1216, SEQ ID NO: 1239, SEQ ID NO: 1362, SEQ ID NO: 1017, SEQ ID NO: 1019, SEQ ID NO: 1360, SEQ ID NO: 149, SEQ ID NO: 167, SEQ ID NO: 349, SEQ ID NO: 209, SEQ ID NO: 990, SEQ ID NO: 185, SEQ ID NO: 883, and SEQ ID NO: 8.

In yet another embodiment, the *H. pylori* cytoplasmic polypeptide is an *H. pylori* chaperone polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1423, SEQ ID NO: 1425, SEQ ID NO: 1374, SEQ ID NO: 887, SEQ ID NO: 350, and SEQ ID NO: 987.

Particularly preferred is an isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* secreted or periplasmic polypeptide or a fragment thereof. Such nucleic acid is selected from the group consisting of SEQ ID NO: 1004, SEQ ID NO: 1138, SEQ ID NO: 1067, SEQ ID NO: 1078, SEQ ID NO: 1314, SEQ ID NO: 1319, SEQ ID NO: 1378, SEQ ID NO: 1105, SEQ ID NO: 1114, SEQ ID NO: 1118, SEQ ID NO: 1120, SEQ ID NO: 1123, SEQ ID NO: 1127, SEQ ID NO: 1212, SEQ ID NO: 1223, SEQ ID NO: 1225, SEQ ID NO: 1246, SEQ ID NO: 1248, SEQ ID NO: 1259, SEQ ID NO: 1264, SEQ ID NO: 1265, SEQ ID NO: 1281, SEQ ID NO: 1285, SEQ ID NO: 1294, SEQ ID NO: 1298, SEQ ID NO: 1299, SEQ ID NO: 1315, SEQ ID NO: 1316, SEQ ID NO: 1317, SEQ ID NO: 1318, SEQ ID NO: 1344, SEQ ID NO: 1351, SEQ ID NO: 1353, SEQ ID NO: 1373, SEQ ID NO: 1380, SEQ ID NO: 1387, SEQ ID NO: 1389, SEQ ID NO: 1393, SEQ ID NO: 1411, SEQ ID NO: 1428, SEQ ID NO: 1431, SEQ ID NO: 1439, SEQ ID NO: 1043, SEQ ID NO: 1183, SEQ ID NO: 1184, SEQ ID NO: 1196, SEQ ID NO: 1197, SEQ ID NO: 1203, SEQ ID NO: 995, SEQ ID NO: 998, SEQ ID NO: 1001, SEQ ID NO: 1022, SEQ ID NO: 1023, SEQ ID NO: 1029, SEQ ID NO: 1040, SEQ ID NO: 1051, SEQ ID NO: 1062, SEQ ID NO: 1154, SEQ ID NO: 1320, SEQ ID NO: 1075, SEQ ID NO: 1106, SEQ ID NO: 1109, SEQ ID NO: 1134, SEQ ID NO: 1221, SEQ ID NO: 1226, SEQ ID NO: 1235, SEQ ID NO: 1301, SEQ ID NO: 1311, SEQ ID NO: 1326, SEQ ID NO: 1341, SEQ ID NO: 1354, SEQ ID NO: 1364, SEQ ID NO: 1366, SEQ ID NO: 1376, SEQ ID NO: 1391, SEQ ID NO: 1395, SEQ ID NO: 1445, SEQ ID NO: 1079, SEQ ID NO: 1186, SEQ ID NO: 1010, SEQ ID NO: 1016, SEQ ID NO: 1172, SEQ ID NO: 1174, SEQ ID NO: 117, SEQ ID NO: 254, SEQ ID NO: 24, SEQ ID NO: 242, SEQ ID NO: 950, SEQ ID NO: 263, SEQ ID NO: 286, SEQ ID NO: 947, SEQ ID NO: 51, SEQ ID NO: 177, SEQ ID NO: 156, SEQ ID NO: 190, SEQ ID NO: 375, SEQ ID NO: 222, SEQ ID NO: 21, SEQ ID NO: 912, SEQ ID NO: 148, SEQ ID NO: 202, SEQ ID NO: 224, SEQ ID NO: 112, SEQ ID NO: 32, SEQ ID NO: 339, SEQ ID NO: 182, SEQ ID NO: 228, SEQ ID NO: 152, SEQ ID NO: 219, SEQ ID NO: 137, SEQ ID NO: 318, SEQ ID NO: 141, SEQ ID NO: 165, SEQ ID NO: 334, SEQ ID NO: 13, SEQ ID NO: 297, SEQ ID NO: 35, SEQ ID NO: 216, SEQ ID NO: 908, SEQ ID NO: 124, SEQ ID NO: 75, SEQ ID NO: 927, SEQ ID NO: 221, SEQ ID NO: 178, SEQ ID NO: 169, SEQ ID NO: 293, SEQ ID NO: 289, SEQ ID NO: 926, SEQ ID NO: 948, SEQ ID NO: 115, SEQ ID NO: 251, SEQ ID NO: 345, SEQ

ID NO: 17, SEQ ID NO: 920, SEQ ID NO: 95, SEQ ID NO: 86, SEQ ID NO: 360, SEQ ID NO: 271, SEQ ID NO: 970, SEQ ID NO: 288, SEQ ID NO: 282, SEQ ID NO: 98, SEQ ID NO: 29, SEQ ID NO: 317, SEQ ID NO: 343, SEQ ID NO: 291, SEQ ID NO: 108, SEQ ID NO: 377, SEQ ID NO: 305, SEQ ID NO: 305, SEQ ID NO: 100, SEQ ID NO: 988, SEQ ID NO: 212, SEQ ID NO: 884, SEQ ID NO: 37, SEQ ID NO: 968, SEQ ID NO: 975, SEQ ID NO: 237, SEQ ID NO: 335, SEQ ID NO: 260, SEQ ID NO: 370, SEQ ID NO: 91, SEQ ID NO: 276, SEQ ID NO: 311, SEQ ID NO: 173, SEQ ID NO: 102, SEQ ID NO: 304, SEQ ID NO: 380, SEQ ID NO: 127, SEQ ID NO: 993, SEQ ID NO: 925, SEQ ID NO: 181, and SEQ ID NO: 171.

Particularly preferred is an isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* surface or membrane polypeptide or a fragment thereof. Such nucleic acid is selected from the group consisting of SEQ ID NO: 1060, SEQ ID NO: 1110, SEQ ID NO: 1112, SEQ ID NO: 1230, SEQ ID NO: 1260, SEQ ID NO: 1280, SEQ ID NO: 1292, SEQ ID NO: 1296, SEQ ID NO: 1307, SEQ ID NO: 1442, SEQ ID NO: 1444, SEQ ID NO: 1122, SEQ ID NO: 1254, SEQ ID NO: 1256, SEQ ID NO: 1272, SEQ ID NO: 1275, SEQ ID NO: 1309, SEQ ID NO: 1313, SEQ ID NO: 1347, SEQ ID NO: 1352, SEQ ID NO: 1356, SEQ ID NO: 1438, SEQ ID NO: 1441, SEQ ID NO: 1009, SEQ ID NO: 1026, SEQ ID NO: 1048, SEQ ID NO: 1063, SEQ ID NO: 1190, SEQ ID NO: 1083, SEQ ID NO: 1113, SEQ ID NO: 1222, SEQ ID NO: 1295, SEQ ID NO: 1343, SEQ ID NO: 1392, SEQ ID NO: 1443, SEQ ID NO: 1085, SEQ ID NO: 1093, SEQ ID NO: 1117, SEQ ID NO: 1121, SEQ ID NO: 1131, SEQ ID NO: 1287, SEQ ID NO: 1440, SEQ ID NO: 1209, SEQ ID NO: 1342, SEQ ID NO: 1381, SEQ ID NO: 1390, SEQ ID NO: 1409, SEQ ID NO: 1035, SEQ ID NO: 1014, SEQ ID NO: 1088, SEQ ID NO: 1242, SEQ ID NO: 1178, SEQ ID NO: 1089, SEQ ID NO: 1340, SEQ ID NO: 1074, SEQ ID NO: 1107, SEQ ID NO: 1204, SEQ ID NO: 1066, SEQ ID NO: 381, SEQ ID NO: 229, SEQ ID NO: 323, SEQ ID NO: 371, SEQ ID NO: 284, SEQ ID NO: 116, SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 907, SEQ ID NO: 193, SEQ ID NO: 145, SEQ ID NO: 59, SEQ ID NO: 322, SEQ ID NO: 94, SEQ ID NO: 306, SEQ ID NO: 939, SEQ ID NO: 205, SEQ ID NO: 123, SEQ ID NO: 906, SEQ ID NO: 928, SEQ ID NO: 346, SEQ ID NO: 129, SEQ ID NO: 307, SEQ ID NO: 133, SEQ ID NO: 131, SEQ ID NO: 886, SEQ ID NO: 179, SEQ ID NO: 104, SEQ ID NO: 213, SEQ ID NO: 359, SEQ ID NO: 140, SEQ ID NO: 146, SEQ ID NO: 327, SEQ ID NO: 365, SEQ ID NO: 33, SEQ ID NO: 331, SEQ ID NO: 175, SEQ ID NO: 200, SEQ ID NO: 292, SEQ ID NO: 23, SEQ ID NO: 336, SEQ ID NO: 301, SEQ ID NO: 28, SEQ ID NO: 941, SEQ ID NO: 103, SEQ ID NO: 231, SEQ ID NO: 176, SEQ ID NO: 31, SEQ ID NO: 917, SEQ ID NO: 151, SEQ ID NO: 922, SEQ ID NO: 265, SEQ ID NO: 142, SEQ ID NO: 259, SEQ ID NO: 122, SEQ ID NO: 206, SEQ ID NO: 96, SEQ ID NO: 353, SEQ ID NO: 38, SEQ ID NO: 89, SEQ ID NO: 77, SEQ ID NO: 954, SEQ ID NO: 264, SEQ ID NO: 937, SEQ ID NO: 226, SEQ ID NO: 283, SEQ ID NO: 88,

SEQ ID NO: 125, SEQ ID NO: 183, SEQ ID NO: 195, SEQ ID NO: 81, SEQ ID NO: 901, SEQ ID NO: 82, SEQ ID NO: 42, SEQ ID NO: 881, and SEQ ID NO: 885.

In one embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least one membrane spanning region encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1060, SEQ ID NO: 1110, SEQ ID NO: 1112, SEQ ID NO: 1230, SEQ ID NO: 1260, SEQ ID NO: 1280, SEQ ID NO: 1292, SEQ ID NO: 1296, SEQ ID NO: 1307, SEQ ID NO: 1442, SEQ ID NO: 1444, SEQ ID NO: 381, SEQ ID NO: 229, SEQ ID NO: 323, SEQ ID NO: 371, SEQ ID NO: 284, SEQ ID NO: 116, SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 907, SEQ ID NO: 193, SEQ ID NO: 145, SEQ ID NO: 59, SEQ ID NO: 322, SEQ ID NO: 94, SEQ ID NO: 306, and SEQ ID NO: 881.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least two membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1122, SEQ ID NO: 1254, SEQ ID NO: 1256, SEQ ID NO: 1272, SEQ ID NO: 1275, SEQ ID NO: 1309, SEQ ID NO: 1313, SEQ ID NO: 1347, SEQ ID NO: 1352, SEQ ID NO: 1356, SEQ ID NO: 1438, SEQ ID NO: 1441, SEQ ID NO: 1009, SEQ ID NO: 1026, SEQ ID NO: 1048, SEQ ID NO: 1063, SEQ ID NO: 1190, SEQ ID NO: 939, SEQ ID NO: 205, SEQ ID NO: 123, SEQ ID NO: 906, SEQ ID NO: 928, SEQ ID NO: 346, SEQ ID NO: 129, SEQ ID NO: 307, SEQ ID NO: 133, SEQ ID NO: 131, SEQ ID NO: 886, SEQ ID NO: 179, SEQ ID NO: 104, SEQ ID NO: 213, SEQ ID NO: 359, SEQ ID NO: 140, SEQ ID NO: 146, SEQ ID NO: 327, and SEQ ID NO: 365.

In yet another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least three membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1083, SEQ ID NO: 1113, SEQ ID NO: 1222, SEQ ID NO: 1295, SEQ ID NO: 1343, SEQ ID NO: 1392, SEQ ID NO: 1443, SEQ ID NO: 33, SEQ ID NO: 331, SEQ ID NO: 175, SEQ ID NO: 200, SEQ ID NO: 292, SEQ ID NO: 23, and SEQ ID NO: 336.

In yet a further embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least four membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1085, SEQ ID NO: 1093, SEQ ID NO: 1117, SEQ ID NO: 1121, SEQ ID NO: 1131, SEQ ID NO: 1287, SEQ ID NO: 1440, SEQ ID NO: 1209, SEQ ID NO: 301, SEQ ID NO: 28, SEQ ID NO: 941, SEQ ID NO: 103, SEQ ID NO: 231, SEQ ID NO: 176, SEQ ID NO: 31, SEQ ID NO: 917, SEQ ID NO: 151, and SEQ ID NO: 922.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least five membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1342, SEQ ID NO: 1381, SEQ ID NO: 1390, SEQ ID NO: 1409, SEQ ID

NO: 1035, SEQ ID NO: 265, SEQ ID NO: 142, SEQ ID NO: 259, SEQ ID NO: 122, SEQ ID NO: 206, and SEQ ID NO: 885.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least six membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1014, SEQ ID NO: 1088, SEQ ID NO: 1242, SEQ ID NO: 1178, SEQ ID NO: 96, SEQ ID NO: 353, SEQ ID NO: 38, SEQ ID NO: 89, SEQ ID NO: 77, SEQ ID NO: 954, SEQ ID NO: 264.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least seven membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1089, SEQ ID NO: 1340, SEQ ID NO: 1074, SEQ ID NO: 1107, SEQ ID NO: 1204, SEQ ID NO: 1066, SEQ ID NO: 937, SEQ ID NO: 226, SEQ ID NO: 283, SEQ ID NO: 88, SEQ ID NO: 125, SEQ ID NO: 183, SEQ ID NO: 195, SEQ ID NO: 81, SEQ ID NO: 901, SEQ ID NO: 82, and SEQ ID NO: 42.

Particularly preferred is a purified or isolated *H. pylori* cell envelope polypeptide or a fragment thereof, wherein the polypeptide is selected from the group consisting of SEQ ID NO: 1471, SEQ ID NO: 1472, SEQ ID NO: 1487, SEQ ID NO: 1501, SEQ ID NO: 1522, SEQ ID NO: 1552, SEQ ID NO: 1586, SEQ ID NO: 1727, SEQ ID NO: 1601, SEQ ID NO: 1638, SEQ ID NO: 1643, SEQ ID NO: 1812, SEQ ID NO: 1830, SEQ ID NO: 1850, SEQ ID NO: 1854, SEQ ID NO: 1851, SEQ ID NO: 1640, SEQ ID NO: 1453, SEQ ID NO: 1664, SEQ ID NO: 1665, SEQ ID NO: 1666, SEQ ID NO: 1685, SEQ ID NO: 1687, SEQ ID NO: 1688, SEQ ID NO: 1675, SEQ ID NO: 1702, SEQ ID NO: 1713, SEQ ID NO: 1600, SEQ ID NO: 1671, SEQ ID NO: 1691, SEQ ID NO: 1615, SEQ ID NO: 1616, SEQ ID NO: 1855, SEQ ID NO: 1595, SEQ ID NO: 1633, SEQ ID NO: 1608, SEQ ID NO: 1611, SEQ ID NO: 1751, SEQ ID NO: 1772, SEQ ID NO: 1774, SEQ ID NO: 1780, SEQ ID NO: 1783, SEQ ID NO: 1796, SEQ ID NO: 1809, SEQ ID NO: 1826, SEQ ID NO: 1868, SEQ ID NO: 1734, SEQ ID NO: 1786, SEQ ID NO: 1819, SEQ ID NO: 1630, SEQ ID NO: 1706, SEQ ID NO: 1709, SEQ ID NO: 1495, SEQ ID NO: 1724, SEQ ID NO: 1670, SEQ ID NO: 1725, SEQ ID NO: 1661, SEQ ID NO: 1873, SEQ ID NO: 1753, SEQ ID NO: 1759, SEQ ID NO: 1761, SEQ ID NO: 1782, SEQ ID NO: 1883, SEQ ID NO: 1503, SEQ ID NO: 1542, SEQ ID NO: 1872, SEQ ID NO: 1520, SEQ ID NO: 1456, SEQ ID NO: 1458, SEQ ID NO: 1617, SEQ ID NO: 1628, SEQ ID NO: 1644, SEQ ID NO: 1657, SEQ ID NO: 1658, SEQ ID NO: 1755, SEQ ID NO: 1756, SEQ ID NO: 1797, SEQ ID NO: 1799, SEQ ID NO: 1801, SEQ ID NO: 1483, SEQ ID NO: 1504, SEQ ID NO: 1532, SEQ ID NO: 1575, SEQ ID NO: 1833, SEQ ID NO: 1888, SEQ ID NO: 1714, SEQ ID NO: 1624, SEQ ID NO: 1856, SEQ ID NO: 1857, SEQ ID NO: 1861, SEQ ID NO: 1537, SEQ ID NO: 1773, SEQ ID NO: 1717, SEQ ID NO: 1733, SEQ ID NO: 1722, SEQ ID NO: 1659, SEQ ID NO: 1577, SEQ ID NO: 1721, SEQ ID NO: 1729, SEQ

ID NO: 1870, SEQ ID NO: 1576, SEQ ID NO: 1632, SEQ ID NO: 1867, SEQ ID NO: 1547, SEQ ID NO: 1533, SEQ ID NO: 1597, SEQ ID NO: 1596, SEQ ID NO: 1559, SEQ ID NO: 1599, SEQ ID NO: 1788, SEQ ID NO: 1789, SEQ ID NO: 1875, SEQ ID NO: 1451, SEQ ID NO: 1478, SEQ ID NO: 1626, SEQ ID NO: 1781, SEQ ID NO: 660, SEQ ID NO: 660, SEQ ID NO: 855, SEQ ID NO: 534, SEQ ID NO: 675, SEQ ID NO: 404, SEQ ID NO: 518, SEQ ID NO: 464, SEQ ID NO: 672, SEQ ID NO: 640, SEQ ID NO: 490, SEQ ID NO: 755, SEQ ID NO: 389, SEQ ID NO: 635, SEQ ID NO: 877, SEQ ID NO: 637, SEQ ID NO: 477, SEQ ID NO: 772, SEQ ID NO: 658, SEQ ID NO: 463, SEQ ID NO: 852, SEQ ID NO: 503, SEQ ID NO: 411, SEQ ID NO: 441, SEQ ID NO: 782, SEQ ID NO: 575, SEQ ID NO: 691, SEQ ID NO: 724, SEQ ID NO: 452, SEQ ID NO: 386, SEQ ID NO: 497, SEQ ID NO: 712, SEQ ID NO: 591, SEQ ID NO: 638, SEQ ID NO: 740, SEQ ID NO: 697, SEQ ID NO: 569, SEQ ID NO: 470, SEQ ID NO: 700, SEQ ID NO: 586, SEQ ID NO: 823, SEQ ID NO: 627, SEQ ID NO: 627, SEQ ID NO: 684, SEQ ID NO: 551, SEQ ID NO: 478, SEQ ID NO: 508, SEQ ID NO: 545, SEQ ID NO: 628, SEQ ID NO: 443, SEQ ID NO: 702, SEQ ID NO: 776, SEQ ID NO: 461, SEQ ID NO: 737, SEQ ID NO: 809, SEQ ID NO: 642, SEQ ID NO: 879, SEQ ID NO: 773, SEQ ID NO: 468, SEQ ID NO: 842, SEQ ID NO: 788, SEQ ID NO: 624, SEQ ID NO: 788, SEQ ID NO: 644, SEQ ID NO: 727, SEQ ID NO: 631, SEQ ID NO: 450, SEQ ID NO: 448, SEQ ID NO: 653, SEQ ID NO: 495, SEQ ID NO: 400, SEQ ID NO: 541, SEQ ID NO: 673, SEQ ID NO: 482, SEQ ID NO: 622, SEQ ID NO: 689, SEQ ID NO: 736, SEQ ID NO: 417, SEQ ID NO: 716, SEQ ID NO: 762, SEQ ID NO: 395, SEQ ID NO: 587, SEQ ID NO: 669, SEQ ID NO: 758, SEQ ID NO: 593, SEQ ID NO: 451, SEQ ID NO: 827, SEQ ID NO: 502, SEQ ID NO: 719, SEQ ID NO: 469, SEQ ID NO: 715, SEQ ID NO: 847, SEQ ID NO: 453, SEQ ID NO: 527, SEQ ID NO: 652, SEQ ID NO: 745, SEQ ID NO: 567, SEQ ID NO: 848, SEQ ID NO: 430, SEQ ID NO: 748, SEQ ID NO: 396, SEQ ID NO: 588, SEQ ID NO: 795, SEQ ID NO: 523, SEQ ID NO: 791, SEQ ID NO: 714, SEQ ID NO: 481, SEQ ID NO: 765, SEQ ID NO: 837, SEQ ID NO: 833, SEQ ID NO: 585, SEQ ID NO: 865, SEQ ID NO: 764, SEQ ID NO: 440, SEQ ID NO: 465, SEQ ID NO: 555, SEQ ID NO: 526, SEQ ID NO: 687, SEQ ID NO: 692, SEQ ID NO: 693, SEQ ID NO: 677, SEQ ID NO: 649, SEQ ID NO: 812, SEQ ID NO: 820, SEQ ID NO: 880, SEQ ID NO: 590, SEQ ID NO:713, SEQ ID NO:750, SEQ ID NO:613, SEQ ID NO: 437, SEQ ID NO: 556, SEQ ID NO: 657, SEQ ID NO: 402, SEQ ID NO: 623, SEQ ID NO: 862, SEQ ID NO: 449, SEQ ID NO: 690, SEQ ID NO: 424, SEQ ID NO: 821, SEQ ID NO: 432, SEQ ID NO: 811, SEQ ID NO: 554, and SEQ ID NO: 809.

In one embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* flagella-associated polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1471, SEQ ID NO: 1472, SEQ ID NO: 1487, SEQ ID NO: 1501, SEQ ID NO: 1522, SEQ ID NO: 1552, SEQ ID NO: 1586, SEQ ID NO: 1727, SEQ ID NO: 1601, SEQ ID NO: 1638, SEQ ID NO: 1643, SEQ ID NO: 1812, SEQ ID NO: 1830,

SEQ ID NO: 1850, SEQ ID NO: 1854, SEQ ID NO: 1851, SEQ ID NO: 1640, SEQ ID NO: 660, SEQ ID NO: 660, SEQ ID NO: 855, SEQ ID NO: 534, SEQ ID NO: 675, SEQ ID NO: 404, SEQ ID NO: 518, SEQ ID NO: 464, SEQ ID NO: 672, SEQ ID NO: 640, SEQ ID NO: 490, SEQ ID NO: 755, SEQ ID NO: 389, SEQ ID NO: 635, SEQ ID NO: 877, SEQ ID NO: 637, SEQ ID NO: 477, SEQ ID NO: 772, and SEQ ID NO: 658.

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: 1453, SEQ ID NO: 1664, SEQ ID NO: 1665, SEQ ID NO: 1666, SEQ ID NO: 1685, SEQ ID NO: 1687, SEQ ID NO: 1688, SEQ ID NO: 1675, SEQ ID NO: 1702, SEQ ID NO: 1713, SEQ ID NO: 1600, SEQ ID NO: 1671, SEQ ID NO: 1691, SEQ ID NO: 1615, SEQ ID NO: 1616, SEQ ID NO: 1855, SEQ ID NO: 1595, SEQ ID NO: 1633, SEQ ID NO: 1608, SEQ ID NO: 1611, SEQ ID NO: 1751, SEQ ID NO: 1772, SEQ ID NO: 1774, SEQ ID NO: 1780, SEQ ID NO: 1783, SEQ ID NO: 1796, SEQ ID NO: 1809, SEQ ID NO: 1826, SEQ ID NO: 1868, SEQ ID NO: 1734, SEQ ID NO: 1786, SEQ ID NO: 1819, SEQ ID NO: 1630, SEQ ID NO: 1706, SEQ ID NO: 1709, SEQ ID NO: 1495, SEQ ID NO: 1724, SEQ ID NO: 463, SEQ ID NO: 852, SEQ ID NO: 503, SEQ ID NO: 411, SEQ ID NO: 441, SEQ ID NO: 782, SEQ ID NO: 575, SEQ ID NO: 691, SEQ ID NO: 724, SEQ ID NO: 452, SEQ ID NO: 386, SEQ ID NO: 497, SEQ ID NO: 712, SEQ ID NO: 591, SEQ ID NO: 638, SEQ ID NO: 740, SEQ ID NO: 697, SEQ ID NO: 569, SEQ ID NO: 470, SEQ ID NO: 700, SEQ ID NO: 586, SEQ ID NO: 823, SEQ ID NO: 627, SEQ ID NO: 627, SEQ ID NO: 684, SEQ ID NO: 551, SEQ ID NO: 478, SEQ ID NO: 508, SEQ ID NO: 545, SEQ ID NO: 628, SEQ ID NO: 443, SEQ ID NO: 702, SEQ ID NO: 776, SEQ ID NO: 461, SEQ ID NO: 737, SEQ ID NO: 809, SEQ ID NO: 642, SEQ ID NO: 879, SEQ ID NO: 773, SEQ ID NO: 468, SEQ ID NO: 842, SEQ ID NO: 788, SEQ ID NO: 624, SEQ ID NO: 788, SEQ ID NO: 644, SEQ ID NO: 727, SEQ ID NO: 631, SEQ ID NO: 450, SEQ ID NO: 448, and SEQ ID NO: 653.

In yet another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* transporter polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1670, SEQ ID NO: 1725, SEQ ID NO: 1661, SEQ ID NO: 1873, SEQ ID NO: 1753, SEQ ID NO: 1759, SEQ ID NO: 1761, SEQ ID NO: 1782, SEQ ID NO: 1883, SEQ ID NO: 1503, SEQ ID NO: 1542, SEQ ID NO: 1872, SEQ ID NO: 1520, SEQ ID NO: 1456, SEQ ID NO: 1458, SEQ ID NO: 1617, SEQ ID NO: 1628, SEQ ID NO: 1644, SEQ ID NO: 1657, SEQ ID NO: 1658, SEQ ID NO: 1755, SEQ ID NO: 1756, SEQ ID NO: 1797, SEQ ID NO: 1799, SEQ ID NO: 1801, SEQ ID NO: 1483, SEQ ID NO: 1504, SEQ ID NO: 1532, SEQ ID NO: 1575, SEQ ID NO: 1833, SEQ ID NO: 1888, SEQ ID NO: 1714, SEQ ID NO: 495, SEQ ID NO: 400, SEQ ID NO: 541, SEQ ID NO: 673, SEQ ID NO: 482, SEQ ID NO: 622, SEQ ID NO: 689, SEQ ID NO: 736, SEQ ID NO: 417, SEQ ID NO: 716, SEQ ID NO: 762, SEQ ID NO: 395, SEQ ID NO: 587, SEQ ID NO: 669, SEQ ID NO: 758, SEQ ID NO: 593, SEQ ID NO: 451, SEQ ID NO: 827.

SEQ ID NO: 502, SEQ ID NO: 719, SEQ ID NO: 469, SEQ ID NO: 715, SEQ ID NO: 847, SEQ ID NO: 453, SEQ ID NO: 527, SEQ ID NO: 652, SEQ ID NO: 745, SEQ ID NO: 567, SEQ ID NO: 848, SEQ ID NO: 430, SEQ ID NO: 748, SEQ ID NO: 396, SEQ ID NO: 588, SEQ ID NO: 795, SEQ ID NO: 523, SEQ ID NO: 791, SEQ ID NO: 714, SEQ ID NO: 481, and SEQ ID NO: 765.

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: 1624, SEQ ID NO: 1856, SEQ ID NO: 1857, SEQ ID NO: 1861, SEQ ID NO: 1537, SEQ ID NO: 1773, SEQ ID NO: 1717, SEQ ID NO: 1733, SEQ ID NO: 1722, SEQ ID NO: 1659, SEQ ID NO: 1577, SEQ ID NO: 1721, SEQ ID NO: 1729, SEQ ID NO: 1870, SEQ ID NO: 1576, SEQ ID NO: 1632, SEQ ID NO: 1867, SEQ ID NO: 1547, SEQ ID NO: 1533, SEQ ID NO: 1597, SEQ ID NO: 1596, SEQ ID NO: 1559, SEQ ID NO: 1599, SEQ ID NO: 1788, SEQ ID NO: 1789, SEQ ID NO: 1875, SEQ ID NO: 1451, SEQ ID NO: 1478, SEQ ID NO: 1626, SEQ ID NO: 1781, SEQ ID NO: 837, SEQ ID NO: 833, SEQ ID NO: 585, SEQ ID NO: 865, SEQ ID NO: 764, SEQ ID NO: 440, SEQ ID NO: 465, SEQ ID NO: 555, SEQ ID NO: 526, SEQ ID NO: 687, SEQ ID NO: 692, SEQ ID NO: 693, SEQ ID NO: 677, SEQ ID NO: 649, and SEQ ID NO: 812.

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 SEQ ID NO: 1598, SEQ ID NO: 1739, SEQ ID NO: 1775, SEQ ID NO: 1814, SEQ ID NO: 1448, SEQ ID NO: 1466, SEQ ID NO: 1535, SEQ ID NO: 1545, SEQ ID NO: 1550, SEQ ID NO: 1680, SEQ ID NO: 1701, SEQ ID NO: 1719, SEQ ID NO: 1744, SEQ ID NO: 1790, SEQ ID NO: 1859, SEQ ID NO: 1880, SEQ ID NO: 1885, SEQ ID NO: 1679, SEQ ID NO: 1482, SEQ ID NO: 1485, SEQ ID NO: 1459, SEQ ID NO: 1512, SEQ ID NO: 1515, SEQ ID NO: 1642, SEQ ID NO: 1668, SEQ ID NO: 1816, SEQ ID NO: 1845, SEQ ID NO: 1865, SEQ ID NO: 1866, SEQ ID NO: 1886, SEQ ID NO: 1509, SEQ ID NO: 1510, SEQ ID NO: 1531, SEQ ID NO: 1579, SEQ ID NO: 1584, SEQ ID NO: 1662, SEQ ID NO: 1703, SEQ ID NO: 1704, SEQ ID NO: 1737, SEQ ID NO: 1740, SEQ ID NO: 1742, SEQ ID NO: 1754, SEQ ID NO: 1847, SEQ ID NO: 1447, SEQ ID NO: 1546, SEQ ID NO: 1607, SEQ ID NO: 1609, SEQ ID NO: 1610, SEQ ID NO: 1728, SEQ ID NO: 1489, SEQ ID NO: 1708, SEQ ID NO: 1808, SEQ ID NO: 1887, SEQ ID NO: 1498, SEQ ID NO: 1506, SEQ ID NO: 1592, SEQ ID NO: 1678, SEQ ID NO: 1778, SEQ ID NO: 1863, SEQ ID NO: 1454, SEQ ID NO: 1538, SEQ ID NO: 1567, SEQ ID NO: 1581, SEQ ID NO: 1583, SEQ ID NO: 1636, SEQ ID NO: 1639, SEQ ID NO: 1649, SEQ ID NO: 1669, SEQ ID NO: 1695, SEQ ID NO: 1757, SEQ ID NO: 1776, SEQ ID NO: 1848, SEQ ID NO: 1849, SEQ ID NO: 1858, SEQ ID NO: 1884, SEQ ID NO: 1667, SEQ ID NO: 1690, SEQ ID NO: 1813, SEQ ID NO: 1468, SEQ ID NO: 1470, SEQ ID NO: 1811, SEQ ID NO: 1874, SEQ ID NO: 1876, SEQ ID NO: 1825, SEQ ID NO: 1479, SEQ ID NO: 1488,

SEQ ID NO: 1528, SEQ ID NO: 1566, SEQ ID NO: 1683, SEQ ID NO: 1692, SEQ ID NO: 1718, SEQ ID NO: 1614, SEQ ID NO: 1519, SEQ ID NO: 1476, SEQ ID NO: 1493, SEQ ID NO: 1497, SEQ ID NO: 1507, SEQ ID NO: 1490, SEQ ID NO: 1523, SEQ ID NO: 1524, SEQ ID NO: 1543, SEQ ID NO: 1551, SEQ ID NO: 1553, SEQ ID NO: 1554, SEQ ID NO: 1555, SEQ ID NO: 1562, SEQ ID NO: 1570, SEQ ID NO: 1587, SEQ ID NO: 1588, SEQ ID NO: 1591, SEQ ID NO: 1593, SEQ ID NO: 1684, SEQ ID NO: 1689, SEQ ID NO: 1694, SEQ ID NO: 1696, SEQ ID NO: 1698, SEQ ID NO: 1700, SEQ ID NO: 1712, SEQ ID NO: 1720, SEQ ID NO: 1730, SEQ ID NO: 1735, SEQ ID NO: 1741, SEQ ID NO: 1748, SEQ ID NO: 1779, SEQ ID NO: 1821, SEQ ID NO: 1823, SEQ ID NO: 1828, SEQ ID NO: 1834, SEQ ID NO: 1835, SEQ ID NO: 1836, SEQ ID NO: 183 SEQ ID NO: 1852, SEQ ID NO: 1853, SEQ ID NO: 1869, SEQ ID NO: 1871, SEQ ID NO: 1878, SEQ ID NO: 1521, SEQ ID NO: 1602, SEQ ID NO: 1627, SEQ ID NO: 1450, SEQ ID NO: 1457, SEQ ID NO: 1463, SEQ ID NO: 1469, SEQ ID NO: 1481, SEQ ID NO: 1484, SEQ ID NO: 1492, SEQ ID NO: 1500, SEQ ID NO: 1505, SEQ ID NO: 1508, SEQ ID NO: 1541, SEQ ID NO: 1548, SEQ ID NO: 1580, SEQ ID NO: 1590, SEQ ID NO: 1594, SEQ ID NO: 1603, SEQ ID NO: 1604, SEQ ID NO: 1606, SEQ ID NO: 1612, SEQ ID NO: 1613, SEQ ID NO: 1620, SEQ ID NO: 1621, SEQ ID NO: 1622, SEQ ID NO: 1631, SEQ ID NO: 1645, SEQ ID NO: 1646, SEQ ID NO: 1650, SEQ ID NO: 1651, SEQ ID NO: 1652, SEQ ID NO: 1653, SEQ ID NO: 1656, SEQ ID NO: 1763, SEQ ID NO: 1787, SEQ ID NO: 1800, SEQ ID NO: 1806, SEQ ID NO: 1810, SEQ ID NO: 1864, SEQ ID NO: 1877, SEQ ID NO: 1881, SEQ ID NO: 390, SEQ ID NO: 876, SEQ ID NO: 547, SEQ ID NO: 678, SEQ ID NO: 729, SEQ ID NO: 786, SEQ ID NO: 654, SEQ ID NO: 734, SEQ ID NO: 646, SEQ ID NO: 522, SEQ ID NO: 696, SEQ ID NO: 807, SEQ ID NO: 683, SEQ ID NO: 790, SEQ ID NO: 763, SEQ ID NO: 806, SEQ ID NO: 799, SEQ ID NO: 434, SEQ ID NO: 743, SEQ ID NO: 804, SEQ ID NO: 733, SEQ ID NO: 826, SEQ ID NO: 562, SEQ ID NO: 420, SEQ ID NO: 664, SEQ ID NO: 850, SEQ ID NO: 857, SEQ ID NO: 861, SEQ ID NO: 872, SEQ ID NO: 544, SEQ ID NO: 830, SEQ ID NO: 446, SEQ ID NO: 397, SEQ ID NO: 699, SEQ ID NO: 459, SEQ ID NO: 509, SEQ ID NO: 818, SEQ ID NO: 488, SEQ ID NO: 438, SEQ ID NO: 831, SEQ ID NO: 667, SEQ ID NO: 429, SEQ ID NO: 680, SEQ ID NO: 597, SEQ ID NO: 460, SEQ ID NO: 709, SEQ ID NO: 822, SEQ ID NO: 466, SEQ ID NO: 584, SEQ ID NO: 388, SEQ ID NO: 631, SEQ ID NO: 787, SEQ ID NO: 532, SEQ ID NO: 619, SEQ ID NO: 723, SEQ ID NO: 641, SEQ ID NO: 698, SEQ ID NO: 630, SEQ ID NO: 869, SEQ ID NO: 601, SEQ ID NO: 415, SEQ ID NO: 542, SEQ ID NO: 704, SEQ ID NO: 572, SEQ ID NO: 467, SEQ ID NO: 399, SEQ ID NO: 579, SEQ ID NO: 739, SEQ ID NO: 849, SEQ ID NO: 824, SEQ ID NO: 871, SEQ ID NO: 547, SEQ ID NO: 633, SEQ ID NO: 695," SEQ ID NO: 405, SEQ ID NO: 394, SEQ ID NO: 761, SEQ ID NO: 574, SEQ ID NO: 596, SEQ ID NO: 832, SEQ ID NO: 651, SEQ ID NO: 867, SEQ ID NO: 614, SEQ ID NO: 401, SEQ ID NO: 393, SEQ ID NO: 413, SEQ ID NO: 835, SEQ ID NO: 863, SEQ

ID NO: 458. SEQ ID NO: 701. SEQ ID NO: 531. SEQ ID NO: 550, SEQ ID NO: 439, SEQ ID NO: 516, SEQ ID NO: 802. SEQ ID NO: 581, SEQ ID NO: 535, SEQ ID NO: 578, SEQ ID NO: 492, SEQ ID NO: 858, SEQ ID NO: 720, SEQ ID NO: 813. SEQ ID NO: 426, SEQ ID NO: 834, SEQ ID NO: 609, SEQ ID NO: 489, SEQ ID NO: 480, SEQ ID NO: 406, SEQ ID NO: 392, SEQ ID NO: 456, SEQ ID NO: 707, SEQ ID NO: 533, SEQ ID NO: 728, SEQ ID NO: 769, SEQ ID NO: 671, SEQ ID NO: 602, SEQ ID NO: 618, SEQ ID NO: 618, SEQ ID NO: 682, SEQ ID NO: 524, SEQ ID NO: 802. SEQ ID NO: 785, SEQ ID NO: 457, SEQ ID NO: 781, SEQ ID NO: 473, SEQ ID NO: 384, SEQ ID NO: 726, SEQ ID NO: 817, SEQ ID NO: 498, SEQ ID NO: 436, SEQ ID NO: 815, SEQ ID NO: 856, SEQ ID NO: 650, SEQ ID NO: 844, SEQ ID NO: 580, SEQ ID NO: 783, SEQ ID NO: 416, SEQ ID NO: 741, SEQ ID NO: 442, SEQ ID NO: 803, SEQ ID NO: 520, SEQ ID NO: 566, SEQ ID NO: 557, SEQ ID NO: 706, SEQ ID NO: 710, SEQ ID NO: 487, SEQ ID NO: 603, SEQ ID NO: 472, SEQ ID NO: 476, SEQ ID NO: 770, SEQ ID NO: 841, SEQ ID NO: 768, SEQ ID NO: 839, SEQ ID NO: 560, SEQ ID NO: 796, SEQ ID NO: 483, SEQ ID NO: 634, SEQ ID NO: 445, SEQ ID NO: 853, SEQ ID NO: 525, SEQ ID NO: 798, SEQ ID NO: 549, SEQ ID NO: 836, SEQ ID NO: 589, SEQ ID NO: 760, SEQ ID NO: 462, SEQ ID NO: 789, SEQ ID NO: 507, SEQ ID NO: 828, SEQ ID NO: 866, SEQ ID NO: 754, SEQ ID NO: 730, SEQ ID NO: 617, SEQ ID NO: 455, SEQ ID NO: 873, SEQ ID NO: 435, SEQ ID NO: 766, SEQ ID NO: 793, SEQ ID NO: 742, SEQ ID NO: 599, SEQ ID NO: 854, and SEQ ID NO: 632.

In one embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in energy conversion selected from the group consisting of SEQ ID NO: 1598, SEQ ID NO: 1739, SEQ ID NO: 1775, SEQ ID NO: 1814, SEQ ID NO: 390, SEQ ID NO: 876, SEQ ID NO: 547, and SEQ ID NO: 678.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in amino acid metabolism selected from the group consisting of SEQ ID NO: 1448, SEQ ID NO: 1466, SEQ ID NO: 1535, SEQ ID NO: 1545, SEQ ID NO: 1550, SEQ ID NO: 1680, SEQ ID NO: 1701, SEQ ID NO: 1719, SEQ ID NO: 1744, SEQ ID NO: 1790, SEQ ID NO: 1859, SEQ ID NO: 1880, SEQ ID NO: 1885, SEQ ID NO: 1679, SEQ ID NO: 1482, SEQ ID NO: 1485, SEQ ID NO: 1459, SEQ ID NO: 729, SEQ ID NO: 786, SEQ ID NO: 654, SEQ ID NO: 734, SEQ ID NO: 646, SEQ ID NO: 522, SEQ ID NO: 696, SEQ ID NO: 807, SEQ ID NO: 683, SEQ ID NO: 790, SEQ ID NO: 763, SEQ ID NO: 806, SEQ ID NO: 799, SEQ ID NO: 434, SEQ ID NO: 743, SEQ ID NO: 804, and SEQ ID NO: 733.

In yet another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in nucleotide metabolism selected from the group consisting of SEQ ID NO: 1512, SEQ ID NO: 1515. SEQ ID NO: 1642, SEQ ID NO: 1668, SEQ ID NO: 1816, SEQ ID NO: 1845, SEQ ID NO: 1865, SEQ ID NO: 1866, SEQ ID NO: 1886, SEQ ID NO: 1509, SEQ ID NO: 1510, SEQ ID NO: 826.

SEQ ID NO: 562, SEQ ID NO: 420, SEQ ID NO: 664, SEQ ID NO: 850, SEQ ID NO: 857, SEQ ID NO: 861, SEQ ID NO: 872, SEQ ID NO: 544, SEQ ID NO: 830, and SEQ ID NO: 446.

In yet a further embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in carbohydrate metabolism selected from the group consisting of SEQ ID NO: 1531, SEQ ID NO: 1579, SEQ ID NO: 1584, SEQ ID NO: 1662, SEQ ID NO: 1703, SEQ ID NO: 1704, SEQ ID NO: 1737, SEQ ID NO: 1740, SEQ ID NO: 1742, SEQ ID NO: 1754, SEQ ID NO: 1847, SEQ ID NO: 1447, SEQ ID NO: 397, SEQ ID NO: 699, SEQ ID NO: 459, SEQ ID NO: 509, SEQ ID NO: 818, SEQ ID NO: 488, SEQ ID NO: 438, SEQ ID NO: 831, SEQ ID NO: 667, SEQ ID NO: 429, SEQ ID NO: 680, and SEQ ID NO: 597.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in cofactor metabolism selected from the group consisting of SEQ ID NO: 1546, SEQ ID NO: 1607, SEQ ID NO: 1609, SEQ ID NO: 1610, SEQ ID NO: 1728, SEQ ID NO: 1489, SEQ ID NO: 460, SEQ ID NO: 709, SEQ ID NO: 822, SEQ ID NO: 466, SEQ ID NO: 584, and SEQ ID NO: 388.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in lipid metabolism selected from the group consisting of SEQ ID NO: 1708, SEQ ID NO: 1808, SEQ ID NO: 1887, SEQ ID NO: 631, SEQ ID NO: 787, and SEQ ID NO: 532.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in mRNA translation and ribosome biogenesis selected from the group consisting of SEQ ID NO: 1498, SEQ ID NO: 1506, SEQ ID NO: 1592, SEQ ID NO: 1678, SEQ ID NO: 1778, SEQ ID NO: 1863, SEQ ID NO: 619, SEQ ID NO: 723, SEQ ID NO: 641, SEQ ID NO: 698, SEQ ID NO: 630, and SEQ ID NO: 869.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in genome replication, transcription, recombination and repair selected from the group consisting of SEQ ID NO: 1454, SEQ ID NO: 1538, SEQ ID NO: 1567, SEQ ID NO: 1581, SEQ ID NO: 1583, SEQ ID NO: 1636, SEQ ID NO: 1639, SEQ ID NO: 1649, SEQ ID NO: 1669, SEQ ID NO: 1695, SEQ ID NO: 1757, SEQ ID NO: 1776, SEQ ID NO: 1848, SEQ ID NO: 1849, SEQ ID NO: 1858, SEQ ID NO: 1884, SEQ ID NO: 601, SEQ ID NO: 415, SEQ ID NO: 542, SEQ ID NO: 704, SEQ ID NO: 572, SEQ ID NO: 467, SEQ ID NO: 399, SEQ ID NO: 579, SEQ ID NO: 739, SEQ ID NO: 849, SEQ ID NO: 824, SEQ ID NO: 871, SEQ ID NO: 547, SEQ ID NO: 633, SEQ ID NO: 695, SEQ ID NO: 405, SEQ ID NO: 394, and SEQ ID NO: 761.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in outer membrane or cell wall

biosynthesis selected from the group consisting of SEQ ID NO: 1667, SEQ ID NO: 1690, SEQ ID NO: 1813, SEQ ID NO: 1468, SEQ ID NO: 1470, SEQ ID NO: 1811, SEQ ID NO: 574, SEQ ID NO: 596, SEQ ID NO: 832, SEQ ID NO: 651, SEQ ID NO: 867, SEQ ID NO: 614, SEQ ID NO: 401, and SEQ ID NO: 393.

In yet another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* chaperone polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1874, SEQ ID NO: 1876, SEQ ID NO: 1825, SEQ ID NO: 413, SEQ ID NO: 835, and SEQ ID NO: 863.

Particularly preferred is a purified or isolated *H. pylori* secreted or periplasmic polypeptide or a fragment thereof, wherein the polypeptide is selected from the group consisting of SEQ ID NO: 1455, SEQ ID NO: 1589, SEQ ID NO: 1518, SEQ ID NO: 1529, SEQ ID NO: 1765, SEQ ID NO: 1770, SEQ ID NO: 1829, SEQ ID NO: 1556, SEQ ID NO: 1565, SEQ ID NO: 1569, SEQ ID NO: 1571, SEQ ID NO: 1574, SEQ ID NO: 1578, SEQ ID NO: 1663, SEQ ID NO: 1674, SEQ ID NO: 1676, SEQ ID NO: 1697, SEQ ID NO: 1699, SEQ ID NO: 1710, SEQ ID NO: 1715, SEQ ID NO: 1716, SEQ ID NO: 1732, SEQ ID NO: 1736, SEQ ID NO: 1745, SEQ ID NO: 1749, SEQ ID NO: 1750, SEQ ID NO: 1766, SEQ ID NO: 1767, SEQ ID NO: 1768, SEQ ID NO: 1769, SEQ ID NO: 1795, SEQ ID NO: 1802, SEQ ID NO: 1804, SEQ ID NO: 1824, SEQ ID NO: 1831, SEQ ID NO: 1838, SEQ ID NO: 1840, SEQ ID NO: 1844, SEQ ID NO: 1862, SEQ ID NO: 1879, SEQ ID NO: 1882, SEQ ID NO: 1890, SEQ ID NO: 1494, SEQ ID NO: 1634, SEQ ID NO: 1635, SEQ ID NO: 1647, SEQ ID NO: 1648, SEQ ID NO: 1654, SEQ ID NO: 1446, SEQ ID NO: 1449, SEQ ID NO: 1452, SEQ ID NO: 1473, SEQ ID NO: 1474, SEQ ID NO: 1480, SEQ ID NO: 1491, SEQ ID NO: 1502, SEQ ID NO: 1513, SEQ ID NO: 1605, SEQ ID NO: 1771, SEQ ID NO: 1526, SEQ ID NO: 1557, SEQ ID NO: 1560, SEQ ID NO: 1585, SEQ ID NO: 1672, SEQ ID NO: 1677, SEQ ID NO: 1686, SEQ ID NO: 1752, SEQ ID NO: 1762, SEQ ID NO: 1777, SEQ ID NO: 1792, SEQ ID NO: 1805, SEQ ID NO: 1815, SEQ ID NO: 1817, SEQ ID NO: 1827, SEQ ID NO: 1842, SEQ ID NO: 1846, SEQ ID NO: 1896, SEQ ID NO: 1530, SEQ ID NO: 1637, SEQ ID NO: 1461, SEQ ID NO: 1467, SEQ ID NO: 1623, SEQ ID NO: 1625, SEQ ID NO: 530, SEQ ID NO: 708, SEQ ID NO: 414, SEQ ID NO: 694, SEQ ID NO: 703, SEQ ID NO: 721, SEQ ID NO: 749, SEQ ID NO: 685, SEQ ID NO: 444, SEQ ID NO: 606, SEQ ID NO: 582, SEQ ID NO: 621, SEQ ID NO: 868, SEQ ID NO: 666, SEQ ID NO: 408, SEQ ID NO: 538, SEQ ID NO: 573, SEQ ID NO: 639, SEQ ID NO: 668, SEQ ID NO: 524, SEQ ID NO: 422, SEQ ID NO: 819, SEQ ID NO: 611, SEQ ID NO: 674, SEQ ID NO: 577, SEQ ID NO: 663, SEQ ID NO: 558, SEQ ID NO: 794, SEQ ID NO: 564, SEQ ID NO: 592, SEQ ID NO: 814, SEQ ID NO: 398, SEQ ID NO: 767, SEQ ID NO: 425, SEQ ID NO: 659, SEQ ID NO: 517, SEQ ID NO: 539, SEQ ID NO: 475, SEQ ID NO: 615, SEQ ID NO: 665, SEQ ID NO: 607, SEQ ID NO: 598, SEQ ID NO: 759, SEQ ID NO: 752, SEQ ID NO: 595, SEQ ID NO: 686, SEQ ID NO: 528, SEQ ID NO: 705, SEQ ID NO: 828, SEQ ID

NO: 403, SEQ ID NO: 561, SEQ ID NO: 500, SEQ ID NO: 491, SEQ ID NO: 846, SEQ ID NO: 732, SEQ ID NO: 778, SEQ ID NO: 751, SEQ ID NO: 744, SEQ ID NO: 504, SEQ ID NO: 419, SEQ ID NO: 792, SEQ ID NO: 825, SEQ ID NO: 756, SEQ ID NO: 519, SEQ ID NO: 870, SEQ ID NO: 777, SEQ ID NO: 808, SEQ ID NO: 506, SEQ ID NO: 864, SEQ ID NO: 655, SEQ ID NO: 407, SEQ ID NO: 427, SEQ ID NO: 774, SEQ ID NO: 797, SEQ ID NO: 688, SEQ ID NO: 815, SEQ ID NO: 718, SEQ ID NO: 859, SEQ ID NO: 775, SEQ ID NO: 874, SEQ ID NO: 543, SEQ ID NO: 878, SEQ ID NO: 594, SEQ ID NO: 610, and SEQ ID NO: 600.

Particularly preferred is a purified or isolated *H. pylori* surface or membrane polypeptide or a fragment thereof, wherein the polypeptide is selected from the group consisting of SEQ ID NO: 1511, SEQ ID NO: 1561, SEQ ID NO: 1563, SEQ ID NO: 1681, SEQ ID NO: 1711, SEQ ID NO: 1731, SEQ ID NO: 1743, SEQ ID NO: 1747, SEQ ID NO: 1758, SEQ ID NO: 1893, SEQ ID NO: 1895, SEQ ID NO: 1573, SEQ ID NO: 1705, SEQ ID NO: 1707, SEQ ID NO: 1723, SEQ ID NO: 1726, SEQ ID NO: 1760, SEQ ID NO: 1764, SEQ ID NO: 1798, SEQ ID NO: 1803, SEQ ID NO: 1807, SEQ ID NO: 1889, SEQ ID NO: 1892, SEQ ID NO: 1460, SEQ ID NO: 1477, SEQ ID NO: 1499, SEQ ID NO: 1514, SEQ ID NO: 1641, SEQ ID NO: 1534, SEQ ID NO: 1564, SEQ ID NO: 1673, SEQ ID NO: 1746, SEQ ID NO: 1794, SEQ ID NO: 1843, SEQ ID NO: 1894, SEQ ID NO: 1536, SEQ ID NO: 1544, SEQ ID NO: 1568, SEQ ID NO: 1572, SEQ ID NO: 1582, SEQ ID NO: 1738, SEQ ID NO: 1891, SEQ ID NO: 1660, SEQ ID NO: 1793, SEQ ID NO: 1832, SEQ ID NO: 1841, SEQ ID NO: 1860, SEQ ID NO: 1486, SEQ ID NO: 1465, SEQ ID NO: 1539, SEQ ID NO: 1693, SEQ ID NO: 1629, SEQ ID NO: 1540, SEQ ID NO: 1791, SEQ ID NO: 1525, SEQ ID NO: 1558, SEQ ID NO: 1655, SEQ ID NO: 1517, SEQ ID NO: 875, SEQ ID NO: 676, SEQ ID NO: 801, SEQ ID NO: 860, SEQ ID NO: 747, SEQ ID NO: 529, SEQ ID NO: 387, SEQ ID NO: 391, SEQ ID NO: 515, SEQ ID NO: 625, SEQ ID NO: 568, SEQ ID NO: 454, SEQ ID NO: 800, SEQ ID NO: 499, SEQ ID NO: 779, SEQ ID NO: 648, SEQ ID NO: 643, SEQ ID NO: 537, SEQ ID NO: 511, SEQ ID NO: 616, SEQ ID NO: 829, SEQ ID NO: 546, SEQ ID NO: 780, SEQ ID NO: 553, SEQ ID NO: 549, SEQ ID NO: 410, SEQ ID NO: 608, SEQ ID NO: 513, SEQ ID NO: 656, SEQ ID NO: 845, SEQ ID NO: 563, SEQ ID NO: 570, SEQ ID NO: 805, SEQ ID NO: 851, SEQ ID NO: 423, SEQ ID NO: 810, SEQ ID NO: 604, SEQ ID NO: 636, SEQ ID NO: 757, SEQ ID NO: 412, SEQ ID NO: 816, SEQ ID NO: 771, SEQ ID NO: 418, SEQ ID NO: 662, SEQ ID NO: 512, SEQ ID NO: 679, SEQ ID NO: 605, SEQ ID NO: 421, SEQ ID NO: 552, SEQ ID NO: 576, SEQ ID NO: 571, SEQ ID NO: 725, SEQ ID NO: 565, SEQ ID NO: 717, SEQ ID NO: 536, SEQ ID NO: 647, SEQ ID NO: 501, SEQ ID NO: 838, SEQ ID NO: 428, SEQ ID NO: 494, SEQ ID NO: 479, SEQ ID NO: 711, SEQ ID NO: 722 ,SEQ ID NO: 645, SEQ ID NO: 670, SEQ ID NO: 746, SEQ ID NO: 493, SEQ ID NO: 540, SEQ ID NO: 612, SEQ ID NO: 629, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 433, SEQ ID NO: 385, and SEQ ID NO: 409.

In one embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least one membrane spanning region selected from the group consisting of SEQ ID NO: 1511, SEQ ID NO: 1561, SEQ ID NO: 1563, SEQ ID NO: 1681, SEQ ID NO: 1711, SEQ ID NO: 1731, SEQ ID NO: 1743, SEQ ID NO: 1747, SEQ ID NO: 1758, SEQ ID NO: 1893, SEQ ID NO: 1895, SEQ ID NO: 875, SEQ ID NO: 676, SEQ ID NO: 801, SEQ ID NO: 860, SEQ ID NO: 747, SEQ ID NO: 529, SEQ ID NO: 387, SEQ ID NO: 391, SEQ ID NO: 515, SEQ ID NO: 625, SEQ ID NO: 568, SEQ ID NO: 454, SEQ ID NO: 800, SEQ ID NO: 499, SEQ ID NO: 779, and SEQ ID NO: 385.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least two membrane spanning regions selected from the group consisting of SEQ ID NO: 1573, SEQ ID NO: 1705, SEQ ID NO: 1707, SEQ ID NO: 1723, SEQ ID NO: 1726, SEQ ID NO: 1760, SEQ ID NO: 1764, SEQ ID NO: 1798, SEQ ID NO: 1803, SEQ ID NO: 1807, SEQ ID NO: 1889, SEQ ID NO: 1892, SEQ ID NO: 1460, SEQ ID NO: 1477, SEQ ID NO: 1499, SEQ ID NO: 1514, SEQ ID NO: 1641, SEQ ID NO: 648, SEQ ID NO: 643, SEQ ID NO: 537, SEQ ID NO: 511, SEQ ID NO: 616, SEQ ID NO: 829, SEQ ID NO: 546, SEQ ID NO: 780, SEQ ID NO: 553, SEQ ID NO: 549, SEQ ID NO: 410, SEQ ID NO: 608, SEQ ID NO: 513, SEQ ID NO: 656, SEQ ID NO: 845, SEQ ID NO: 563, SEQ ID NO: 570, SEQ ID NO: 805, and SEQ ID NO: 851.

In yet another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least three membrane spanning regions selected from the group consisting of SEQ ID NO: 1534, SEQ ID NO: 1564, SEQ ID NO: 1673, SEQ ID NO: 1746, SEQ ID NO: 1794, SEQ ID NO: 1843, SEQ ID NO: 1894, SEQ ID NO: 423, SEQ ID NO: 810, SEQ ID NO: 604, SEQ ID NO: 636, SEQ ID NO: 757, SEQ ID NO: 412, and SEQ ID NO: 816.

In yet a further embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least four membrane spanning regions selected from the group consisting of SEQ ID NO: 1536, SEQ ID NO: 1544, SEQ ID NO: 1568, SEQ ID NO: 1572, SEQ ID NO: 1582, SEQ ID NO: 1738, SEQ ID NO: 1891, SEQ ID NO: 1660, SEQ ID NO: 771, SEQ ID NO: 418, SEQ ID NO: 662, SEQ ID NO: 512, SEQ ID NO: 679, SEQ ID NO: 605, SEQ ID NO: 421, SEQ ID NO: 552, SEQ ID NO: 576, SEQ ID NO: 571.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least five membrane spanning regions selected from the group consisting of SEQ ID NO: 1793, SEQ ID NO: 1832, SEQ ID NO: 1841, SEQ ID NO: 1860, SEQ ID NO: 1486, SEQ ID NO: 725, SEQ ID NO: 565, SEQ ID NO: 717, SEQ ID NO: 536, SEQ ID NO: 647, and SEQ ID NO: 409.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least six membrane spanning regions selected from the group consisting of SEQ ID NO: 1465, SEQ ID NO: 1539, SEQ ID NO: 1693, SEQ ID NO: 1629, SEQ ID NO: 501, SEQ ID NO: 838, SEQ ID NO: 428, SEQ ID NO: 494, SEQ ID NO: 479, SEQ ID NO: 711, and SEQ ID NO: 722.

In yet another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least seven membrane spanning regions selected from the group consisting of SEQ ID NO: 1540, SEQ ID NO: 1791, SEQ ID NO: 1525, SEQ ID NO: 1558, SEQ ID NO: 1655, SEQ ID NO: 1517, SEQ ID NO: 645, SEQ ID NO: 670, SEQ ID NO: 746, SEQ ID NO: 493, SEQ ID NO: 540, SEQ ID NO: 612, SEQ ID NO: 629, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, and SEQ ID NO: 433.

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 antibodies have 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. 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* polypeptide 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*.

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 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 preferred embodiments: the polypeptide has biological activity; the polypeptide has an amino acid sequence at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% identical to an amino acid sequence of the invention contained in the Sequence Listing, preferably it has about 65% sequence identity with an amino acid sequence of the invention contained in the Sequence Listing, and most preferably it has about 92% to about 99% sequence identity with an amino acid sequence of the invention contained in the Sequence Listing; the polypeptide has an amino acid sequence essentially the same as an amino acid sequence of the invention contained in the Sequence Listing; the polypeptide is at least 5, 10, 20, 50, 100, or 150 amino acid residues in length; the 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 the invention contained in the Sequence Listing. In yet another preferred embodiment, the amino acid sequence which differs in sequence identity by about 7% to about 8% from the *H. pylori* amino acid sequences of the invention contained in the Sequence Listing is also encompassed by the invention.

In preferred embodiments: the *H. pylori* polypeptide is encoded by a nucleic acid of the invention contained in the Sequence Listing, or by a nucleic acid having at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with a nucleic acid of the invention contained 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 of the invention contained in the Sequence Listing. The differences, however, are such that the *H. pylori* polypeptide exhibits an *H. pylori* 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 of the invention contained in the Sequence Listing; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the invention contained in the Sequence Listing.

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 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 postranslational events.

The invention also encompasses an immunogenic component which includes an *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 of the invention contained in the Sequence Listing.

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 of the invention contained in the Sequence Listing; the encoded polypeptide has an amino acid sequence essentially the same as an amino acid sequence of the invention contained 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 of the invention contained in the Sequence Listing.

In preferred embodiments: the nucleic acid of the invention is that contained in the Sequence Listing; the nucleic acid is at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% homologous with a nucleic acid sequence of the invention 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 acid sequence at 1, 2, 3, 5, 10 or more residues, from a sequence of the invention contained 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 of the invention contained in the Sequence Listing; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the invention 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., 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 the invention contained in the Sequence Listing; more preferably to at least 12 consecutive nucleotides of the invention contained in the Sequence Listing; more preferably to at least 20 consecutive nucleotides of the invention contained in the Sequence Listing; more preferably to at least 40 consecutive nucleotides of the invention contained in the Sequence Listing.

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

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

In another aspect, the invention encompasses: a vector including a nucleic acid 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.

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 of the invention 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 which hybridizes under stringent conditions to at least 10 consecutive nucleotides of sense or antisense sequence of the invention 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.

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 # 55679) as strain HP-J99.

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 of the invention contained 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 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.

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 characterized as shown in Table 1 below, including: *H. pylori* cell envelope proteins, *H. pylori* periplasmic/secreted proteins, *H. pylori* cytoplasmic proteins, and other *H. pylori* surface and membrane proteins. Members of these groups were identified by BLAST homology searches and by searches for secretion signal or transmembrane protein motifs. (Polypeptides in the same row of Table 1, i.e., rows 1 and 3, or rows 2 and 4, are related to one another as described in Table 3 below.)

TABLE 1

TABLE OF FUNCTIONAL GROUPS					
	nt	aa		nt	aa
ORF Name	SeqID #	SeqID #	ORF Name	SeqID #	SeqID #
Row	1	2		3	4
A. CELL ENVELOPE					
A.1. Flagella-associated					
01gp10401orf1	1020	1471	26588588.aa	217	660
01gp10401orf5	1021	1472	26588588.aa	217	660
02ae11612orf21	1036	1487	6288949.aa	367	855
02ce10213orf7	1050	1501	22692187.aa	911	534
02ge20116orf34	1071	1522	29454837.aa	944	675
04ge11713orf5	1101	1552	1171928.aa	18	404
04ge11713orf5	1101	1552	21699087.aa	107	518
05ep20322orf11	1135	1586	16219090.aa	894	464
12ge20305orf11	1276	1727	29298130.aa	943	672
06cp20302orf12	1150	1601	25525277.aa	203	640
07ge20415orf27	1187	1638	19557055.aa	85	490
07ge20415orf27	1187	1638	36111066.aa	290	755
07ge31107orf2	1192	1643	104792.aa	5	389
29zp10241orf6	1361	1812	24882763.aa	199	635
hp2e10911orf5	1379	1830	917152.aa	992	877
hp3e11122orf1	1399	1850	25478375.aa	934	637
hp3e11168orf2	1403	1854	16984442.aa	899	477
hpe11122orf5	1400	1851	3942217.aa	302	772
07ge20415orf34	1189	1640	26380318.aa	215	658
A.2. Inner membrane proteins					
01ce11016orf1	1002	1453			
09ap11406orf14	1213	1664	16131887.aa	893	463
09ap11406orf15	1214	1665	6093906.aa	984	852
09ap11406orf5	1215	1666	2082012.aa	97	503
11ce11603orf16	1234	1685	1204418.aa	22	411
11ce11603orf16	1234	1685	14455461.aa	49	441
11ce11603orf25	1236	1687	4035783.aa	309	782
11ce11603orf6	1237	1688	23915877.aa	150	575
09cp10502orf22	1224	1675	30730068.aa	240	691
09cp10502orf22	1224	1675	3385833.aa	957	724
11gp10904orf29	1251	1702	14713512.aa	57	452
12ap10324orf2	1262	1713	10353192.aa	2	386
06cp20302orf10	1149	1600	203192.aa	92	497
09ap20802orf5	1220	1671	32704686.aa	255	712
11ge10309orf14	1240	1691	24222885.aa	164	591
11ge10309orf14	1240	1691	2548562.aa	201	638
06gp10409orf7	1164	1615	34666680.aa	278	740
06gp10409orf8	1165	1616	3203142.aa	245	697

hp3e11168orf29	1404	1855	23853165.aa	921	569
06cp11118orf6	1144	1595	16412593.aa	896	470
06cp11118orf6	1144	1595	32236462.aa	248	700
07ee20513orf28	1182	1633	24132293.aa	159	586
07ee20513orf28	1182	1633	486075.aa	979	823
06ep10306orf12	1157	1608	24651083.aa	194	627
06ep10306orf3	1160	1611	24651083.aa	194	627
06ep10306orf3	1160	1611	30089217.aa	946	684
13ep12003orf20	1300	1751	23493756.aa	916	551
14ge10705orf11	1321	1772	17086587.aa	76	478
14ge10705orf11	1321	1772	21486677.aa	905	508
14ge10705orf11	1321	1772	23468781.aa	914	545
14ge10705orf11	1321	1772	24708129.aa	931	628
14gp11820orf13	1323	1774	14494077.aa	50	443
14gp11820orf13	1323	1774	3242337.aa	250	702
14gp11820orf13	1323	1774	3962777.aa	969	776
14gp12015orf12	1329	1780	15824052.aa	66	461
14gp12015orf12	1329	1780	34489543.aa	275	737
14gp12015orf16	1332	1783	4698838.aa	330	809
27ze10351orf17	1345	1796	25605166.aa	204	642
29zp10241orf14	1358	1809	9776562.aa	383	879
hp1p13947orf2	1375	1826	3953143.aa	303	773
hp4p11352orf4	1417	1868	16406265.aa	70	468
13ap11517orf20	1283	1734	5267037.aa	983	842
16ae10113orf1	1335	1786	423131.aa	972	788
hp1p13922orf22	1368	1819	24611590.aa	929	624
07ee11620orf2	1179	1630	423131.aa	972	788
12ae10622orf9	1255	1706	259665.aa	936	644
12ae10622orf9	1255	1706	34097707.aa	267	727
12ae11404orf15	1258	1709	24806290.aa	197	631
02ce10213orf14	1044	1495	14645905.aa	55	450
12ge10305orf15	1273	1724	14642202.aa	54	448
01xe21717orf18	1024	1475	26261040.aa	210	653
A.3. Transporters					
09ap20802orf27	1219	1670	20032561.aa	90	495
12ge10305orf16	1274	1725	11132778.aa	15	400
09ae11601orf14	1210	1661	23439633.aa	913	541
09ae11601orf14	1210	1661	29302003.aa	227	673
hp5e11726orf7	1422	1873	179677.aa	79	482
14ce11113orf1	1302	1753	24609593.aa	191	622
14cp10119orf12	1308	1759	30662792.aa	238	689
14cp10119orf15	1310	1761	34427317.aa	274	736
14gp12015orf14	1331	1782	12617677.aa	27	417
hp5e15440orf16	1432	1883	33203192.aa	258	716
hp5e15440orf16	1432	1883	36573502.aa	295	762
02ce11022orf7	1052	1503	1071890.aa	10	395
04ep10811orf4	1091	1542	24215.aa	160	587

04ep10811orf4	1091	1542	289711.aa	225	669
hp5e11726orf4	1421	1872	36203402.aa	964	758
02ge20116orf28	1069	1520	24238762.aa	166	593
01ce11513orf21	1005	1456	1464715.aa	56	451
01ce11513orf21	1005	1456	4882763.aa	980	827
01ce11618orf10	1007	1458	207817.aa	903	502
06gp11202orf7	1166	1617	33399142.aa	261	719
07cp21714orf13	1177	1628	16406581.aa	71	469
07gp11807orf25	1193	1644	3319687.aa	955	715
07gp11807orf8	1206	1657	5875152.aa	361	847
07gp11807orf9	1207	1658	14714687.aa	58	453
14ce20219orf1	1304	1755	22441050.aa	114	527
14ce20219orf2	1305	1756	26258562.aa	940	652
27ze10351orf18	1346	1797	35345228.aa	960	745
27ze10351orf24	1348	1799	23728388.aa	144	567
27ze10351orf29	1350	1801	5878208.aa	362	848
02ae11611orf11	1032	1483	13726562.aa	40	430
02ae11611orf11	1032	1483	35428912.aa	285	748
02ce11022orf8	1053	1504	10723412.aa	11	396
02ce11022orf8	1053	1504	24218968.aa	161	588
02ce11022orf8	1053	1504	4455467.aa	974	795
03ee11215orf29	1081	1532	22265691.aa	111	523
05cp11911orf41	1124	1575	4338438.aa	316	791
hp2p10625orf28	1382	1833	32952.aa	257	714
hp5p15641orf12	1437	1888	17787558.aa	78	481
12ap10324orf3	1263	1714	3906712.aa	966	765
A.4. Outer membrane proteins					
07ap80601orf8	1173	1624	5083193.aa	352	837
hp3e11168orf30	1405	1856	4960952.aa	981	833
hp3p10156orf12	1406	1857	24104558.aa	158	585
hp4e13394orf2	1410	1861	7116626.aa	989	865
04ce11617orf2	1086	1537	36126938.aa	963	764
14ge10705orf5	1322	1773	1431462.aa	48	440
14ge10705orf5	1322	1773	16225006.aa	68	465
12ap10324orf7	1266	1717	23531562.aa	135	555
13ae10712orf9	1282	1733	22379952.aa	910	526
12ge10305orf1	1271	1722	30478562.aa	236	687
12ge10305orf1	1271	1722	31250333.aa	241	692
07gp31516orf4	1208	1659	31262.aa	949	693
05cp20518orf33	1126	1577	29479681.aa	945	677
12ap11614orf8	1270	1721	26054702.aa	207	649
12ge20305orf2	1278	1729	4721061.aa	977	812
A.5. Other cell envelope proteins					
hp4p11352orf9	1419	1870	4821082.aa	978	820
05cp20518orf3	1125	1576	978477.aa	994	880
07ee20513orf14	1181	1632	24220627.aa	163	590
hp4p11352orf2	1416	1867	32705252.aa	256	713

hp4p11352orf2	1416	1867	35445843.aa	287	750
04ge11713orf11	1096	1547	24427340.aa	184	613
03ee11215orf30	1082	1533	1416312.aa	45	437
06cp11722orf15	1146	1597	23535937.aa	136	556
06cp11722orf15	1146	1597	26366312.aa	214	657
06cp11722orf12	1145	1596	114505.aa	16	402
05ae20220orf32	1108	1559	2461062.aa	192	623
06cp11722orf21	1148	1599	6828218.aa	373	862
16ae10508orf13	1337	1788	14642217.aa	892	449
16ae10508orf14	1338	1789	30703183.aa	239	690
hp5e12982orf14	1424	1875	1365943.aa	34	424
01ae22001orf2	1000	1451	4826401.aa	340	821
01xe21717orf5	1027	1478	1385937.aa	41	432
01xe21717orf5	1027	1478	4714375.aa	332	811
07ce10203orf22	1175	1626	23526667.aa	134	554
14gp12015orf13	1330	1781	4698838.aa	330	809
B. CYTOPLASAMIC PROTEINS					
B.1. Proteins involved in energy conversion					
06cp11722orf16	1147	1598	10553192.aa	882	390
13ee10216orf55	1288	1739	914087.aa	382	876
14gp11820orf20	1324	1775	23475342.aa	130	547
hp1p11244orf7	1363	1814	29500075.aa	230	678
B.2. Proteins involved in amino acid metabolism					
01ae12021orf1	997	1448	34109763.aa	269	729
01ee11621orf6	1015	1466	4177212.aa	312	786
03ge31106orf1	1084	1535	26301059.aa	211	654
04ep71403orf15	1094	1545	34194093.aa	959	734
04ge11713orf37	1099	1550	25992137.aa	938	646
09gp10903orf3	1229	1680	21976637.aa	110	522
11gp10904orf27	1250	1701	31681556.aa	244	696
12ap11614orf4	1268	1719	45914063.aa	328	807
13ee12016orf10	1293	1744	30082267.aa	235	683
16ae10508orf21	1339	1790	429192.aa	315	790
hp3p10349orf16	1408	1859	36594167.aa	296	763
hp5e15211orf22	1429	1880	4578469.aa	976	806
hp5e15440orf19	1434	1885	4492217.aa	321	799
09cp10713orf29	1228	1679	1408.aa	43	434
02ae11611orf1	1031	1482	35269000.aa	281	743
02ae11612orf13	1034	1485	4570262.aa	326	804
01ce11618orf18	1008	1459	34189716.aa	272	733
B.3. Proteins involved in nucleotide metabolism					
02cp20821orf10	1061	1512	4882652.aa	344	826
02ep30607orf10	1064	1515	23598962.aa	139	562
07ge20415orf6	1191	1642	12897656.aa	30	420
09ap20802orf1	1217	1668	2738378.aa	220	664
hp1p13852orf5	1365	1816	598933.aa	364	850
hp3e11024orf24	1394	1845	6517040.aa	369	857

hp4e14535orf3	1414	1865	677088.aa	372	861
hp4e14535orf4	1415	1866	867183.aa	991	872
hp5e15440orf21	1435	1886	23442642.aa	128	544
02cp11822orf22	1058	1509	4895327.aa	347	830
02cp11822orf26	1059	1510	14574201.aa	52	446
B.4. Proteins involved in carbohydrate metabolism					
03ee11215orf26	1080	1531	10737627.aa	12	397
05cp20518orf5	1128	1579	32144532.aa	247	699
05cp20518orf64	1133	1584	15807794.aa	64	459
09ae11601orf3	1211	1662	2149041.aa	101	509
11gp11422orf1	1252	1703	4787562.aa	338	818
11gp11422orf2	1253	1704	19541302.aa	83	488
13ee10216orf43	1236	1737	14257751.aa	46	438
13ee10216orf56	1289	1740	4897177.aa	348	831
13ee10216orf9	1291	1742	2855006.aa	223	667
14ce11519orf2	1303	1754	13723593.aa	39	429
hp3e11060orf11	1396	1847	29557266.aa	232	680
01ae11421orf1	996	1447	24300682.aa	168	597
B.5. Proteins involved in cofactor metabolism					
04ge10816orf2	1095	1546	1581937.aa	65	460
06ee10709orf5	1156	1607	3261306.aa	952	709
06ep10306orf13	1158	1609	485375.aa	341	822
06ep10306orf14	1159	1610	16251627.aa	69	466
12ge20305orf14	1277	1728	24089437.aa	924	584
02ae11612orf26	1038	1489	10407625.aa	4	388
B.6. Proteins involved in lipid metabolism					
12ae11404orf14	1257	1708	24806290.aa	197	631
29zp10241orf11	1357	1808	422937.aa	313	787
hp5e15440orf22	1436	1887	22667967.aa	119	532
B.7. Proteins involved in mRNA translation and ribosome biogenesis					
02ce10213orf2	1047	1498	24500088.aa	188	619
02cp11404orf11	1055	1506	33601578.aa	956	723
06ce10515orf4	1141	1592	25595387.aa	935	641
09cp10713orf28	1227	1678	32036462.aa	246	698
14gp11820orf5	1327	1778	24803280.aa	196	630
hp4e14522orf11	1412	1863	785437.aa	376	869
B.8. Proteins involved in genome replication, transcription, recombination& repair					
01ce11016orf14	1003	1454	24396937.aa	172	601
04ce11617orf27	1087	1538	12520952.aa	25	415
05ap11505orf1	1116	1567	23440814.aa	126	542
05cp20518orf56	1130	1581	32431687.aa	951	704
05cp20518orf63	1132	1583	23880087.aa	147	572
07ge11504orf4	1185	1636	16305252.aa	895	467
07ge20415orf30	1188	1639	10745275.aa	14	399
07gp11807orf35	1198	1649	24036302.aa	154	579

09ap20802orf22	1218	1669	34574062.aa	277	739
09ap20802orf22	1218	1669	5879160.aa	363	849
11ge10309orf51	1244	1695	487750.aa	342	824
14ce21516orf1	1306	1757	85786.aa	378	871
14gp11820orf27	1325	1776	23475342.aa	130	547
hp3e11060orf2	1397	1848	24818802.aa	198	633
hp3e11060orf9	1398	1849	3166040.aa	243	695
hp3p10156orf8	1407	1858	11719687.aa	19	405
hp5e15440orf18	1433	1884	10677187.aa	9	394
hp5e15440orf18	1433	1884	36523442.aa		761
B.9. Proteins involved in outer membrane or					
cell wall biosynthesis					
09ap11406orf8	1216	1667	23912807.aa	149	574
09ap11406orf8	1216	1667	24298127.aa	167	596
11ep12011orf9	1239	1690	495312.aa	349	832
29zp10241orf7	1362	1813	26197187.aa	209	651
01ep30520orf16	1017	1468	7225666.aa	990	867
01ep30520orf27	1019	1470	24441412.aa	185	614
01ep30520orf27	1019	1470	11253.aa	883	401
29zp10241orf4	1360	1811	10675632.aa	8	393
B.10. Chaperones					
hp5e12982orf13	1423	1874	12343763.aa	887	413
hp5e15211orf10	1425	1876	50253.aa	350	835
hp1p13947orf1	1374	1825	6845425.aa	987	863
B.11 Other cytoplasmic proteins					
01xe21717orf9	1028	1479	156587.aa	63	458
02ae11612orf25	1037	1488	32422343.aa	249	701
03ee11215orf10	1077	1528	22542803.aa	118	531
05ae20220orf99	1115	1566	23492181.aa	132	550
11ce10917orf14	1232	1683	14313885.aa	47	439
11ge10309orf15	1241	1692	21647676.aa	106	516
12ap11614orf2	1267	1718	4562712.aa	324	802
06ge10115orf15	1163	1614	24070250.aa	155	581
02ge20116orf22	1068	1519	22704567.aa	121	535
02ge20116orf22	1068	1519	24003758.aa	153	578
02ge20116orf22	1068	1519	19626250.aa	87	492
02cp11404orf9	1056	1507	6517192.aa	986	858
03ae10516orf11	1072	1523	33476715.aa	262	720
03ae10516orf11	1072	1523	4726503.aa	333	813
03ap21820orf10	1073	1524	13673328.aa	36	426
04ep71403orf10	1092	1543	50062.aa	982	834
04gp11213orf36	1102	1553	24414687.aa	180	609
04gp11213orf60	1103	1554	19556290.aa	84	489
05ae10307orf1	1104	1555	17497107.aa	900	480
05ae20220orf54	1111	1562	1179838.aa	20	406
05cp11911orf11	1119	1570	10664078.aa	7	392
05gp11901orf20	1136	1587	15039062.aa	61	456

05gp11901orf24	1137	1588	32600912.aa	253	707
06ae11405orf10	1140	1591	22687687.aa	120	533
06ce11002orf2	1142	1593	34099062.aa	268	728
11ce10917orf9	1233	1684	391313.aa	299	769
11cp12006orf17	1238	1689	291700.aa	942	671
11ge10309orf25	1243	1694	24406401.aa	173	602
11ge10309orf56	1245	1696	24495312.aa	187	618
11ge10309orf66	1247	1698	24495312.aa	187	618
11gp10904orf12	1249	1700	29844512.aa	234	682
12ae11404orf9	1261	1712	22303918.aa	112	524
12ap11614orf6	1269	1720	4562712.aa	324	802
12ge20305orf30	1279	1730	4095342.aa	971	785
13ap11517orf31	1284	1735	15126875.aa	62	457
13ee10216orf82	1290	1741	4035262.aa	308	781
13ee12016orf24	1297	1748	16459375.aa	74	473
14gp12015orf1	1328	1779	10009666.aa	1	384
hp1p13922orf30	1370	1821	34089087.aa	266	726
hp1p13939orf13	1372	1823	4766691.aa	337	817
hp2e10911orf25	1377	1828	2035936.aa	93	498
hp2p10625orf30	1383	1834	1411681.aa	44	436
hp2p10625orf7	1384	1835	4740887.aa	335	815
hp2p10625orf8	1385	1836	6495137.aa	368	856
hp3e10349orf18	1388	1839	260941.aa	208	650
hp3e11168orf14	1401	1852	5325005.aa	358	844
hp3e11168orf15	1402	1853	24039587.aa	923	580
hp4p11352orf8	1418	1869	4040928.aa	310	783
hp4p13402orf1	1420	1871	1256885.aa	26	416
hp5e15211orf15	1427	1878	35156938.aa	279	741
02ge20116orf33	1070	1521	14480927.aa	890	442
06cp20302orf8	1151	1602	4569693.aa	325	803
07ce11409orf4	1176	1627	21742157.aa	109	520
01ae12021orf8	999	1450	23646885.aa	143	566
01ce11513orf24	1006	1457	23539006.aa	918	557
01cp11710orf27	1012	1463	32595137.aa	252	706
01ep30520orf20	1018	1469	32627125.aa	953	710
02ae11211orf19	1030	1481	19537968.aa	902	487
02ae11611orf5	1033	1484	24407533.aa	174	603
02ce10114orf1	1041	1492	16440842.aa	73	472
02ce10213orf32	1049	1500	16839562.aa	898	476
02ce11220orf2	1054	1505	3930468.aa	300	770
02cp11721orf13	1057	1508	5265957.aa	356	841
04ep10811orf1	1090	1541	3907042.aa	298	768
04ge11713orf27	1097	1548	5111308.aa	354	839
05cp20518orf50	1129	1580	23573294.aa	138	560
06ae11020orf2	1139	1590	4486092.aa	319	796
06ce11002orf8	1143	1594	194415.aa	80	483
06cp30603orf11	1152	1603	24824087.aa	933	634

06ee10207orf2	1153	1604	14572133.aa	891	445
06ee10709orf17	1155	1606	6136430.aa	366	853
06ep11108orf20	1161	1612	22370182.aa	113	525
06ge10115orf12	1162	1613	4491093.aa	320	798
07ap11111orf3	1169	1620	23490686.aa	915	549
07ap80601orf10	1170	1621	5078593.aa	351	836
07ap80601orf12	1171	1622	24219012.aa	162	589
07ee20513orf1	1180	1631	36520792.aa	965	760
07gp11807orf28	1194	1645	16100038.aa	67	462
07gp11807orf29	1195	1646	42683.aa	314	789
07gp11807orf38	1199	1650	214812.aa	904	507
07gp11807orf41	1200	1651	4882842.aa	345	828
07gp11807orf42	1201	1652	719606.aa	374	866
07gp11807orf44	1202	1653	35949212.aa	962	754
07gp11807orf54	1205	1656	34161500.aa	270	730
14cp10923orf1	1312	1763	24492192.aa	186	617
16ae10508orf10	1336	1787	14864452.aa	60	455
27ze10351orf25	1349	1800	875042.aa	379	873
29gp10119orf6	1355	1806	14094816.aa	889	435
29zp10241orf18	1359	1810	3906937.aa	967	766
hp4e14535orf2	1413	1864	43490713.aa	973	793
hp5e15211orf13	1426	1877	35163962.aa	280	742
hp5e15211orf29	1430	1881	24329712.aa	170	599
			625277.aa	985	854
			24816915.aa	932	632
C. SECRETED OR PERIPLASMIC PROTEINS					
C.1. Secreted or periplasmic proteins					
01ce11016orf19	1004	1455	22460468.aa	117	530
05gp11901orf25	1138	1589	32609403.aa	254	708
02ge20116orf20	1067	1518	12505125.aa	24	414
03ee11215orf15	1078	1529	3157067.aa	242	694
14cp10923orf3	1314	1765	3242952.aa	950	703
14ee11217orf1	1319	1770	33595708.aa	263	721
14ee11217orf1	1319	1770	35442513.aa	286	749
hp2e10911orf30	1378	1829	30100332.aa	947	685
05ae20220orf124	1105	1556	14570443.aa	51	444
05ae20220orf92	1114	1565	24410643.aa	177	606
05ap21216orf7	1118	1569	24078837.aa	156	582
05cp11911orf12	1120	1571	24609431.aa	190	621
05cp11911orf27	1123	1574	783432.aa	375	868
05cp20518orf41	1127	1578	2843912.aa	222	666
09ae11601orf4	1212	1663	11876471.aa	21	408
09cp10502orf17	1223	1674	23438887.aa	912	538
09cp10713orf25	1225	1676	23912707.aa	148	573
11ge10309orf63	1246	1697	25501501.aa	202	639
11ge10309orf9	1248	1699	289077.aa	224	668
12ae11404orf3	1259	1710	22303918.aa	112	524

12ap10324orf4	1264	1715	13178562.aa	32	422
12ap10324orf5	1265	1716	4805318.aa	339	819
13ae10712orf4	1281	1732	24416083.aa	182	611
13ap11517orf7	1285	1736	29386577.aa	228	674
13ee12016orf15	1294	1745	23958179.aa	152	577
13ee12016orf5	1298	1749	272058.aa	219	663
13ee12016orf8	1299	1750	23564012.aa	137	558
14cp10923orf8	1315	1766	4414000.aa	318	794
14cp11121orf6	1316	1767	23631292.aa	141	564
14ee10308orf8	1317	1768	24230058.aa	165	592
14ee10308orf9	1318	1769	4728193.aa	334	814
16ep10117orf8	1344	1795	10742963.aa	13	398
27ze10351orf5	1351	1802	3906963.aa	297	767
29ge10111orf1	1353	1804	1367157.aa	35	425
hp1p13939orf9	1373	1824	26423583.aa	216	659
hp2e11858orf5	1380	1831	21687842.aa	908	517
hp3e10349orf17	1387	1838	23439055.aa	124	539
hp3e10349orf24	1389	1840	16603418.aa	75	475
hp3e11024orf22	1393	1844	2445812.aa	927	615
hp3e11024orf22	1393	1844	2774062.aa	221	665
hp4e13394orf5	1411	1862	24411011.aa	178	607
hp5e15211orf21	1428	1879	24328910.aa	169	598
hp5e15276orf14	1431	1882	36335436.aa	293	759
hp5p15641orf8	1439	1890	35837767.aa	289	752
02ce10213orf11	1043	1494	24276587.aa	926	595
07ge11504orf2	1183	1634	30283516.aa	948	686
07ge11504orf3	1184	1635	22447252.aa	115	528
07gp11807orf32	1196	1647	32462543.aa	251	705
07gp11807orf33	1197	1648	4882842.aa	345	828
07gp11807orf48	1203	1654	116018.aa	17	403
01ae11403orf1	995	1446	23594838.aa	920	561
01ae12021orf7	998	1449	20415937.aa	95	500
01ce10516orf2	1001	1452	1962590.aa	86	491
01gp11016orf14	1022	1473	5869090.aa	360	846
01xe21717orf12	1023	1474	34179577.aa	271	732
02ae11211orf10	1029	1480	3987580.aa	970	778
02ae11612orf4	1040	1491	35704718.aa	288	751
02ce10216orf1	1051	1502	35336707.aa	282	744
02cp20821orf12	1062	1513	20836042.aa	98	504
02cp20821orf12	1062	1513	12698442.aa	29	419
06ee10709orf16	1154	1605	4339708.aa	317	792
14ep11115orf1	1320	1771	4882318.aa	343	825
C.2. Proteins likely to be secreted or periplasmic					
03ap21820orf5	1075	1526	36131282.aa	291	756
05ae20220orf24	1106	1557	21720017.aa	108	519
05ae20220orf50	1109	1560	80257.aa	377	870
05cp20518orf9	1134	1585	3964593.aa	305	777

05cp20518orf9	1134	1585	4687507.aa	305	808
09cp10502orf14	1221	1672	2111040.aa	100	506
09cp10713orf26	1226	1677	7031343.aa	988	864
11ce11603orf22	1235	1686	26306340.aa	212	655
14ce10720orf2	1301	1752	1181418.aa	884	407
14cp10119orf7	1311	1762	1370202.aa	37	427
14gp11820orf4	1326	1777	3953952.aa	968	774
16cp30109orf6	1341	1792	4490717.aa	975	797
29gp10119orf5	1354	1805	30603402.aa	237	688
hp1p11256orf7	1364	1815	4740887.aa	335	815
hp1p13868orf24	1366	1817	33397538.aa	260	718
hp1p14013orf4	1376	1827	663530.aa	370	859
hp3e11024orf16	1391	1842	20173437.aa	91	496
hp3e11024orf16	1391	1842	34573431.aa	276	738
hp3e11024orf6	1395	1846	4062813.aa	311	784
hp6p10723orf7	1445	1896	24406401.aa	173	602
03ee11215orf20	1079	1530	2150290.aa	102	510
07ge20415orf22	1186	1637	3958537.aa	304	775
01ce11618orf20	1010	1461	882827.aa	380	874
01ep10216orf6	1016	1467	23441078.aa	127	543
07ap80601orf5	1172	1623	917200.aa	993	878
04ge11713orf35	1098	1549	24256572.aa	925	594
03ap21820orf9	1076	1527	24415917.aa	181	610
07ce10203orf14	1174	1625	24395801.aa	171	600
D. OTHER SURFACE AND MEMBRANE PROTEINS					
D.1. Proteins likely to contain a single membrane spanning region					
02cp11822orf8	1060	1511	907827.aa	381	875
05ae20220orf51	1110	1561	29458178.aa	229	676
05ae20220orf6	1112	1563	4548792.aa	323	801
11ae10305orf4	1230	1681	6696887.aa	371	860
12ae11404orf8	1260	1711	35417942.aa	284	747
12ge20305orf35	1280	1731	22453166.aa	116	529
13ee11718orf2	1292	1743	1038312.aa	3	387
13ee12016orf19	1296	1747	10580417.aa	6	391
13ee12016orf19	1296	1747	21618785.aa	907	515
14ce21516orf3	1307	1758	24634750.aa	193	625
hp6p10723orf20	1442	1893	23831562.aa	145	568
hp6p10723orf5	1444	1895	14726542.aa	59	454
02ce10213orf1	1042	1493	4531568.aa	322	800
02ae11612orf36	1039	1490	2040717.aa	94	499
04ge11713orf41	1100	1551	3991067.aa	306	779
			10037799.aa	881	385
D.2. Proteins likely to contain two membrane spans					
05cp11911orf15	1122	1573	26052137.aa	939	648
12ae10622orf16	1254	1705	25925.aa	205	643
12ae11404orf12	1256	1707	23438840.aa	123	537

12ge10305orf10	1272	1723	21503772.aa	906	511
12ge10305orf10	1272	1723	24488537.aa	928	616
12ge10305orf21	1275	1726	489057.aa	346	829
14cp10119orf14	1309	1760	23473437.aa	129	546
14cp10119orf14	1309	1760	40339452.aa	307	780
14cp10923orf14	1313	1764	23515833.aa	133	553
27ze10351orf22	1347	1798	23486342.aa	131	548
27ze10351orf7	1352	1803	11924177.aa	886	410
29gp10119orf7	1356	1807	24413512.aa	179	608
hp5p15641orf5	1438	1889	21563752.aa	104	513
hp6p10723orf13	1441	1892	26351567.aa	213	656
01ce11618orf19	1009	1460	55843.aa	359	845
01xe21717orf40	1026	1477	23610905.aa	140	563
02ce10213orf23	1048	1499	23867207.aa	146	570
02cp20821orf8	1063	1514	4572168.aa	327	805
07ge20415orf39	1190	1641	5993958.aa	365	851
D.3. Proteins likely to contain 3 membrane spanning regions					
03ge10505orf14	1083	1534	1364378.aa	33	423
05ae20220orf88	1113	1564	4708337.aa	331	810
09cp10502orf16	1222	1673	24409577.aa	175	604
13ee12016orf18	1295	1746	25398250.aa	200	636
16ep10117orf7	1343	1794	36134661.aa	292	757
hp3e11024orf17	1392	1843	1206675.aa	23	412
hp6p10723orf43	1443	1894	4744128.aa	336	816
D.4. Proteins likely to contain 4 membrane spanning regions					
03xe11215orf5	1085	1536	3933437.aa	301	771
04ep71403orf12	1093	1544	12694087.aa	28	418
05ap11505orf10	1117	1568	26758437.aa	941	662
05cp11911orf13	1121	1572	21511555.aa	103	512
05cp11911orf13	1121	1572	29531590.aa	231	679
05cp20518orf61	1131	1582	24409641.aa	176	605
13ee10216orf5	1287	1738	12969218.aa	31	421
13ee10216orf5	1287	1738	23494043.aa	917	552
hp5p15641orf9	1440	1891	23945317.aa	151	576
09ae11601orf11	1209	1660	23867687.aa	922	571
D.5. Proteins likely to contain 5 membrane spanning regions					
16ep10117orf6	1342	1793			
hp2p10625orf14	1381	1832	33986087.aa	265	725
hp3e10349orf25	1390	1841	23631317.aa	142	565
hp3p10349orf32	1409	1860	33218912.aa	259	717
02ae11612orf14	1035	1486	23437502.aa	122	536
			25995917.aa	206	647
			11878127.aa	885	409
D.6. Proteins likely to contain 6 membrane spanning regions					
01cp11710orf34	1014	1465	2042312.aa	96	501
01cp11710orf34	1014	1465	5083577.aa	353	838
04ep10206orf22	1088	1539	13704718.aa	38	428

04ep10206orf22	1088	1539	20023400.aa	89	494
11ge10309orf18	1242	1693	17089217.aa	77	479
07cp21714orf14	1178	1629	32663212.aa	954	711
07cp21714orf14	1178	1629	3360130.aa	264	722
D.7. Proteins likely to contain 7 or more membrane spanning regions					
04ep10206orf23	1089	1540	25976418.aa	937	645
04ep10206orf23	1089	1540	2915903.aa	226	670
16ae10508orf3	1340	1791	35360843.aa	283	746
03ap21820orf13	1074	1525	197166.aa	88	493
03ap21820orf13	1074	1525	234391.aa	125	540
03ap21820orf13	1074	1525	24417212.aa	183	612
05ae20220orf31	1107	1558	24798427.aa	195	629
07gp11807orf49	1204	1655	19531291.aa	81	484
07gp11807orf49	1204	1655	19536375.aa	901	485
02ep30607orf31	1066	1517	19536458.aa	82	486
02ep30607orf31	1066	1517	13865928.aa	42	433

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

Definitions

A purified or isolated polypeptide or a substantially pure preparation of a polypeptide are used interchangeably herein and, as used herein, mean 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 purified or isolated or a substantially pure nucleic acid, e.g., a substantially pure DNA, (are terms used interchangeably herein) 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 and can be determined from a stop to stop codon or from a start to stop codon.

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 referes 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 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. 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 stingency (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).

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* infection, it can promote, or mediate the attachment of *H. pylori* to a cell; (2) it has an enzymatic activity, structural or regulatory function 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-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 of the invention contained 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 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 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 preferably the fragment or analog possesses 10%, preferably 40%, more preferably 60%, 70%, 80% or 90% or greater of the activity of *H. pylori*, in any *in vivo* or *in vitro* assay.

Analogs 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 analogs 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 can be made in view of the table 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-I-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 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 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 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* 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 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, 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 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 a process of transformation of competent cells or 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.

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 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 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-transitional modification, or biological activity of the expressed polypeptide; a pattern of 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 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 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 include a

promoter, ribosomal binding site, terminators. and in some cases operators; 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 isloated 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 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*.

To determine the genomic sequence of *H. pylori*, DNA was isolated from a strain of *H. pylori* (ATCC # 55679) 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 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 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 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 Genome Program Contractor-Grantee Workshop V, Jan. 1996, p.157). The average contig length was about 3-4 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 designed that are complementary to sequences at the end of each contig. These oligonucleotides may be hybridized to libaries 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 primers in polymerase chain reaction (PCR) to amplify junctional fragments, the nucleotide sequence of which is then determined.

The *H. pylori* sequences were analyzed for the presence of open reading frames (ORFs) comprising at least 180 nucleotides. 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).

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, the authenticity of amplified products can be checked by conventional sequencing methods. Clones carrying the desired sequences described in this invention may also 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 strain. 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 of the invention are contained 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 of the invention contained in the Sequence Listing. These uses are described in further detail below.

Probes

A nucleic acid isolated or synthesized in accordance with the sequence of the invention contained 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 of the invention contained in 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 of the invention 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 of the invention contained 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 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 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 acid sequences of $\geq$ 10-15 nucleotides of the invention contained in the Sequence Listing have utility in conjunction with suitable enzymes and reagents to create copies of *H. pylori*

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 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 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 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. 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 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 acid of the invention exemplified in the 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 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 not produce the

same gene product(s). This includes, but is not limited to other *Helicobacter* strains, or other bacterial strains such as *E. coli*, *Norcardia*, *Corynebacterium*, *Campylobacter*, 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. 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 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 introduced 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. cerivisae* 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 NH_2 terminal amino acids to the expressed target gene. These NH_2 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 complexes. 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 micelle 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 an *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

This invention encompasses isolated *H. pylori* polypeptides encoded by the disclosed *H. pylori* genomic sequences, including the polypeptides of the invention 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 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 acheived, 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 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 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 Table 3 below. Most polypeptides described in Table 3 are over 90% identical to one another as noted in the last two columns; some are between 70% and 90% identical to one another; and very few share between 60% and 70% identity with each other. The polypeptides represented by the sequence identification numbers in the third column of Table 3 result from translations carried out from stop codon to stop codon in the genomic nucleotide sequence of the invention, while those in the first column result from translations carried out from the first methionine or valine codon following the prior stop codon and proceeding to the final stop codon in the nucleotide sequence. In some cases, the nucleotide sequence encoding the related polypeptides is slightly different, resulting in some differences in amino acid residues of the related polypeptides. In many cases, the related polypeptides differ significantly in length, with one polypeptide containing amino acid residues in addition to those in common between the two

polypeptides. In all cases, the relationships described in Table 3 are highly significant, and the nucleotide sequences encoding these related polypeptides are also very similar to one another. For example, the nucleotide probes derived from the coding sequence of the polypeptides in column one can be used in PCR or hybridization experiments to identify clones carrying the nucleotide sequence encoding the polypeptides of column three.

The relationships between the polypeptides shown in Table 3 can be classified in five broad categories as follows. First, for many polypeptides (designated "A" in the last column of the Table 3), the polypeptide denoted in column one is identical to the polypeptide denoted in column three except for an occasional addition of a few putative amino acid residues at the N-terminus which result from the fact that the polypeptides of column three were derived by translating from stop codon to stop codon instead of from a predicted start codon (i.e., Met or Val) to a stop codon as was done for the polypeptides in column one.

Second, for most polypeptides (designated "B" in the last column of the Table 3), the polypeptide of column one is at least 95% identical to the polypeptide of column three except that the polypeptide in column three is longer (at either or both ends) by one or more amino acid residues which do not result from the difference between reading from stop to stop instead of from start to stop.

Third, for some polypeptides (designated "C" in the last column of Table 3), the converse is true, the polypeptide of column one is at least 95% identical to the polypeptide of column three except that the polypeptide in column three is shorter (at either or both ends).

Fourth, for some polypeptides (designated "D" in the last column of Table 3), the polypeptide of column one shares a high level of amino acid identity (i.e., at least 95%) with the polypeptide of column three in the region in which they overlap, but shares little or no identity (i.e., less than 95%) at one or both ends. The level of identity of the polypeptides in columns one and three in categories "B", "C" and "D" is highly significant. For example, a typical *H. pylori* gene product will exhibit amino acid sequence identities of between 92% to 100% among strains of *H. pylori* isolated from human patients (*see* Table 10 below).

Finally, a fifth class of polypeptides in column one (designated "E" in the last column of Table 3) are closely related but differ significantly (i.e., less than 95% identical) from the polypeptide of column three. These polypeptides are likely "paralogs," members of related gene families in *H. pylori*.

TABLE 3

SeqID #	Length (aa)	SeqID #	Length (aa)	% Identity: Overlap Length	Category
384	509	1779	593	100.0 : 504 aa	B
386	133	1713	205	99.2 : 127 aa	B
387	158	1743	340	98.7 : 155 aa	B
388	112	1489	330	100.0 : 105 aa	B
389	650	1643	369	95.4 : 65 aa	D
390	62	1598	327	90.2 : 61 aa	E
391	619	1747	991	99.3 : 608 aa	B
392	110	1570	183	93.1 : 101 aa	E
393	68	1811	85	97.1 : 68 aa	B
394	446	1884	594	99.5 : 433 aa	B
395	84	1503	347	100.0 : 84 aa	B
396	40	1504	519	88.2 : 34 aa	E
397	300	1531	273	98.9 : 267 aa	C
398	214	1795	197	99.0 : 192 aa	C
399	137	1639	199	96.4 : 137 aa	B
400	272	1725	285	99.3 : 271 aa	B
401	287	1470	455	98.9 : 277 aa	D
402	106	1596	302	99.1 : 106 aa	B
403	157	1654	197	99.3 : 150 aa	B
404	278	1552	362	100.0 : 277 aa	B
405	120	1858	529	100.0 : 116 aa	B
406	226	1562	297	100.0 : 216 aa	B
407	62	1752	157	77.6 : 58 aa	E
408	50	1663	74	97.9 : 47 aa	B
410	188	1803	351	87.1 : 155 aa	E
411	130	1685	497	100.0 : 129 aa	B
412	183	1843	185	100.0 : 183 aa	A
413	194	1874	508	97.6 : 169 aa	D
414	235	1518	246	100.0 : 235 aa	B
415	88	1538	676	97.5 : 80 aa	B
416	109	1871	335	99.1 : 109 aa	B
417	107	1782	593	94.4 : 90 aa	E
418	136	1544	441	100.0 : 135 aa	B
419	54	1513	175	97.0 : 33 aa	E
420	125	1642	539	96.7 : 122 aa	B
421	249	1738	346	99.6 : 249 aa	B
422	86	1715	128	97.5 : 79 aa	B
423	128	1534	149	100.0 : 128 aa	B
424	93	1875	178	100.0 : 93 aa	B
425	88	1804	105	97.7 : 88 aa	B
426	128	1524	116	62.4 : 117 aa	E
427	108	1762	109	100.0 : 108 aa	A
428	118	1539	276	100.0 : 118 aa	B
429	54	1754	113	89.6 : 48 aa	E
430	288	1483	377	95.5 : 286 aa	B
431	303	1785	248	98.2 : 170 aa	D
431	303	1784	148	96.4 : 138 aa	D
432	192	1478	408	99.5 : 192 aa	B
433	168	1517	426	99.3 : 151 aa	D

434	153	1679	403	100.0 : 153 aa	B
435	162	1806	173	98.1 : 161 aa	B
436	59	1834	80	37.5 : 24 aa	E
437	222	1533	288	100.0 : 221 aa	B
438	53	1737	260	93.5 : 31 aa	E
439	109	1683	121	100.0 : 109 aa	B
440	73	1773	280	100.0 : 73 aa	B
441	237	1685	497	96.0 : 198 aa	D
442	92	1521	646	100.0 : 84 aa	D
443	97	1774	327	100.0 : 96 aa	B
444	280	1556	284	100.0 : 280 aa	A
445	187	1604	253	95.5 : 155 aa	D
446	58	1510	198	96.4 : 55 aa	B
447	85	1496	155	100.0 : 85 aa	B
448	90	1724	90	100.0 : 90 aa	A
449	105	1788	141	98.0 : 100 aa	D
450	172	1495	239	100.0 : 172 aa	B
451	212	1456	139	81.7 : 126 aa	E
452	182	1702	192	97.0 : 166 aa	D
453	224	1658	228	100.0 : 224 aa	A
454	131	1895	159	100.0 : 131 aa	B
455	73	1787	370	100.0 : 54 aa	D
456	92	1587	295	96.6 : 87 aa	B
457	205	1735	310	100.0 : 195 aa	B
458	41	1479	144	97.6 : 41 aa	B
459	219	1584	297	100.0 : 219 aa	B
460	188	1546	375	89.3 : 187 aa	E
461	231	1780	438	97.3 : 225 aa	B
462	63	1645	71	100.0 : 63 aa	B
463	183	1664	242	97.8 : 182 aa	B
464	117	1586	234	99.1 : 113 aa	B
465	153	1773	280	98.0 : 153 aa	B
466	43	1610	308	100.0 : 43 aa	B
467	240	1636	255	97.0 : 237 aa	B
468	209	1868	240	96.6 : 206 aa	B
469	95	1628	321	98.5 : 65 aa	D
470	229	1595	375	96.5 : 228 aa	B
471	92	1713	205	90.1 : 71 aa	E
472	96	1492	352	95.4 : 87 aa	B
473	1178	1748	1183	100.0 : 1178 aa	A
474	163	1822	113	92.7 : 109 aa	E
474	163	1820	88	93.1 : 58 aa	E
475	466	1840	467	100.0 : 466 aa	A
476	60	1500	90	97.0 : 33 aa	D
477	249	1854	254	100.0 : 248 aa	B
478	44	1772	528	100.0 : 44 aa	B
479	421	1693	421	99.8 : 421 aa	A
480	167	1555	340	98.1 : 162 aa	B
481	89	1888	236	100.0 : 89 aa	B
482	237	1873	461	97.5 : 236 aa	B
483	471	1594	428	99.3 : 301 aa	C
484	123	1655	366	87.9 : 107 aa	E
485	127	1655	366	99.2 : 127 aa	B
486	259	1517	259	100.0 : 259 aa	A
487	17	1481	101	93.3 : 15 aa	E
488	77	1704	246	100.0 : 77 aa	B

489	180	1554	180	100.0 : 180 aa	A
490	213	1638	577	92.3 : 209 aa	E
491	148	1452	157	100.0 : 148 aa	B
492	281	1519	849	99.6 : 281 aa	B
493	144	1525	377	94.9 : 118 aa	D
494	73	1539	276	95.8 : 71 aa	B
495	311	1670	446	99.0 : 311 aa	B
496	115	1842	384	99.1 : 114 aa	B
497	200	1600	459	100.0 : 200 aa	B
498	264	1828	458	100.0 : 264 aa	B
499	339	1490	362	99.7 : 339 aa	B
500	146	1449	430	94.4 : 142 aa	E
501	60	1465	240	98.3 : 58 aa	B
502	351	1458	532	98.6 : 346 aa	B
503	233	1666	296	94.3 : 230 aa	E
504	32	1513	175	100.0 : 32 aa	B
505	171	1462	452	91.8 : 171 aa	B
506	33	1672	121	100.0 : 24 aa	D
507	100	1650	192	80.0 : 90 aa	E
508	79	1772	528	80.8 : 78 aa	E
509	70	1662	88	96.2 : 53 aa	D
510	130	1530	131	100.0 : 130 aa	A
511	53	1723	163	91.8 : 49 aa	E
512	79	1572	189	98.5 : 65 aa	D
513	102	1889	114	99.0 : 100 aa	B
514	15	1516	407	100.0 : 12 aa	B
515	378	1747	991	97.9 : 377 aa	B
516	1027	1692	2440	100.0 : 1027 aa	B
517	155	1831	182	89.6 : 154 aa	E
518	62	1552	362	74.5 : 47 aa	E
519	237	1557	241	100.0 : 237 aa	A
520	83	1627	424	100.0 : 83 aa	B
522	64	1680	227	98.4 : 63 aa	B
523	228	1532	241	100.0 : 228 aa	B
524	273	1710	189	97.2 : 180 aa	C
524	273	1712	115	100.0 : 99 aa	C
525	15	1612	65	100.0 : 15 aa	B
526	115	1733	112	94.6 : 111 aa	C
527	67	1755	156	100.0 : 62 aa	D
528	323	1635	336	100.0 : 322 aa	B
529	10	1731	101	50.0 : 10 aa	B
530	12	1455	284	100.0 : 12 aa	B
531	79	1528	101	94.9 : 79 aa	B
532	95	1887	279	100.0 : 95 aa	B
533	154	1591	168	100.0 : 152 aa	B
534	68	1501	283	100.0 : 67 aa	B
535	313	1519	849	95.5 : 313 aa	B
536	319	1486	325	100.0 : 319 aa	A
537	118	1707	154	90.9 : 110 aa	E
538	89	1674	161	88.2 : 76 aa	E
539	92	1838	100	100.0 : 92 aa	A
540	138	1525	377	86.9 : 137 aa	B
541	277	1661	394	96.0 : 273 aa	D
542	254	1567	392	98.0 : 254 aa	B
543	185	1467	594	99.5 : 185 aa	B
544	37	1886	326	100.0 : 37 aa	B

545	94	1772	528	89.1 : 92 aa	E
546	182	1760	366	100.0 : 182 aa	B
547	247	1776	150	100.0 : 146 aa	C
547	247	1775	88	100.0 : 87 aa	C
548	422	1798	426	100.0 : 422 aa	A
549	61	1620	78	96.7 : 60 aa	B
550	54	1566	309	37.8 : 45 aa	E
551	298	1751	518	98.0 :297 aa	B
552	91	1738	346	95.5 : 88 aa	D
553	111	1764	130	100.0 : 111 aa	B
554	137	1626	93	100.0 : 84 aa	D
555	124	1717	114	89.2 : 111 aa	E
556	86	1597	432	89.7 : 78 aa	E
557	87	1457	97	100.0 : 86 aa	B
558	108	1750	154	99.1 : 108 aa	B
559	142	1619	211	97.9 : 141 aa	B
560	231	1580	315	99.6 : 231 aa	B
561	186	1446	275	88.3 : 180 aa	E
562	183	1515	198	100.0 : 183 aa	B
563	154	1477	188	100.0 : 154 aa	B
564	288	1767	303	100.0 : 288 aa	B
565	420	1841	424	100.0 : 420 aa	A
566	72	1450	486	98.5 : 67 aa	D
567	205	1799	270	99.5 : 199 aa	D
568	328	1893	338	100.0 : 328 aa	B
569	140	1855	614	84.8 : 125 aa	E
570	76	1499	184	98.1 : 53 aa	D
571	194	1660	201	100.0 : 193 aa	B
572	140	1583	163	96.9 : 130 aa	D
573	308	1676	316	100.0 : 308 aa	B
574	339	1667	468	99.1 : 335 aa	B
575	207	1688	208	98.1 : 207 aa	A
576	251	1891	267	100.0 : 251 aa	B
577	69	1745	109	96.7 : 61 aa	D
578	112	1519	849	99.1 : 112 aa	B
579	152	1649	543	98.7 : 152 aa	B
580	130	1853	220	98.3 : 120 aa	D
581	113	1614	134	100.0 : 113 aa	B
582	174	1569	209	100.0 : 174 aa	B
583	35	1752	157	34.4 : 32 aa	E
584	308	1728	316	100.0 : 307 aa	B
585	702	1857	797	99.9 : 702 aa	B
586	293	1633	664	96.2 : 293 aa	B
587	52	1542	429	100.0 : 52 aa	B
588	182	1504	519	100.0 : 182 aa	B
589	251	1622	262	99.6 : 251 aa	B
590	40	1632	61	97.5 : 40 aa	B
591	122	1691	717	99.1 : 113 aa	D
592	113	1768	121	100.0 : 113 aa	B
593	437	1520	448	100.0 : 437 aa	A
594	146	1549	200	93.2 : 146 aa	E
595	128	1494	131	99.2 : 127 aa	B
596	95	1667	468	100.0 : 93 aa	B
597	102	1447	149	100.0 : 91 aa	D
598	127	1879	138	100.0 : 127 aa	B
599	502	1881	928	99.2 : 500 aa	B

600	42	1625	91	100.0 : 42 aa	B
601	341	1454	381	99.7 : 341 aa	B
602	465	1694	442	98.2 : 433 aa	D
602	465	1896	259	99.6 : 238 aa	D
603	193	1484	229	99.4 : 170 aa	D
604	141	1673	130	97.6 : 126 aa	D
605	159	1582	358	83.3 : 156 aa	E
606	376	1565	382	100.0 : 376 aa	B
607	352	1862	363	99.1 : 352 aa	B
608	88	1807	144	98.7 : 77 aa	D
609	86	1553	181	72.0 : 82 aa	E
610	76	1527	77	100.0 : 76 aa	A
611	98	1732	118	98.9 : 95 aa	B
612	162	1525	377	91.3 : 161 aa	E
613	58	1547	152	98.3 : 58 aa	B
614	66	1470	455	85.2 : 61 aa	E
615	117	1844	982	95.5 : 111 aa	D
616	83	1723	163	96.3 : 82 aa	B
617	77	1763	275	89.6 : 77 aa	E
618	176	1696	149	93.6 : 125 aa	E
618	176	1698	231	92.3 : 65 aa	E
619	144	1498	577	96.0 : 124 aa	D
620	90	1516	407	98.9 : 90 aa	B
621	268	1571	275	100.0 : 268 aa	B
622	171	1753	206	99.4 : 171 aa	B
623	102	1559	256	100.0 : 84 aa	D
624	117	1819	640	94.2 : 104 aa	E
625	237	1758	842	99.6 : 233 aa	B
626	199	1464	200	100.0 : 198 aa	C
627	225	1611	347	97.7 : 221 aa	B
627	225	1608	97	97.8 : 91 aa	C
628	86	1772	528	90.4 : 83 aa	E
629	496	1558	539	100.0 : 496 aa	B
630	142	1778	332	99.1 : 116 aa	D
631	153	1709	111	76.9 : 108 aa	E
631	153	1708	76	60.9 : 46 aa	E
633	93	1848	106	100.0 : 93 aa	B
634	177	1603	531	98.9 : 175 aa	B
635	88	1812	93	100.0 : 88 aa	A
636	115	1746	122	100.0 : 115 aa	B
637	261	1850	304	98.5 : 260 aa	B
638	191	1691	717	99.5 : 185 aa	B
639	351	1697	373	99.7 : 351 aa	B
640	351	1601	355	100.0 : 342 aa	D
641	146	1592	320	96.6 : 145 aa	B
642	190	1796	376	100.0 : 190 aa	B
643	489	1705	957	99.4 : 468 aa	D
644	249	1706	249	100.0 : 248 aa	A
645	120	1540	269	100.0 : 104 aa	D
646	109	1550	350	100.0 : 108 aa	B
648	158	1573	237	95.5 : 155 aa	D
649	312	1721	312	100.0 : 312 aa	A
650	56	1839	242	98.1 : 52 aa	D
651	199	1813	261	99.5 : 196 aa	B
652	82	1756	99	96.3 : 81 aa	D
653	89	1475	227	100.0 : 89 aa	B

654	111	1535	119	98.2 : 111 aa	B
655	65	1686	276	98.3 : 59 aa	D
656	268	1892	272	100.0 : 268 aa	A
657	100	1597	432	100.0 : 84 aa	D
658	80	1640	276	97.2 : 72 aa	D
659	205	1824	217	100.0 : 205 aa	B
660	124	1471	67	98.4 : 64 aa	D
660	124	1472	186	96.7 : 60 aa	D
661	93	1618	95	98.9 : 93 aa	B
662	80	1568	170	98.7 : 79 aa	B
663	214	1749	224	100.0 : 214 aa	B
664	78	1668	214	97.3 : 75 aa	D
665	177	1844	982	78.6 : 173 aa	E
666	258	1578	275	94.1 : 254 aa	E
667	75	1742	360	100.0 : 75 aa	B
668	421	1699	421	99.5 : 421 aa	A
669	81	1542	429	100.0 : 81 aa	B
670	112	1540	269	76.1 : 113 aa	E
671	326	1689	246	92.8 : 208 aa	E
672	272	1727	279	100.0 : 271 aa	A
673	78	1661	394	100.0 : 78 aa	B
674	400	1736	419	100.0 : 400 aa	B
675	91	1522	273	95.5 : 88 aa	D
676	126	1561	131	100.0 : 126 aa	A
677	195	1577	301	76.5 : 196 aa	E
678	72	1814	90	98.6 : 72 aa	B
679	111	1572	189	100.0 : 111 aa	B
680	142	1847	207	92.6 : 135 aa	E
681	63	1516	407	96.4 : 56 aa	D
682	310	1700	446	99.3 : 301 aa	B
683	169	1744	219	100.0 : 169 aa	B
684	85	1611	347	88.1 : 84 aa	E
685	77	1829	251	97.3 : 75 aa	D
686	197	1634	425	99.0 : 194 aa	D
687	142	1722	197	100.0 : 136 aa	D
688	86	1805	87	100.0 : 86 aa	A
689	121	1759	356	97.5 : 118 aa	B
690	59	1789	77	84.6 : 52 aa	E
691	142	1675	420	97.1 : 140 aa	B
692	80	1722	197	83.3 : 60 aa	E
693	180	1659	187	100.0 : 179 aa	B
694	75	1529	159	100.0 : 75 aa	B
695	99	1849	119	100.0 : 99 aa	B
696	209	1701	430	99.5 : 205 aa	B
697	75	1616	196	100.0 : 75 aa	B
698	121	1678	460	100.0 : 121 aa	B
699	102	1579	139	99.0 : 100 aa	B
700	131	1595	375	99.2 : 131 aa	B
701	441	1488	444	96.9 : 426 aa	D
702	127	1774	327	99.1 : 116 aa	D
703	287	1765	327	93.9 : 279 aa	E
704	46	1581	111	95.2 : 21 aa	D
705	115	1647	117	100.0 : 115 aa	A
706	86	1463	111	100.0 : 86 aa	B
707	44	1588	68	100.0 : 44 aa	B
708	560	1589	1413	98.8 : 560 aa	B

709	125	1607	443	95.8 : 118 aa	D
710	96	1469	540	100.0 : 73 aa	D
711	81	1629	244	96.3 : 80 aa	D
712	141	1671	375	100.0 : 125 aa	D
713	51	1867	193	96.1 : 51 aa	B
714	233	1833	240	99.5 : 218 aa	D
715	266	1644	271	100.0 : 265 aa	B
716	158	1883	226	94.7 : 150 aa	E
717	191	1860	240	100.0 : 189 aa	B
718	243	1817	256	99.6 : 243 aa	B
719	236	1617	667	98.3 : 236 aa	B
720	175	1523	592	97.1 : 172 aa	B
721	226	1770	340	92.7 : 218 aa	E
722	79	1629	244	100.0 : 74 aa	D
723	65	1506	229	100.0 : 49 aa	D
724	138	1675	426	93.2 : 132 aa	E
725	210	1832	215	100.0 : 210 aa	A
726	296	1821	223	100.0 : 190 aa	D
726	296	1819	640	99.1 : 106 aa	D
727	94	1706	249	97.8 : 91 aa	D
728	83	1593	171	100.0 : 83 aa	B
729	203	1448	268	100.0 : 202 aa	B
730	220	1656	242	100.0 : 220 aa	B
731	116	1818	196	100.0 : 115 aa	B
732	248	1474	248	100.0 : 248 aa	A
733	150	1459	347	100.0 : 118 aa	D
734	228	1545	302	96.9 : 227 aa	B
735	187	1597	432	100.0 : 172 aa	D
736	198	1761	354	100.0 : 198 aa	B
737	208	1780	438	93.8 : 208 aa	E
738	201	1842	384	100.0 : 193 aa	D
739	127	1669	405	21.6 : 74 aa	E
740	79	1615	280	97.3 : 75 aa	D
741	49	1878	443	91.3 : 46 aa	E
742	412	1877	425	97.8 : 412 aa	B
743	89	1482	111	100.0 : 89 aa	B
744	192	1502	222	98.4 : 189 aa	B
745	109	1797	304	96.3 : 109 aa	B
746	116	1791	359	94.8 : 116 aa	B
747	163	1711	321	100.0 : 163 aa	B
748	40	1483	377	100.0 : 40 aa	B
749	45	1770	340	95.2 : 42 aa	D
750	118	1867	193	92.2 : 116 aa	E
751	200	1491	211	100.0 : 200 aa	B
752	79	1890	80	100.0 : 79 aa	A
753	98	1837	268	98.7 : 79 aa	D
754	146	1653	413	100.0 : 141 aa	B
755	206	1638	577	93.7 : 206 aa	B
756	97	1526	89	100.0 : 66 aa	D
757	197	1794	198	100.0 : 197 aa	A
758	149	1872	94	97.5 : 80 aa	D
759	68	1882	291	100.0 : 68 aa	B
760	135	1631	162	99.3 : 134 aa	B
761	93	1884	594	100.0 : 69 aa	D
762	73	1883	226	100.0 : 73 aa	B
763	268	1859	430	95.4 : 263 aa	B

764	274	1537	277	100.0 : 273 aa	B
765	134	1714	136	99.2 : 133 aa	A
766	72	1810	74	95.8 : 71 aa	A
767	147	1802	285	100.0 : 147 aa	B
768	144	1541	241	100.0 : 144 aa	B
769	47	1684	75	100.0 : 47 aa	B
770	129	1505	183	90.2 : 122 aa	E
771	242	1536	235	99.1 : 232 aa	C
772	97	1851	129	99.0 : 97 aa	B
773	143	1826	259	96.5 : 143 aa	B
774	218	1777	383	99.5 : 217 aa	B
775	84	1637	143	100.0 : 84 aa	B
776	76	1774	327	95.9 : 73 aa	D
777	155	1585	263	79.7 : 133 aa	E
778	192	1480	299	91.5 : 189 aa	E
779	171	1551	186	99.4 : 171 aa	B
780	141	1760	366	99.2 : 129 aa	D
781	70	1741	95	100.0 : 70 aa	B
782	153	1687	223	98.0 : 153 aa	B
783	183	1869	184	100.0 : 183 aa	A
784	67	1846	231	100.0 : 67 aa	B
785	254	1730	256	100.0 : 253 aa	B
786	173	1466	251	100.0 : 166 aa	D
787	259	1808	322	100.0 : 238 aa	D
788	294	1786	131	93.7 : 126 aa	E
788	294	1630	163	94.0 : 116 aa	E
789	194	1655	366	99.2 : 122 aa	D
789	194	1646	75	100.0 : 72 aa	C
790	132	1790	273	100.0 : 132 aa	B
791	213	1575	216	98.1 : 213 aa	A
792	47	1605	86	100.0 : 47 aa	B
793	143	1864	342	93.0 : 143 aa	E
794	69	1766	93	100.0 : 69 aa	B
795	144	1504	519	95.7 : 138 aa	D
796	190	1590	193	100.0 : 190 aa	A
797	84	1792	215	83.5 : 79 aa	E
798	135	1613	138	100.0 : 135 aa	A
799	255	1885	424	99.6 : 253 aa	B
800	243	1493	205	87.1 : 140 aa	E
800	243	1497	131	100.0 : 126 aa	C
801	252	1563	255	100.0 : 252 aa	A
802	165	1720	91	100.0 : 88 aa	C
802	165	1718	99	92.7 : 82 aa	E
803	171	1602	297	85.5 : 159 aa	E
804	62	1485	165	100.0 : 61 aa	B
805	199	1514	219	100.0 : 199 aa	B
806	131	1880	391	86.2 : 130 aa	E
807	101	1719	257	95.0 : 100 aa	B
808	80	1585	263	98.8 : 80 aa	B
809	447	1781	344	99.7 : 331 aa	D
809	447	1783	118	98.3 : 117 aa	C
810	218	1564	250	100.0 : 218 aa	B
811	192	1478	408	99.5 : 192 aa	B
812	341	1729	354	100.0 : 340 aa	B
813	201	1523	592	100.0 : 158 aa	D
814	130	1769	306	92.3 : 130 aa	E

815	144	1835	548	78.4 : 116 aa	E
815	144	1815	377	84.3 : 121 aa	E
816	309	1894	310	100.0 : 309 aa	A
817	164	1823	156	96.7 : 153 aa	D
818	54	1703	87	100.0 : 53 aa	B
819	202	1716	215	99.5 : 202 aa	B
820	169	1870	115	100.0 : 110 aa	D
821	186	1451	254	100.0 : 186 aa	B
822	72	1609	180	96.6 : 58 aa	D
823	122	1633	664	94.9 : 118 aa	D
824	13	1695	70	100.0 : 13 aa	B
824	13	1567	392	100.0 : 13 aa	B
825	99	1771	144	100.0 : 86 aa	D
826	71	1512	154	98.6 : 71 aa	B
827	150	1456	139	93.7 : 127 aa	E
828	255	1651	155	100.0 : 155 aa	C
828	255	1648	109	98.0 : 102 aa	D
829	106	1726	147	99.1 : 106 aa	B
830	527	1509	567	99.8 : 524 aa	B
831	124	1740	214	99.2 : 123 aa	B
832	110	1690	400	98.2 : 110 aa	B
833	326	1856	325	100.0 : 325 aa	C
834	253	1543	191	96.7 : 184 aa	D
835	597	1876	638	100.0 : 594 aa	B
836	156	1621	345	99.4 : 154 aa	B
837	157	1624	253	97.4 : 155 aa	B
838	191	1465	241	96.8 : 190 aa	B
839	90	1548	231	92.9 : 85 aa	E
840	277	1682	298	99.6 : 277 aa	B
841	58	1508	270	98.1 : 54 aa	D
842	139	1734	139	88.4 : 129 aa	E
843	279	1476	276	100.0 : 269 aa	C
844	36	1852	83	94.4 : 36 aa	B
845	129	1460	196	100.0 : 129 aa	B
846	127	1473	172	100.0 : 105 aa	D
847	276	1657	319	100.0 : 276 aa	B
848	126	1801	187	98.4 : 126 aa	B
849	242	1669	405	97.0 : 236 aa	D
850	151	1816	217	100.0 : 151 aa	B
851	154	1641	194	100.0 : 154 aa	B
852	496	1665	327	97.5 : 314 aa	C
853	179	1606	272	97.2 : 179 aa	B
855	160	1487	198	96.9 : 160 aa	B
856	94	1836	420	100.0 : 93 aa	B
857	146	1845	371	99.3 : 146 aa	B
858	205	1507	366	98.5 : 202 aa	B
859	173	1827	198	100.0 : 149 aa	D
860	193	1681	294	100.0 : 175 aa	D
861	104	1865	253	100.0 : 104 aa	B
862	355	1599	358	100.0 : 355 aa	B
863	93	1825	236	97.8 : 92 aa	B
864	82	1677	315	97.5 : 81 aa	B
865	234	1861	249	99.1 : 233 aa	B
866	239	1652	405	99.2 : 238 aa	B
867	86	1468	201	77.4 : 84 aa	E
868	289	1574	395	94.4 : 284 aa	E

869	436	1863	662	100.0 : 436 aa	B
870	114	1560	121	100.0 : 114 aa	B
871	173	1757	362	98.8 : 173 aa	B
872	116	1866	145	98.1 : 105 aa	D
873	127	1797	304	63.9 : 83 aa	E
873	127	1799	270	89.7 : 58 aa	E
873	127	1800	62	97.4 : 38 aa	D
873	127	1801	187	82.0 : 50 aa	E
874	150	1461	179	100.0 : 150 aa	B
875	209	1511	339	98.9 : 188 aa	D
876	234	1739	615	99.6 : 230 aa	B
877	395	1830	879	99.7 : 379 aa	D
878	103	1623	413	97.0 : 99 aa	D
879	265	1809	566	89.8 : 265 aa	B
880	364	1576	442	98.6 : 346 aa	D

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 nucleic acids encoding immunogenic components of vaccines and targets for agents effective against *H. pylori*. Identification of said immunogenic components involved in the determination of the function of the disclosed sequences, which can be achieved using a variety of approaches. Non-limiting examples of these approaches 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 useful 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 indicates 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 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. 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. 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.

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

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.

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

lower than $1x10^{-6}$ that the homology is only due to random chance) to membrane or exported proteins represent protein antigens for vaccine development. Possible functions can be provided to *H. pylori* genes based on sequence homology to genes cloned in other organisms.

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 antigens for vaccine development.

Infrequently it is not possible to distinguish between multiple possible 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)

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

Based on the discovery of the *H. pylori* gene products of the invention provided in the Sequence Lsiting, 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 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 the identification of inhibitors of *H. pylori*.

Generation of Fragments

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 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 complimentary 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).

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.

(A) Alanine Scanning Mutagenesis

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.

(B) Oligonucleotide-Mediated Mutagenesis

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

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 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 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 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 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 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 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 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 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. Sehon and co-workers (Wie et al., supra) to produce a protein conjugated with 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 (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 immobilized metal ion affinity chromatography (Hochuli, E. et al., (1988) *Bio/Technology*, 6: 1321 - 1325). In addition, to facilitate isolation of peptides free of 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 homologs 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 NH_2-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 peptide 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 *Staphylococcus*

protein A and the outer membrane IgA protease 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 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 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, 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. 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)

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 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 though 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 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. diazepine 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 gama 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 of the invention contained in the Sequence Listing which encode *H. pylori* surface proteins. For example, the preferred nucleic acid for a vaccine composition of the invention is isolated from the group of nucleic acids which encode cell envelope proteins as outlined in Table 1. More specifically, the amino acids of SEQ ID NO:812, SEQ ID NO:820, SEQ ID NO:880, SEQ ID NO:658, SEQ ID NO:865, SEQ ID NO:1729, SEQ ID NO:1861, or fragments thereof, can be used alone or in combination for the formulation of vaccine compositions of the invention, as well as, their corresponding nucleic acids of SEQ ID NO:977, SEQ ID NO:978, SEQ ID NO:994, SEQ ID NO:215, SEQ ID NO:989, SEQ ID NO:1278, and SEQ ID NO:1410. 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 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.

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. 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 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 thymidine incorporation. The proliferation of T cells can be measured *in vitro* by determining the amount of ^{3}H-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 (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 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 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 and health of the patient, and the therapeutic activity of the particular protein or DNA.

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 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 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-sn-glycero-3-hydroxyphos-phoryloxy)-ethylamine (CGP 19835A, referred to a MTP-PE); RIBI, which contains three components from bacteria; monophosphoryl lipid A; trehalose dimycoloate; 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 genetically engineered fusions of the *H. pylori* polypeptide with cholera toxin or its B subunit, procholeragenoid, 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 immuno-stimulating complexes (ISCOMs), cochleates, 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 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 in an insoluble form as fusion proteins. Suitable carriers for the vaccines of the 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)).

In a preferred embodiment, a vaccine composition of the invention can be based on a killed whole *E. coli* preparation with an immunogenic fragment of an *H. pylori* protein of the invention expressed on its surface or it can be based on an *E. coli* lysate, wherein the killed *E. coli* acts as a carrier or an adjuvant.

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, or an increase in the production of antibodies in the serum or mucous of patients.

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 of the invention contained 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 of the invention contained 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 of the invention 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 λgt11, λgt18-23, λZAP, and λORF8. Messenger libraries of this type, having coding sequences inserted in the correct reading frame and orientation, can produce fusion proteins. For instance, λgt11 will produce fusion proteins whose amino termini consist of ß-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

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 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 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 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.

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 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 active compounds may directly, or with chemical alterations to promote membrane permeability or solubility, also inhibit or potentiate the same activity (e.g., enzymatic activity) in whole, live *H. pylori* cells.

EXEMPLIFICATION

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 (NH_4Ac) 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.

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.).

The purified DNA fragments were then blunt-ended using T4 DNA polymerase. The healed DNA was then ligated to unique BstXI-linker adapters (5' TCTAGACCACCTGC and 5' GTGGTCTAGA 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.

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 DH5α competent cells (Gibco/BRL, DH5α 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 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 μg of DNA was obtained per pool. Fifteen 96-well plates of DNA were generated to obtain a 5-10 fold sequence redundancy assuming 250-300 base average read-lengths.

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. 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*). 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 had been probed 38 times for chemical sequencing membranes and 10 times for the dideoxy sequencing membranes. 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 computer workstations (VaxStation 4000's) using the program REPLICA™ (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 REPLICA™ and displayed for 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. Many of the sequence errors could be detected and corrected because multiple sequence reads covering the same portion of the genomic DNA provide adequate sequence redundancy for editing. Each sequence automatically received an identification number (corresponding to microtiter plate, probe information, and lane set number). 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 database.

Routine assembly of *H. pylori* sequences was done using the program FALCON (Church, Church et al., *Automated DNA Sequenicng 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 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 sequence reads in the assembly.

II. Identification, cloning and expression of recombinant *H. pylori* DNA sequences

To facilitate the cloning, expression and purification of membrane and secreted proteins from *H. pylori* a powerful gene expression system, the pET System (Novagen), for cloning and expression of recombinant proteins in *E. coli*, was selected. Also, a DNA sequence encoding a peptide tag, the His-Tag, was fused to the 3' end of DNA sequences of interest in order to facilitate purification of the recombinant protein products. The 3' end

was selected for fusion in order to avoid alteration of any 5' terminal signal sequence. The exception to the above was ppiB, a gene cloned for use as a control in the expression studies. In this study, 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 DNA sequences containing ORF's for membrane and secreted proteins from the J99 Strain of Helicobacter pylori.

Sequences chosen (from the list of the DNA sequences of the invention) for cloning from the J99 strain of *H. pylori* were prepared for amplification cloning by polymerase chain reaction (PCR). Synthetic oligonucleotide primers (Table 4) specific for the 5' and 3' ends of open reading frames (ORFs) were designed and purchased (GibcoBRL Life Technologies. Gaithersburg, MD, USA). All forward primers (specific for the 5' end of the sequence) were designed to include an NcoI cloning site at the extreme 5' terminus, except for HpSeq. 4821082 (SEQ ID NO: 820) where NdeI was used. These primers were designed to permit initiation of 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. An exception is *H. pylori* sequence 4821082 (SEQ ID NO: 820) where the initiator methionine is immediately followed by the remainder of the native *H. pylori* DNA sequence. All reverse primers (specific for the 3' end of any *H. pylori* ORF) included 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-terminal amino acids (only 19 amino acids in HpSeq. 26380318 (SEQ ID NO: 658)and HpSeq.14640637 (SEQ ID NO: 447)) 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 encoded a BamHI site at its extreme 5' terminus and the primer for the 3' end of the ppiB gene encoded a XhoI site at its extreme 5' terminus.

TABLE 4

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

Outer membrane Proteins	**Forward primer 5' to 3'**	**Reverse Primer 5' to 3'**
16225006 (SEQ ID NO: 465)	5'-TATACCATGGTGGG CGCTAA-3' (SEQ ID NO:1897)	5'-ATGAATTCGAGTAAG GATTTTTG-3' (SEQ ID NO:1898)
26054702 (SEQ ID NO: 649)	5'-TTAACCATGGTGAAA AGCGATA-3' (SEQ ID NO:1899)	5'-TAGAATTCGCATAAC GATCAATC-3' (SEQ ID NO:1900)
7116626 (SEQ ID NO: 865)	5'-ATATCCATGGTGAGT TTGATGA-3' (SEQ ID NO:1901)	5'-ATGAATTCAATTTTT TATTTTGCCA-3' (SEQ ID NO:1902)
29479681 (SEQ ID NO: 677)	5'-AATTCCATGGTGGGG GCTATG-3' (SEQ ID NO:1903)	5'-ATGAATTCTCGATAG CCAAAATC-3' (SEQ ID NO:1904)
14640637 (SEQ ID NO: 447)	5'-AATTCCATGGTGCAT AACTTCCATT-3' (SEQ ID NO:1905)	5'-AAGAATTCTCTAGCA TCCAAATGGA-3' (SEQ ID NO:1906)
Periplasmic/ Secreted Proteins		
30100332 (SEQ ID NO: 685)	5'-ATTTCCATGGTCATG TCTCATATT-3' (SEQ ID NO:1907)	5'-ATGAATTCCATCTTT TATTCCAC-3' (SEQ ID NO:1908)
4721061 (SEQ ID NO: 812)	5'-AACCATGGTGATTT TAAGCATTGAAAG-3' (SEQ ID NO:1909)	5'-AAGAATTCCACTCA AAATTTTTTAACAG-3' (SEQ ID NO:1910)
Other Surface Proteins		
4821082 (SEQ ID NO: 820)	5'-GATCATCCATATGTT ATCTTCTAAT-3' (SEQ ID NO:1911)	5'-TGAATTCAACCATTT TAACCCTG-3' (SEQ ID NO:1912)
978477 (SEQ ID NO: 880)	5'-TATACCATGGTGAA ATTTTTTCTTTTA-3' (SEQ ID NO:1913)	5'-AGAATTCAATTGCG TCTTGTAAAAG-3' (SEQ ID NO:1914)
Inner Membrane Protein		
26380318 (SEQ ID NO: 658)	5'-TATACCATGGTGAT GGACAAACTC-3' (SEQ ID NO:1915)	5'-ATGAATTCCCACTT GGGGCGATA-3' (SEQ ID NO:1916)
Cytoplasmic Protein		
ppi	5'-TTATGGATCCAAAC CAATTAAAACT-3' (SEQ ID NO:1917)	5'-TATCTCGAGTTATA GAGAAGGGC-3' (SEQ ID NO:1918)

Genomic DNA prepared from the J99 strain of *H. pylori* (ATCC #55679) 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., eds., 1994). To amplify a DNA sequence containing an *H. pylori* ORF, genomic DNA (50 nanograms) was introduced into a reaction vial containing 2 mM $MgCl_2$, 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:

Sequences 26054702 (SEQ ID NO: 649), 7116626 (SEQ ID NO: 865), 29479681 (SEQ ID NO: 677), 30100332 (SEQ ID NO: 685), 4821082 (SEQ ID NO: 820) and 978477 (SEQ ID NO: 880);
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.

Sequence 16225006 (SEQ ID NO: 465);
Denaturation at 94°C for 2 min,
25 cycles at 95°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min
Reaction was concluded at 72°C for 6 minutes.

Sequence 4721061 (SEQ ID NO: 812);
Denaturation at 94°C for 2 min,
2 cycles at 94°C for 15 sec, 36°C for 15 sec and 72°C for 1.5 min
23 cycles at 94°C for 15 sec, 60°C for 15 sec and 72°C for 1.5 min
Reactions were concluded at 72°C for 6 minutes.

Sequence 26380318 (SEQ ID NO: 658);
Denaturation at 94°C for 2 min,
2 cycles at 94°C for 15 sec, 38°C for 15 sec and 72°C for 1.5 min
23 cycles at 94°C for 15 sec, 62°C for 15 sec and 72°C for 1.5 min
Reactions were concluded at 72°C for 6 minutes.

Sequence 14640637 (SEQ ID NO: 447):
Denaturation at 94°C for 2 min.
2 cycles at 94°C for 15 sec, 33°C for 15 sec and 72°C for 1.5 min
30 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.

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, each sample of amplified DNA was washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA). All amplified DNA samples were subjected to digestion with the restriction endonucleases, NcoI and EcoRI (New England BioLabs, Beverly, MA, USA), or in the case of HpSeq. 4821082 (SEQ ID NO: 820), with NdeI and EcoRI (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). DNA samples were then subjected to electrophoresis on 1.0 % NuSeive (FMC BioProducts, Rockland, ME USA) agarose gels. 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 of H. pylori DNA sequences into the pET-28b prokaryotic expression vector.

The pET-28b vector was prepared for cloning by digestion with NcoI and EcoRI, or in the case of *H. pylori* sequence 4821082 (SEQ ID NO: 820) with NdeI 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, was used and the cloning site prepared for cloning with the ppiB gene by digestion with BamHI and XhoI restriction endonucleases.

Following digestion, DNA inserts were 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 was cloned into the pET-28a expression vector. Products of the ligation reaction were 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), were 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 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 25 microgram/ml kanamycin sulfate 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

Individual BL21 clones transformed with recombinant pET-28b-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 expression vector (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994).

Isolation and Preparation of plasmid DNA from BL21 transformants

Individual clones of recombinant pET-28b vectors carrying properly cloned *H. pylori* ORFs were picked and incubated in 5 mls of LB broth plus 25 microgram/ml kanamycin sulfate overnight. The following day plasmid DNA was isolated and purified 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 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 a T7 promoter and a gene of interest. Strains used include: BL21(DE3) (Studier, F.W., Rosenberg, A.H.. 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 was 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) was expressed in the pET-System as described for the *H. pylori* recombinant constructions. Transformed cells were cultured in SOC medium for 1 hour,

and the culture was then plated on LB plates containing 25 micrograms/ml kanamycin sulfate. The following day, bacterial colonies were 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 for 3 hours 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 3500 x g for 15 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. Wet pellets were 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 were quantified spectrophotometrically using absorbance coefficients calculated from amino acid content (Perkins, S.J. 1986 Eur. J. Biochem. 157, 169-180). Protein concentrations were 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) were purchased from BioRad (Hercules, CA, USA), and stained with Coomassie blue. Molecular weight markers included 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 were carried out at 4°C. Frozen cells were 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 % 2-mercaptoethanol, 200 µg/ 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 was 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 µm Supor filter (Gelman Sciences, ERG) the crude extract was loaded directly onto a Ni^{2+}- nitrilotriacetate-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 was washed with 250 ml (50 bed volumes) of lysis buffer containing 10 % glycerol. 0.1 % Brij 35, and was eluted with sequential steps of lysis buffer containing 10 % glycerol, 0.05 % Brij 35, 1 mM PMSF, and 20, 100, 200, and 500 mM imidazole in succession. Fractions were monitored by absorbance at OD_{280} nm, and peak fractions were analyzed by SDS-PAGE. Fractions containing the recombinant protein eluted at 100 mM imidazole.

Recombinant protein 14640637 (SEQ ID NO: 447) and proteins, beta-galactosidase (lacZ) and peptidyl-prolyl cis-trans isomerase (ppiB)

Fractions containing the recombinant proteins from the Ni^{2+}-NTA-agarose columns were pooled and then concentrated to approximately 5 ml by centrifugal filtration (Centriprep-10. Amicon, MA), and loaded directly onto a 180-ml column (1.6 X 91 cm) of Sephacryl S-100 HR gel filtration medium equilibrated in Buffer A (10 mM Hepes, pH 7.5, 150 mM NaCl, 0.1 mM EGTA) and run in Buffer A at 18 ml/h. Fractions containing the recombinant protein were identified by absorbance at 280 nm and analyzed by SDS-PAGE. Fractions were pooled and concentrated by centrifugal filtration.

Recombinant protein 7116626 (SEQ ID NO: 865)

Fractions containing the recombinant protein from the Ni^{2+} -NTA-agarose column were pooled and dialyzed overnight against 1 liter of dialysis buffer (10 mM MOPS, pH 6.5, 50 mM NaCl, 0.1 mM EGTA, 0.02% Brij 35 and 1 mM PMSF). In the morning, a fine white precipitate was removed by centrifugation and the resulting supernatant was loaded onto an 8 ml (8 x 75 mm) MonoS high performance liquid chromatography column (Pharmacia Biotechnology, Inc., Piscataway, NJ, USA) equilibrated in buffer B (10 mM MOPS, pH 6.5, 0.1 mM EGTA) containing 50 mM NaCl. The column was washed with 10 bed volumes of buffer B containing 50 mM NaCl, and developed with a 50-ml linear gradient of increasing NaCl (50 to 500 mM). Recombinant protein 7116626 (SEQ ID NO: 865) eluted as a sharp peak at 300 mM NaCl.

2. Purification of insoluble proteins from inclusion bodies

The following steps were carried out at 4°C. Cell pellets were resuspended in lysis buffer with 10% glycerol 200 µg/ ml lysozyme, 5 mM EDTA, 1mM PMSF and 0.1 % -mercaptoethanol. After passage through the cell disrupter, the resulting homogenate was made 0.2 % deoxycholate, stirred 10 minutes, then centrifuged at 20,000 x g, for 30 min. The pellets were 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 % 2-mercaptoethanol. The resulting

white pellet was composed primarily of inclusion bodies, free of unbroken cells and membranous materials..

Recombinant proteins 26054702 (SEQ ID NO: 649), 16225006 (SEQ ID NO: 465), 30100332 (SEQ ID NO: 685), 4721061 (SEQ ID NO: 812)

The following steps were carried out at room temperature. Purified inclusion bodies were dissolved in 20 ml 8.0 M urea in lysis buffer with 1 mM PMSF and 0.1 % 2-mercaptoethanol, and incubated at room temperature for 1 hour. Materials that did not dissolve were removed by centrifugation. The clear supernatant was filtered, then loaded onto a Ni^{2+} -NTA agarose column pre-equilibrated in 8.0 M urea in Lysis Buffer. The column was washed with 250 ml (50 bed volumes) of lysis buffer containing 8 M urea, 1.0 mM PMSF and 0.1 % 2-mercaptoethanol, and developed with sequential steps of lysis buffer containing 8M urea, 1 mM PMSF, 0.1 % 2-mercaptoethanol and 20, 100, 200, and 500 mM imidazole in succession. Fractions were monitored by absorbance at OD_{280} nm, and peak fractions were analyzed by SDS-PAGE. Fractions containing the recombinant protein eluted at 100 mM imidazole.

Recombinant proteins 29479681 (SEQ ID NO: 677), 978477 (SEQ ID NO: 880), 26380318 (SEQ ID NO: 658)

The pellet containing the inclusion bodies was solubilized in buffer B containing 8 M urea, 1 mM PMSF and 0.1 % 2-mercaptoethanol, and incubated for 1 hour at room temperature. Insoluble materials were removed by centrifugation at 20,000 x g for 30 min, and the cleared supernatant was loaded onto a 15 ml (1.6 x 7.5 cm) SP-Sepharose column pre-equilibrated in buffer B, 6 M urea, 1 mM PMSF, 0.1 % 2-mercaptoethanol. After washing the column with 10 bed volumes, the column was developed with a linear gradient from 0 to 500 mM NaCl.

Dialysis and concentration of protein samples

Urea was 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 concentration as follows; 6M, 4M, 3M, 2M, 1M, 0.5 M and finally TBS without any urea. Each dialysis step was conducted for a minimum of 4 hours at room temperature.

After dialysis, samples were concentrated by pressure filtration using Amicon stirred-cells. Protein concentrations were 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).

The recombinant proteins purified by the methods described above are summarized in Table 5 below.

SUBSTITUTE SHEET (RULE 26)

TABLE 5

J99 Sequence Identifier	Homolog Identified by Blast	Gene symbol of Homolog	Bacterial cell fraction used to purify recombinant proteins	Method of purification	Relative MW on SDS-PAGE gel	Final concentration of purified protein	Composition of buffer
Outer Membrane Proteins							
16225006 (SEQ ID NO: 465)	P28635	**YEAC**	Inclusion bodies	His-Tag	18 kDa	5 mg/ml	B
26054702 (SEQ ID NO: 649)	P15929	**flgH**	Inclusion bodies	His-Tag	37 kDa	1.18 mg/ml	B
						----	as dry pellet
7116626 (SEQ ID NO: 865)	P26093	**e(P4)**	Soluble fraction	His-Tag	29 kDa	0.8 mg/ml	A
						1.85 mg/ml	C
29479681 (SEQ ID NO: 677)	P13036	**fecA**	Inclusions bodies	SP-Sepharose	23 kDa	2.36 mg/ml	B
						0.5 mg/ml	B
						----	as dry pellet
14640637 (SEQ ID NO: 447)	P16665	**TPF1**	Soluble fraction	His-Tag	17 kDa	2.4 mg/ml	A
				gel filtration S100 HR			

TABLE 5 (continued)

Periplasmic/Secreted Protein							
3010032 (SEQ ID NO: 685)	P23847	dppA	Inclusion bodies	His-Tag	11 kDa	2.88 mg/ml	B
4721061 (SEQ ID NO: 812)	P36175	GCP	Inclusion bodies	His-Tag	38 kDa	2.8 mg/ml	B
Other Surface Proteins							
4821082 (SEQ ID NO:820)	P08089	M protein	Inclusion bodies	His-Tag	20 kDa	1.16 mg/ml	B
978477 (SEQ ID NO: 880)	L28919	FBP54	Inclusion bodies	SP-Sepharose	44 kDa	2.56 mg/ml	B
						0.3 mg/ml	B
Inner Membrane Proteins							
26380318 (SEQ ID NO: 658)	P15933	fliG	Inclusion bodies	SP-Sepharose	11 kDa	22 mg/ml	B
Control Proteins with His-Tag							
	P00722	lacZ	Soluble fraction	His-Tag	116 kDa	10 mg/ml	A
				gel filtration S200 HR			
		ppiB	Soluble fraction	His-Tag	21 kDa	4.4 mg/ml	A
				gel filtration S100 HR			
Buffer compositions							
A 10 mM Hepes pH 7.5, 150 mM NaCl, 0.1 mM EGTA							
B 10 mM Tris pH 8.0, 150 mM NaCl, 0.5 % DOC							
C 10 mM MOPS pH 6.5, 300 mM NaCl, 0.1 mM EGTA							

SUBSTITUTE SHEET (RULE 26)

IV. 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.

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% CO_2, 5%O_2). 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 10^8 cfu/animal). Positive take of the infection was checked in some animals 2-3 weeks after the inoculation.

Antigens

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 6 below.

Table 6
Helicobacter pylori proteins

Outer membrane Proteins
SEQ ID NO:447
SEQ ID NO:677
SEQ ID NO:865
SEQ ID NO:812
SEQ ID NO:465

Periplastic/Secreted proteins
SEQ ID NO:685

Other cell envelope proteins
SEQ ID NO:820
SEQ ID NO:880

Flagella-associated proteins
SEQ ID NO:658

Control proteins
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 µg/mouse. As an adjuvant, the animals were also given 10 µg/mouse of Cholera toxin (CT) with each immunization. Omeprazole (400 µmol/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 7 below.

Table 7
Study outline, therapeutic immunization:

Mice were all infected with *H. pylori* strain Ah244 at day 30. Proteins are listed by their SeqID #'s.

Substance	Mouse strain n=10	Dose/mouse	Dates for dosing
1. Controls, PBS	Balb/c	0,3 ml	0, 14, 24, 34
2. Cholera toxin, 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
3. Protein 447, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
4. Protein 465, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
5. Protein 649, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
6. Protein 658, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
7. Protein 677, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
8. Protein 685, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
9. Protein 812, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
10. Protein 820, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
11. Protein 880, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
12. Protein 865, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34

Analysis of infection

Mucosal infection: The mice were sacrificed by CO_2 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 $25mm^2$ 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 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 µl 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'-Tetramethyl-p-Phenylenediamine, was purchased from Sigma, St. Louis, MO (Catalog # T3134). A solution of the regent (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 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 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 *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 SEQ ID NOs:865, 812, 658, 447, and 820 (see Figure 1).

Antibodies in mucus: In the mucus scrapings, specific antibodies against all antigens tested were seen. By far the strongest response was seen with SEQ ID NOs.685, followed by 447, 865, and 658 (see Figure 2).

Therapeutic immunization effects:

All control animals (BALB/c mice) were well colonized with *H. pylori* (strain AH244) in both antrum and corpus of the stomach. Of the antigens tested 3 proteins (SEQ ID NOs: 812, 820, and 447) 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 SEQ ID NOs: 880, 658, and 865 compared to control. The effect of SEQ ID NOs:465, 677, and 685 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.

V. 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 10) 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 OD_{600} 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 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 $MgCl_2$, 1 micromolar synthetic oligonucleotide primers (forward and reverse primers, see Table 8) 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 8
Oligonucleotide primers used for PCR amplification of *H. pylori* DNA sequences.

Outer membrane Proteins	**Forward primer 5' to 3'**	**Reverse Primer 5' to 3'**
SEQ ID NO:649 (for strains AH4, AH15, AH61, 5294, 5640, AH18, and AH244)	5'-TTAACCATGGTGAAAAGC GATA-3' (SEQ ID NO:1919)	5'-TAGAATTCGCCTCTAAAACT TTAG-3' (SEQ ID NO:1920)
SEQ ID NO:649 (for strains AH5, 5155, 7958, AH24, and J99)	5'-TTAACCATGGTGAAAAGC GATA-3' (SEQ ID NO:1921)	5'-TAGAATTCGCATAACGATCA ATC-3' (SEQ ID NO:1922)
SEQ ID NO:865	5'-ATATCCATGGTGAGTTTGA TGA-3' (SEQ ID NO:1923)	5'-ATGAATTCAATTTTTTATTTT GCCA-3' (SEQ ID NO:1924)
SEQ ID NO:677	5'-AATTCCATGGCTATCCAAA TCCG-3' (SEQ ID NO:1925)	5'-ATGAATTCGCCAAAATCGTA GTATT-3' (SEQ ID NO:1926)
SEQ ID NO:764	5'-GATACCATGGAATTTATGA AAAAG-3' (SEQ ID NO:1927)	5'-TGAATTCGAAAAAGTGTAGT TATAC-3' (SEQ ID NO:1928)

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:

Sequences (by SEQ ID NO:) 865 and 764;
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.

Sequence (by SEQ ID NO:) 649 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
Reaction was concluded at 72°C for 6 minutes.

Sequences (by SEQ ID NO:) 677 and 649 for strains AH4, AH15, AH61, 5294, 5640, AH18, and Hp244 ;
Denaturation at 94°C for 2 min,
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 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 (pCRII in the case of *H. pylori* sequence 865) 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. pylori sequence 865) 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 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 "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 ampicillan 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

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 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 PCRII or pCR2.1, Invitrogen, San Diego, CA) and sequencing primers specific to the ORF as listed in Table 9 below.

Table 9
Oligonucleotide primers used for sequencing of *H. pylori* DNA sequences.

Outer membrane Proteins	Forward primers 5' to 3'	Reverse Primers 5' to 3'
SEQ ID NO:649	5'-CCCTTCATTTTAGAAATCG-3' (SEQ ID NO:1929) 5'-ATTTCAACCAATTCAATGCG-3' (SEQ ID NO:1930) 5'-GCCCCTTTTGATTTGAAGCT-3' (SEQ ID NO:1931) 5'-TCGCTCCAAGATACCAAGA AGT-3' (SEQ ID NO:1932) 5'-CTTGAATTAGGGGCAAAGA TCG-3' (SEQ ID NO:1933) 5'-ATGCGTTTTTACCCAAAGA AGT-3' (SEQ ID NO:1934) 5'-ATAACGCCACTTCCTTATT GGT-3' (SEQ ID NO:1935)	5'-CTTTGGGTAAAAACGCATC-3' (SEQ ID NO:1936) 5'-CGATCTTTGATCCTAATTCA-3' (SEQ ID NO:1937) 5'-ATCAAGTTGCCTATGCTGA-3' (SEQ ID NO:1938)
SEQ ID NO:865	5'-TTGAACACTTTTGATTATG CGG-3' (SEQ ID NO:1939) 5'-GGATTATGCGATTGTTTTAC AAG-3' (SEQ ID NO:1940)	5'-GTCTTTAGCAAAAATGGC GTC-3' (SEQ ID NO:1941) 5'-AATGAGCGTAAGAGAGCC TTC-3' (SEQ ID NO:1942)
SEQ ID NO:677	5'-CTTATGGGGGTATTGTCA-3' (SEQ ID NO:1943) 5'-AGCATGTGGGTATCCAGC-3' (SEQ ID NO:1944)	5'-AGGTTGTTGCCTAAAGACT-3' (SEQ ID NO:1945) 5'-CTGCCTCCACCTTTGATC-3' (SEQ ID NO:1946)
SEQ ID NO:764	5'-ACCAATATCAATTGGCACT-3' (SEQ ID NO:1947) 5'-ACTTGGAAAAGCTCTGCA-3' (SEQ ID NO:1948)	5'-CTTGCTTGTCATATCTAGC-3' (SEQ ID NO:1949) 5'-GTTGAAGTGTTGGTGCTA-3' (SEQ ID NO:1950)
	5'-CAAGCAAGTGGTTTGGTTT TAG-3' (SEQ ID NO:1951) 5'-TGGAAAGAGCAAATCATTG AAG-3' (SEQ ID NO:1952)	5'-GCCCATAATCAAAAAGCC CAT-3' (SEQ ID NO:1953) 5'-CTAAAACCAAACCACTTGC TTGTC-3' (SEQ ID NO:1954)
Vector Primers	5'-GTAAAACGACGGCCAG-3' (SEQ ID NO:1955)	5'-CAGGAAACAGCTATGAC-3' (SEQ ID NO:1956)

Results

To establish the PCR error rate in these experiments, five individual clones of SEQ ID NO:649, 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 SEQ ID NO:649 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: SEQ ID NO:649, homologous to the val A & B genes encoding an ABC transporter in F. novicida; SEQ ID NO:865, homologous to lipoprotein e (P4) present in the outer membrane of H. influenzae; SEQ ID NO:677, homologous to fecA, an outer membrane receptor in iron (III) dicitrate transport in *E. coli*. SEQ ID NO:764 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 10 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 (SEQ ID NO:764, J99 strain) to approximately 7% change (SEQ ID NO:649, strain AH5). The deduced protein sequences show either no variation (SEQ ID NO:764, strains AH18 and AH24) or up to as much as 7.66% amino acid changes (SEQ ID NO:649, Strain AH5).

Table 10

Multiple Strain DNA Sequence analysis of H. pylori Vaccine Candidates

J99 Seq. ID #:	649	649	865	865	677	677	764	764
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%

n.d. = not done

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

Therapeutic targets are 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.

The protocol for the deletion of portions of *H. pylori* genes/ORFs and the insertional mutagenesis of a kanamycin-resistance cassette in order to identify genes which are essential to the cell is 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). The result is a gene "knock-out."

Identification and Cloning of H. pylori Gene Sequences

The sequences of the genes or ORFs (open reading frames) selected as knock-out targets are identified from the *H. pylori* genomic sequence and used to design primers to specifically amplify the genes/ORFs. All synthetic oligonucleotide primers are designed with the aid of the OLIGO program (National Biosciences, Inc., Plymouth, MN 55447, USA), and can be purchased from Gibco/BRL Life Technologies (Gaithersburg, MD, USA). If the ORF is smaller than 800 to 1000 base pairs, flanking primers are chosen outside of the open reading frame.

Genomic DNA prepared from the *Helicobacter pylori* HpJ99 strain (ATCC 55679) is 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 Example I. PCR amplification is 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 $MgCl_2$, 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., Branchburg, NJ, USA) in a final volume of 40 microliters. The PCR is carried out with Perkin Elmer Cetus/GeneAmp PCR System 9600 thermal cyclers.

Upon completion of thermal cycling reactions, each sample of amplified DNA is 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 is then washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA).

PCR products are 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 ligation of the PCR product into the vector is 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. Ligation is allowed to proceed for 16 hours at 16°C.

Ligation products are 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 is mixed with 40 microliters of electrocompetent cells and subjected to a high voltage pulse (25 microFarads, 2.5 kV, 200 ohms) after which the samples are incubated in 0.45 ml SOC medium (0.5% yeast extract, 2% tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM $MgCl_2$, 10 mM $MgSO_4$ and 20 mM glucose) at 37°C with shaking for 1 hour. Samples are then spread onto LB (10 g/l bacto tryptone, 5 g/l bacto yeast extract, 10 g/l sodium chloride) plates containing 100 microgram/ml of Ampicillin, 0.3% X-gal, and 100 microgram/ml IPTG. These plates are incubated overnight at 37°C. Ampicillin-resistant colonies with white color are selected, grown in 5 ml of liquid LB containing 100 microgram/ml of Ampicillin, and plasmid DNA is isolated using the Qiagen miniprep protocol (Qiagen, Gaithersburg, MD, USA).

To verify that the correct *H.pylori* DNA inserts had been cloned, these pT7Blue plasmid DNAs are used as templates for PCR amplification of the cloned inserts, using the same forward and reverse primers 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 are confirmation that the correct inserts had been cloned. Two to six such verified clones are 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 are pooled, and used in subsequent cloning steps.

The sequences of the genes/ORFs are again used to design a second pair of primers which flank the region of *H. pylori* DNA to be either interrupted or deleted (up to 250 basepairs) within the ORFs but are oriented away from each other. The pool of circular plasmid DNAs of the previously isolated clones are used as templates for this round of PCR. Since the orientation of amplification of this pair of deletion primers is away from each other, the portion of the ORF between the primers is not included in the resultant PCR product. The PCR product is a linear piece of DNA with *H. pylori* DNA at each end and the pT7Blue vector backbone between them which, in essence, resultes in the deletion of a portion of the ORFs. The PCR product is visualized on a 1% TAE, ethidium bromide stained agarose gel to confirm that only a single product of the correct size has been amplified.

A Kanamycin-resistance cassette (Labigne-Roussel et al., 1988 J. Bacteriology 170, 1704-1708) is 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 is 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) is isolated on a 1% TAE gel, and isolated using the QIAquick gel extraction kit (Qiagen, Gaithersburg, MD, USA). The fragment is 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 is then purified through a Qiaquick column (Qiagen, Gaithersburg, MD, USA) to eliminate nucleotides. The "T" overhang is then generated by mixing 5 micrograms of the blunt-ended kanamycin cassette, 10 mM Tris pH 8.3, 50 mM KCl, 2 mM $MgCl_2$, 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 is purified using a QIAquick column (Qiagen, Gaithersburg, MD, USA). The PCR product of the deletion primers (F2 and R2) is 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 and incubating for 16 hours at 16°C.

The ligation products are transformed into XL-1 Blue or DH5-α *E.coli* cells by electroporation as described previously. After recovery in SOC, cells are plated onto LB plates containing 100 microgram/ml Ampicillin and grown overnight at 37°C. These plates are then replica plated onto plates containing 25 microgram/ml Kanamycin and allowed to grow overnight. Resultant colonies have both the Ampicillin resistance gene present in the pT7Blue vector, and the newly introduced Kanamycin resistance gene. Colonies are picked into LB containing 25 microgram/ml Kanamycin and plasmid DNA is isolated from the cultured cells using the Qiagen miniprep protocol (Qiagen, Gaithersburg, MD, USA).

Several tests by PCR amplification are conducted on these plasmids to verify that the Kanamycin is 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 is inserted into the *H. pylori* sequence, the plasmid DNAs are used as templates for PCR amplification with the set of primers originally used to clone the *H. pylori* gene/ORFs. The correct PCR product is 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 is determined and both orientations are eventually used in *H. pylori* transformations (see below). To determine the orientation of insertion of the kanamycin resistance gene, primers are designed from the ends of the kanamycin resistance gene ("Kan-1" 5'-ATCTTACCTATCACCTCAAAT-3', and "Kan-2" 5'-AGACAGCAACATCTTTGTGAA-3'). By using each of the cloning primers in conjunction with each of the Kan primers (4 combinations of primers), the orientation of the Kanamycin cassette relative to the *H.pylori* sequence is determined. Positive clones are classified as either in the "A" orientation (the same direction of transcription is 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 is opposite to that of the Kanamycin resistance gene). Clones which share the same orientation (A or B) are pooled for subsequent experiments and independently transformed into *H. pylori*.

Transformation of Plasmid DNA into H. pylori cells

Two strains of *H. pylori* are used for transformation: ATCC 55679 the clinical isolate which provided the DNA from which the *H. pylori* sequence database is obtained, and AH244, an isolate which had been passaged in, and has the ability to colonize the mouse stomach. Cells for transformation are grown at 37°C, 10% CO_2, high humidity,

either on Sheep-Blood agar plates or in Brucella Broth liquid. Cells are grown to exponential phase, and examined microscopically to determine that the cells are "healthy" (actively moving cells) and not contaminated. If grown on plates, cells are 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 are 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 is taken to determine the optical density at 600 nm, in order to calculate the concentration of cells. An aliquot (1 to 5 OD_{600} units/25 microliter) of the resuspended cells is placed onto a prewarmed Sheep-Blood agar plate, and the plate is further incubated at 37°C, 6% CO_2, 100% humidity for 4 hours. After this incubation, 10 microliters of plasmid DNA (100 micrograms per microliter) is spotted onto these cells. A positive control (plasmid DNA with the ribonuclease H gene disrupted by kanamycin resistance gene) and a negative control (no plasmid DNA) are done in parallel. The plates are returned to 37°C, 6% CO_2 for an additional 4 hours of incubation. Cells are then spread onto that plate using a swab wetted in Brucella broth, and grown for 20 hours at 37°C, 6% CO_2. Cells are 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% CO_2, 100% humidity. If colonies appear, they are picked and regrown as patches on a fresh Sheep-Blood agar plate containing 25 micrograms/ml Kanamycin.

Three sets of PCR tests are done to verify that the colonies of transformants have arisen from homologous recombination at the proper chromosomal location. The template for PCR (DNA from the colony) is obtained by a rapid boiling DNA preparation method as follows. An aliquot of the colony (stab of the colony with a toothpick) is 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) is added and vortexed. The mixture is microfuged for 5 minutes and the supernatant is used as DNA template for PCR with combinations of the following primers to verify homologous recombination at the proper chromosomal location.

TEST 1. PCR with 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 Kanamycin cassette. A PCR product of just the size of the gene/ORF is proof that the gene had not been knocked out and that the transformant is 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 not present on the plasmid), and either primer Kan-1 or Kan-2 (primers designed from the ends of the kanamycin resistance gene), depending on whether the plasmid DNA used

was of "A" or "B" orientation. Homologous recombination at the correct chromosomal location will result in a single PCR product of the expected size (i.e., from the location of F3 to the insertion site of kanamycin resistance gene). No PCR product or PCR product(s) of incorrect size(s) will prove that the plasmid had not 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 not present on the plasmid) and either primer Kan-1 or Kan-2, depending on whether the plasmid DNA used was of "A" or "B" orientation. Homologous recombination at the correct chromosomal location will result in a single PCR product of the expected size (i.e., 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) will prove that the plasmid had not integrated at the correct site and that the gene had not been knocked out.

Transformants showing positive results for all three tests above indicate that the gene is not essential for survival *in vitro*.

A negative result in any of the three above tests for each transformant indicates that the gene had not been disrupted, and that the gene is essential for survival *in vitro*.

In the event that no colonies result from two independent transformations while the positive control with the disrupted ribonuclease H plasmid DNA produces transformants, the plasmid DNA is further analyzed by PCR on DNA from transformant populations prior to plating for colony formation. This will verify that the plasmid can enter the cells and undergo homologous recombination at the correct site. Briefly, plasmid DNA is incubated according to the transformation protocol described above. DNA is extracted from the *H. pylori* cells immediately after incubation with the plasmid DNAs and the DNA is used as template for the above TEST 2 and TEST 3. Positive results in 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

VII. High-throughput drug screen assay

Cloning, expression and protein purification

Cloning, transformation, expression and purification of the *H. pylori* target gene and its protein product,e.g., an *H. pylori* enzyme, to be used in a high-throughput drug screen assay, is carried out essentially as described in Examples II and III above. Development and application of a screening assay for a particular *H. pylori* gene product, peptidyl-propyl *cis-trans* isomerase, is described below as a specific example.

Enzymatic Assay

The assay is 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 spectophotometer. The data are collected every second with an average scanning of time of 0.5 second. Assays are carried out in 35 mM Hepes, pH 8.0, in a final volume of 400 ul, with 10 μM α-chymotrypsin (type 1-5 from bovine Pancreas, Sigma # C-7762, lot 23H7020) and 10 nM PPIase. To initiate the reaction, 10 μl of the substrate (2 mM N-Succinyl-Ala-Ala-Pro-Phe-p-nitroanilide in DMSO) is added to 390 μl of reaction mixture at room temperature.

Enzymatic assay in crude bacterial extract.

A 50 ml culture of *Helicobacter pylori* (strain J99) in Brucella broth is harvested at mid-log phase ($OD_{600\ nm}$ ~ 1) and resuspended in lysis buffer with the following protease inhibitors: 1 mM PMSF, and 10 μg/ml of each of aprotinin, leupeptin, pepstatine, TLCK, TPCK, and soybean trypsin inhibitor. The suspension is 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 is centrifuged (12,000 g x 30 minutes) and the supernatant is assayed for enzymatic activity as described above.

Many *H. pylori* enzymes 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.

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 following claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME: Astra Aktiebolag
(B) STREET: S-151 85
(C) CITY: Sodertalje
(D) STATE:
(E) COUNTRY: Sweden
(F) POSTAL CODE (ZIP):

(ii) TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS

(iii) NUMBER OF SEQUENCES: 1956

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 8-mm cartridge tape
(B) COMPUTER: SPARC station LX
(C) OPERATING SYSTEM: SunOS Release 4.1.3
(D) SOFTWARE: tar

(v) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US96/09122
(B) FILING DATE: June 6, 1996

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/630,405
(B) FILING DATE: 01-APR-1996

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/561,469
(B) FILING DATE: 17-NOV-1995

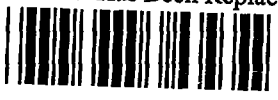
(viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/487,032
(B) FILING DATE: 07-JUNE-1995

(ix) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: LAHIVE & COCKFIELD
(B) STREET: 60 State Street, Suite 510
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02109-1875

(x) ATTORNEY/AGENT INFORMATION:
(A) NAME: Mandragouras, Amy E.
(B) REGISTRATION NUMBER: 36,207
(C) REFERENCE/DOCKET NUMBER: GTN-001C5PC

(xi) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (617)227-7400
(B) TELEFAX: (617)227-5941

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1527 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

```
ATGTGTTCTC AGGAAATTTT ATCAAGCTTG CAAACCATTA TTGCCGAACA ATTTTCTATA      60
AATATCATCA CTCAGCTTGC TAATAAACTC ACACAAGTTA AAAATCTAAA TTTTTTTGAG     120
AATAAAGACC ATACTATCAA GCTTAACACT ATCCATAACG GACTGCACAT CCGCCCCCTA     180
AATTATGTCA GTAATCTTTT TTTCAATCTA CAACGCATTA TAGGGCTTAT CAGTCTGTTT     240
GGGATATTAT TTTCCATTAG TATTTATCTA CCCTTTATAA TGATTTTTGC AACAGTGCCT     300
TGTATTCTCA TTTCCAACCA TATAGCAAAA AAACATAGTG CTTCCATAGA TAAACTTCAA     360
GACCAAAAAG AAAGCATGCA AAATTACTTA TACTCTGGAC TAGATAACCA AAAGAACAAG     420
GACAACCTAT TATTTAACTT CATGCTAAAT TTTCACCATA AATTTATTGA AACAAAAGAA     480
TTGTATCTCA ATAATTTTGT GAAAGTAGCC CAAAAAAACT TAATATTTAC CATATATGCT     540
GATGTTTTAA TCACCACTCT AAGTATTGCA CTATTTTTTC TAATGGTTTT TATTATCCTT     600
TCAAAATTAA TTGGTGTGGG AGCAATTGCT GGGTATATCC AAGCATTTAG CTCTACCCAA     660
CAACAACTAC AAGATTTATC ATTTTATGGA AAGTGGTTTT TTGCTATCAA TAAATACTTT     720
GAAAATTATT TCTGTATTTT AGATTACAAA ATACCGAAAC CAGAAACACA AATCAAATTA     780
GAAGAAAAAA TCCATAGCAT TACATTTGAA AATATTAGTT TCTCTTATCC TAATTCAAAA     840
CTTATTTTTG AAAACTTTAA TCTCTCTTTA CACTCTAATA AAATTTATGC ATTAGTCGGC     900
AAGAATGCTA GCGGAAAAAG CACGCTGATT AATTTATTAT TAGGTTTTTA TACCCCAAAT     960
TCAGGTCAAA TTATCATTAA TAACAAATAC CCATTACAAG ACTTGGAACT AAATAGCTAC    1020
CATCAACAAA TGAGTGCCAT ATTTCAAGAT TTTTCTCTTT ATGCTGGGTA TAGCATTGAT    1080
GATAATCTTT TTATGCAAAA CAATATCACT AAAGAGCAAT TGAAGCAAAA AAGAGAAATA    1140
CTAAAATCTT TTGATGAGAA TTTTCAAAAT TGTCTTAATG ATTGCAACAA CACACTATTT    1200
GGAGCGCAAT ATAATGGGGT AGATTTTTCT TTAGGTCAAA AGCAACGCAT AGCTACCATG    1260
AGAGCCTTTT TAAAACCAAG TAATTGCATT GTTTTAGATG AGCCAAGCAG CGCCATCGAT    1320
CCCATTATGG AAAAAGAGTT TTTAGATTTT ATTTTTAAAA AATCGCAATC TAAGATGGCT    1380
TTAATTATTA CACACCGCAT GAATAGTGTC AAGCAAGCTA ATGAAATTAT CGTGTTAGAT    1440
CAAGGCAAAC TAATAGAACA GGGCAACTTT GAAACCCTTA TGAAAAAACA GGGATTATTT    1500
TGCGAATTGT TTTTGAAACA ACAATAC                                        1527
```

(2) INFORMATION FOR SEQ ID NO:2:

(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

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

```
ATGGAGCGCA AGACGCTCCA GAGCATTTTA TGTTTAATAA AAAAAGAAAT GATGAGACCA      60
AAAGGTATTC TAATGAATTG TTGCAGGSCT TGGAAACACC AGGTTCTTAA GCAAAGCACG     120
ACAGGTTTAG TGGTGTTGAG CATTATCTCT TCTACAGCCC CCTTTATTGG TTTGTTTGGG     180
ACGGTAGTTG AAATTTTAGA AGCGTTTAAC AATTTGGGCG CGTTAGGTCA AGCTTCTTTT     240
GGAGTGATCG CACCCATTAT TTCTAAGGCG CTTATCGCCA CCGCTGCAGG GATTTTAGCA     300
GCCATTCCAG CCTATTCTTT TTACTTGATC TTAAAGCGCA AGGTGTATGA TTTATCGGTT     360
TATGTGCAGA TGCAAGTGGA TATTTTGTCT TCTAAAAAA                            399
```

(2) INFORMATION FOR SEQ ID NO:3:

(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:3

```
ATGCATGAAC GCATTGAAAG AGGTATTRGA AATAATGAAT GTAAAGAAAT TTTTGGCAAT      60
GAACTCAAAC AAAGAAAGAC AAAATTGATT GAAGACATAG AACGGCGGTT CAAAGAATGC     120
GAGGAACAAT TCCGTGGAAG TGTAGGAAAA AATATTGAAC AACTTGAAGA AAGAGTTAAA     180
GATTCTCTAG CGATTATAAA ACGCATCAAT AACCTTGGTC TTAATCCTAA TTCTAATTTT     240
AATATGGATA GCGGCATTGA TACAATAGGC TTATTTAGTT CAATAGGAGG TTTGGTGTTG     300
CTTCTATTGA CGCCTGTAGT AGGTGAGTTT GCGTTAATTG CAGGAGTGGG TTTAGCATTA     360
GTGGGGGTAG GTAAATCAAT ATGGAGTTTT TTTGATTCAG ATTATAAAAA ATCCCAACAA     420
AGAAAAGAAG TGGATAAGAA TTTACATCAA ATTTGCGAAA AATTGTGCAG GATG           474
```

(2) INFORMATION FOR SEQ ID NO:4:

(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

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

ATGCCTGGCG TGTATCAAAT GAGTATAGAG CCTCTTTTAA AAGAATGCGA AGAATTAGTG 60
GGTTTAGGCA TAAAAGCCGT TTTATTGTTT GGCATTCCTA AACATAAGGA CGCTACAGGA 120
AGCCATGCGT TAAATAAGGA TCACATTGTC GCAAAAGCTA CGAGAGAAAT TAAAAAACGA 180
TTTAAGGATT TGATCGTTAT AGCGGATTTG TGTTTTTGCG AATACACCGA CCATGGGCAT 240
TGCGGGATTT TAGAAAACGC TTCTGTGTCT AACGATAAAA CGCTAAAGAT TTTAAATCTT 300
CAAGGGCTTA TTTTGCTGAA AGCGGTGTGG ATATTC 336

(2) INFORMATION FOR SEQ ID NO:5:

(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:5

GTGGAAAACA ACAAGAGTTT AAAGCATGCG AATGAGTTAA GGGATAAGCG AGATGAATTA
GAGTTTCATT TGCGAGAGCT TTTCGGGGGG AATGTTTTTA AAAGCAGCAT TAAAACCCAT
TCGCTCACAG ATAAAGACTC AGCGGACTTT GATGAGAGCT ATAACCTTAA TATCGGGCAT
GGGYTCAATA TSATA

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1857 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

This Sheet Has Been Replaced



(A) NAME/KEY: misc_feature
(B) LOCATION 1...1857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

GTGTTTGTGG CAAGCAAACA AGCTGACGAA CAAAAAAAGC TAGTTATAGA GCAAGAGGTT 60
CAAAAGCGGC AGTTTCAAAA AATAGAAGAA CTTAAAGCAG ACATGCAAAA GGGTGTCAAT 120
CCCTTTTTTA AAGTCTTGTT TGATGGGGGG AATAGGTTGT TTGGTTTCCC TGAAACTTTT 180
ATTTATTCTT CTATATTTAT ATTGTTTGTA ACAATTGTAT TATCTGTTAT TCTTTTTCAA 240
GCCTATGAAC CTGTTTTGAT TGTAGCGATT GTTATTGTGC TTGTAGCTCT TGGATTCAAG 300
AAAGATTACA GGCTTTATCA AAGAATGGAG CGAGCGATGA AATTTAAAAA ACCTTTTTTG 360
TTTAAGGGCG TGAAAAACAA AGCGTTCATG AGCATTTTTT CCATGAAGCC TAGTAAAGAA 420
ATGGCTAATG ACATCCACTT AAATCCAAAC AGAGAAGACA GGCTTGTGAG CGCTGCAAAC 480
TCCTATCTAG CGAATAACTA TGAATGTTTT TTAGATGATG GGGTGATCCT TACTAACAAC 540
TATTCTCTTT TAGGCACAAT CAAATTGGGG GGCATTGATT TTTTAACCAC TTCCAAAAAA 600
GATCTCATAG AGTTACACGC TTCTATTTAT AGCGTTTTTA GGAATTTTGT TACCCCTGAA 660
TTCAAATTTT ATTTTCACAC TGTTAAAAAG AAAATCGTTA TTGATGAAAC CAATAGGGAT 720
TATGGTCTTA TTTTTTCTAA TGATTTCATG CGAGCCTATA ATGAGAAGCA AAAGAGAGAA 780
AGTTTTTATG ATATTAGTTT TTATCTCACC ATAGAGCAAG ATTTATTAGA CACTCTCAAT 840
GAACCCGTTA TGAATAAAAA GCATTTTGCA GACAATAATT TTGAAGAGTT TCAAAGGATT 900
ATTAGAGCCA AGCTTGAAAA CTTCAAAGAT AGGATAGAGC TCATAGAAGA GCTACTGAGT 960
AAATACCACC CCACTAGATT AAAAGAATAC ACTAAAGATG GCATTATTTA CTCCAAACAA 1020
TGCGAATTTT ACAATTTTCT TGTGGGAATG AATGAAGCCC CTTTTATTTG CAACAGAAAA 1080
GACTTGTATC TCAAGGAAAA AATGCATGGT GGGGTGAAAG AAGTTTATTT TGCCAATAAG 1140
CATGGAAAAA TCTTAAATGA CGATTTGAGT GAAAAATATT TTAGCGCTAT TGAGATCAGT 1200
GAATACGCCC CTAAATCACA GAGCGATTTG TTTGATAAAA TCAACGCTCT AGACAGCGAA 1260
TTTATCTTTA TGCATGCTTA TTCGCCTAAA AACTCACAAG TTTTAAAGGA CAAACTAGCT 1320
TTCACCTCTA GAAGGATTAT TATTAGTGGA GGCTCCAAAG AGCAAGGCAT GACTTTGGGT 1380
TGCTTGAGCG AATTAGTGGG TAATGGTGAT ATTACGCTAG GCAGTTATGG TAATTCTTTA 1440
GTGCTGTTTG CTGATAGCTT TGAAAAAATG AAACAAAGCG TTAAGGAATG CGTCTCTAGT 1500
CTTAACGCTA AAGGTTTTTT AGCCAACGCA GCGACTTTCT CTATGGAAAA TTACTTTTTT 1560
GCCAAACATT GCTCTTTTAT CACGCTTCCT TTTATTTTTG ATGTAACTTC TAACAATTTT 1620
GCTGATTTCA TAGCGATGAG AGCGATGAGT TTTGATGGCA AAGAAGACAA TAACGCTTGG 1680
GGCAATAGCG TGATGACGTT AAAAAGCGAG ATCAATTCGC CTTTTTATTT GAACTTCCAC 1740
ATGCCCACTG ATTTTGGTTC AGCTTCAGCA GGACACACTT TGATACTTGG CTCAACCGGT 1800
TCAGGTAAGA ACAGTGTTTA TGTCCATGAC TCTAAACGCT ATGGGGCAAT TTGCCTA 1857

(2) INFORMATION FOR SEQ ID NO:7:

(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

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

GTGAAAACAT CGTGTTTGGT TACAATAGGG AGGATCCGGG GCGTTTTTAT CATTAAGGCG 60
CAGTTGTTGC TTCGTGAGGG AGGTTTTATG AATTTTACCG CTTATAACAC GAAGACGCCA 120
GGGCATTTGC ATTTGTATGT GCATAAGGGG CATACGGAAT TAGGCGAGGG TGAAAGGCTG 180
ATTAAAACTT TATCCATGAA ATTAGCGCAA GGGTTGCCTA AAGAATGGAG GGTTTTCCCT 240

AGCAATGAAT GGCCTAAGGA ATTTAATATT TTAGCTTTAC CTTATGAAGT GTTTGCAAAA 300
GAGCGCGGGA GCTCTTGGGC GAAGCATTTA 330

(2) INFORMATION FOR SEQ ID NO:8:

(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:8

GTGGCTAAAG ACATCATCAG CGAGTCTCAA AACCTTTGCG CAAGAAAATT CCGCCGTTTG 60
TATGCGTTAT TGAAAGAAAA TGAAATGCTC ATTCGCATCG GATCTTATCA AATGGGGAAC 120
GATAAAGAGC TTGATGAAGC GATTAAGAAA AAGGCTCTAA TGGAGCAATT TTTAGTGCAA 180
GATGAAAACG CTTTACYAGC CTTT 204

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

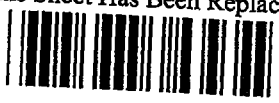
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

ATGAAATCAC GCCCAATCCT CGCACAAGCT TACGCGCTCC AAATGATGGT CAAACAGATC 60
GCTTTTTTAG AAACCATTTT AGTGGAAAAC GAGCAAGACG CTTTGATTTT GGAAAATTCT 120
TTGATCAAGC AGCTCAAGCC TAAATACAAC ATTCTTTTAA GAGACGATAA AACTTACCCT 180
TATATTTACA TGGATTTTTC TATTGATTTC CCTATCCCTT TAATCACACG AAAAATCTTA 240
AAACAGCCTG GCGTTAAATA TTTTGGCCCT TTTACGAGCG GGGCTAAGGA TATTTTGGAC 300
AGCTTGTATG AATTGCTCCC TTTGGTTCAA AAGAAAAATT GCATCAAGGA TAAAAAGGCA 360
TGCATGTTTT ATCAAATAGA GCGTTGTAAA GCCCCATGCG AGGATAAAAT CACTAAAGAA 420
GAATATTTAA AAATCGCTAA AGAATGTTTA GAAATGATTG AAAATAAAGA CAGGCTCATC 480
AAAGAGCTTG AATTGAAAAT GGAGCGCCTT TCTAGTAACT TGCGTTTTGA AGAAGCCTTA 540

This Sheet Has Been Replaced



```
ATTTATAGGG ATAGGATTGC AAAAATCCAA AAAATCGCCC CTTTCACTTG CATGGATTTA      600
GCCAAACTCT ACGATTTGGA TATTTTTGCT TTTTATGGTG GGAACAACAA GGCGGTGTTA      660
GTGAAAATGT TCATGCGTGG GGGTAAAATC ATTTCTTCAG CGTTTGAAAA AATCCACTCT      720
CTCAACGGGT TTGACACTGA TGAAGCGATG AAACAAGCCA TTATCAATCA TTACCAATCG      780
CATTTGCCTT TGATGCCTGA ACAAATCTTA TTGAGCGCTT GTTCTAATGA AACGCTTAAA      840
GAATTGCAAG AGTTTATCTC TCACCAATAT TCTAAAAAAA TCGCTCTTAG CATTCCTAAA      900
AAGGGTGATA AGCTCGCTTT AATAGAAATC GCTATGAAAA ACGCTCAAGA GATTTTTAGC      960
CAAGAAAAAA CCTCTAATGA AGATCGGATC TTAGAAGAAG CGCGATCGCT CTTCAATTTA     1020
GAGTGCGTGC CTTATAGGGT AGAAATCTTT GACACAAGCC ACCATTCAAA CAGCCAATGC     1080
GTGGGGGGAA TGGTCGTGTA TGAAAACAAT GCATTTCAAA AAGACTCTTA TCGGCGCTAC     1140
CATCTAAAAG GCTCTAACGA ATATGATCAA ATGAGCGAAT TGCTCACCAG AAGGGCTTTA     1200
GACTTTGCTA AAGAGCCACC GCCTAATTTG TGGGTGATAG ATGGAGGGAG GGCGCAATTA     1260
AACATCGCTT TAGAAATTTT AAAAAGCAGC GGGAGTTTTG TAGAAGTGAT CGCTATTTCT     1320
AAAGAAAAAA GGGGATTC                                                   1338
```

(2) INFORMATION FOR SEQ ID NO:10:

(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:10

```
GTGAGTTTGG GGGCGTTTCA GGGGTATTAT GGAGGGCTAG TGGATTTAGT GGGGCAAAGG       60
TTGAGCGAAA TTTGGAGCGC GATCCCCATG CTTTTTTTAC TCATTGTGAT TTCTAGCGCG      120
TTCAATTCTA ATTTTTGGAT CATCTTGTTT TTAGTCTTGC TCTTTAGCTG GATGGGGCTT      180
TCTCAAGTCG TGCGCACGGA GTTTTTAAAA GCAAGGAATA TGGACTACAC CAAAGCCGCT      240
AGAGCGTTGG GG                                                          252
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature

This Sheet Has Been Replaced



(B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

ATGAGTGAAG CCTATTTTTT ACACCATAAA AACGCTTCTC AAGTGTCTCT TAATGAACAA 60
GTTTTAAACG TTATGAAACA AGTTCAATTG GATGAAAATT TTTGGAATGT TTCTCTTATG 120

(2) INFORMATION FOR SEQ ID NO:12:

(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:12

GTGATCCTGA TATTTATCAT CGTGGTGGAA GATCAGAAAG GCATTTTCCC TATCGCAGCG 60
TCAAAAAGAA AAAGCCAAAG CTCTGTGATC ATTGAAGACG TGTGCTTCAG CAAAGAGGAT 120
TTTGTAGAAG GGGCAAAAGC GATTGAGGGG CTTTTAAAAA AACATGGCTT TAAGGATAAT 180
GGCATTATTT TTGGGCATGC GTTAAGCGGG AATTTGCACT TTGTCGTTAC GCCGATTCTA 240
GAAAATGAAG CTGAAAGAAA AGCGTTTGAA AATTTAGTTT CTGAGATGTT TTTAATGGTG 300
AGCAAAAGCT CTGGCTCTAT TAAAGCCGAA CATGGCACAG GCAGGATGGT AGCCCCTTTT 360
GTGGAAATGG AGTGGGGAGA AAAAGCTTAT AAGATCCACA AACAAATCAA GGAATTGTTT 420
GATCCTAATG GCCTTTTAAA CCCTGATGTG ATCATCACAA ACGATAAAGA AATCCACACT 480
AAAAATTTAA AGAGCATTTA CCCTATTGAA GAGCATTTGG ACATGTGCAT GGAATGTGGG 540
TTTTGTGAAA GGATCTGCCC CAGTAAAGAT TTATCCTTAA CGCCACGACA ACGCATCGTC 600
ATCCACAGAG AGGTAGAGCG TTTGAAAGAA AGGGTAAGTC ATGGTCATGA TGAAGATCAG 660
GTTTTACTAG ATGAGCTTTT AAAAGAGTCT GAATACTTAG CGCATGCCAC TTGCGCGGTG 720
TGCCATATGT GTTCCACTTT ATGCCCTTTA GGGATTGATA CCGGGAGYAT CGCTTTAAAT 780
CATTATCAAA AAAACCCTAA AGGCGAAAAG ATCGCTTCAA AGATTCTTAA ATCACATGCA 840
AACGACCACA AGCGTGGCTC GTTTTTCTTT AAAARGCGCT TTCGTGGTTT CAAAAACTCA 900

(2) INFORMATION FOR SEQ ID NO:13:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

```
ATGAAAGAAA AAAACTTTTG GCCTTTAGGA ATCATGAGCG TGCTTATTTT TGGGCTTGGG      60
ATCGTGGTGT TTTTAGTGGT GTTTGCCCTA AAAAATTCGC CTAAAAATGA TTTAGTGTAT     120
TTCAAGGGTC ATAACGAAGT GGATTTAAAC TTTAACGCCA TGCTTAAAAC TTATGAAAAC     180
TTTAAATCCA ATTATCGTTT TTCAGTGGGT TTAAAGCCTC TTACCGAAAG CCCTAAAACC     240
CCCATTTTGC CCTATTTTTC TAAAGGCACG CATGGGGATA AAAAAATCCA AGAAAACCTT     300
TTAAACAACG CTTTGATTTT AGAAAAGTCC AACACGCTTT ATGCACAATT GCAACCGCTC     360
AAACCCGCTT TAGATTCGCC AAATATTCAA GTGTATTTAG CGTTCTATCC CAGCCAATCC     420
CAGCCCAGAT TATTAGGAAC GCTTGATTGT AAAAACGCAT GCGAACCTTT AAAATTTGAT     480
TTGTTAGAGG GCGATAAAGT GGGGCGCTAT AAGATCCTTT TTAAATTTGT TTTTAAAAAT     540
AAAGAAGAAT TGATTTTGGA GCAACTGCTT TTTTTAAGTA GCATGGCTTG TATGGGTATA     600
TCAATTTTAA AAAACGCTAA AGCATTTTTT AAATACAAAA TA                        642
```

(2) INFORMATION FOR SEQ ID NO:14:

(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:14

```
ATGCCCATTA AAGGCTCTTT TTTAGCCAGA AACCGCCTGG TGATCGCTTT AACCGATGCG      60
GTGATTATCC CCCAAGCGGA TTTAAAAAGC GGCTCTATGA GCAGTGCGAG ATTAGCCCAG     120
AAATACCAAA AACCCTTGTT TGTTTTACCC CAACGCCTGA ATGAGAGCGA CGGCACTAAT     180
GAGCTTTTAG AAAAAGGGCA GGCTCAAGGG ATATTTAATA TTCAAAATTT TATAAACACC     240
CTTTTAAAAG ATTACCATTT AAAAGAAATG CCTGAAATGA AAGATGAATT TTTAGAATAT     300
TGCGCGAAAA ACCCTAGCTA TGAAGAAGCG TATCTCAAAT TTGGGGATAA GCTTTTAGAA     360
TACGAGCTGT TGGGTAAGAT TAAGCGCATC AATCATCTCG TGGTGTTAGC A              411
```

(2) INFORMATION FOR SEQ ID NO:15:

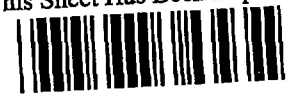
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 816 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

```
ATGGTAGTAG AATTAAAAAA CATTGAAAAG ATTTATGAAA ACGGGTTTCA TGCTCTAAAA      60
GGCGTGAATT TGGAATTGAA AAAAGGCGAT ATTTTGGGCG TGATAGGCTA TTCAGGGGCG     120
GGGAAATCCA CGCTCATTCG CTTGATCAAT TGTTTAGAGC GCCCCAGTTC TGGCGAAGTT     180
TTAGTCAATG GGGTCAATCT GTTAAACTTA AAGCCTAAAG AATTGCAAAA AGCGCGCCAA     240
AAAATAGGCA TGATTTTCCA GCATTTCAAT TTATTGAGCG CTAAAAACGT GTTTGAAAAC     300
GTCGCTTTCG CTCTAGAAAT CGCCCGATGG GAAAAAACTA AGATTAAATC AAGGGTGCAT     360
GAATTGTTGG AATTAGTGGG GTTAGAAGAT AAAGTGCATT TTTATCCTAA ACAGCTCAGC     420
GGCGGGCAAA AACAACGAGT GGCGATCGCT AGGAGTTTAG CGAATTGCCC TAATTTGTTG     480
CTTTGCGATG AAGCCACATC CGCTTTGGAT TCTAAAACCA CGCATTCTAT TTTAACGCTT     540
CTAAGCGGCA TTCAAAAAAA GTTTGATTTG AGCATCGTTT TCATCACACA CCAGATTGAA     600
GTGGTTAAAG AATTGTGCAA TCAAATGTGT GTGATCAGCA GCGGCGAAAT CGTAGAAAGA     660
GGCTCGGTGG AAGAAATTTT TGCTAACCCT AAACATGCTG TTACTAAAGA ATTGCTTGGC     720
ATCAAAAACG AACATGCGGA TCAAAAATCG CAAGACATTT ATCGCATCGT GTTTTTAGGG     780
GAGCATTTAG ACGAGCCGAT CATTTCTAAW TTTTGW                               816
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

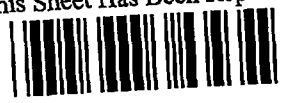
```
ATGGGGGCTT TGATAGCCAT GTTTTTTTTA ATGCTCATTA AAAAGACTAT CGCTTATAAA      60
GAAGATAAAA AGAGCGCGGC TTTAAAGGTC GTGCCTTATT TGGTGGCGTT GATGAGCTTA     120
GCCTTTAGCT GGTATTTGAT CGTGAAGGTT TTAAAACGCC TCTATGCGGT GAGTTTTGAA     180
ATCCAGCTCG CTTGCGGTTG TGTCCTTGCG CTTTTGATTT TTATCCTTTT TAAAAGATTT     240
GTGTTAAAAA AAGCCCCGCA ATTAGAAAAT AGCCACGAAA GCGTCAATGA GCTTTTTAAT     300
GTCCCTTTGA TTTTTGCC                                                   318
```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 471 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(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:17

```
ATGATTAAAA GAATTGCTTG TATTTTAAGC TTGAGCGCGA GTTTAGCGTT AGCTGGCGAA     60
GTGAATGGGT TTTTCATGGG TGCGGGTTAT CAACAAGGTC GTTATGGCCC TTATAACAGC    120
AATTACTCTG ATTGGCGTCA TGGCAATGAC CTTTATGGTT TGAATTTCAA ATTAGGTTTT    180
GTAGGCTTTG CCAATAAATG GTTTGGGGCT AGGGTGTATG GCTTTTTAGA TTGGTTTAAC    240
ACTTCAGGGA CTGAACACAC CAAAACCAAT TTGCTCACCT ATGGCGGCGG TGGCGATTTG    300
ATTGTCAATC TCATTCCTTT GGATAAATTC GCTCTAGGTC TCATTGGTGG CGTTCAATTA    360
GCCGGAAACA CTTGGATGTT CCCTTATGAT GTCAATCAAA CCAGATTCCA GTTCTTATGG    420
AATTTAGGCG GAAGAATGCG TGTTGGGGAT RCAGTGCGTT TGAAGCGGGC G            471
```

(2) INFORMATION FOR SEQ ID NO:18:

(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:18

```
ATGTATCGCC ATGTGTTGAA AGATTTCTCC CTAGATTTTA GCAAAGAAAG CGTTCAAGAG     60
CTGTTTAACC AGCTGGCTAA AGACACTTTT TTATTGCTTT TGCCTGTTTT AATCATTTTA    120
ATGGTGGTGG CGTTTTTGTC TAATGTCTTG CAATTTGGCT GGCTCTTTGC CCCTAAAGTC    180
ATTGAGCCTA AATTTTCTAA AATCAACCCT ATCAATGGCG TCAAAAACCT TTTTTCTTTA    240
AAAAAGATCC TTGATGGGAG TTTGATCACT TTAAAAGTTT TTTTAGCTTT TTTTCTGGGG    300
TTTTTCATCT TTTCCTTATT TTTAGGGGAA TTAAACCATG CGGCTCTTTT GAATTTGCAA    360
GGCCAGTTGT TGTGGTTTAA AAGCAAGGCG TTATGGCTCA TTTCTTCGCT TTTATTTTTA    420
TTTTTTGTCT TGGCTTTTGT GGATTTAATC ATCAAACGCC GCCAATACAC TAACTCTTTA    480
AAAATGACTA AACAAGAAGT TAAGGACGAA TACAAACAGC AAGAAGGAAA CCCAGAAATC    540
AAAGCCAAAA TCCGCCAGAT GATGGTAAAA AACGCCACGA ATAAAATGAT GCAAGAAATC    600
CCCAAATCCA ATGTCGTGGT GACTAACCCT ACCCATTATG CCGTCGCTCT CAAATTTGAT    660
GAAGAACACC CTGTGCCTGT GGTAGTGGCT AAAGGCACGG ATTATTTAGC CATTAGGATT    720
AAGGGTATCG CCAGAGAGCA TGACATAGAA ATTATAGAAA ATAAAACGCT CGCTAGAGAG    780
CTTTATAGAG ACGTGAAATT GAACGCCACC ATACCAGAAG AATTGTTTGA GCGG          834
```

(2) INFORMATION FOR SEQ ID NO:19:

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

```
ATGAATACAA GSCCCTTAAT CGCTACGCTT TTGCAAGCGC CTTTGCATGT TTTAGGGATT      60
AGAGAGCCAG TTTCTTTTCA GCCTTTTTAC CCCAAAACAG AAAAGCCTAA TCGCCCTCAA     120
AAGTTCGCGC ATGTTTCTAG CATGCCCAGT TTGGAATTTT TAGAAAAATT GGTGATCCGC     180
TACCTTTTAG AAGACAGAAG CCTATTGGAT TTAGCGGTGG GTTATATCCA TAGTGGGGTA     240
TTCTTGCATA AAAAACAAGA ATTTGACGCT TTATGTCAAG AAAAATTGGA CGACCCTAAA     300
TTAGTTGCGT TATTATTAGA TGCGAATTTA CCCCTAAAAA AAGGGGGTTT TGAAAAGGAA     360
```

(2) INFORMATION FOR SEQ ID NO:20:

(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:20

```
ATGGGGCAGG CATTTTTTAA AAAAATTGTT GGCTGTTTCT GTCTTGGTTA TTTATTTTTA      60
TCTAGCGCAA TAGAAGCAGT AGCACTTGAC ATTAAGAATT TTAATCGTGG TAGGGTGAAA     120
GTGGTGAATA AGAAGATTGC TTATTTGGGA GATGAAAAAC CTATTACGAT TTGGACTTCA     180
TTAGACAATG TTACCGTGAT CCAACTTGAA AAAGATGAAA CTATTTCTTA CATCACAACA     240
GGTTTCAATA AAGGTTGGAG TATTGTGCCT AATTCTAATC ATATATTCAT TCAACCTAAA     300
TCGGTAAAAA GTAATCTCAT GTTTGAAAAA GAAGCAGTGA ATTTTGCCCT AATGACAAGA     360
GATTACCAAG AATTTTTAAA GACAAAAAAA CTTATCGTAG ATGCGCCTGA CCCTAAAGAA     420
TTAGAAGAAC AAAAAAAAGC TCTAGAAAAA GAAAAAGAAG CTAAAGAACA GGCGCAAAAG     480
GCACAAAAAG ATAAAAGAGA AAAAAGAAAG GAGGAGCGTG CAAAAAATAG AGCCAATTTA     540
GAAAATCTCA CTAACGCTAT GAGTAACCCA CAAAATTTGA GCAATAACAA AAATCTTAGC     600
GAATTGATCA AGCAACAGAG AGAAAATGAA TTAGACCAAA TGGAACGAAC TAGAGGACAT     660
GCAAGAGCAG GCTCAAGC                                                  678
```

This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

```
ATGAATACAG AAATTTTAAC CATCATGTTA GTTGTCTCCG TGCTTATGGG ATTGGTAGGC      60
TTAATAGCGT TTTTATGGGG GGTTAAAAGC GGTCAGTTTG ACGATGAAAA ACGCATGCTT     120
GAAAGCGTGT TGTATGACGC GCGAGCGACT                                      150
```

(2) INFORMATION FOR SEQ ID NO:22:

(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:22

```
ATGTTTGTAG CGGCCGGGCT TGGGGCTTAT GCGATCGCGC TTTTCCACCT CTTTACGCAT      60
GCGTTCTTCA AATCCCTCCT TTTCTTAGGC TCAGGCAATG TCATGCATGC GATGGAAGAC     120
AATCTGGATA TTACTAAAAT GGGCGCTTTA TACAAGCCTA TGAGGATCAC AGCTGTCTTT     180
ATGATTATAG GGTCAGTGGC TTTGTGTGGG ATCTACCCCT TTGCGGGCTA TTTCTCCAAA     240
GACAAGATTT TAGAGGTCGC CTTTGGGATG CACCACCACA TTTTATGGTT TGTTCTTTTG     300
ATTGGGGCGA TCTTTACCGC TTTTTATAGC TTCAGACTCA TCATGCTGGT GTTTTTTGCA     360
CCCAAACAAC ATGAAATCAA CCACCCCCCA                                      390
```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 549 base pairs

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

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

```
ATGTTTATAT CTTCTTCTTA CACGCTGAGT TTTGTATGGC TTTTTTTAAT TTTCTTTTTT      60
TTCAAAAATA AGCCATTGGG TTTGAGGTTT TCGCTCTCTT TGATAAGCGT GATTTTAAGC     120
AATATCGCTT TGAAAGACTC CCTATCGCTC AATGAATTTT TAAGCAGTTT TACAGCCCCC     180
TTAAGCCCCT TTAGCTGTCT TTTGATCCTT GCTTATGCAA GCTTTTCTTG CCATATACTC     240
AAAAAGCCCC CTTTAGAAAC CTTGCAATCT TATAGCGTCA TGCTGTTTTT CAATCTGTTG     300
CTTTTGACAG ATATTTTAGG GTTTTTGCCT TTTTCAATCT ACCATCATTT CATGGCTTCT     360
CTGATTTTTA GCGCGCTTTT TTGCAGCAGT TTGTTTTTGA GTAGCCCCTT ATTAGGCGTG     420
ATCGCTTTAG TGGCTTTATC CAGTTCGCTT TTGATGCGTT CTAATTTTCA AATCTTAGAT     480
TCTTTATTGG ATTTCCCATT ATTTCTTTTT GTCTTTTTTA AGACTTTATA TCTTGCTAAA     540
AAAAGGTTA                                                             549
```

(2) INFORMATION FOR SEQ ID NO:24:

(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:24

```
ATGCGCCTAG ATTACGCCCT ATTCAACCAG CATTTAGCAA ATAGCAGAGA AAAAGCTAAA
GCGTTGGTTT TAAAAAAACA GGTTTTAGTC AATAAAATGG TGGTTTCTAA ACCCTCTTTT
ATCGTTAAAG AGGGCGATCA AATTGAACTC ATCGCTCCCA ATCTATTCGT TAGCAGGGCT
GGGGAAAAAT TAGGGGCTTT TTTAGAAGAT CATTTTATAG ATTTTAAAGA AAAGGTTGTT
TTAGATGTGG GAGCGAGTAA GGGAGGCTTT AGTCAAGTGG CTCTTTTAAA AGGGGCTAAA
AAGGTGCTTT GCGTGGATGT GGGGAAAATG CAATTAGATG AAAGTTTGAA AAACGACCAA
CGCATAGAAT GTTACGAAGA ATGCGATATT AGAGGGTTTA AAACGCCAGA AAAAATTGAT
TTAGCACTTT GTGATGTGAG CTTTATTTCT TTATATTGTA TTTTAGAAGC GATTTTGCCT
TTAAGCGGTG AATTTTTAAC GCTTTTCAAA CCGCAATTTG AAGTGGGCAG AACAATAAAA
CGCAATAAAA AGGGGGTGGT GATGGATAAA GAAGCCATTT TGAACGCTTT AGAAAACTTT
AAAAACCATT TAAAAACAAA GGATTTTCAA ATCTTAACGA TCCAAGAAAG CTTAGTGAAA
```

GGGAAAAACG GGAATGTTGA ATTTTTTATC CATTTCAAGC GAGCC 705

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:25

ATGAGCCTAC CACCGGTTTG CATTTTGAAA GATGTGAATC ACCTTTTACA AGTCTTRCAT 60
TCTTTGGTGG CGTTAGGCAA TTCCATGCTA GTGATTGAGC ATAATTTAGA CATCATCAAA 120
AACGCTGACT ACATTATAGA CATGGGGCCT GATGGGGGGG ATAAGGGCGG GAAAGTCATT 180
GCGAGCGGCA CGCCTTTAGA AGTGGCGCAA AATTGCGAAA AAACCCAAAG CTATACGGGA 240
AAATTTTTAG CTTTGGAATT GAAA 264

(2) INFORMATION FOR SEQ ID NO:26:

(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:26

ATGCAAAATC GATCGCATGA AATACAAGGC GTATCACACA TTAAGAATAA TTATAAATTT 60
TTCACCAAAG AGCTTGACAA TTATATCAGC AAAGGGTATC GCATTGAAGA GATTTATGGC 120
GCGTTTTTGT GGCTCAAAAT CGTAGCCATA GGTTTAGAGT TGGGCGAAGA CGATCCGCAA 180
GTGGTGTTTG AGAGCATCAA CGCTACAGGC GTGCAATTAA AAGGGCTGGA TCTCATCCGC 240
AACTATTTGA TGATGGGGGA AAATYCTGAC AACCAGAATC GTCTTTATAA TACTTATTGG 300
GTGCCTTTAG AAAATTGGCT TGGTGAAAAG GATTTGAATG ATTTCATCAA AACCTATTTG 360
AGAATCTATT TTGAGGATAG AGTTACAAGA GGGAGAGCGC GAAGTGTATT ACGCGCTAAA 420
AGCCCACCAC AGAGACAATT TCCC 444

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:27

```
ATGGATACCA TAAAAAGCAT TCCCATAAGA ACTTTTATTT TACTCTATAA AAGCTCACCA      60
AAATGTGTTG TGTTGGCATC AATTACAGTG CTATTTGTCG GCATTCTTYC ATCTCTGAAT     120
ATTCTTGTTA TGATAAAATT GATTGATATT GTGGTGAATC TATTACAAAA GCATACGCAT     180
TTTGAATACA GCTTGCTGTT ACCAACTTTA CTACTATGGG GAGCCTTGCT GTTTTTAACG     240
CATGTGTTCT CAGGAAATTT TATCAAGCTT GCAAACCATT ATTGCCGAAC AATTTTCTAT     300
AAATATCATC ACTCAGCTTG C                                               321
```

(2) INFORMATION FOR SEQ ID NO:28:

(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

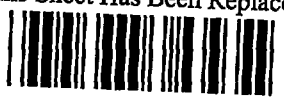
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

```
ATGATCTTTT ACACCACCAT TAAAGAGCCT TTAAAAAACC TCCAATACCG CTATGCGCAA      60
TTTTTTGGCA AGATCAAGCC TTGTTCGTTC TTAGAGTCTC TAAAATCATG CTTTTTTCAA     120
ACCTATTCTT TTTCTTTAAC GCGAAAACAA GATTTCAAAT CGCATTTGCG CCATTTCATT     180
GACAGCGCCC ATTCCAACGC CTTAGTGGGT AATTTGTATC GAGCGTTATT CATAGGGGAT     240
AGCTTGAATA AAGACTTAAG AGACAGGGCT AACGCGCTAG GGATCAACCA CTTACTGGCC     300
ATTAGCGGGT TTCATTTAGG GATTTTGAGC GCGAGCGTGT ATTTTCTTTT CTCTCTTTTT     360
TATACCCCCT TACAAAAACG CTATTTCCCT TACAGGAACG CTTTTTWA                   408
```

(2) INFORMATION FOR SEQ ID NO:29:

This Sheet Has Been Replaced



(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:29

ATGAATAAAC CATTTTTAAT CTTACTCATA GCCCTAATTG CCTTTAGCGG CTGTAACATG 60
AGAAAATACT TCAAACCCGC TAAACACCAA ATTAAAGCGA AGCGTATTTC CCTAACCATT 120
TGCAAGAAAG CATCGTTTCG TCTAATCGTT ATGGAGCCAT TT 162

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 375 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

ATGGCGGCTT GGAACACTTT AGTAGAAAAA ATCATCGCTC CTAAACACAA GGTCAAAATT
GGTTTTGTGG GCAAGTATTT AAGCTTAAAA GAATCTTATA AATCCTTGAT TGAAGCCCTA
ATCCATGCGG GGGCGCATCT GGATACGCAA GTCAATATTG AATGGCTGGA TAGCGAGAAT
TTTAATGAAA AGACTGATTT AGAGGGCGTT GATGCGATTT TAGTGCCGGG GGGCTTTGGA
GAAAGGGGGA TTGAGGGCAA AATTTGCGCC ATTCAAAGGG CTAGGTTAGA AAAACTCCCC
TTTTTAGGGA TTTGTTTGGG CATGCAATTA GCGATCGTTG AATTTTGTCG CAAATGTTTT
AGGCTTGAAA GGGGC

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 747 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

This Sheet Has Been Replaced



(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

```
ATGACTAAAG CGTTTGTGCC TTTAAGTTTG TTAGTGAGCG CGATTTTATT AGCGTTTTCG     60
CTCATCTTAA TCCCCACTTC TAAGAGCGCT TATTACGGGT TTTTGCGTCA AAAAAAAGAC    120
AAGATTGACA TTAACATCAG AGCGGGTGAA TTCGGGCAAA AATTAGGCGA TTGGCTCGTG    180
TATGTGGATA AGACTGAAAA CAATTCCTAT GATAATTTGG TGCTTTTTTC TAATAAAAGT    240
CTCTCTCAAG AAAGCTTTAT TTTGGCTCAA AAAGGCAATA TCAACAATCA AAACGGCGTG    300
TTTGAATTGA ATTTGTATAA CGGGCATGCG TATTTCACTC AAGGCGATAA AATGCGTAAG    360
GTTGATTTTG AAGAATTGCA TTTGCGCAAC AAGCTCAAGT CTTTCAATTC TAATGATGCG    420
GCTTATTTGC AAGGCACGGA TTATTTGGGT TATTGGAAAA AAGCCTTTGG TAAAAACGCT    480
AATAAAAATC AAAAACGCCG TTTTTCTCAA GCGATCTTAG TTTCCTTGTT CCCTTTAGCG    540
AGCGTGTTTT TAATCCCCTT ATTTGGCATC GCCAACCCGC GATTCAAAAC GAATTGGAGT    600
TATTTCYAWG TCCTTGGAGC GGTTGGGGTW TATTTTTTAA TGGTGCATGT GATTTCTACG    660
GATTTGTTTT TGATGACCTT TTTCTTCCCC TTTATTTGGG CGTTTATTTC TTATTTATTG    720
TTTAGAAAAT TCATTTTAAA GCGTTAT                                        747
```

(2) INFORMATION FOR SEQ ID NO:32:

(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

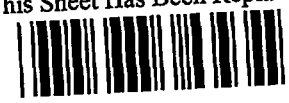
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

```
ATGAGTAAGA GCGCGATTTT TGTTCTTTCT GGCTTTTTAG CGTTCTTGCT CTATGCTTTG     60
TTATTATATG GTTTGTTGTT AGAAAGGCAT AATAAAGAAG CAGAGAAAAT CCTTTTAGAT    120
TTAAATAAAA AGGACGAACA AGCCATTGAC TTGAATTTAG AAGATCTGCC AAGCGAGAAA    180
AAGAATGAAA AAATTRAAAA AGTAACGGAA AAACAGGACG ATTTTTTAGA GCCTAAAAGA    240
AGAACCCAAA GAGGAGCC                                                  258
```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

This Sheet Has Been Replaced



(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:33

```
GTGATGGCTC AATCCTTGCT TGTYCATGCC TTTTTTGCCG CCTTGCTCGC CCTAGCCTTT      60
ATGATCAATC TTTACACCCT TTTTAAAGAA AAGAATTTCA TCCAATTGAA CCGGAAAATC     120
TATCTTGTCA TGCCAGCGAT TTATATTCTT TTAAGCATCG CTCTTTTGAG TGGGGTTTTT     180
ATTTGGGCGA TGCAACAATT TGAATTTTCT TTTAGCGCTG TTGTCATGCT TTTGGGGTTG     240
TTGTTGATGC TCATTGCAGA AATCAAACGC CATAAAAGCG TGAAATTCGC TATCACTAAA     300
AAAGAAAGGA TGAAAGCCTA TATCAAAAAA GCTAAAATCC TGTATTTTTT AGAAACGATT     360
CTTATCATCG TGTTAATGGG CATT                                            384
```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...306

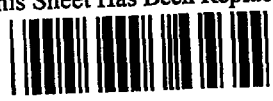
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

```
GTGCGTAATG TGGTTTTATT CATTTTAACA GCGATCTTTT TAGCGTTCAT GCTTTTAGTG      60
AGTTATTGCA TGCCCCATTA TAGCGTGGCT GTCATTAGCG GGGTGGAAGT CAAAAGAATG     120
AATGAAAATG AAAACACGCC CAATAATAAG GAAGTAAAAA CCCTTGCTAG AGATGTCTAT     180
TTTGTGCAAA CTTACGACCC TAAGGATCAA AAAAGCGTGA CCGTCTATCG TAACGAAGAC     240
ACGCGCTTTG GCTTCCCTTT TTATTTTAAG TTTAATTCGG CTGATATTTC AGCTCTCGCC     300
AAAGTT                                                                306
```

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid

This Sheet Has Been Replaced



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

(ii) MOLECULE TYPE: DNA (genomic)

(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:35

```
ATGTTTAAAA AAATCATTTT TTTGTGCGTT TTTTTGATAG GGGGATTTGT CATTCCACCC      60
CTTGAAGCCA TGCCTATTTT GCGCAATAAA ACCCCCAAAA AAAATTACCA AGAAGCCCAT     120
GAAAAGCTCT ATAGAAGCAT CATTAACCGC CAAAASSTCA CGCGTAAAAA AAGCGGGTGG     180
TATTTTTTAG GGGGGGTTGG CGCTGTAGAA GCCATTAAGG ACTATCAAGG CAAGGAAATG     240
AAAGATTGGA TGCCACGCTC AATT                                            264
```

(2) INFORMATION FOR SEQ ID NO:36:

(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:36

```
GTGCATTTTA CGTGTATCTT TCTAACCCTA TTAAAATGGA TTTTGCCAGC CAAAAACAAG      60
CAGGCGTGCA AAAAGGCCAC CAACCAGATC CATTCAAGGY YTGCAAAACA TCCAGCAAAA     120
TATCCCCCCT CAAGTATTAA CCCCTCAATC CAAGCGGGTA TACAAGGGGT GATGCAAGGT     180
TTTGGGGCTT TGAGCAGCAY YTTAGAAGYC CCCYTATTTG TTTTYYAAGC AAAATGTGGG     240
TGGATTGGGG GCTTTGAGCA TTATTTATCC CCTTTATATG GGTGGGGCAA GATTCACGAT     300
GGTGCGCATT GCGATTTGAT GCAAAAAGAC GCCAATGGAA GGGGTATCGG CTTGGAAAAA     360
GGTCTTCCAC CTTTCAAGGG GCTG                                            384
```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:37

```
ATGCAGAAGT TTTTCTCTCG TTTTAGAAGG TGGGCGTTGC CCTTTTATTT TGTGAGCGCT      60
TTAGCAGCGA TTGATATTGA TGAAGTAACA GAAGCTCAAG CTAATAGCAT TAAATTAAGC     120
GATCAGTTAG TGAGCCTGAG CGATAAGCTT TTAGAAAAAG CGGTGGATAG GGGGCGCAAT     180
ACCGATCACT TAAAAGATCT TAACGATTTG CATGAAAAAA TCAAACATTT GCGCTTGATT     240
TTAGAGCCTA AGCCTAAGGG CAAAGAAGAT AGTCCTAACT TGGGAGGTAA TAAGGATATG     300
AAAACGGTTG AAATCGGAAG CGGT                                            324
```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38

```
GTGATTTTAG CGTTCGCCTT TGGCATGAGT CTTCTTGGAT TAGCGGGCAT GTTCATTGAT      60
ATTCCTTTTT TATCCACAGG CGTTCATATC CCTAGAAAAG AGGATATTTT ATGGATTTCT     120
TTAATAGGGA TTAGCGGGAC TTTAGGGCAG TATTTCTTAA CCTATGCTTA CATGAACGCT     180
CCTGCTGGGA TCATCGCCCC CATTGAATAC ACCCGCATTG TTTGGGGGCT ATTGTTTGGG     240
CTGTATTTAG GCGATACATT TTTGGATCTT AAAAGCTCTT TAGGGGTGGC TTTGATCTTA     300
TGTTCAGGCT TGCTCATTGC CTTGCCCGCT CTTTTAAAAG AATTAAAAAA AATT           354
```

(2) INFORMATION FOR SEQ ID NO:39:

(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

This Sheet Has Been Replaced



(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:39

```
ATGATCTATT TAGGGAAGAA AAATTTTAAC GCCCTTTTGA AAGGGGCGTA TTTAATGGAT      60
GAGCATTTTA GAAACGCCCC TTTTGAAAGC AATTTACCCG TTTTAATGGG ATTAATCTGG     120
CGTGTGGTAT ATCTAACTTT TTTTCCAATC CAAAAAGCCA CT                        162
```

(2) INFORMATION FOR SEQ ID NO:40:

(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:40

```
ATGGCCGCCA AATCCAAAGC GYAAACGCTT AAAGTCTTTT CAAAATTTTT CAGCAATTTC      60
AAAATCACTA AACTCAAAGA CAACCACGAA GAAGCCCACA AACTTTTTGG AGAAAATAGC     120
CGTAAAGCCC ATGACACTGA GATCATTTAC TCCACTTTGC AAGTGGTCCC CAGGTATTCA     180
ATAGAAACCG TGGGCTTTAG TTTGTTGATT TTAGCGGTCG CTTACATCTT ATTCAAATAC     240
GGCGAAGCTA GAATGGTACT CCCTACCATT TCTATGTATG CCCTAGCGCT TTATCGCATA     300
CTCCCTTCTG TAACTGGAGT GATCAGCTAT TATAATGAAA TCGCTTACAA CCAGCTTGCA     360
ACCAATGTTG TTTTTAAAAG CCTTTCTAAG ACCATCGTTG AAGAGGATTT AGTCCCTTTA     420
GACTTTAATG AAAAAATCAC TCTCCAAAAC ATTTCATTCG CTTATAAGTC AAAACACCCG     480
GTTTTAAAAA ATTTCAACCT CACCATTCAA AAAGGTCAAA AAATCGCTCT CATAGGCCAT     540
AGCGGGTGCG GAAAATCCAC GCTGGCGGAT ATTATTATGG GGCTTACCTA CCCTAAAAGT     600
GGGGAAATTT TTATTGATAA CACCCTTTTA ACCAGCGAAA ACAGGCGCTC ATGGCGTAAA     660
AAAATAGGCT ATATCCCCCA AAATATTTAC CTTTTTGATG GCACTGTGGG GGATAATATC     720
GCTTTTGGGA GTGCTATAGA TGAAAAACGC TTGATTAAGG TGTGCAAAAT GGCTCATATC     780
TATGATTTTT TATGCGAGCA TGAGGGCCTT AAAACCCAAG TGGGCGAAGG GGCGCTAAGC     840
TTAGCGGCGG TCAAAAACAG CGCA                                            864
```

(2) INFORMATION FOR SEQ ID NO:41:

(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:41

```
ATGCTTGATA TATGGATAGA TATGATAATC TGTATTTTTT ATTTGCTCTT TTTTACGACT     60
CCTTACATTG TAGGCGATAT TTTGCAATTG AAATTTATCC GTCAAAAACT CTGCGAGAAG    120
CCTGTTTTAC TCCCACAAAA GGATTATGAA GAAGCGGGAA ATTATGCTAT TAGGAAAATG    180
CAATTATCCA TTATTTCTCA AATTTTAGAT GGGGTGATCT TTGCTGGTTG GGTCTTTTTT    240
GGTTTGACGC ATTTAGAAGA TCTCACGCAT TATTTAAACC TTCCTGAAAC GCTAGGTTAC    300
TTGGTGTTTG CCTTGTTGTT TTTAGCGATT CAAAGCGTTT TAGCTTTACC CATTAGCTAC    360
TATACTACCA TGCATTTGGA TAAGGAATTT GGCTTTTCTA AGGTGAGTTT ATCGTTGTTT    420
TTTAAGGATT TTTTCAAAGG ATTATTGCTC ACTTTAGGCG TGGGGTTGTT GTTGATTTAC    480
ACTCTCATAA TGATCATTGA ACATGTGGAG CATTGGGAGA TCAGCTCGTT TTTTGTCGTG    540
TTTGTTTTCA TGATTTTGGC TAATCTTTTT TTACCC                              576
```

(2) INFORMATION FOR SEQ ID NO:42:

(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:42

```
ATGCTAAAAA AAATATTTTT AACCAACAGC TTAGGGATTT TATGCTCTAG GATTTTTGGC     60
TTTTTACGGG ATTTAATGAT GGCCAATATC CTAGGGGCTG GGGTGTATAG CGATATTTTC    120
TTTGTGGCTT TCAAATTGCC TAATCTATTC AGGCGTATTT TTGCGGAGGG CTCTTTTTCT    180
CAAAGCTTTT TACCGAGCTT CATACGGAGT TCCATTAAGG GGGGTTTTGC GAGTTTGGTG    240
GGGCTTATTT TTTGTGGCGT TTTATTCATG TGGTGCTTAT TAGTAGCGCT CAATCCCTTA    300
TGGCTAACCA AACTCCTAGC TTACGGCTTT GATGAAGAAA CGCTCAAACT ATGCACCCCT    360
ATTGTAGCGA TCAATTTTTG GTATCTTTTA TTGGTGTTTA TCACCACTTT TTTAGGCGCG    420
CTTTTACAAT ACAAACACAG CTTTTTTGCC GCGCTTATGC GCAAGCTTAC TCAATTTATG    480
CATGATTTTA GCCCTTTTGA TTTC                                           504
```

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 459 base pairs

This Sheet Has Been Replaced



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

(ii) MOLECULE TYPE: DNA (genomic)

(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:43

```
ATGAATTTAG AAGTGGCTCT AAAGGCGTTT GAAACGCTAT TGCCATGCAA TAAACAAGAA      60
GTTTTAAAAA ACCTAAAGCC CCTAGATTTA ATCGGCCGTT GCGAGCTTTT AAGCCCTAAC     120
ATTTTAATAG ATGTGGGGCA TAACCCCCAT AGCGCTAAAG CCTTAAAAGA AGAAATCAAA     180
CGCATCTTTA ACGCTCCAAT CGTTTTGATT TATAATTGCT ATCAAGATAA AGACGCTTTT     240
TTGGTGCTAG AAATTTTAAA GTCTGTGGTT AAAAAGGTTT TGATTTTAGA ATTGCATAAT     300
GAAAGAATTA TCCAATTAGA AAAACTTAAA GGGATTTTAG AAACTTTAGG GTTAGAACAC     360
GCCTTGTTTG AAGAACTGAA AGAAAATGAA AATTATTTGG TGTATGGCTC ATTTCTGGTA     420
GCCAACGCTT TTTATGAACG CTATCCAAAG AAGAGGGAT                            459
```

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44

```
ATGGCTATCG GGTTTCCGTT AGTGTTTGGG ATTTTACTCA CCCTTTTTAG CCGTTCTTAT      60
TGGCGTGAGT TTGGGGGCGT TTCAGGGGTA TTATGGAGGG CTAGTGGATT TAGTGGGGCA     120
AAGGTTGAGC GAAATTTGGA GCGCGATCCC CATGCTTTTT TTACTCATTG TGATTTC        177
```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 666 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:45

```
ATGAAGAAAA AAGCAAAAGT CTTTTGGTGT TGTTTTAAAA TGATTCGTTG GTTGTATTTG    60
GCGGTCTTTT TTTTGTTGAG CGTATCAGAC GCTAAAGAAA TCGCTATGCA ACGATTTGAC   120
AAACAAAACC ATAAGATTTT TGAAATCCTT GCGGATAAAG TGAGCGCCAA AGACAATGTG   180
ATAACCGCCT CAGGGAATGC GATCCTATTG AATTATGACG TGTATATTCT AGCGGRTAAG   240
GTGCGTTATG ACACCAAGAC TAAAGAAGCG TTATTAGAAG GCAATATTAA GGTTTATAGG   300
GGCGAGGGCT TGCTCGTTAA AACCGATTAT GTGAAATTGA GTTTGAACGA AAAATATGAG   360
ATCATTTTCC CCTTTTATGT CCAAGACAGC GTGAGCGGGA TTTGGGTGAG CGCGGATATT   420
GCTAGCGGGA AGGATCAAAA ATATAAGATT AAAAACATGA GCGCTTCAGG GTGCAGCATT   480
GACAACCCCA TTTGGCATGT CAATGCGACT TCAGGCTCAT TTAACATGCA AAAATCGCAT   540
TTGTCAATGT GGAATCCTAA GATTTATGTC GGCGATATTC CTGTATTGTA TTTGCCCTAT   600
ATTTTCATGT CCACGAGCAA TAAAAGAACT ACCGGGTTTT TATACCCTGA GTTTGGCACT   660
TCCMAC                                                              666
```

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46

```
ATGCTGGATT TTGATTTGGT TCTTTTTGGC GCGACTGGGG ATTTAGCCAT GCGAAAGCTC    60
TTTGTTTCGC TTTATGAAAT TTATATTTCA TTTATGGTTT TAAAAACGAT TCTAGGATTA   120
TCGCATCGGG GCGTAAGGAG CTATCCAATG AAGAGTTTT                          159
```

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:47

```
ATGCAAGATT TACCCCCATG CCCTAAACGC AACGACGCCT ACACCTACCA TGATGGCACG    60
CAGTTCGTTT GCTCTAGCTG TTTGTATGAA TGGAATGGAA ATGAAATTAG TAATGAAGAA   120
TTGATCGTTA AAGATTGCCA TAATAATCTT TTACAAAATG GGGACTCGGT CATTCTCATT   180
AAAGATTTAA AGGTTAAAGG CTCATCTTTG GTGCTTAAAA AAGGCACTAA AATCAAAAAT   240
ATCAAGCTTG TCAATAGCGA TCACAATGTG GATTGTAAAG TGGAAGGGCA GAGCTTGTCT   300
TTAAAATCTG AATTCCTTAA AAAAGCT                                       327
```

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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:48

```
GTGGATGGGG CTATCATAAC AGGGAATTAT GCCTTGCAAG CAAAACTCAC CGGAGCCTTA    60
TTTTCAGAAG ATAAGGACTC GCCTTATGCT AATCTTGTAG CCTCTCGTGA GGATAATGCG   120
CAAGATGAAG CGATAAAAGC GTTGATTGAA GCCTTACAGA GCGAAAAGAC CAGGAAATTC   180
ATTTTGGATA CCTATAAGGG GGCGATTATC CCGGCTTTT                          219
```

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 711 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49

GTGTTTYCCA TGCTGGTGTT GGTGTTGAGC GATAATTTTT TAGGGCTTTT CATTGGCTGG 60
GAAGGGGTGG GGCTATGCTC TTACTTGCTC ATTGGCTTTT GGTATCATAA AAAAAGCGCG 120
AATAACGCTT CTATTGAAGC CTTTGTGATG AATCGAATCA CGGATTTAGG CATGCTCATG 180
GGGATTATTT TGATCTTTTG GAATTTTGGC ACCCTCCAGT ATAAAGAAGT CTTTAGCATG 240
CTCAATAACG CCGATTATTC CATGCTCTTT TACATTAGCG TGTTTCTTTT TATTGGCGCT 300
ATGGGGAAGA GTGCTCAATT CCCTATGCAC ACATGGTTAG CCAACGCTAT GGAGGGGCCT 360
ACCCCTGTAT CCGCTCTCAT CCATGCARCG ACGATGGTAA CCGCTGGGGT GTATCTAATC 420
ATCAGAGCCA ATCCTTTGTA TAGTGCGGTG TTTGAAGTGG GTTATTTTAT CGCATGCTTA 480
GGAGCGTTTG TGGCTCTTTT TGGAGCGAGC ATGGCTTTAG TCAATAAGGA TTTAAAACGC 540
ATCGTGGSYT ATTCCACGCT TTCTCAATTA GGGCTATATG TTTGTAGCGG CCGGGCTTGG 600
GGCTTATGCG ATCGCGCTTT TCCACCTCTT TACGCATGCG TTCTTCAAAT CCCTCCTTTT 660
CTTAGGCTCA GGCAATGTCA TGCATGCGAT GGAAGACAAT CTGGATATTA C 711

(2) INFORMATION FOR SEQ ID NO:50:

(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:50

ATGATGATAA CCAAACAATC GTATCAAAGA TTCGCTTTAA TGCGGGTTTT TGTGTTTTCG
CTTTCGGCGT TTATTTTTAA CACCACGGAG TTTGTCCCTG TTGCACTTCT GTCAGACATT
GCGAAAAGCT TTGAAATGGA GAGCGCAACA GTGGGGCTTA TGATCACTGC TTATGCATGG
GTGGTGTCTC TTGGCTCATT GCCCTTGATG CTGCTTAGCG CTAAAATTGA AAGGAAACGC
TTATTGCTTT TTCTTTTCGC TCTTTTTATT TTCAGCCATA TCCTTTCGCG T

(2) INFORMATION FOR SEQ ID NO:51:

(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

This Sheet Has Been Replaced



(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:51

```
ATGAAACTGA GAGCAAGTGT TTTAATCGGT GTGGCAATTC TGTGCTTAAT TTTAAGTGCG      60
TGCAGTAACT ATGCGAAAAA AGTGGTGAAA CAAAAGAACC ATGTTTATAC GCCTGTGTAT     120
AATGAACTGA TAGAGAAGTA TAGTGAGATC CCCTTAAATG ACAAACTCAA AGACACACCA     180
TTCATGGTGC AAGTGAAGTT GCCAAATTAC AAGGACTATT TGTTGGATAA TAAACAAGTT     240
GTACTAACTT TCAAACTTGT TCACCATTCT AAAAAGATTA CGCTCATAGG CGATGCCAAT     300
AAGATCCTCC AATACAAGAA TTACTTCCAA GCTAACGGGG CAAGATCTGA CATTGATTTT     360
TACTTGCAAC CCACTTTGAA TCAAAAGGGT GTGGTGATGA TAGCGAGTAA CTACAATGAT     420
AATCCCAACA ACAAAGAAAA ACCACAGACC TTTGATGTGT TGCAAGGAAG TCAGCCAATG     480
CTAGGAGCTA ACACAAAAAA CTTGCATGGC TATGATGTGA GTGGAGCAAA CAACAAGCAA     540
GTGATCAATG AAGTGGCAAG AGAAAAAGCT CAGCTAGAAA AAATCAATCA GTATTACAAG     600
ACTCTCTTGC AAGACAAGGA ACAAGAATAT ACCACTAGGA AAAATAACCA ACGAGAAATT     660
TTAGAAACAT TGAGTAATCG TGCAGGTTAT CAAATGAGGC AGAATGTGAT TAGTTCTGAG     720
ATTTTTAAGA ATGGCAACTT GAACATGCAA GCCAAAGAAG AAGAAGTTAG GGAGAAGCTA     780
CAAGAAGAAA GAGAGAATGA ATACTTGCGC AATCAAATCA GAAGTTTGCT CAGTGGTAAG     840
```

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52

```
ATGTGGTTAG ATCACATCGC TAAAGAGATC AGAAGTTTAG TGGAAAACGA TATTGAAGTG      60
GGTATTGTGA TTGGTGGAGG CAATATCATT AGGGGGGTTA GCGCGGCTCT AGGGGGGATC     120
ATTAGGCGCA CCAGTGGGGA TTATATGGGC ATGTTAGCCA CCGTGATTAW GCGG           174
```

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 372 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(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:53

```
GTGCATAACT TCCATTGGAA TGTGAAAGGC ACCGATTTTT TCAATGTGCA TAAAGCCACT     60
GAAGAAATTT ATGAAGGGTT TGCGGACATG TTTGATGATC TCGCTGAAAG GATCGTTCAA    120
TTAGGACACC ACCCCCTAGT CACTTTATCC GAAGCGATCA AACTCACTCG TGTTAAAGAA    180
GAAACTAAAA CGAGCTTCCA CTCTAAAGAC ATCTTTAAAG AAATTCTAGA GGACTACAAA    240
CACCTAGAAA AAGAATTTAA AGAGCTCTCT AACACCGCCG AAAAAGAAGG CGATAAAGTT    300
ACCGTAACTT ATGCGGACGA TCAATTAGCC AAGTTGCAAA AATCCATTTG GATGCTAGAA    360
GCCCATTTAG CT                                                        372
```

(2) INFORMATION FOR SEQ ID NO:54:

(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:54

```
ATGAATAAAA CCATAAAAGC CGCCGCCCTA GCCTATAACA TGGGGCAAGA TCATGCCCCA     60
AAAGTGATCG CAAGCGGGGT GGGCGAAGTG GCTAAAAGGA TCATTCAAAA AGCTAAGGAA    120
TACGATATAG CGCTCTTTTC TAACCCCATG CTGGTGGATT CGCTCTTAAA GGTGGAATTA    180
GACTGCGCGA TACCTGAAGA ATTGTATGAA AGCGTGGTGC AAGTGTTTTT ATGGCTCAAC    240
AGCGTGGAAA ATAACGCGCA AATGTCCAAG                                      270
```

(2) INFORMATION FOR SEQ ID NO:55:

(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

This Sheet Has Been Replaced



(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:55

```
ATGGGGAAAA TTTCAGCGCA TTTAGCCCAT GAAATCAGAA ACCCCGTAGG CTCTATCTCT      60
CTTTTAGCTT CGGTGTTATT AAAGCATGCG AACGAAAAAA CTAAACCCAT TGTTGTAGAA     120
TTGCAAAAAG CTTTATGGCG CGTAGAAAGG ATCATTAAAG CCACCTTGCT TTTTTCTAAA     180
GGCATTCAAG CCAACCGCAC CAAGCAAAGT TTGAAAACGC TAGAGAGCGA TCTCAAAGAA     240
GCCCTAAACT GCTACACTTA CTCTAAAGAC ATTGATTTTC TTTTTAATTT TAGCGATGAA     300
GAAGGGTTTT TTGACTTTGA TTTAATGGGG ATTGTGTTAC AAAATTTCTT GTATAACGCC     360
ATTGATGCGA TTGAAGCCTT AGAAGAGAGC GAACAAGGTC AGGTCAAAAT TGAAGCGTTC     420
ATTCAAAATG AATTTATTGT CTTCACCATT ATTGATAATG GCAAGGAAGT GGAAAATAAA     480
AGCGCTTTAT TTGAGCCTTT TGAAACCACT AAATTAAAGG GGAATGGCTT AGGGTTAGCC     540
CTGTCTTTGC AAGTCGTTAA AGCCCATGAA GGGAGCATTG CGCTATTAGA AAATCAAGAA     600
AAAACCTTTG AAATTAAGAT TCTTAACGCT TCT                                  633
```

(2) INFORMATION FOR SEQ ID NO:56:

(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

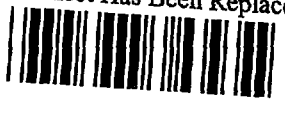
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56

```
GTGTCAGAAT TTCATCAAGT TTATGACCCT TTGGGTAATA TTTGGCTGAG CGCTCTTGTG      60
GCCTTATTGC CGATTTTGTT ATTTTTCTTA TCTTTAATGG TTTTTAAACT CAAAGGTTAT     120
ACAGCGGCCT TTTTGAGCGT GGCCTTTATCA GCCATTATTG CGGTTTTAGT GTATAAAATG     180
CCTGTTAGCA TGGTGGGTTC AAGCTTCCTT TATGGCTTTC TTTATGGCCT ATGGCTATTC     240
GCTTGGATCA TTATTGCCGC GATTTTTTTA TACAAACTCA GCGTTAAATC CGGCTATTTT     300
GAAATCTTAA AAGAAAGCGT TCAGTCCATC ACTTTAGATC ACCGCATTTT AGTGATTTTG     360
ATTGGCTTTT GTTTTGGCTC ATTTTTAGAA GGGGCGATCG GCTTTGGAGG GCCTATTGCC     420
ATCACAGCGG CGATTTTAGT GGGGTTGGGG TTAAGCCCTT TGTATTCTGC TGGGTTATGT     480
TTGATCGCTA ACACCGCTCC TGTGGCCTTT GGCGCGGTGG GTATCCCTAT AAGCGCGATG     540
GCGAGCGCGG TAGGGGTGCC AGCGATCTTA ATTTCAGCCA TGACGGGTAA AATCCTCTTT     600
TTTGTGAGCT TGTTAGTGCC GTTTTTTTATT GTGTKT                              636
```

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 546 base pairs
(B) TYPE: nucleic acid

This Sheet Has Been Replaced



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

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

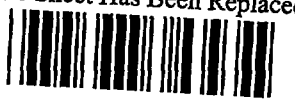
(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57

This Sheet Has Been Replaced



```
ATGGAAATTA AAATGGCTAA GGATTATGGT TTTTGTTTTG GCGTCAAAAG AGCGATACAA      60
ATCGCTGAAA AAAATCAAAA CAGCTTGATT TTTGGCTCGC TCATTCATAA CGCTAAAGAA     120
ATCAATCGTT TGGAAAAAAA TTTCAATGTG AAAATTGAAG AAGATCCTAA AAAAATCCCT     180
AAAAATAAGA GCGTGATCAT AAGAACCCAT GGCATTCCTA AACAGGATTT AGAATACTTG     240
AAAAATAAGG GGGTTAAAAT CACTGACGCG ACTTGCCCGT ATGTGATCAA ACCTCAGCAA     300
ATTGTGGAAT CCATGAGTAA AGAAGGGTAT CAAATCGTGC TTTTTGGGGA CATTAACCAC     360
CCTGAAGTCA AGGGCGTGAT CAGCTATGCC ACTAACCAGG CTTTAGTCGG CAATTCGTTA     420
GAAGAATTGC AAGAAAAAAA ATTGCAACGG AAAGTGGCTT TAGTCTCTCA AACCACCCAA     480
GCAAACCCCA AAACTCTTGC AAATCGCTTC TTATTTGGTG GARGRTGCAC TGAAGTGCGT     540
ATTTTT                                                                546
```

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 672 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

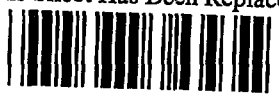
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58

```
ATGGATCATG AGTTTTTGAT TACCATGCGT TTGAGCTTTT CTTTAGCTTT GATTACCACC      60
CTTATTTTAC TCCCTATAGG GATTTTTTTA GGCTATTTTT TAAGCCTTAA ACGCAATCTT     120
TTAACGAGCT TAACAGAAAC GCTTGTGTAT ATGCCTTTAG TTTTACCCCC AAGCGTGCTA     180
GGGTTTTTATC TTCTTTTAAT CTTTTCGCCT TCTTCTTTTT TGGGAGCGTT TTTACAAGAT     240
GTGTTAAATG TGAAACTCGT TTTTAGTTTC CAAGGGCTTA TCTTAGGGAG CGTGATTTTT     300
TCCTTGCCCT TTATGGTAAG CCCTATTAAA AGCGCGTTAA TTTCCTTGCC CACTTCTTTA     360
AAAGAAGCCA GTTATAGCTT GGGTAAAGGG GAATACTACA CCCTTTTTTT TGTCCTACTC     420
CCTAACATCA AACCCAGTGT GTTGATGGCT ATCATTACAA CTTTTATGCA CACTATAGGT     480
GAATTTGGCG TGGTGATGAT GCTTGGGGGT GATATATTAG GGGAAACAAG AGTGGCTAGC     540
ATTACGATCT TTAACGAAGC TGAAGCACTC AATTATTCTA AAGCCCATCA ATACGCCTTA     600
ACGCTCACGC TTATTAGTTT TAGCCTCTTG TTTGTTACCC TATTTTTAAA TAAAAAACAA     660
AGCTCGTTTT TA                                                         672
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59

```
ATGCATCCTA TAATGTTTGC CTATATCGCT AACGCGCTCG CTCAAGCTAG AAAGATCAAC      60
GGAACACTTT GCATGGCGTT TCAAAAAATA TCTCAAGTCA AAGAATTAGG CATTGATAAA     120
GCAAAGAGTT TGATAGGCAA CCTTTCTCAA GTGATTATCT ACCCCACAAA AGATACTGAT     180
GAATTAATAG AATGTGGCGT CCCATTAAGC GATAGTGAAA TCAATTTCTT ACACAACACG     240
GACATGAGAG CCAGACAAGT GCTAGTAAAA AATATCGTTA CAAACGCTTC AGCTTTTATT     300
GAAATTGATT TAAAAAAGAT TTGCAAGAAC TACTTTATAT TCTTGATAGC AATGCTGGTA     360
ATAGAAAAAT CCTCAATGAT CTTAAAAAAG CAAACCAAGA AACTTATAAG GAAGAGTATT     420
```

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

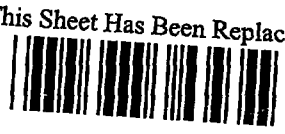
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60

```
ATGTGCCTGA CAGGCGGCTT GATGCGTTGG CTCAAATCGG TAAAGCCTGA ACGAATCTTG      60
CATTCTGTGG TGGAATTTGT GGATATTGCC GGATTGATTA AGGGGGCGAG CAAGGGGGAG     120
GGTTTAGGCA ATCAGTTTTT AGCCAATATC AAGGAATGCG AAGTGATCTT GCAAGTGGTG     180
CGCTGTTTTG AAGATGACAA TYATCACGCA TGTGAACGA                            219
```

(2) INFORMATION FOR SEQ ID NO:61:

This Sheet Has Been Replaced



(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:61

```
ATGCATGTTG CTTGTCTTTT GGCTTTAGGG GATAACCTCA TCACGCTTAG CCTTTTAAAA     60
GAAATCGCTT CCAAACAGCA ACAGTCCCTT AAAATCCTAG GCACTCATTT GACTTTAAAA    120
ATCGCCAAGC TTTTAGAATG CGAAAAACAT TTTGAAATCA TTCCTGTTTT TGAAAATATC    180
CCTGCTTTTT ATGACCTTAA AAAACAAGGC GTTTTTTGGG CGATGAAGGA TTTTTTATGG    240
TTATTAAAGC AATTAAAAAA CATCAAATCA AACGTT                               276
```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 615 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62

```
ATGAAAAAGA AGCCATTGAT GTGGCGTATC TGTGCGTTAA GGAGACTTCT TCTAGGGTTC     60
AAGAGAGAGA GAGAGTTATT AAGCTTCGCT AAACATTGGA ATATCCCAAC GATTGTCGTT    120
TTCACACACA CTCAAGCCGA AGCCGGCGAT GCGTTTGTCC AAGAAACTAA AGGGATCATA    180
GACGAAGAAT GGGGGTTTAA AGGTTTTGTC AGAGCCTATG TGAGGGTCAA TTCCGTTGCC    240
TTTTCATTTA GGGGGTTGAA AGTCCCTGTT GAAGGTTTAG AAGAATTGGT AGATGAAACG    300
AAAAAATGCC TTTCAGACGC TGAAAAAAAT AAGAAAAGGC ATTTCTTGAG TATTCAAAGA    360
GTTAAGATTC AAGAAAGAAA ACAGGCTATG ATAGAGGAAT GTAAAACCAT TATCCATGTT    420
GCATCAGGCG CTGCAGGAGT TGCTGGGCTT ATCCCCATAC CTTTTAGCGA TGCGCTCGCT    480
ATCGCACCCA TTCAAGCAGG GATGATCTAT AAAATGAATG ACGCTTTTGG AATGGATTTG    540
GATAAATCTG TGGGCGCGAG TTTGGTCGCA GGATTGTTAG GCGTAAACTG TCGCGCAAGT    600
GGGGAGGACT CTCGT                                                     615
```

(2) INFORMATION FOR SEQ ID NO:63:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63

GTGCTTGGCG TGTTYAATTT AAGGGGCAAT GTCTTCCCTT TGATCAGTTT GCGTTTAAAG 60
TTTGGCTTGA AAGCCGAAAA ACAAAACAAA GACACTCGTT ATTTGGTGGT ACGCCATAAC 120
GAT 123

(2) INFORMATION FOR SEQ ID NO:64:

(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:64

GTGAAAAGCG TTTTTAGCGA AGAAAAAGAA ACGCCTGTTA CTAAAGAAAA CGGCTCTTAT
TTGATCGCTT ATGACCCCCT AGATGGGAGT TCAGTGATGG AGGCGAATTT CTTAGTAGGC
ACGATTATAG GGGTTTATGA AAAGGATTAT AAGGCGCAAA ATTTAGTTGC AAGCCTTTAT
GTGGTTTTTG GGCATAAAAT AGAATTGGTG GTGGCTTTAG AAGAAGTTTA TCGTTACGCT
TTTTATCAAA ACAAGTTTCA TTTTATAGAA ACCATCGTTT TAGAAAATAA GGGTAAAATC
ATCGCTAGCG GAGGCAATCA AAAGGATTTT TCYTTGGGCT TAAAAAAGGC TTTAGAAGGG
TTTTTTGCAG AAAATTACCG CTTGCGATAC TCAGGATCTA TGGTGGCTGA TGTCCATCAT
GTGTTGGTTA AAAAGGGCGG AATGTTTTCC TACCCGCAAA AGAAATTGCG AAAGCTTTTT
GAAGTCTTTC CTTTAGCCTT GATGGTTGAA AAAGCTAAAG GGGAAGCGTT TTATTTTGAT
AAGGGGGTTA AAAAGCGTTT GCTAGATCAA AGCGTAGAAA GCTACCATGA AAAAAGCGAA
TGCTATTTAG CCAGCCCGCA TGAAGCTCAG ATTTTAGAAA AACATTTAAA GGGAGAA

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 564 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:65

```
ATGAAAAGCA TTGGAGAAGT GATGGCGATA GGGGGCAATT TCTTAGAAGC CTTACAAAAA      60
GCGTTATGCT CTTTGGAAAA CAATTGGCTA GGGTTTGAAT CGTTAAGCAA AGATTTAGAG     120
GCGATAAAAA AGGAAATCCG CCGGCCCAAT CCCAAACGCT TGCTCTATAT TGCTGATGCG     180
TTCAGGTTGG GCGTTTCTGT GGATGAAGTG TTTGAATTAT GCCAGATTGA CAGGTGGTTT     240
TTATCTCAAA TTCAAAAACT AGTCAAAGCA GAAGAGGGCA TCAATTCTAG CGTTTTAACG     300
GACGCCAAAA AATTGAGAGG GCTTAAAAAT TTAGGCTTTA GCGATGCCAG GATTGCCACT     360
AAAATCAAAG AAAATGAAAA TTTAGAGGTC AGCCCTTTTG AAGTGGAATT AGCTAGATCT     420
AATTTACAAA TCGCGCCCCA TTTTGAAGAA GTGGACACTT GCGCGGCGGA GTTTTTATCG     480
CTCACGCTTA TTTGTATTCC ACCTATGCCC CTAACCCTTT GCCCCCTATT GGAAACAAAC     540
AAGAAAAACA AGAAAAGAAA ATCC                                            564
```

(2) INFORMATION FOR SEQ ID NO:66:

(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:66

```
ATGTTTGGGA ATAAGCAGTT ACAGCTTCAA ATCAGTCAAA AAGATTCTGA GATTGCGGAG      60
TTAAAAAAAG AAGTCAATCT CTATCAAAGC CTTTTAAATT TGTGCTTGCA TGAGGGTTTT     120
GTAGGTATTA AAAACAATAA AGTCGTTTTT AAAAGCGGGA ATCTTGCAAG CTTAAACAAT     180
TTAGAAGAAC AAAGCGTTCA TTTTAAAGAA AACGCAGAAA GCGTTAATTT ACAAGGGGTT     240
TCTTATTCTT TGAAAAGCCA AAATATTGAC GGCGTGCAGT ATTTTTCATT GGCTAAAAAA     300
ACAGGGGGTG TGGGGGAATA CCATAAAAAT GATTTGTTTA AGACTTTTTG CACGAGCTTA     360
AAAGAGGGCT TAGAGAACGC GCAAGAAAGC ATGCAGTATT TCCATCAAGA AACAGGCTTG     420
CTCTTGAATG CGGCTAAAAA TGGCGAAGAG CATTCTAATG AAGGATTAAT AACCGTTAAT     480
AAAACGGGTC AAGACATTGA ATCGCTTTAT GAAAAGATGC AAAACGCCAC TTCGTTAGCG     540
```

GACTCCCTCA ACCAACGGAG CAATGAAATC ACTCAAGTCA TTTCTTTGAT TGATGATATT 600
GCAGAGCAAA CCAATCTCTT AGCCCTAAAC GCCGCTATTG AGGCCGCACG AGCGGTGAAC 660
ATGGCAGAGG GTTTGCGGTG GTGGCTGATG AGG 693

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:67

ATGTGGATTA TGTCTTCACT TTCTAGTTCA TTCTTTCATT CGCTCTTCTT CATCAAATCA 60
AACCCTGGCC AACTCTTAAA AGGTTGGGGT TCAAAAATCT TTTTCATAAA TAGAAAGTTT 120
GTTTTAGCAC AGTATAATCC TAGCGTTTCA ATTTTTATTT TACTCAATAG GGTGTTTGGT 180
GTTGGCGTT 189

(2) INFORMATION FOR SEQ ID NO:68:

(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:68

GTGGGCGCTA ACCCTGTGCC GCATGCGCAA ATCTTGCAAT CAGTTGTGGA TGATTTGAAA 60
GAGAAAGGGA TCAAATTAGT GATCGTGTCT TTTACGGATT ATGTGTTGCC TAATTTAGCG 120
CTCAATGACG GCTCTTTAGA CGCGAATTAC TTCCAGCACC GCCCTTATTT GGATCGGTTT 180
AATTTGGACA GAAAAATGCA CCTTGTTGGT TTGGCCAATA TCCATGTGGA GCCTTTAAGA 240
TTTTATTCTC AAAAAATCAC AGACATTAAA AACCTTAAAA AAGGCTCAGT GATTGCTGTG 300
CCAAATGATC CGGCCAATCA AGGCAGGGCG TTGATTTTAC TCCATAAACA AGGCCTTATC 360
GCTCTCAAAG ACCCAAGCAA TCTATACGCT ACGGAGTTTG ATATTGTCAA AAATCCTTAC 420
AACATCAAAA TCAAACCCCT AGAAGCTGCG GTTATTGCC 459

This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:69:

(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:69

ATGGGGCTTG TTGCGAGCGG CATTAACGAT GAAGAGCTTT TAAAATGGCT TCAGGCTTTT 60
GGGTTAAAAA TGGGTCTTTG TTTTCAAGTG CTAGATGATA TTATAGACGT TACACAAGAT 120
GAAAAAGAAA GCGGTAAAAC CACGCATTTA GACAGCGCTA AAAACAGCTT TGTGAATTTA 180
TTGGGGCTAA AAAAGGCAGC GGTTACGCCC AAACTT 216

(2) INFORMATION FOR SEQ ID NO:70:

(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:70

ATGGGGTTTA ACCGCTTGGT GGATAGAGAC ATTGATAAGG ATAACCCAAG GACGAAAAAC
CGCCCGAGCG TGGATGGTAG GATCAGCGTT AAAGGCATGG TCATTTTTAG CGTTTCAAAC
GCTCTTTTGT TCGTGGGAGT GAGTTATTTC ATCAACCCTT TAGCTTTCAA GCTTTCGTTA
CCTTTTTTAA TCATTTTAGG GGGTTATTCG TATTTCAAGC GCTTTTCTTC TTTGGCGCAT
TTTGTCGTGG GTTTGGCTTT GGGTTTAGCC CCCATTGCAG GAAGCGTGGC GGTTTTAGGG
GATATTCCTT TATGGAATGT CTTTTTGGCY TTAGGGGTGA TGTTGTGGGT GGCTGGGTTT
GATTTGCTCT ATTCTTTACA GGATATGGAG TTTGATAAAG AAAGGGGCTT GTTTTCCATT
CCTAGCCAAT TAGGGGAAAA ATGGTGCTTG AATCTTTCAA GGCTCTCGCA CCTTGTGGCA
CTGATCTGCT GGCTTTGTTT TGTGAAATGC TATCATGGGG GGCTTTTTGC GTATTTGGGC
TTAGGGGTTT CAGCCTTGAT CTTACTCTAT GAGCAGATTT TAGTGGCCAG AGATTATAAA
AACATTCCTA AAAGCCTTTT TTGTGAG

(2) INFORMATION FOR SEQ ID NO:71:

This Sheet Has Been Replaced



(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:71

GTGGAGCAAA ATAAAATCAT TAAACTCTTC ACTGTGGCGA CTATGGCGAT GATGCCCCCC 60
ACATTGATTG GCACGATTWA TGGCATGAAT TTTAAATTCA TGCCGGAGTT AGAATGGCAA 120
TACGGGTATC TTTTTGCGCT GATTGTCATG GCGATTTCTA CGATTTTGCC GGTGATTTAT 180
TTCAAAAAGA AAGGGTTGGT TGTAGCCTTT CATGGAATTT TTATCCTCAC TCTTAGACGC 240
TCTTTCTACA CCGCATGGCA TAGTCTCCTT GGCTACGCCA CGCTT 285

(2) INFORMATION FOR SEQ ID NO:72:

(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:72

ATGTTCGATT CAATCGTTTA TTTTTTCAAT AAGAGCGGGT TTGTTACCAC GCTTGTTTTA 60
GTTTGGATTT CGCTTTATTT GGTGATGACT TTATGGGTCT TTTTGTATAA AAGCATTGTA 120
TTAAAGATTG AACTCAGGCG CGAGATGCAA TCTTTGTCTA ACATTCTTAA TGGAGCGCAA 180
GACGCTCCAG AGCATTTTAT GTTTAATAAA AAAAGAAATG ATGAGACCAA AAGGTATTCT 240
AATGAATTGT TGCAGGSCTT GGAAACACCA GGTTCT 276

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

This Sheet Has Been Replaced



(A) LENGTH: 375 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73

```
ATGGCGATGC TYTATTGCAT GCGGTTATTG ATGCCGATTT TAGGAGCGAT TAAAGGGGGG      60
GATATTGGCG AATGGTTCCC TGATAATGAC CCCAAATACA AAAACGCCTC TTCTAAAGAG     120
CTTTTAAAAA TCGTGTTGGA TTTTTCTCAA AGCATTGGGT TTGAATTGCT TGAAATGGGA     180
GCGACCATCT TTAGCGAAAT CCCTAAAATC ACTCCTTACA AACCGGCGAT TTTAGAGAAT     240
TTGAGCCAAC TTTTGGGTTT AGAAAAATCT CAAATCAGCT TGAAAGCCAC TACAATGGAA     300
AAAATGGGGT TCATTGGCAA ACAAGAAGGG CTGTTAGTCC AAGCGCATGT GAGCATGCGT     360
TATAAACAAA AACTT                                                      375
```

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3534 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...3534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74

```
ATGATACCAA ATTTAGATAT AGAAGGAGAA ACAATGACTA ACGAAGCCAT TAACCAACAA      60
CCACAAACCG AAGCGGCTTT TAACCCGCAG CAATTTATCA ATAATCTTCA AGTGGCTTTT     120
ATTAAAGTTG ATAATGTTGT CGCTTCATTT GATCCTAATC AAAAACCAAT CGTTGATAAG     180
AATGATAGGG ATAATAGGCA AGCTTTTGAG AAAATCTCGC AGCTAAGGGA GGAATTCGCT     240
AATAAAGCGA TCAAAAATCC TACCAAAAAG AATCAGTATT TTTCAAGCTT TATCAGTAAG     300
AGCAATGATT TAATCGACAA AGACAATCTC ATTGATACAG GTTCTTCCAT AAAGAGCTTT     360
CAGAAATTTG GGACTCAGCG TTACCAAATT TTTATGAATT GGGTGTCCCA TCAAAACGAT     420
CCGTCTAAAA TCAACACCCA AAAAATCCGA GGTTTTATGG AAAATATCAT ACAACCCCCT     480
ATCTCTGATG ATAAAGAGAA AGCGGAGTTT TTGAGGTCTG CCAAACAAGC TTTTGCAGGA     540
ATTATCATAG GAAACCAAAT CCGATCGGAT CAAAAATTCA TGGGCGTGTT TGATGAATCT     600
TTGAAAGAGA GGCAAGAAGC AGAAAAAAAT GGAGAGCCTA ATGGAGATCC TACTGGTGGG     660
GATTGGCTTG ATATTTTTTT ATCATTTGTG TTTAACAAAA AACAATCTTC CGATCTCAAA     720
GAAACGCTCA ATCAAGAACC AGTTCCTCAT GTCCAACCAG ATGTAGCCAC TACCACCACT     780
```

```
GACATACAAA GCTTACCGCC TGAAGCTAGG GATTTGCTTG ATGAAAGGGG TAATTTTTCT    840
AAATTCACTC TTGGCGATAT GAACATGTTA GATGTTGAGG GAGTCGCTGA CATTGATCCT    900
AATTACAAGT TCAACCAATT ATTGATCCAC AATAACGCTC TGTCTTCTGT GTTAATGGGG    960
AGTCATAATG GCATAGAACC TGAAAAAGTT TCATTGTTGT ATGGAAACAA TGGTGGTCCT   1020
GAAGCTAGGC ATGATTGGAA CGCCACCGTT GGTTATAAAA ACCAACGAGG CGACAATGTG   1080
GCTACACTCA TTAATGTGCA TATGAAAAAT GGCAGTGGGT TAGTCATAGC AGGTGGTGAG   1140
AAAGGGATTA ACAACCCTAG TTTTTATCTC TACAAAGAAG ACCAACTCAC AGGCTCACAA   1200
CGAGCATTGA GTCAAGAAGA GATCCAAAAC AAAGTGGATT TCATGGAATT TCTTGCACAA   1260
AATAATGCTA AATTAGACAA CTTGAGCAAG AAAGAGAAAG AAAAATTCCA AAATGAGATT   1320
GAAGATTTTC AAAAAGACTC TAAGGCTTAT TTAGACGCCC TAGGGAATGA TCACATTGCT   1380
TTTGTTTCTA AAAAAGACAA AAAACATTTA GCTTTAGTTG CTGAGTTTGG TAATGGGGAA   1440
TTGAGCTACA CTCTCAAAGA TTATGGGAAA AAAGCAGATA AAGCTTTAGA TAGGGAGGCA   1500
AAAACCACTC TTCAAGGTAG CCTAAAACAT GATGGCGTGA TGTTTGTTGA TTATTCTAAT   1560
TTCAAATACA CCAACGCCTC CAAGAGTCCT GATAAGGGTG TGGGTGCTAC GAATGGCGTT   1620
TCCCATTTAG AAGCAGGCTT TAGCAAGGTA GCTGTCTTTA ATTTGCCTAA TTTAAATAAT   1680
CTCGCTATCA CTAGTGTCGT AAGGCAGGAT TTAGAGGATA AACTAATCGC TAAAGGATTG   1740
TCCCCACAAG AAGCTAATAA GCTTGTCAAA GATTTTTTGA GCAGCAACAA AGAATTGGTT   1800
GGAAAAGCTT TAAACTTCAA TAAAGCTGTA GCTGAAGCTA AAAACACAGG CAACTATGAC   1860
GAGGTGAAAC AAGCTCAGAA AGATCTTGAA AAATCTCTAA AGAAACGAGA GCGTTTGGAG   1920
AAAGATGTAG CGAAAAATTT GGAGAGCAAA AGCGGCAACA AAAATAAAAT GGAAGCAAAA   1980
TCTCAAGCTA ACAGCCAAAA AGATGAGATT TTTGCGTTGA TCAATAAAGA GGCTAATAGG   2040
GATGCAAGAG CAATCGCTTA CGCTCAGAAT CTTAAAGGCA TCAAAAGGGA ATTGTCTGAT   2100
AAACTTGAAA ATATCAACAA GGATTTGAAA GACTTTAGTA AATCTTTTGA TGAATTCAAA   2160
AATGGCAAAA ATAAGGATTT CAGCAAGGCA GAAGAAACAC TAAAAGCCCT TAAAGGCTCG   2220
GTGAAAGATT TAGGTATCAA TCCAGAATGG ATTTCAAAAG TTGAAAACCT TAATGCAGCT   2280
TTGAATGAAT TCAAAAATGG CAAAAATAAG GATTTCAGCA AGGTAACGCA AGCAAAAAGC   2340
GACCTTGAAA ATTCCATTAA AGATGTGATC ATCAATCAAA AGATAACGGA TAAAGTTGAT   2400
AATCTCAATC AAGCGGTATC AGTGGCTAAA GCAACGGGTG ATTTCAGTGG GGTAGAGCAA   2460
GCGTTAGCCG ATCTCAAAAA TTTCTCAAAG GAGCAATTGG CTCAACAAGC TCAAAAAAAT   2520
GAAGATTTCA ATACTGGAAA AAATTCTGCA CTATACCAAT CCGTTAAGAA TGGTGTAAAC   2580
GGAACCCTAG TCGGTAATGG GTTATCTAAA GCAGAAGCCA CAACTCTTTC TAAAAACTTT   2640
TCGGACATCA AGAAAGAGTT GAATGCAAAA CTTGGAAATT TCAATAACAA TAACAATAAT   2700
GGACTCGAAA ACAGCACAGA ACCCATTTAT ACTCAAGTTG CTAAAAGGT AAAAGCAAAA   2760
ATTGACCGAC TCGATCAAAT AGCAAGTGGT TTGGGTGATG TAGGGCAAGC AGCGAGCTTC   2820
CTTTTGAAAA GGCATGATAA AGTTGATGAT CTCAGTAAGG TAGGGCTTTC AGCTAACCAT   2880
GAACCCATTT ACGCTACGAT TGATGATCTC GGCGGACCTT TCCCTTTGAA AAGGCATGAT   2940
AAAGTTGATG ATCTCAGTAA GGTAGGGCTT TCAAGGGAGC AAAAATTGAC TCAGAAAATT   3000
GACAATCTCA ACCAGGCGGT ATCAGAAGCT AAAGCAAGTC ATTTTGACAA CCTAGATCAA   3060
ATGATAGACA AGCTCAAAGA TTCTACAAAA AAGAATGTTG TGAATCTATA TGTTGAAAGT   3120
GCAAAAAAAG TGCCTACTAG TTTGTCAGCG AAATTGGACA ATTACGCTAC TAACAGCCAC   3180
ACACGCATTA ATAGCAATGT CAAAAATGGA ACAATCAATG AAAAAGCGAC CGGCATGCTA   3240
ACGCAAAAAA ATTCTGAGTG GCTCAAGCTC GTGAATGATA AGATAGTTGC GCATAATGTG   3300
GGAAGTGCTC CTTTGTCAGC GTATGATAAA ATTGGATTCA ACCAAAAGAA TATGAAAGAT   3360
TATTCTGATT CGTTCAAGTT TTCCACCAGG TTGAGCAATG CCGTAAAAGA CATTAAGTCT   3420
GGCTTTGTGC AATTTTTAAC CAATATATTT TCTATGGGAT CTTACAGCTT GATGAAAGCA   3480
AGTGTGGAAC ATGGAGTCAA AAATACTAAT ACAAAAGGTG GTTTCCAAAA ATCT         3534
```

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1398 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

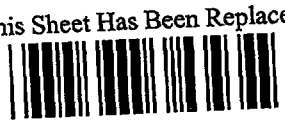
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75

ATGAAAGCGT TGAAGACTTT TTTAAAAAAA TCCCTTATTC TGTTACTAGC AATTGCCTTA 60
AACCACTTAA ACGCTGTGGC TATGATTGTG GATAATCCTA CGCAGAACGC TTGGAATGGT 120
GCTAAAAGAG CATGGGATGA AAGCAAGTGG GCTAAACATT TAGCCACTAT TACTGAAAGG 180
ATCAAGCTCG CTCAAGACAC ATTAGATAGG GCTAATCAGA CGCTTAATTC CATCAACAAA 240
GTGAATGATG TTTTGAACAA AACCAATCAA TTTCTAACAG GCAGTATTTT AAGCATCCCC 300
AATCCCATGC AGTATGTAGA AAAAATCCAA AGTTTTGCCA AGCAAGTTCA AGCCAATACT 360
GAAAGGATCA AAGAAAATGC ACAAAACTAT GATATACGCA ATCAAATTGC AGCCAAACGC 420
ATCTCTGAAA AATGCCCTGA ACTCAATTGG GATGTCAGTC AAGACGCGAG CCCTACAGAG 480
AAAAACTTAC ACCAATTTTT CACGAGCAAG GGGAAAGAAA GCGCTAACAC AAAGGCTCTA 540
AAGGATTTTG CTAACGCCAT AGGTAACACT CAAATCAGCA CGGCGAACGA TTTAGGAGCT 600
GGACTTAGAG GCAGAGCCTT ATTAGAATAC ATTTGCATTC AAAAAGGCAA TTTAGAAGCG 660
GCTAAAAAAA TCCAATTATT AGACAGCCAA ATGACTTTAG CTCTACTCAA TAACGACTAT 720
ACGGCTTATG AAAAACTTAG AGCTGAAAAA GAAGAATTAA AAAGACAAAT CGCTTCAAAT 780
GTGTATGCGA AAGTCAAACA GCTTGTTGTA GCTTCCCAAG ATAGAGCGTT TAGTCAAATG 840
GATAATGAGT TGGGCGTTAA AACTTTTGGG TTCAACGATG AGAATGTTAA AAAAGGTTAT 900
TGCAAGAAAG AAAACAGAAA TGGCAAAAGC GAGTGCATCC CTAACATGCT CAATGTTAAT 960
CGCTTAAAAG CGCAATTTGA TGAGCTTAAT TTAGATTATA GTAGGGATAT TGCTGGTAAA 1020
AAAGGTGAAG CAGCCGCTAA AGTGTTCAAT GACTACAAAC ACCGATTCCA ACAATTAAGC 1080
GTAGAAACTG CTTTAGAAAT CGCTCAAAAT TTAAGTTTTA TGAATAAGAC GCTAGGTTTA 1140
ATGGTGCAAA TGCAAAGCTA TGCATTCAAG CAACAAATGG GCTATTTTGA AGATATTATT 1200
CCTGCTGACG CCCTAAAAGA TGACAAAGAG CATCAAGAAA ATCTTGAACA AAAACAACAA 1260
GAAATAGAGA AAGTCTATAG GGCTAAATTA GACGCTTATG GTTTCCCTAA TGGTAGTGTA 1320
GGAAAGGCAA GTGGCGTGAA TTCAAATAGT AATAATGAAG CCCCAAGCTC TGATAATATC 1380
CAGTCGTTTA ATCCGTAT 1398

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(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:76

GTGATGGATG CAGAAAATGG GGAATTGCTC GTTGCAGGAA GTTACCCTGA ATACAATTTG 60
AACGATTTTG TAGGCGGGAT CAGTCAAGAC AAATGGCAAA AACTCCAAGA TGATATTTAT 120
AACCCTTTAT TAAACCGCTT CGCAATGCCT TGTATCCGCC GGGATCTGTG GTTAAAATGG 180
GCGTGGGGT 189

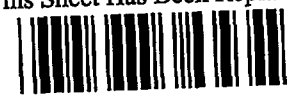
(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1263 base pairs

This Sheet Has Been Replaced



This Sheet Has Been Replaced



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

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77

```
ATGAATTTTT TTGACACCCT TATGGGTATG TTTGTTGAGC CATCTCAAAA AGTAGCCAAA      60
AGTCTTGCTG AACATGTGGG TAGCTTTTTT CATGCACAAC TCATTTTAAA CACAATTATT     120
ACTATTTTAT TTATGATATG GGCGTATAAG CGTGTGAAAG AGGGCGATAT GTTTGAGTTT     180
AAAACCGCTA TGGGTGTGGT TGTATTTATA GCGTTTGTAG GATTTATCAA TTGGGGGATT     240
AAAAATCCTA ATGATTTTAA CACTTATTTT ATCAATACGA TATTCTACCC ATCTGAAAAA     300
CTAGCCATAC TTATCGCTCA AAGCCTAAAT GATGGCTTAG AAATCCCCAC TAACACTAAT     360
TTAAGTCCTA GTGAAATTTT TAGCATAGGA AATTTAGCCT CAAGTGCGTA TGCAATGATA     420
GTTAATCTGT GGGATAATGC TTTTGATGGT ATTAACATGT TTAATTGGCT CACAATGATA     480
CCTAAAATAA TTATGTTTTT TTTAGTGATT TTAGGGGAAT TATTGTTTTT AGGCTTATTG     540
CTTATTATTG TGTTATTAGT TACAGCAGAA ATTTTTATGT GGTCAGCATT AGGTTTAATT     600
GTATTGCCTT TAGGTTTAAT CCCCCAAACC AAAGGCATGT TATTTAGCTA TCTTAAAAAG     660
CTCATTTCCC TTACTCTTTA TAAACCTTGT ATGATGTTAG TAGCTTTTTT TAATTATGGA     720
ATAATCTATA AAGTCAATAC TTTAATCCCC ACTAAACACG AAGTCACACA AGGCTTTTAT     780
GGCAATGCGG ATAAAATGGC AAATGAGGGA AAAATTATTG ATGTCTTTGG CAATGTCTTA     840
GAAGGAGATT GGAACTCTTA TATAGCCCAT AGTTCTATTG TAGGCTTTTT AACCATTATT     900
GTTTTAGGTT CTGTGATTTG TTTCTTTCTA GTCAAACGAG TGCCTGATTT TATCAATAAT     960
ATCTTTGGCA CAAGTGGAGG CGTGGGGGCA GTAACAGAAA TGATGCAAAA AATTGGCATG    1020
ACAATAGGCG GAGCTGTATT TGGGGGTAGT GCAGTTATGG TTGCTAATCA AGTTAAGCAA    1080
GCCTATCAGA GTGCTGGGGG CGGACTAGCA GGACTTCAAG CTGGAGCTAA AGCTTTTGGG    1140
CTTGGAGCAA TCAGTGGAGG GGCAAGTGCT ATGGCAAACC ACAGGAGTGT TAAAGCTGGG    1200
GTGAAACACT TTGTAGCAAG TGTTAAAAGT GGCTTTGGAT TTGATAATGA TAAAAATAAT    1260
AAA                                                                  1263
```

(2) INFORMATION FOR SEQ ID NO:78:

(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:78

```
ATGGATGAAC CAGAAACCAG TTTAGAGCAA AACGCTCTTA TAAGACTATC AAATCTCATA      60
AGCTTGCGCA ACACCCAACA ACTTACAAGT ATCATCGCCA CTCATGATCC TATTGTCTTA     120
GATAGTTGCG AATGGGTATT GCTCCTTAAG AATGGCAACA TTGCTCAATA CAAACCTTTA     180
AATTCTATAT TAAAATCTGT AGCTAAAACT TTTAACTTTA AAGAAAAACC AACCACAAAA     240
GACTTATTAG CGTTACTAAA GGATATT                                         267
```

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 711 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79

```
GTGAAAACCT TAGGATTGTC TTCGCTTGGT GGGACTTTAG AATTTTACGA TTTTATCATC      60
TTTGTATTTT TTACAAGTAT CATTGCCAAA CACTTTTTCC CAAACACGCT TAGCCCTATC     120
TGGTCTGAAA TCAACACTTA TGGGATCTTT GCTGCAGGTT ATCTGGCGCG CCCGCTTGGT     180
GGCATAGTGA TGGCCCACTT TGGGGATAAA TTCGGTCGTA AAAACATGTT CATGCTCTCT     240
ATTTTATTAA TGGTAATCCC AACCTTTGCG CTAGCTTTGA TGCCAACTTT TAATGATTTG     300
GTGGGTTTTG GCGTGGATAG CATGGGGCTT ACCCCTAAAA ACGCTCATTA TCTTGGTTAC     360
ATAGCTCCTG TTTTTTTRGT RCTTGTTAGG ATTTGTCAAG GCGTCGCTGT GGGTGGTGAA     420
TTGCCTGGCG CTTGGGTTTT TGTCCATGAA CATGCCCCAC AAGGACAAAA AAACACTTAT     480
ATCGGTTTTT TAACCGCTTC CGTAGTTTCT GGGATTTTGC TTGGGAGTTT GGTTTATATC     540
GGGATTTACA TGGTTTTTGA CAAGCCTGTT GTTGAAGATT GGGCTTGGCG GGTTGCCTTT     600
GGGCTTGGAG GAATTTTTGG TATCATTTCT GTGTATTTGA GGCGCTTTTT AGAAGAAACT     660
CCCGTTTTTC AGCAAATGAA GCAGGGACGA TGCCTTAGTC AAATTCCCGC T              711
```

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1413 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1413

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80

```
ATGCGCAAAT TTTTGGATGG GGCAAAAAGT GAGGTTTTAA AATACGATGT GATTTCTTTT      60
GATATTTTTG ATACCCTCCT TCTAAGACCT TTCATTAAAC CCACAGATTT ATTTTTGTAT     120
ATTGAGACTA AATACAATAT TAAAGGTTTT CATCAAGCAA GGATCCTGGC AGAAATGCAA     180
TCCAGAAAAT TAAGTAAAAG ACAAGACATT ACTCTAGATG AAATTTATCA TCAAATCCCA     240
AAAGAGTTTC ATTCATATAA GGGAGTAGAA ATCGCTACTG AAAAAGAGGT GCTTGTTCCA     300
AACTTGGAGA TGTTAGAACT CTATCGTTTC GCTAAAGAGA ACAATAAGAG AGTGATTATT     360
GTATCAGATA TGTATTTACC TTTAGAGGTT CTTGAAGATA TTTTAATTTC TAAGGGTTTT     420
GATGGTTATA CAAATTTCTA TCTTAGTAAC CATATAATGC TCACTAAACA TTCAAAGGAT     480
TTGTTTAAGC ATGTTTTAAA ACAAGAAAAT ATTACTAATA CGCAGATATT GCATATCGGT     540
GATAATTCTT GGGCAGATGA CGCTATGCCT AAAAGTTTAG GCATAGCAAC GCTATTTAGA     600
AAAAGCGTGT TGAAACAATT AGAAGAAGTT TTTCCTAAAT ACAAAACATT TAATCCAACC     660
AGTGTTGCGC AAAGTTTTAT TTTAGGATCT TTATGCGTTT TTTATAAAAA TTATATTCAA     720
AAACATGAAA AATTTGATTA TTGGTTTCTT TTAGGAGCGA TGCAGGCAGG AATTGCAGCC     780
GTTGCTTATT GCCAGTTTAT CTATAAGGAG ATTCACAAAA GAAATATTGA TACTTTAGTG     840
TTTGTTGCGC GAGATGGTTA TTTATTGCAA AAAATTTTTA ATATTTTATA TCCAAATTCA     900
TATAAAACTA CTTATGTCTA TGCTCCCAGA ATTTTAAAAA AAGCGGTATT TTTAGAAGTC     960
GTAGAGGGCG AGAGTTTGGA AATTTTGCGT ATTTTAGAAG GCGAAGAAGA AGTTAAAAAG    1020
AAGCAAATCA CCACCAACCA ACAGGCGTAT GTATATCTCT ATAGCAATTT TGAACATTGC    1080
CGCCATTTAG CGTTAAAATG TTTAGATAAT TACAGAAAAT ACTTGTTTTC ATCAAATTTA    1140
GAAGGAAATA TCGCTATTGT AGATACGATT ACTTTAGGCT ATTCTTCGCA AGGGTTAATC    1200
CAAAAAGCTT TAAATAAAGA AGTTTTTGGG TGCTATGTGG ATCTCCTAAG AATTTTAAAT    1260
TATGATTGCG TGAGTTTCTT ACCTTTTTCA CACCCTAAAC CCGTTTATTT TCATAATTGG    1320
GATTTTATGG AGTTTTTGCT AACAAGCCCT GAATACCCTA TTTTAAATGT AGAAAATGGC    1380
GTTCCAATCT TATCAAAAAG ACGTTTCATC TTG                                 1413
```

(2) INFORMATION FOR SEQ ID NO:81:

(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:81

```
GTGTTGAAAT TCTTTGAAGA TTCCAAACAG CTTAGCACGC CTATGGGAAA GAGCGCGGTT      60
GGGATTTTGA TTTTCCAAGA TATTGCAGCC ATTCCCATGC TTTTAATTTT GACGATTCTA     120
GGCAGTAAGG ATTCTCATGT CAATTTGCTC ATTCTTAAAA CCCTTATTTC AGCGGGGATT     180
ATTTTAATTC TTTTATTATT GCCTGGAAAA AAAGGGGCTA ATCTCATCTT AGAGCAAGCT     240
AAAGACACGC GCTTGCCTGA AATCTTTATA GGCACGGATT TTAGTGATTG TTTGCAGCGT     300
GGCGGGGTTG AGCCATTTTT TTGGGTTTTC TATGTCTTTG GGGGCGTTCA TTGTGGGCAT     360
GGCGATTTC                                                            369
```

(2) INFORMATION FOR SEQ ID NO:82:

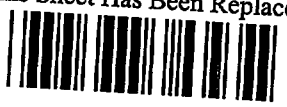
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 777 base pairs

This Sheet Has Been Replaced



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

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:82

```
ATGATTTTAG CCCTTTTGAT TTCTAAAGAA AAAACGCATT TAGAAGCGTT GTATTATTTG      60
AGCTATGGCG TGCTTTTAGG GGGCGTGGCT CAAATCTTAT TACACTTTTA TCCTTTAGTA     120
AAATTAGGCT TATGGGATTT ATTATTTAAA GGGTTGTTGG GTTTTAAGAC TAAAAATACA     180
AACAAAAAAG AATATCGTTT GAATAGGGCT AAAAAGGATC TAAAAGCGTT TTTCAAGCAA     240
TTCTTCCCCA GCGTCTTAGG CAATTCTAGC GCTCAGATCG CTTCTTTTTT AGACACCACA     300
ATCGCTTCTT TTCTGGCGAG CGGGAGCGTG TCTTATTTGT ATTACGCCAA TAGAGTCTTC     360
CAGCTCCCTT TAGCCTTATT CGCTATCGCT ATCTCCACAG CTCTTTTCCC TAGCATTGCG     420
ATCGCGCTTA AAAACAACCA GCAGGATTTA ATCTTACAAC GCTTGCAAAA GGCGTGGTTT     480
TTTTTGGTGG GGGTTTTGCT TCTTTGCAGC ATTGGGGGGA TAATGTTAAG CAAAGAAATC     540
ACCGAACTTT TATTTGAAAG GGGGCAATTT AGCCCTAAAG ACACCCTAAT CACTTCGCAA     600
GTCTTTTCGC TCTATCTTTT AGGCTTGCTC CCTTTTGGGC TAACCAAACT CTTTTCTTTA     660
TGGCTTTATG CGAAATTAGA GCAAAAAAAA GCGGCTAAAA TCTCTTTAAT TTCGCTTTTT     720
TTAGGTTTAG CGGCTTCTTT GAGTTTAATG CCTTTGTTAG GGGTTTTGGG TTTGCGT        777
```

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

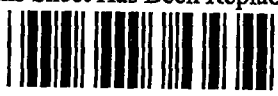
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83

```
GTGCTAAAAT ACCCTACRRT GTTCATGTGT GCGGATGCGG TCATTATCAG TAAGGCGGAC      60
ATGATTGAAG TGTTTAATTT TAGGGTTTCT CAAGTCAAAG AAGACATGCA AAAATTAAAG     120
CCTGAAGCGC CCATTTTTTT AATGAGCTCC AAAGACCCTA AAAGCTTGGA AGATTTTAAA     180
AATTTCCTTT TAGAAAAAAA GCGTGAAAAT TACCAATCCA CGCATTCGTT T               231
```

(2) INFORMATION FOR SEQ ID NO:84:

This Sheet Has Been Replaced



(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:84

```
ATGCTGCTTT GCGCGGGAAG GAATGAGACT TTAAAAAAAG CGGTGCCTAT TGGTGTGGGC      60
TTGATAGAGA GCGCGATCAA TTTAACGAGA ATGTGCCTTA AAAACCCTGA TACAGAAAGC     120
CTTATTTTTA TAGGGAGCGC GGGGAGTTAT AGCCCAGAAA CGGAGATTTT GAGCGTGTTT     180
GAAAGCATTG AAGGCTATCA AATTGAAGAG AGTTTTAGCC ATTTAAACAG CTACACGCCT     240
TTGGATAATT TCATTCACAT AGAAACTAAA GAGCAGGCTC TTTTTGAAAG GGTGCGTGTG     300
AATAGCAGTA ACTACATCCA CACCAGCGAA ATGTTTGCTA AAAAAATGGT TCAAAAGGGC     360
GTTTTATTAG AAAACATGGA GTTTTTTAGC GTCTTAAGCG TGGCTAAAAT TTTTTCTTTA     420
AAGGCTAAAG GGATTTTTTG CGTGAGCAAT CATGTAGGGC TTAACGCGCA TAAGGAATTT     480
AAAGAAAACC ACGCCAAAGT CAAACAGATT CTAGAAAACA TCATTGATAG TTTGATAGTT     540
```

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 639 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85

```
GTGTATGAAG AAAGGATCAC TCTGGCTTCT CAAGGGATCC CTAAAACGAG TAAAGTGGGC      60
TTTGAAATCT TTGACACTAA AGACTTTGGG GCGACTGATT TTGATCAAAA CATCAAACTC     120
ATTCGCGCCA TTGAGGGGGA ATTGTCGCGC ACGATTGAAA GTTTAAACCC CATTCTTAAA     180
GCCAATGTGC ATATTGCAAT CCCTAAAGAC AGCGTGTTTG TGGCTAAAGA AGTCCCTCCT     240
AGCGCTTCAG TGATGCTCAA GCTTAAGCCT GACATGAAGC TTTCACCCAC TCAAATTTTA     300
GGGATTAAAA ATTTAATCGC TGCAGCTGTG CCTAAACTCA CGATAGAAAA CGTGAAAATC     360
GTGAATGAAA ATGGCGAATC AATAGGCGAG GGCGATATAC TAGAAAACTC CAAAGAATTA     420
GCCTTAGAGC AATTGCGCTA CAAACAAAAT TTTGAAAACA TTTTAGAAAA TAAGATCGTC     480
AATATCTTAG CCCCTATTGT GGGGRGTAAA AACAARGTRG TCRCAARRGT CAATRCGGAG     540
TTTRATTTCA RCCAAAAGAA AAGCACCAAA GAGACTTTTG ATCCCAATAA TGTCGGTAAG     600
```

GAGCGAGCAA AATTTAGAAG AAAAAAAAGA AGGCGCTCC 639

(2) INFORMATION FOR SEQ ID NO:86:

(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:86

GTGATAARGA AAGGCTATAT AAGAGGAGAT CTTATGCGTA TAGTTAGAAA TTTATTTCTT 60
GTATCGTTTG TGGCGTATAG TAGTGCGTTC GCAGCGGATT TAGAAACCGG AACCAAAAAC 120
GACAAAAAGA GCGGTAAAAA ATTTTACAAA CTCCATAAAA ACCATGGCTC AGAAACCGAG 180
ACTAAAAACG ATAAAAAGCT TTATGATTTC ACTAAAAATA GCGGATTAGA AGGCGTGGAT 240
TTAGAAAAAA GCCCTAACCT TAAAAGCCAT AAAAAAAGCG ATAAAAAGTT TTATAAACAA 300
CTCGCTAAAA ACAATATCGC TGAAGGGGTG AGCATGCCGA TTGTGAATTT CAATAAAGCC 360
CTATCTTTTG GGCCTTATTT TGAAAGGACT AAAAGCAAAA AAACCCAATA CATGGACGGC 420
GGGTTGATGA TGCACATCCG TTTT 444

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 843 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87

GTGATGATCG ATCCCAAAAT GGTGGAATTT AGCATTTATG CGGACATCCC TCATTTACTC
ACGCCCATTA TCACTGACCC TAAAAAAGCT ATCGGGGCTT TGCAAAGCGT GGCTAAAGAA
ATGGAGCGCC GATACTCTTT AATGAGCGAA TACAAGGTTA AAACCATTGA TTCTTATAAT
GAACAAGCCC AAAGTAACGR CGTTGAAGCG TTCCCCTATT TGATTGTGGT GATTGATGAA
TTAGCGGATT TGATGATGAC AGGGGGCAAA GAAGCGGAGT TTCCTATCGC TAGAATCGCT
CAAATGGGGC GAGCGAGCGG CTTGCACCTC ATTGTGGCGA CCCAACGCCC GAGCGTGGAT

This Sheet Has Been Replaced



```
GTCGTAACCG GCTTGATTAA AACCAACTTG CCTTCAAGGG TGAGTTTTAG GGTAGGCACT      420
AAGATTGATT CTAAAGTGAT TTTAGACACC GATGGGGCGC AAAGCTTACT AGGAAGGGGC      480
GATATGCTCT TTACCCCCCC AGGAACAAAC GGGTTAGTGC GCTTGCATGC CCCCTTTGCC      540
ACTGAAGATG AAATCAAAAA AATCGTGGAT TTTATTAAAG CCCAAAAAGA GGTGGAATAC      600
GATAAAGATT TCTTGCTAGA AGAATCGCGC ATGCCTTTAG ACACCCCTAA CTATCAAGGC      660
GATGACATTC TAGAAAGGGC TAAAGCGGTG ATTTTAGAAA AAAAGATCAC TTCTACGAGC      720
TTTTTACAAC GCCAATTAAA AATCGGCTAC AACCAAGCCG CCACCATTAC TGACGAATTA      780
GAAGCTCAAG GCTTTCTATC CCCAAGAAAC GCCAAAGGCA ACAGAGAGAT TTTGCAAAAT      840
TTT                                                                    843
```

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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:88

```
ATGAATTTTT TTAAAATCCT TTTAATGGAG TTAAGAGCCA TTGTTTCTCA TAAGGGCGTT       60
TTATTGATCC TTATAGGCGC TCCTTTAATC TATGGCTTGT TATACCCTTT GCCTTATTTG      120
AAAGACATCG TAACGCAGCA AAAAATCGCC CTTGTAGATG AAGACAATTC CTTCCTTTCT      180
AGGCAATTAG CCTTCATGGT GCAAAGCTCC AACGAGTTAG AAATCGCTTT CTTTAGCCCC      240
TCTATGCTGG AAGCCAAAAA GCTTTTAAAA GAAGAAAAAA TTTATGGGAT CTTACACATT      300
CCCTCTCATT TTGAAGCCAA TATTTATAAA CAAAGTGCCT GTAACGATAG ATTTTTATGC      360
GAACGCCAAT TACTTTTTGA TTTATGGTGC GTTAGCGAAT GCGGTGGTGG GGAGCATCAA      420
CGCCTTAAAC GA                                                          432
```

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89

GTGGGGGGCT TAGCCATGCT GGGCTTTTTT TATAATATTG AAAAAATTTC GCTCGCCACA 60
GCGACGGCTT TCTCGCAATG CGCGCCTAWT TATACGGTGC TCCTTTCCCC TTTGCTTTTG 120
AAAGAAAAGC TCAAAAGAAG CGCGTTAATT TCCGCATGCA TCGGGCTAGT GGGGGTGGTG 180
TTGATTTCAG ATCCTAGCGT GGAAAATGTA GGACCTAGT 219

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 933 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90

GTGTGCTGGA CGGATTTGAT TCAAGGGCTT TTGATGATGA GCGCTTTAAT CGTGGTGCCG 60
ATTGTTATGA TAATCCATCT TGGAGGGATT GGAGAGGGGA TTAAAATCAT TAGAGAGATC 120
AAGCCTGAAA ACCTWTCTTT CTSGCAAGGC TCTAGCGTAG TCGCTATTAT TTCAAGCCTT 180
GCTTGGGGGT TAGGCTATTT TGGGCAACCC CATATTTTAG TGCGCTTCAT GTCTATCCGC 240
TCCATTAGAG ATGTGCCTAA AGCGACCACT ATTGGGATTT CTTGGATGGT TATTTCTTTA 300
ATTGGGGCAT GCGTTATGGG GCTTTTAGGC GTTGCTTATG TACATAAATY TGACTTGAGT 360
TTAGAAGACC CTGAAAAGAT TTTCATTGTA ATGAGTCAAT TGCTCTTTAA CCCTTGGATC 420
ACAGGCATTT TATTGAGCGC GATTTTAGCG GCGGTGATGA GCACGGCCAG TTCGCAACTG 480
CTTGTAAGCT CTTCTACCAT TGCTGAAGAT TTCTATGCGA CGATTTTCAA TAAAAACGCC 540
CCCCAAAAAT TAGTGATGAC GATTTCTAGG CTTTCGGTTT TAGGGGTGGC TTGCATCGCT 600
TTTTTCATTT CAACGGATAA AAACGCTAGC ATCCTCAGCA TCGTGAGTTA CGCATGGGCT 660
GGCTTTGGCG CGAGTTTTGG CTCTGTGATT TTGTTTTCAC TTTTTTGGTC AAGAATGACG 720
CGCATTGGCG CGATTGCTGG CATGCTCTCT GGGGCTAGCA CGGTGATTTT ATACGATAAA 780
TTTGGCAAAA GCTTTTTGGA TATTTATGAA ATCGTTCCGG GCTTTATTGT AGCGAGCGTA 840
GCTATTGTTG CGTTTAGTTT GTTTTCTAGC GTGCGATCAG GCACTAAAGA GGCCTTTGAA 900
ACCATGCTTA AAGAAATTGA GAGCTTAAAG CAT 933

(2) INFORMATION FOR SEQ ID NO:91:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91

```
GTGGGGCTTT TTATCGTTTT GTTTTTAATT ATAATGAAGC ACCAAACCTC CCCCTATGCT      60
TTCACGCATA ATCAAGCCCT TGTCACTCAA ACCCCCCCCT ATTTCACGCA ACTCACTATC     120
CCTAAACCAA ATGACGCTTT AAGCGCGCAT GCGAGCTCTT TAATCAGCTT GCCTAACGAC     180
AATCTTTTGA GCGCTTATTT TAGCGGCACT AAAGAAGGGG CAAGGGATGT GAAAATCAGC     240
GCGAATCTTT TTGACAGCAA GACTAATCGC TGGAGCGAAG CCTTCATTCT TTTAACCAAA     300
GAAGAGCTTT CTCATCATTC GCATGAATAC ATCAAAAAAA TTAGG                      345
```

(2) INFORMATION FOR SEQ ID NO:92:

(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:92

```
ATGCTTGTAG GGCCAACAGG CGTGGGGAAA ACGACGACTT TGGCTAAATT AGCCGCACGC      60
TATTCTAGAA TGCTGGCTAA AAAATACAAG GTGGGCATTA TCACTTTAGA CAATTATCGC     120
ATTGGGGCTT TGGAGCAATT GAGTTGGTAT GCTAATAAAA TGAAAATGAG TATAGAAGCG     180
GTGATTGACG CTAAGGATTT TGCTAAAGAA ATTGAAGCTT TGGAATACTG CGATTTTATT     240
TTAGTGGATA CGACAGGGCA TTCGCAATAC GATAAGGAAA AAATTGCCGG TTTGAAAGAG     300
TTTATAGATG GGGGTTATAA TATTGATGTA TCCTTAGTGC TTTCGGTTAC CACTAAGTAT     360
GAAGACATGA AAGATATTTA TGATTCTTTT GGGGTGTTAG GGATTGACAC TTTAATCTTT     420
ACGAAATTAG ATGAGAGTAG GGGGTTAGGG AATTTGTTTT CTTTAGTGCA TGAAAGCCAA     480
AAGCCTATCA GTTATCTTTC TGTCGGCCAA GAAGTGCCTA TGGATTTGAA AGTGGCTACT     540
AATGAGTATT TAGTGGATTG CATGCTAGAT GGCTTTAGTA ACCCTAATAA GGAACAAGCA     600
```

(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:

This Sheet Has Been Replaced



(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93

```
GTGGGAGGAG CGAGCTTTAT TTCTGGGGGC AATGGCACGC TTTATGGCTT GAATGTGGGC      60
TATGACCGAT TGGTTAAAAG CGTGATCCTT GGGGGTTATG TGGCTTATGG CTATAGCGGT     120
TTTAACGGGA ACATCATGCA TTCTTTGGCT AATAATGTGG ATGTGGGGAT GTATGCGAGG     180
GCTTTTTTGA AAAGAAACGA ATTCACTTTG AGCGCGAATG AAACTTATGG AGGCAATGCG     240
AGTCATATCA ATTCTTCTAA TTCCTTGCTC TCTGTGTTGA ACCAACGCTA CAACTACAAC     300
ACCTGGACAA CGAGCGTGAA TGGGAATTAC GGCTATGATT TCATGTTCAA ACAAAAAAGC     360
GTGGTGCTAA AACCTCAAGT GGGCTTGAGC TATCATTTCA TAGGCTTGAG CGGGATGAAA     420
GGTAAAATGC AAAATCCAGC TTACCAACAA TTCGTCATGC ATTCAAACCC TTCTAACGAA     480
TCGGTTTTAA CGCTCAACAT GGGGTTAGAG AGCCGTAAAT ATTTTGGTAA AAATTCCTAT     540
TATTTTGTAA CGGCGAGGTT GGGTAGGGAT CTTTTGATCA AAGCTAAAGG CGACAATGTG     600
GTGCGTTTTG TGGGTGAAAA CACTTTATTG TACCGCAAGG GGGAAATTTT TAACACTTTT     660
GCGAGCGTGA TCACAGGAGG CGAAATGCAT TTGTGGCGTT TGATGTATGT GAATGCGGGG     720
GTGGGGCTTA AAATGGGCTT GCAATACCAA GATCTTAATA TCACTGGGAA TGTGGGCATG     780
CGAGTGGCGT TT                                                        792
```

(2) INFORMATION FOR SEQ ID NO:94:

(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:94

```
ATGGACGGCT ATGGGTTTAA AATGCAAGAC TTGGGCCAAA AAACTCAAGT TATCCAACAC      60
ATCTTTGCCG GGGATGATGT GAGCGCTTTA GAAGTCAAAG AAAATGAATG CGTTAAAATC     120
RTGACTGGAG CGATGGTGCC AAAGGGAATA GAAACGATTG TTCCCATAGA ATGCATGCTA     180
GAGAGTCATA AAGATTTCGC CCTAGCTCCT AAAGATTTTA AAATTCACGC TAATATCCGT     240
CAAAAGGGCG AGAACGCTTC TTTAAACAGC GTTTTAGTCC CTAAAAATAC CCGTTTGAAT     300
TATGGCCATA TCGCGCTCAT TGCCTCTCAA GGGTTCAAAG AAATCAAAGC GTTTAGAAAA     360
TTAAAAATCG CTCTCTTTAG TAGCGGCGAT GAATTAGTGC CTTTAGGGCA AAACGCCCTA     420
GAGTGCCAGG TTTATGATGT TAATTCAGTG GGTGTTTTTA ACATGCTTAA AAACTACAAC     480
ACGCATTTTC TAGGGGTTTT AAAAGATGAT AAAAATTTAC AGCTTAAAAT ACTTGAATTG     540
CAAGGCTATG ATGTCATCCT TTCAAGTGCG GGGGTGAGCG TAGGGGATAA AGACTTTTTT     600
AAAGACGCTT TGAAAGAAAG AAACGCCCTT TTTTATTACG AAAAAGTCAA TCTCAAACCT     660
GGAAAGCCGG TAACTTTAGC CCAACTCAAT CAAAGCATTA TTATAGGCTT ACCGGGTAAT     720
CCTTTAAGTT GCTTACTGGT TTTACGAGTT TTGATTCTAC CCTTATTGGA GCGCTTATCC     780
TTAAATAAAG ATTTTAAATT AAAACCCTTT AAGGCTCAAA TCAATGCCCC TTTAAAGCTT     840
AATAACAAAC GGACGCATTT AATCTTAGGC AACTATTCAA ACCACCAATT CATTCCTTAC     900
AACAACCGCT ATGAATCAGG AGCGATTCAA GCCCTTGCGC AAGTGGATTC TATCRCTTTA     960
ATTGATGAAG GAGTGGGATT GGTTCAGGGC GAAATTGAAA TTTTAAGGTT TGAAAAT      1017
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 438 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:95

```
ATGCCATACG CCTTAAGAAA AAGATTTTTC AAACGCCTTT TATTGTTTTT TTTAATTGTT      60
TGTATGATAA ATTTGCATGC CAAAAGCTAT CTGTTTTCTC CTTTGCCCCC AGCGCACCAG     120
CAAATCATTA AGACAGAGCC TTGCTCTTTG GAGTGCTTGA AAGACTTGAT GCTGCAAAAT     180
CAAATCTTTT CTTTTGTATC CCAATACGAT GATAACAACC AAGATGAGAG CCTTAAAACT     240
TATTACAAGG ACATCTTAAA CAAACTCAAC CCCGTATTCA TCGCTTCTCA AACTCCAGCT     300
AAAGAAAGCT ATGAGCCTAA GATTGAATTA GCGATTTTAC TGCCTAAAAA GGTGGTGGGC     360
CGTTATGCGA TTTTAGTGAT GAACACCCTT TTAGCGTATT TTGAACACCA GAAACAACGA     420
TTTCAATATC CAAGTCTT                                                  438
```

(2) INFORMATION FOR SEQ ID NO:96:

(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

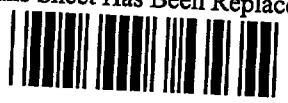
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

```
ATGCCTATTA ACCCTCTCTA TCTTTTCCCC AATCTTTTTA CCGCTAGCAG TATTTTTTTA      60
GGCATGATGA GTATTTTTTA CGCTTCCAGT TACCAATTTG TCATGGCGTG TTGGTTAGTG     120
GTGGCGAGTC TTATTTTAGA TGGGCTTGAT GGGCGTGTCG CAAGGCTTAC CAAACACCAC     180
```

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

This Sheet Has Been Replaced



(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:97

```
ATGCTTTCAG CCTTGCTTTC TAAAATGGGG ACTTACGCCT TATTACGCTT CTTGCTCCCG      60
CTTTTTCCTG AACTTTCAGA AATTTATTTA ACCCCCATAG CCATTGTGGC GCTGTGCATG     120
ATCATTTATG GAGGTTTTCT AGCCTACGCT CAAAAAGATT TAAAAACCCT CATCGCTTAT     180
AGCTCTTTCT CGCACATGGG AGTCGTGGTG CTTGGGGTTT TTTCTTTCAA TGTTGAAGGG     240
GTTTCAGGGG CGGTGTTTAT GATGTTTGCG CATGGCGTTA TCGTCATGGG ATTATTTTTA     300
CTCGCTGGTA TCTTGGAAGA ACGCGCCAGC AGTTTAGAAA TCGCTCGCTT TGGATCGATC     360
GCTAAAAGCG CTCCTGTTTT TGCAGCCTTT TTTATGATCG TTTTAATGGC GAATGTGGGC     420
ATGCCTTTAA GCATTGGTTT TGTGGGAGAG TTTTTGARCT TGTTAGGGTT TTTTGCCACT     480
TACCCTCTTT TGGCTATCAT TGCCGGGACA AGCCTCATTC TATCAGCGGT TTACATRCTC     540
ACTTCATATA AAGATGTGTT CTTTGGCAAC TTAAAAACCG GGAACAACCA AATCAGCGTG     600
TTTGAAGATT TAAACGCTCG TGAGGTAGGG GTTTTAAGCG TGATTTTAGC CTTTGATCTT     660
AATTTTAGGG ATTTATYCYA AAGCGCTTTT AAAACCGAT                            699
```

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 96 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98

```
GTGGAATTGA TTAGCAATAA CCCTAACGCC AGCCAACAAT CTATCGTTAT TCCTTTGGAG      60
ACTTTTGCCT TGGCGCGAGC GTTAAAGGGA ATCTTT                               96
```

(2) INFORMATION FOR SEQ ID NO:99:

(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:99

This Sheet Has Been Replaced



```
ATGAAAATTT TTGGGACTGA TGGCGTGAGG GGTAAAGCAG GGGTGAAACT CACCCCCATG      60
TTTGTGATGC GTTTAGGCAT TGCTGCCGGA TTGTATTTTA AAAAACATTC TCAAACGAAT     120
AAAATTCTAA TCGGTAAAGA CACCAGAAAG AGCGGCTATA TGGTAGAAAA CGCTTTAGTG     180
AGCGCTCTCA CTTCCATAGG CTATAATGTG ATCCAAATAG GGCCTATGCC TACCCCTGCG     240
ATCGCTTTTT TAACCGAAGA CATGCGCTGT GATGCGGGCA TTATGATAAG CGCGAGCCAC     300
AACCCTTTTG AAGACAATGG CATCAAGTTT TTCAATTCCT ATGGTTATAA ACTCAAAGAA     360
GAAGAAGAAA GAGCGATTGA AGAAATCTTT CATGATGAAG AATTACTGCA TTCTAGCTAT     420
AAAGTGGGCG AGAGCGTCGG TAGCGCTAAA AGGATAGACG ATGTGATAGG GCCGCTATAT     480
CGCGCATTTG AAGCACTCTY TYCCCAAACA TTT                                  513
```

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100

```
GTGCGAGCCG TGTTTGTCTT TGGTTTGAAA GCGGCGTTTT GTATAGGGAT TTTTTTCTAT
GGCGCTTATT ATTTCCTAGA TGAGTTTTTA ATCAAGCTC
```

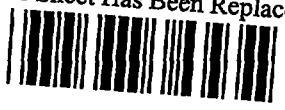
(2) INFORMATION FOR SEQ ID NO:101:

(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

This Sheet Has Been Replaced



(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:101

GTGAGGAGCG GTAAAAGATT AGGCTATACC AATCAAGTGA TCACCGATAT TGTCAATATC 60
GGTATTGGGG GGTCAGATTT AGGCGCTTTA ATGGTTTGCA CCGCCCTAAA ACGCTACGGC 120
CACCCAAGAT TARRAATGCA TTTTGTGTCT AATGTGGAAT GGCACGCAGA TTTTAGACGT 180
TTTGGAAAAA ATCAACCCGG CCAGCGCGCT 210

(2) INFORMATION FOR SEQ ID NO:102:

(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:102

ATGAATCTTG TCTTTTTTGTG GGCCGCTCTA GGAGGGGCTA TAGGGAGCTC GTTAAGGTAT 60
TTTGTGGGCA AAATGATGCC CAGTAAATTT TTAATGTTTG AAAGTTTCCC TTTAGGGACT 120
TTTAGCGTGA ATCTCATAGG GTGTTTTATC ATCGGCTTTA TGGGGCATTT GGCCGCTAAA 180
AAAGTTTTTG GTGATGATTT TGGGATTTTC TTTGTAACCG GAGTTTTAGG GGGTTTTACG 240
ACCTTTTCTT CTTATGGGTT AGACACTTTA AAACTCTTGC AAAAATCCCA ATACCTTGAA 300
GCCATTTCTT ATGTCTTAGG CACTAACCTT TTAGGGCTTA TTGGGGTAGC TATCGGTTGG 360
TTTTTGGCTA AGAATTTTGT AGGCGTTAAT 390

(2) INFORMATION FOR SEQ ID NO:103:

(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:103

ATGTTGGAAA AACTGATTGA AAGAGTGTTG TTTGCCACTC GTTGGTTGCT AGCCCCTTTA 60
TGCATTGCCA TGTCGTTAGT GTTGGTGGTT TTAGGCTATG TGTTCATGAA AGAGTTGTGG 120
CACATGCTCA GCCATTTARA CACCATTAGT GAAACGGATT TGGTTTTATC AGCCTTAGGT 180
TTAGTGGATT TGTTGGTTCA TGGCCGGGCT TGTTTTGATG GTGCTGCTCG CCAGTTA 237

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104

ATGCACTATC AATTAACAAG TTTCAATATA ATACAAGATC TTTTTATAAC TTGTCATGTG 60
TTAAGGATCA AAATGCGCGT GTTTGTTTGC TTTTTAGGGG TTTTTGTATC TAACGGCTTG 120
GCTCGTTTTG GCTATGTGGT TTTAATCCCC CTACTCATTT TATCAGGGAG TTTAACCCCA 180
CACCAAAGCT TCCAACTGGG TATTGCGGTG CTAATGGGCT ATGTTTTTGG GAGCTTTTTA 240
ATCCAATTTT TAAGCCCGTT AATGTCATTA SAAAGCATCG CTAAAATCAG TTTTAAATTA 300
ACACTT 306

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105

GTGGATATGA AAGACGCTGT AGGGACTTAT AAACTAYTCA GGGCT 45

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3081 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...3081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106

GTGTGTTTAG ACCATCAGGT TGGAGCAGGC AAGACTTTGT GCGCTATAGC CAGCTGCATG 60
GAACAAAAAC GCATGGGATT AGTGAATAAA ACGCTCATTG CCGTGCCTAA CCATTTAACC 120
AAGCAATGGG GCGATGAATT TTATAAGGCT TACCCTAACG CTAATGTGTT AGTTGTTGAT 180
AGCAAGGACA CCACTGAAAA AGAAAAGAGAA CTTTTATTCA ATCAAATCGC TAACAACAAT 240
TATGACGCTG TGGTTATCGC GCACACCCAT TTGGAATTAT TGTCTAACCC TAGAGGAATC 300
ATAGAAGAAT TGAAAGAAGA AGAGCTAGTG AATGCTGAAA AAAACTTTGA AAGGCAAGAA 360
TTAGCTTATA AAAATAACCC TAGAGAAACT AAAAAACCCA ATGAAAGAGC CTTTAAAAAC 420
AAGTTGGATA AAATCCGTGC TAAATACGAT GCGATTTTAG AAAAACAAGG CTCTCATATT 480
GATATTAGTC AAATGGGGAT TGACAATTTG ATTGTGGATG AAGCCCACTT ATTCAAAAAT 540
CTAGCCTTTG AAACTTCTAT GGAAAAAATT GCAGGACTTG GTAACCAACA AGGCTCTAAT 600
CGCGCTAGAG ATTTGTTTAT TAAAACGCGC TACTTGCATC AAAACGATAA GAAAATCATG 660
TTTTTAACCG GCACGCCTAT AGCTAATTCC TTGAGTGAAA TGTATCACTT GCAACGCTAT 720
TTAACCCCTG ATGTGTTAAA AGAAAGAGGG TTAGAATTCT TTGATGATTG GGCTAAGACT 780
TATGGGGAAG TGGTGAATGA TTTTGAATTA GACACTTCCG CTCAAAGTTA TAAAATGGTT 840
AATCGCTTTT CTAAATTTAG CGATGTGCAA GGCTTAAGCA CCATGTATAG AGCTTTTGCG 900
GATATTGTCT CTAATGATGA TATTTTAAAG CATAACCCCC ACTTTGTGCC TAAAGTGTAT 960
GGGGATAAAC CTATCAATGT GGTGGTGAAA AGAAGCGAAG AAGTGGCTCA ATTCATTGGA 1020
GTGGCTTTAG AAAATGGAAA ATATAATGAA GGCTCTATCA TTGATAGGAT GCAAAAATGC 1080
GAGGGCAAGA AAAGCCAAAA AGGGCAAGAC AATATCCTTT CTTGCACCAC AGACGCTAGA 1140
AAAGTGGCTT TGGATTACCG CTTGATTGAC CCTAACGCTA AAGTAGAAAA AGAATTTTCT 1200
AAAAGCTATG CTATGGCAAA AAATATCTAT GAGAATTATT TAGAAACTCA TGCCACTAAA 1260
GGCACACAAC TTGGTTTCAT AGGGCTATCC ACACCCAAAA CCCATAGCCA AAAAGTCAGT 1320
TTAGAAGCGC TAGATAACGC TCACGAAACT GAAAATAAAA ATCCCCTAGA TAAAGCTCAA 1380
GAACTTTTAG AAAGCTTGTC TAGTTATGAT GAAAAGGGCA ATCTTATCGC TCCTAGCAAG 1440
AAAGAATTAG AGAACGAGCT CAAAGAGAAA GAAGCTAAAA GCGTCAATTT AGATGAAGAG 1500
ATAGCTAAAG GCTGTTCGTT TGATGTTTAT AGCGATGTTT TAAGGCATTT AGTCCAAATG 1560
GGTATCCCAC AAAATGAAAT CGCTTTCATC CATGACGCTA AAACCGAAGA GCAAAAGCAG 1620
GATTTGTTTA AAAAGCTCAA TCGTGGCGGA GTCAGGGTAT TATTGGGCAG TCCTGCTAAA 1680
ATGGGCGTAG GCACTAATGT GCAAGAAAGA TTAGTCGCTA TGCATGAATT AGATTGCCCA 1740
TGGAGACCTG ATGAATTGTT GCAAATGGAA GGGCGTGGGA TAAGGCAAGG CAATATTTTA 1800
CACCAAAATG ATCCTGAAAA CTTTAGAATG AAAATCTATC GTTACGCCAC TGAAAAGACT 1860
TACGATAGCC GTATGTGGCA AATCATAGAA ACTAAATCTA AAGGCATAGA GCAATTTAGA 1920
AACGCGCACA AATTAGGCTT GAATGAATTA GAAGACTTTA ATATGGGTAG CTCTAATGCG 1980

```
AGCGAGATGA AAGCAGAAGC GACAGGCAAT CCCTTGATTA TTGAAGAAGT CAAATTGAGA    2040
GCGGAGATTA AAAGCGAAGA ATCAAAATAC AAAGCCTTCA ATAAAGAGCA TTACTTCAAT    2100
GAAGAAAGCT TAAAAAACAA CGCTTCTAAA TTGGATTATC TAAAACAGGA ATTGAAAGAT    2160
TTAGAAACGC TTCAAAGATC CGTAATAATC CCCACTCATA CAGAGATCAA GCTCTATGAT    2220
TTGAAAAATG AAGAAAGTAA GGATTATGAG CTTATCAAAG TTAAAGAGGT AGAGCCTTTA    2280
AAAGAAAACG CCTCTATGAG TGAAGAATTA ACGCACAAGA AACTCAAAGA ACAAAACAAG    2340
CAAATAGCCG AACAAAATAA AGAAAAGCTA GACGCTATTA AAAAGCAATT TGCAAGCAAT    2400
TTGAACACCT TGTTTGTGAA TGAAGAAGAA GATTATAAGC TTTTAGAATA CAAGGGCTTT    2460
GTGGTGAATG CTTATAAAAC TAAGTATCAA GTGGAGTTTA GTTTAAGCCC TAAAGACAAT    2520
CCCAATATTG CCTATAGCCC TAGCAATATG GTTTATAAAA ACGATACTAT CAACATGTTT    2580
AGCTCTTATA ATTTCTGCGC TGAGATCAAG TTTGATGGGT TTTTAAAAAG GTTGGATAAC    2640
GCTATCACTA AACTCCCTGA AAAAATCAAG GAATTAGAAA ACTCCATTGA AATCACGAAA    2700
AAAAATATCG CTAAATACAC AAGATTAGTG GAGCAAAAAC CTTCTTACCC ACGACTAGAA    2760
TACCTGCAAG CTTTAAAATG GGATCATAAA ACTCTAATAG ATGATTTAGC TAAAATGAGC    2820
AAAGACAGAA ATTATAAGCC TGCGTTCAAC CCTAAATCTA AAGAAGTCTT AAAGAATTTG    2880
AACGCTGAAA AAAGAGCGAG TTTAGAGAAT GAGAGGGAAG AGCAAGGGGT TAAGGGGAAC    2940
ACAAAGAGTC ATGATGAAAT AGAGCCAGCT ACAGAACAAG TGATTGAAAA AGAAATAGAA    3000
AAAGGAGATG AAATCGCTAA TAATGTTGAT TACTACGAGA ACGAACAAGA AGTGGAAATT    3060
ACTAAATCAA TGGGTAGAAG A                                              3081
```

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107

```
ATGGCCGAAG AAGAAAAGAC CGAACTCCCT AGCGCGAAAA AAATCCAAAA AGCCAGAGAA      60
GAAGGCAATG TGCCTAAAAG CATGGAAGTG GTGGGGGTTT TTAGGGTTAT TGGCTGGGCT     120
AATGAGTATT TTTGTTTTTT TTATATGGTG GGTGGGATGG CTTTAGCGAG ATGTATCGCC     180
ATGTGT                                                                186
```

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 711 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

This Sheet Has Been Replaced



(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108

```
ATGAAAACAC TCGTGAAAAA TACCATATAT TCTTTTTTGC TATTGTCTGT TTTGATGGCA      60
GAAGATATAA CAAGCGGCTT AAAGCAACTG GATAACACCT ACCAAGAGAC CAACCAACAA     120
GTGCTCAAAA ACCTAGATGA GATTTTTTCA ACCACTAGCC CTAGCGCTAA TAATAAAATA     180
GGTCAAGAAG ATGCTCTAAA CATCAAAAAA GCGGCCATTG CTTTGAGAGG AGATTTAGCG     240
TTATTGAAAG CCAATTTTGA AGCGAATGAG TTATTTTTCA TCTCAGAAGA TGTGATTTTT     300
AAGACTTATA TGTCTAGCCC TGAACTTTTA TTAACCTATA TGAAAATCAA TCCCTTAGAC     360
CAAAAGACTG CTGAGCAACA ATGCGGAATA TCCGATAAAG TTTTAGTTCT TTATTGTGAG     420
GGGAAGCTGA AAATCGAGCA AGAAAAACAA AATATAAGAG AGCGTTTAGA AACTTCTCTA     480
AAGGCATATC AGAGCAACAT TGGAGGTACA GCTTCCTTAA TCACTGCTTC ACAGACGCTT     540
GTAGAAAGCC TAAAAAATAA AAATTTCATC AAAGGAATCA AAAAGCTTAT GTTAGCTCAC     600
AACAAGGTCT TTTTAAATTA TTTAGAGGAG TTGGACGCAT TAGAAAGATC CCTAGAACAA     660
AGTAAGCGAC AATACCTACA AGAAAGGCAA TCAAGTAAGA TCATTGTTAA A              711
```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109

```
GTGAGCGAAA AAGACAGGGC GTTTCTTTTA GCGAGCTTGT CTTGCGTGGA TTATGTTGTG      60
GTGTTTGGAG AAGACACGCC CATAAAATTG ATTCAAGCCC TAAAGCCTGA TATTTTAGTC     120
AAGGGAGCGG ACTACCTCAA TAAAGAAGTC ATAGGGAGCG AGTTGGCTAA AGAAACCCGT     180
TTGATAGAAT TTGAAGAAGG TTATTCCACA AGCGCTATCA TAGAAAAAAT TAAAAGGACA     240
CATAATGAT                                                             249
```

(2) INFORMATION FOR SEQ ID NO:110:

(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

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110

GTGTATGACA AATCCTTGTG TAAGACCATG GCGCTAGCGT TGAAGGCTTT AGGCGTTAAA 60
AGGGCGATGG TGGTTAATGG AGGGGGGACA GGTGAAATCG TGTTGCATGA CATTACGCAT 120
GCGTGCGAAT TGAAAAATAA CGAAATTTTA GAGTATGATT TGAGCGCTAA AGATTTTGRT 180
TTRCCCCCCT CA 192

(2) INFORMATION FOR SEQ ID NO:111:

(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:111

ATGCTAGTAG AAATAGAGAA TTTGACTAAA ACTTATGGGA GTTTAAAAGC GCTAGACAAT 60
ATCAGTTTGA AACTACCCAA ACAGCAATTT ATAGGGCTTT TAGGGCCTAA TGGGGCGGGT 120
AAAACCACTC TGTTAAAAAT TTTAGCCGGA TTGAATTTGA ACTATCAAGG GGAAGTGAAA 180
ATTTTAAACC AAAAGATTGG TATAGAGACT AAAAAAAGCG TGGCGTTTTT AAGCGATGGC 240
GATTTTTTAG ATCCTAAATT AACGCCTTTA AAAGCGATCG CTTTTTATAA GGATTTTTTT 300
AGCGATTTTG ATGAATCAAA AGCCCTAAAT TTGTTAAAAC GCTTCAGCGT GCCTTTAAAA 360
AGAGAGTTCA AAGCCCTTTC AAAAGGCATG AGGGAAAAAT TGCAGCTGAT TTTAACCCTA 420
TCACGAAACG CTTCTTTGTA TCTTTTTGAT GAGCCGGTGG CTGGGATTGA CCCTATTGCA 480
AGAGAAGAGA TTTTTGAGTT AATCGCTAAG GAGTTTAGCC AAAACGCAAG CTTGCTAGTC 540
TCTACGCATT TGGTGGTGGA TGTGGAAAAG TATTTAGACA GCGCGATTTT TTTAAAAGAA 600
GCTAAAGTGG TGGCTTTTGG GGATGTGGGG GAATTAAAAA AAGGGTATAG CAGTTTGGAG 660
GCAGCGTATA AAGAAAGGTT GAAA 684

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

This Sheet Has Been Replaced



(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112

```
ATGAACAAGC TTTTTTTAGC TTTTATTGTT GGGGGAATGC TTTTAAGTGC TGATGCTTTA      60
AACGATAAGA TTGAGAATTT AATGGGGGAG CGATCCTACC ACATGAACAA GCTTTTTTTA     120
GAGCGTTTGT TTAAAAATCG TAAGGATTTC TATGAAATGG GGCGTTTGGA TTCCTTAAAA     180
CTACTCAACA CTCTCAAAGA AAACGGGCTT TTATCGTTTA ATTTTGACAA ACCAAGCGTG     240
TTAAAAATCA CTTTCAAGGC TTCAAGTAAT CCCCTAGCGT TTGCCAAAAG CATCAACAAT     300
TCTTTGAATA TGATGGGGTA TTCGTATGTT TTGCCTATTA GAATGCAAAG CTCTTCAGGC     360
GAGAATGTTT TTTCATACGA GCTTAAAACG GAATACGTTT TAGACCCTAA CATTTTGATA     420
GAGACGATGA AAAGGCATGG TTTTGATTTT ATGGATATTA GACGGGTGTC TTTAAAGGAG     480
TGGGAATACG ACTTTGCCTT ACAAAAGATC AAGCTCCCTA ACGCGAGAGC CTTAGTTTTG     540
AGTAGCGATC CTGTGGAGTT TAAGGAAGCG AGCGGGAAAT ATTGGCTGAG CGTGAATCAA     600
AACGCGTATT TAAAAATAAG CTCCAATAAC CCTTTGTGGC AACCCAAAAT CATTTTTTAT     660
GATGAAAACT TAAAGATCAT TCAAATCATT GCTAAAGAAA ACAGACAACA AGAAATCGCT     720
CTTAACTTGC TTGATGGCGT GCGTTTTATC CATATCACTG ACGCAAAAAA CCCTATCATT     780
TTAAAAAATG GGATTAGCGT GGTTTTTGAT GCGATGCCT                            819
```

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113

```
GTGTCTCGCC CGTTCAAAAC GATCAAAAAA CCCCCACAAC CCCCT                     45
```

(2) INFORMATION FOR SEQ ID NO:114:

(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

This Sheet Has Been Replaced



(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:114

```
ATGATCGCTG TATTACCGCC CTTGTTTTCT ATGGGGAGCT TTGATGAGTG GATTTATAGG      60
GGGCTTGTGG CTTTAATGGT GAGCTGTCCT TGCGCGTTAG TGATTTCTGT GCCTTTAGGG     120
TATTTTGGAG GCGTGGGAGC GGCGAGCCGA AAGGGGATTT TAATGAAAGG AGTGCATGTT     180
TTAGAGGGTG CTTACCCAAA C                                               201
```

(2) INFORMATION FOR SEQ ID NO:115:

(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:115

```
GTGCAACACT TCAATTTCCT CTATAAAGAT TCTTTATTTT CTATCGCTTT ATTCACTTTC      60
ATTATCGCTC TTGTGATTTT ATTAGAACAG GCTAGAGCGT ATTTCACCCG AAAGAGAAAC     120
AAAAAATTTT TGCAAAAATT CGCCCAAAAT CAAAACGCCT ATGCGAGCAG CGAGAATTTA     180
GACGAGCTTT TAAAGCATGC TAAAATTTCC AGTTTGATGT TTTTAGCTAG GGCGTATTCT     240
AAAGCGGATG TGGAAATGAG CATTGAAATC TTAAAAGGGC TTTTGAATCG CCCCTTAAAA     300
GATGAAGAAA AAATCGCTGT TTTAGATTTA TTGGCTAAAA ATTATTTTAG CGTGGGGTAT     360
TTGCAGAAAA CAAAAGACAC CGTGAAAGAA ATTTTGCGCT TTTCCCCAAG GAATGTGGAA     420
GCGTTGTTGA AGCTTTTGCA TGCGTATGAA TTAGAAAAAG ATTATTCAAA GGCTTTAGAA     480
ACTTTGGAAT GTTTGGAAGA ATTAGAGGTG CCTAAAATTG AAACGATTAA AAATTACCTC     540
TATTTAATGC ATTTAATAGA GAATAAGGAA GATGCGGCTA AAATCTTGCA TGTTTCAAAA     600
GCGTCGTTAG ATTTGAAAAA AATCGCTCTG AATCACTTAA AATCGCATGA TGAAAATCTT     660
TTTTGGCAAG AAATTGATAC AACCGAACGG CTAGAAAATG TGATCGATCT TTTATGGGAT     720
ATGAATATCC CTGCTTTTAT TTTAGAAAAA CATGCCCTTT TGCAGGACAT CGCGCGATCT     780
CAAGGGTTGC TTTTGGATCA CAAACCTTGC CAAATTTTTG AATTAGAGGT TTTACGCGCT     840
CTATTGCATA GCCCTATAAA AGCGAGTCTG ACTTTTGAAT ACCGCTGCAA GCATTGCAAA     900
CAAATCTTTC CTTTTGAAAG CCATAGGTGT CCTGTGTGTT ACCAGTTAGC GTTTATGGAT     960
ATGGTGGCT                                                             969
```

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

This Sheet Has Been Replaced



(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116

ATGGAACACC TTACAAGGGG AATTAAGCAC 30

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117

GTGGTTATCT TAGGCTCRCA TGGCAAGGAA GAGTATTACG CTAGCAAGAT TGCAGCCCCC 60
ATTTTTAAAG AAATCACCGA AATTTTAGTG CGTTACAATT ACCTATCGCC CTCTATTGCG 120
ATTCAAAACG CTTTGGAAAA AAACCGCTTA AAA 153

(2) INFORMATION FOR SEQ ID NO:118:

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

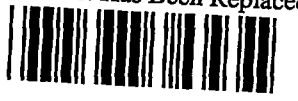
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118

ATGAAAAAGG TTATTGTGGC TTTAGGCGTT TTGGCGTTCG CAAATGTTTT AATGGCAACC 60
GATGTTAAGG CTCTTGTAAA AGGTTGTGCC GCTTGCCATG GGGTTAAGTT TGAAAAGAAA 120
GCTTTAGGTA AAAGCAAAAT CGTTAACATG ATGAGCGAAA AAGAGATTGA AGAGGATCTT 180
ATGGCTTTTA AAAGCGGTGC CAACAAGAAT CCTGTCATGA CCCGCAAGCT AAAAAAT 237

(2) INFORMATION FOR SEQ ID NO:119:

(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:119

ATGGGGATTG CAACCAGTCT CATCAGTGAG GTTTCTAAGT TTTATTACGC TTTAAAATAC 60
CATGCGAAAT TTATGAGCTT GGGGGAGCTT GGGTGCTATG CGAGCCATTA TTCGTTGTGG 120
CAAAAATGCA TAGAGCTCAA TGAAGCGATC TGTATTTTAG AAGACGATAT AACCTTGAAA 180
GAGGATTTTA AAGAGGGCTT GGATTTTTTA GAAAAACACA TCCAAGAGTT AGGCTATGCG 240
CGTTTGATGC ATTTATTGTA TGATGCCAGC GTGAAAAGTG AGCCT 285

(2) INFORMATION FOR SEQ ID NO:120:

(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:120

This Sheet Has Been Replaced



```
ATGCACCTTA AAAGTGGGGC TGTTTTTATC TCTGATGCGC ATTTTTTGCC CAAAAGCCCT      60
CATTTAATCC ATACGCTTAA AGAACTTTTA AGCGCCAAAC CCCCGCAAGT CTTTTTCATG     120
GGCGATATTT TCCATGTTCT TGTGGGCTAT TTACCCCTAG ATAAAGAGCA GCAAAAAATC     180
ATTGATTTAA TCCATGCGTT GAGCGAAATT TCACAAGTCT TTTACTTTGA AGGCAACCAT     240
GATTTTTCCA TGCGTTTTGT ATTCAATTCC AAAGTAATGG TTTTTGAGCG CCAAAACCAA     300
CCCGCATTAT TCCAGTATGA TAACAAACGC TTTTTGCTAG CCCATGGGGA TTTATTCATC     360
ACTAAAGCGT ATGAATTTTA CATCACGCAG CTCACTTCCA CTTGGGCTAG ATTTTTTTTA     420
ACTTTTTTAA ATTTATTAAG TTTTAAAACC TTATACCCTT TT                        462
```

(2) INFORMATION FOR SEQ ID NO:121:

(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:121

```
GTGCAACCGA TGAAATCTAA AAAACTTTAT TTAGCTTTAA TCATAGGGGT TTTATTAGCG      60
TTTTTAACCC TATCTTCATG GCTAGGTAAT AGCGGTTTAG TGGGGCGTTT TGGGGTGTGG     120
TTTGCCGCAA TCAATAAAAA ATATTTTGGG TATCTTTCAT TGATTAATTT ACCCTATTTG     180
GCGTGGGTTT TATTCCTTTT ATACAGGGCT AAAAACCCTT TTACAGAAAT CGTTTTAGAA     240
AAAACTTTAG GGCATCTATT AGGCATTTTA TCTTTACTCT TTTTGCAATC TAGCCTGTTG     300
AATCAAGGGG AAATCGGCAA CAGCGCGCGT TTGTTTTTAC ACCCTTTTAT AGGGGACTTT     360
GGGCTTTATG TGCTGATAAT GCTTATGGTA GTTATCTCTT ATTTAATTTT ATTCAAACTG     420
CCCCCTAAAA GCGTTTTTTA CCCTTATATG AACAAAACAC AAAGCCTTTT AAAAGAGATT     480
TACAAACAAT GCTTGCAGGC CTTTAGCCCT AATTTTAGCC TGAAAAAAGA GGGTTTTGAA     540
AACACCCCAT CAGATTCTCA AAAAAAAGAA ACCAACAACG ACAAAGAAAA AGAAAACCTC     600
AAAGAAAACC CTATTGATGA AAACCACAAC ACCCCTAACG AAGAATCGTT TTTAGCGATC     660
CCTACCCCCT ATAACACGAC CTTAAATAAT TCAGAGCCGC AAGAAGGCTT AGTCCAAATT     720
TCCCCACACC CCCCTACCCA TTACACCATT TACCCTAAAA GAAACCGATT TGATGATTTG     780
ACTAACCCCA CTTTAAAAGA ACCTAAGCAA GAAACCAAAG AAAGAGAACC CACGCTAAAA     840
AAAGAAACGC CCACCACACT CAAACCTATC ATGCCCATAT CCGCATCCAC ACAGAAAATC     900
ATGACAAAAC RGAAAACCAC AAAACCCCTA ACCACCCCA                            939
```

(2) INFORMATION FOR SEQ ID NO:122:

(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

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122

GTGATGTTAA GTAGAGACAT TGTCCAATAT TCCAAGATCC GCACCGAGTT ATACGCCTAC 60
CTCACTTATT TGTTTTCGCA CAATATCCGC AACCACCTTC CTGAAATCAC TTTGGATTAT 120
TTAAACAGGC AAATCAGTAA GATGCAAGCT GAAATCAAAA TGGCAAAAAG TTTTTTTGTT 180
TTAGACGCTA AGGGCATGCT CATGCTTAAG CCAAGCCAAT TTAAAGAGCA GGGGCATAAG 240
GAAGGGCTAT TAGAGCATGA TTTAACAGAA GGGATTGAAT TAGAATCGCA TGTCAGTTTT 300
AGCGATAAGT ATTATTTTTA TCAAGCCGTG AATGAAAAGC GTTGCATTTT AACCGACCCC 360
TATCCTTCTA AAAAAGGGAA CCATTTGGTA GTGAGCGCGT CTTACCCGGT GTATGATCAA 420
AATAACGATC TAGCGTTTGT GGTGTGCTTG CAAATCCCTT TGAGGGTGGC GATTGAAATC 480
AGCTCGCCTT CAAAGTATTT TAAAACTTTT AGCGAAGGGA GCATGGTCAT GTATTTTATG 540
ATTTCTATCA TGCTCACTTT AGTGTCGCTG CTTTTATTCG TGAAATGCAT TTCTAGCTTT 600
TGGACAGCGA TCGTGCATTT TAGCAGTTTT GACATTAAAG AAGTGTTCCA CCCCATTGTG 660
CTTTTAACCC TAGCTTTAGC CACCTTTGAT TTGGTCAAGG CGATTTTTGA AGAAGAAGTG 720
TTGGGTAAAA ATAGCGGGGA CAACCACCAT GCGATCCACC GCACCATGAT CAGGTTTTTA 780
GGCTCTATCA TTATCGCATT AGCCATTGAA GCGTTAATGC TCGTGTTTAA ATTCAGCGTG 840
AGCGAGCCGG ATAAAATCAC TTATGCGGTG TATTTGGCTA TCGGCGTGGC GGTGCTTTTG 900
ATCAGTTTGG CGATTTATGT TAAATTCGCT TATAGCGTGT TGCCCAAACG AGAACGC 957

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123

ATGGTTATAC ATGAAAAAAT CAAAAGCCGC TTTTCTAGGA ATTGGTCTTT AAGGAATAGG 60
GGCAGGCATT TTGCATCTTC AAGCGTGTAT TTTTTCTCAC TTCTTGTCAT TACAGCGGTT 120
AATAGAAGTA GTGCAGTTGC TTGGTTATTG ATGCCTGAAC ATTTGATTGG GTGGTTTTTG 180
ATTTCTTTTA GTGGGGAATT TGTAGCAGAC ATGGCGTTTG GCAAAAAAAG TAAGATTTTT 240
AAAACCCGCT TTGGAATTTC TATTGTGAGC GGCGTTTCAC TATTGCTTGG CGCTTACCAG 300
CGCTTTTATT TTTTGTATGG TTTGGCTTTA TTAATTGGTG GGCTGTCTTT TTTA 354

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:124

```
ATGTTTAAAA GCAGATTAAA TTCATGGATT TTATTAGGGA TTTTAGGGGT TTTAGTGGTG      60
GTTTTTTGGG ATGTCATAAA ATACAAAATA GAAGATTTGC AACATGATCA TTATCTATCA     120
CAAGTGAAAG AAAGGGAAGA ATATTATAAA AACCACATAG AAGAAGCTTT GAAAAAGGAT     180
AGCGAATGCT TTGAAAAAGG AGGCGATAAA GTGGATTGCT CGGCTGCTAT GAGAATAGCT     240
GCTGGTGAAA GAAATAGAAG AATGTTAGAG ATTAAA                               276
```

(2) INFORMATION FOR SEQ ID NO:125:

(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:125

```
ATGGTATTTT GGGGCGCTGT TTTCTTTTTA TGGGATCGAA CGGCATGGAA GCGCTTAATG
GTGTTTTTGA ACAGCTTGAW TTYCATGCTT GCGGCCTTGA GTTTGGGGTC GTTTTTAGGG
GCATGGATCA AAAATGAAGC CCACACCACT CAAATCGTTT TGATTTCTTC TTTGCCCTTG
ATTTTTATGA TGGGTTTTGT GTGGCCTTTT GAATCCTTGC CCTCTTATTT GCAAGTCTTC
GTTCAAATAG TGCCTGCTTA TCATGGGATC AGTTTGCTCG GGCGATTGAA TCAAATGCAT
GCGGAATTTA TAGATGTTTC TATCCATTTT TACGCGCTTA TTGCGATTTT TATCGTGAGT
TTTATAGGGT GCGTGTTCAA ACTCAGCTCT TTAAAGAAAG CTTGTGAAAA CGCT
```

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 762 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(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:126

```
ATGCATGAGC AAGGTTCTAT AAGCTTTRTA GGCGRACAGG GAGCTAAAAG ATTATTATAC      60
ATACTCTACA AGCTCGCATT TAATGCTAAG TCTAATAAGA TTGCCCTAGA TAGACATTAC     120
GCCAAAATGT TTTTGCAAGT TGTAGCAAGA ACTCTAATAA AGAATGTCAA TATATTAGAA     180
GAGCAAGGTT TTATTGAAGT CATTAAAGGA AAACAAAGAT ACTTGTATGT GTATCTTAAA     240
GATTACAGAG AATTAGAATG CTTAGTGAAG AGCAAGATGG CTAAGTATGT GATGTATTTA     300
AGACAATTCT TTGATTATTT GGATAGAAAA AGGCGTTATG GCTTTGATTT TACGCTTAAA     360
AACCTAGCCT TTGCTAAGAC CAAAGAAAGC TTACCCAGAC ATTTAAACGA TAAAGACTTA     420
AAGAGTTTTT TAAAAACACT CTTAGACTAT AAGCCAGCTA CAAGCTTTGA AAAACGCAAT     480
AAGTGTATTC TACTTATTGT AATACTTGGG GGACTTAGAA AATGCGAAGT GTTAAACATA     540
GAATTAAAAC ACATTCAAGT AGAAGAGCAA AACTACTCTA TTTTAATTCA AGGTAAAGGT     600
AGAAAAGAGA GAAAAGCTTA TATTAAAAAG AGTTTGTTAG AACCAAGCTT GAATGCTTGG     660
ATTAGTGATG ATTACAGACT AAAATATTTC AATGGAGCAT ATCTCTTTAA AAAGGATAAG     720
CAAAAATCAC AAAATTCTTT AACGCTTTAT AATTTATCCC CT                        762
```

(2) INFORMATION FOR SEQ ID NO:127:

(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

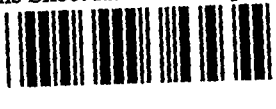
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127

```
GTGGTCTTTA AAATTTTAAG TTTATGGTTA GGGGTGTTTT GTTTCCTTAG GGCTACGCAT      60
TTATACTTAG GCGAAGAACC CAAATATAAA GACAATTTCA CGCATTTTGA ATACGCTAAC     120
CCTAACGCTA GAAAAGGCGG TGTTTTGAGA AATGACGCTA TAGGGACTTT TGATAGCCTT     180
AACCCTTTTG CGCTTAAAGG CACTAAAGCC GAAGGCTTGG ATCTCATTTA TGACACTTTA     240
ATGGTGCAAA GCTTAGACGA ACCTTTTGCA GAATACCCCT TAATCGCTAA AGACGCCGAA     300
GTGGCTAAGG ATAACAGCTA TGTGATTTTT ACCCTAGATA AAAGAGCGAG ATTCAGCAAT     360
AACGCTCCCA TTTTAGCGAG CGATGTGAAG TTTAGCTTTG ATACGATAAT GAAATTAGGA     420
TCGCCCCTTT ATAGGCAGTA TTACCAAGAT GTTAAAAAGG CGGTTATCTT AGACAAGCAC     480
CATGTTAAAT TCATTTYCAA AACCACTGAA AATAAAGAAT TGCCCCTCAT TTTAGGGCAG     540
TTGCAGATCT TTTCC                                                      555
```

(2) INFORMATION FOR SEQ ID NO:128:

This Sheet Has Been Replaced

SUBSTITUTE SHEET (RULE 26)



(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:128

GTGGCCATGA TAGATTGCGC GATTATTGGA GGTGGTCCTG CAGGTTTGAG TGCGGGGCTT 60
TATGCCACTA GAGGCGGTGT TAAAAACGCC GTTTTATTTG AAAAAGGAAT GCCTGGGGGG 120
CAAATCACTG GCAGTAGTGA GATTGAAAAT TATCCGGGCG TTAAGGAAGT GGTGAGCGGA 180
TTGGATTTCA TGCAACCA 198

(2) INFORMATION FOR SEQ ID NO:129:

(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

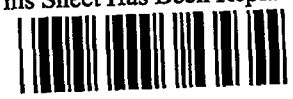
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129

GTGGGGAAAA GCTTGAGATA CAGCTTGAAT TTAGATCTCA ATCAAAAAGC CGATTTGTTT 60
TTCACCGAAT TAGAGCCAAC AGGTCTCACG CTCTCCCCCA TCATGAAACG CTTTACTATC 120
AAAGGCGATT TTGATTCAGG GCTAAAATCC TATGACATGA GCTACATGTA TGCGAGCCTT 180
CAAGCTATAA GCGCGATCAG GAGATTACCC TTAGGGCTTT ATGATGGGGT GCATGTCTAT 240
TCTAAAACGC CCATGAAGGA TATTGAAAAA TTACGCAACG CTTTAAAAAC AATCAACCAC 300
CATGGCATAG GCATTGAAGG GTGGTGGCAA CAAAACGGGA ATTTTTTCTC GGCGATGGAA 360
TTGGAAAAAA GAGCGTTATT CATTGTGCTC ATGCTCATTA TTTTAATGGC GTCTTTGAAT 420
ATCATCAGCT CGCTTTTAAT GGTGGTGATG AACAGGCGTA AAGAAATCGC CCTACTCTTT 480
AGCATGGGGA GCAGTCAAAA AGAAATCCAA AAAACCTTTT TTTATTTGGG TAATATCATT 540
AGTTTA 546

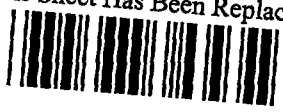
(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(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:130

```
ATGAAAAAAA CTTTTTTGAT CGCTTTAGCG CTTACGGCTT CTCTTATAGG CGCTGAAAAC      60
ACCAAATGGG ATTATAAAAA TAAAGAAAAT GGCCCGCACC GCTGGGACAA ATTGCACAAA     120
GATTTTGAAG TGTGCAAAAG CGGTAAAAGC CAATCGCCCA TCAACATTGA GCATTACTAC     180
CACACGCAAG ATAAAGCCGA TTTGCAATTC AAATACGCCG CTTCTAAACC TAAAGCGGTC     240
TTTTTCACCC ACCATACTTT AAAGGCTTCG TTTGAGCCGA CTAACCACAT CAATTATAGA     300
GGGCATGACT ATGTGTTGGA TAATGTGCAT TTCCACGCCC CTATGGAGTT TTTAATCAAT     360
AATAAAACCA GGCCTTTGAG CGCGCATTTC GTGCATAAAG ACGCTAAAGG GCGTTTGTTG     420
GTGTTAGCGA TTGGTTTTGA AGAAGGGAAA GAAAACCCCA ACCTTGATCC TATTTTAGAA     480
GGCATTCAAA AGAAACAAAA TCTTAAAGAG GTGGCTTTAG ACGCTTTCTT GCCTAAAAGC     540
ATCAATTACT ACCATTTTAA CGGCTCTCTC ACCGCTCCTC CTTGCACAGA GGGGGTGGCA     600
TGGTTTGTCA TAGAAGAACC TTTGGAAGTT TCTGCCAAAC AATTGGCTGA AATCAAAAAA     660
CGCATGAAAA ATTCGCCCAA CCAACGCCCC GTCCAGCCTG ACTACAACAC CGTGATCATT     720
AAAAGCTCGG CTGAGACCCG C                                               741
```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131

```
ATGAAAATTT CTTTATTGGG GCATGGAAAA ACCACTCTAG CCCTAGGGCG TTTTTTTAAA      60
AAAAACCATA ATGAAGTCAA ATTTTTTGAT GATAAATTCC CTGCATTTTT TAAGGATAGC     120
GAGGGTTTTC TTTGCTACCC TAGTAAGGAT TTTAACCCTA ATGATTCCCA ACTAGAAATC     180
GTCAGCCCTG GCATTAGTTT CACGCACCCT TTAGTCATGA AAGCCAAGCA TTTAATGAGC     240
GAATACGATT ATATTGATAG TTTGTTTGAT CATTCTTTCA CGCCTACGAT GATAAGTATT     300
AGCGGCACTA ACGGGAAAAC CACCACGACC GAAATGCTCA CCACACTTTT AGAAGATTTT     360
AAGGCTGTGA GTGGGGGGAA TATCGGCACG CCCTTGATTG AATTGTTTGA AAAACGATCG     420
```

```
CCCTTGTGGG TGCTAGAAAC AAGCTCCTTT TCTTTGCATT ACACTAATAA GGCTTACCCT     480
TTAATCTACT TGCTCATCAA TGTGGAAGCC GATCATTTGA CTTGGCATTG CAATTTTGAA     540
AATTATTTGA ACGCTAAACT CAAGGTTTTA ACATTGATGC CTAAAACTTC GCTCGCTATC     600
CTCCCTTTAA AATTCAAAGA ACACCCTATT GTTCAAAACT CGCAAGCGCA AAAAATCTTT     660
TTTGACAAAA GCGAAGAGGT TTTAGAGTGT TTAAAAATCC CTTCTAACGC CCTTTTTTTT     720
AAGGGAGCGT TTTTATTAGA CGCGGCTTTA GCCCTTTTAG TTTATGAGCA ATTTTTAAAA     780
ATAAAGAATT TAAAATGGCA AGATTATAGA GAAAACGCCC TTAAAAGACT GAACGCTTTT     840
AAAATCGGCT CGCATAAAAT GGAAGAATTT AGGGATAAAC AAGGGCGTTT GTGGGTAGAT     900
GACAGCAAAG CCACGAATAT TGATGCCACC TTACAAGCCC TAAAAACCTT TAAAAACCAA     960
AAAATCCATT TGATTTTAGG GGGCGATATT AAAGGGGTCA ATTTAACCCC CCTTTTTGAA    1020
GAGTTTAAAA ACTATAAAAT AAGCCTTTAT GCCATAGGAT CAAGCGCTTC TATCATACAA    1080
GCCTTAGCGT TAGAATTTAA TGTTTCTTGT CAGGTTTGTT TGAAGTTAGA AAAAGCGGTT    1140
CAAGAAATTA AAAGCGTTTT ATTACAAAAT GAAGTCGCTT TGCTTTCACC TAGCGCGGCC    1200
AGTTTGGATC AATTTTCTTC GTATAAAGAA AGGGGTGAAA AATTCAAAGC GTTTGTTTTA    1260
AAAGAT                                                               1266
```

(2) INFORMATION FOR SEQ ID NO:132:

(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:132

```
ATGAAAGAAA TCATTGTCGC CCTTGTGGGC CAGCCTAATG TGGGGAAATC GTCCTTAATC      60
AACGCTTTGA GTAACSCCCA TTTRAAAGTG GGGAATTTTA CCGRGGTTAC CGTGGATAAA     120
ATGGAAGTGA GTTTGATCCA WAAAGATCAT CAARTSWYTM TC                        162
```

(2) INFORMATION FOR SEQ ID NO:133:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133

GTGCATCGTT TTTCTAGAAA CCCATGCGCA TCTTGCAATC GCGCTCGCTC TTGTTCGAGA 60
CTATCTCGCT CATTAGTGAG CGCGGTAACT TGGTGGTTGA GCTTGTCGTT TTCGGTGGTT 120
AGTGCTTTAT TTTCTTTAGT CAGCTCGGTG ATTTTATGGG TTAGCTCGGT GTTTTCTCTT 180
TTTAGCCTTT CTTTTTCTGT TGTCAATTCT CTTTTTTCTT CAGTCAGCCG ATCTCTGGCT 240
GCTAATAAGC GTGTGTTTTC TTTAGCTAAA ATGTCTTTTT CCGTTTTCAG TTCTGCTTTT 300
TCTTTAGTGA GCTTGTTATT GTTTTGCCAT AAT 333

(2) INFORMATION FOR SEQ ID NO:134:

(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:134

ATGCAAAAAA TGGGCGTTGT CTCTTATTCC GTGTTTCAAG CGTTTGAAAA GGCTTTGAGT 60
CGGTTTAAAG AGGGCGTTGT TTTGATTGTG GATTCTTTAA GGCGTTTGAT TATGGGGAGC 120
GCTTCAGTTA AAGAATTGAG TGGGGTAATA GGCATTGTGG GGGCGTTAAG CCATGCCAAT 180
AGCGTGAGCA TGCTTTTGTT GTTTGGGGCG TTTTTATCTA TCAATCTAGG GATTTTAAAT 240
TTATTACCCA TTCCAGCCTT AGATGGGGCG CAAATGCTAG GGGTCGTTTT TAAAAATATT 300
TTTCATATCG CTTTGCCAAC GCCCATACAA AATGCGTTGT GGCTAGTGGG GGTGGGGTTT 360
TTGGTTTTTG TCATGTTTTT AGGGCTTTTT AATGACATTA CTCGTTTGCT A 411

(2) INFORMATION FOR SEQ ID NO:135:

(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

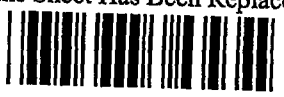
(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135

This Sheet Has Been Replaced



GTGATGGCTT TGTTGAAAAT TAGTGTGGTA GTTCCTGAGG GGGAAGTTTA TACAGGAGAG 60
GTTAAAAGCG TTGTGTTGCC AGGAGTGGAA GGGGAATTTG GGGTGCTTTA TGGGCATAGC 120
AACATGATCA CCTTGCTTCA GGCGGGAGTG GTTGAGATTG AAACCGAAAA CCAAAAAGAG 180
CACATTGCTA TCAATTGGGG TTATGCAGAA GTTACTAATG AACGGGTGGA TATTTTAGCC 240
GATGGAGCGG TCTTTATTAA AAAAGGATCA GATGACAGAG ATGATGCTAT CTCTAGGGCT 300
AAAAAGCTTT TAGAGGACGC AAGCTCTGAC AGGTTAGCGG TCTCTAGCGT GCTGGCTAAG 360
ATTGAGTCTC TT 372

(2) INFORMATION FOR SEQ ID NO:136:

(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:136

ATGTATTCCT TGCTCTTAGA TTTGAATAAA AAGACCGCTC TTTTAGGCAC AAGAGGGTTT 60
TTTATCGACG ACAAACACAT CAAAGAAAAG GGCTTGACCA CGCCCACTCT TTTAGAGCTT 120
TATAGCGATT TGGAAGAAGC GATTCGTTTA AAATGCGAAT ACTTCATTAT GGAGGTGAGC 180
TCCCATGCGA TTGTCCAAAA CGCATCGCTG GGCTTGATTT CGCTCTTAAA ATTCTCACCA 240
ATATCACAAG CGATCATT 258

(2) INFORMATION FOR SEQ ID NO:137:

(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:137

ATGAAAACGA ACTTTTATAA AATTAAATTA CTATTTGCTT GGTGTCTTAT CATTGGCATG 60
TTTAACGCTC CGCTTAACGC TGACCAAAAC ACGGATATAA AAGATATTAG TCCTGAAGAT 120

This Sheet Has Been Replaced



ATGGCGCTAA ATAGCGTGGG GCTTGTTTCT AGAGATCAGC TAAAAATAGA GATCCCTAAA 180
GAAACCCTAG AGCAAAAAGT GACCATACTC AATGACTATA ATGATAAGAA TGTTAATATC 240
AAGTTTGACG ACATAAGTTT AGGGAGTTTC CAACCTAATG ATAATCTAGG TATCAATGCG 300
ATGTGGGGCA TTCAAAATCT TCTM 324

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 720 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138

ATGATTGATA SCCTTGATGG GGCAAAAGAT GCACAATTGA TAAAAAAAGC TTACGCGTTT 60
TTGTGTTTAG GAGGCGATGG CACGATTTTA GGGGCTTTAA GAATGACGCA TGCTCACAAT 120
AAGCCATGCT TTGGGGTGAG GATTGGGAAT TTAGGGTTTT TGAGCGCGGT TGAATTGAAC 180
GGGTTGAAAG ATTTCTTACA AGATCTCAAG CAAAACAGGA TCAAATTAGA AGAGCATTTG 240
GCTTTGGAGG GCCGTATTGG AAACACTTCT TTTTATGCGA TCAATGAAAT CGTGATCGCT 300
AAAAAAAAAG CTTTAGGGGT TTTAGACATC AAAGCGTGCG CGGGCCATAC GCCCTTTAAC 360
ACTTATAAAG GCGATGGGCT TATCATTGCC ACGCCCCTAG GCTCAACCGC TTATAATTTG 420
AGCGCTCATG GGCCCATTGT GCATGCTTTA AGCCAAAGCT ATATTTTAAC GCCCTTGTGC 480
GATTTTTCTT TAACGCAACG CCCTTTAGTG TTAGGGGCGG AATTTTGCTT GAGTTTTTGC 540
GCTCATGAAG ACGCTCTTGT GGTTATTGAT GGGCAAGCCA CCTACGATTT AAAAGCCAAC 600
CAACCCCTAT ACATTCAAAA AAGCCCCACG ACCACCAAGC TCTTACAAAA AAATTCAAGC 660
GATTATTTTA AAGTGCTTAA AGAAAAGCTG TTATGGGGGG AAAGCCCTAA CAAAAAAAGA 720

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 549 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139

This Sheet Has Been Replaced

```
ATGATAGTGG GTTTGATAGG GGTTGTGGAA AAAATCTCTG CTTTAGAAGC GCATATAGAA      60
GTGCAAGGGG TTGTTTATGG GGTGCAAGTT TCTATGCGAA CGGCTGCTTT GCTCCAAACG     120
GGCCAAAAAG CGCGTTTTGA AATCTTACAA GTGATTAAAG AAGATGCGCA TCTTTTATAC     180
GGGTTTTTAG AAGAGAGCGA AAAAATTCTC TTTGAAAGGC TTTTGAAAAT CAATGGGGTA     240
GGGGGGCGTA TCGCTTTAGC CATTCTTTCA AGCTTTTCGC CGAATGAATT TGAAAACATT     300
ATCGCTACTA AAGAAGTCAA AAGACTCCAG CAAGTCCCAG GCATAGGGAA AAAGCTCGCC     360
GATAAGATCA TGGTGGATTT GATTGGCTTT TTCATTCAAG ATGAAAACAG ACCCGCGCGC     420
AATGAAGTCT TTTTAGCCCT AGAGAGTTTG GGCTTTAAAA GCGCTGAAAT CAATCCAGTT     480
TTAAAAACCC TAAAACCCCA TCTCAGCATA GAGGCAGCGA TTAAAGAAGC CTTACAGCAA     540
CTGCGCTCT                                                             549
```

(2) INFORMATION FOR SEQ ID NO:140:

(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:140

```
GTGGGGGTTT TGTTRGCGTT GTTTTTCTTT TATGCGAAAA ATAACCTTTT GGAAAACACC      60
CAAATACGCA TGCAATACAC CGCTGATGCG ATCGCTAAAA GCCTTTTAGA ATTAAATAAT     120
GCCTCTTCTT TAGAGCCTTT AAAAATCTTA GAAGAACGAT TCAAAAACAC CCCCTTTGTT     180
TTGTTGGACG CAGACAACAG AGTCAAGTTT TCTAATATCG GGGTGTTTGT GGCCTCTTTT     240
AAAAATGACG CCTTAATCAA AACCCCTTAT TTTGCGCTTA AAAAACAGGG CTTTTACCTC     300
ACAGACAGCG CCCCAACTAA CCGCTTAGGG GTTTCTAAAA TCATTATTGC AGAAGAAGAA     360
ATTCAAAAAA TCTTTATCCC CCTTTATAAA ATGATAGGCT ATGTGTTTTT GGGCGCGAGT     420
TTGTTTGTCG CGCTAATAGC CATGTGGCTT TATAAAATCC CA                        462
```

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 864 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

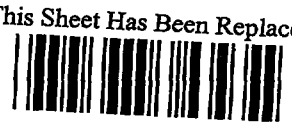
(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature

This Sheet Has Been Replaced



(B) LOCATION 1...864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141

```
GTGGTAATAA TGATTTTAGT CTGCTTTTTA GCTTGCTCGC AAGAGAGCTT TATCAAAATG      60
CAAAAAAAAG CCCAAGAGCA AGAAAATGAC GGCTCTAAAC GCCCCAGCTA TGTGGATTCG     120
GATTATGAAG TCTTTAGCGA AACGATTTTT TTACAAAACA TGGTGTATCA GCCTATAGAG     180
GAAAGAAACG CTTTTTTCCA ACTGACTAAA GATGAAGACA ATTCTTTTAA CCCTGAAAAT     240
TCCGTGATTT TACTGAATGA GCCAAGCGAT AATAGTGAAA AAAACCTACT CTCATACCCA     300
AACGATCCCA ATAACAATGA AGACAACGCT AATAATAGTC AAAAAAATCC GTTCCTTTAC     360
AAGCCCAAAA GAAAAACAAA AAACCCAAAA CTCATTGAAT ATTCCCAACA AGATTTCTAC     420
CCCCTAAAAA ATGGGGATAT TATCATGAGT AAAGAAGGGG ATCAATGGTT GATAGAAATC     480
CAATCCAAAG CCTTGAAGCG TTTTTTAAAA GATCAAAACG ATAAAGATCG CCAGATCCAA     540
ACTTTCACTT TTAATGACAC TAAAACGCAA ATCGCGCAAA TTAAGGGCAA AATTTCTTCG     600
TATGTTTATA CCACCAATAA CGGTAGCTTG AGTTTAAGGC CYTTTTATGA ATCGTTTTTG     660
TTAGAAAAAA AGAGCGATAA TGTTTATACG ATAGAGAATA AGGCTTTAGA TACTATGGAG     720
ATTTCAAAGT GTCAAATGGT GTTAAAAAAG CATTCAACCG ATAAATTAGA CAGCCAGCAT     780
AAAGCCATCA GTATTGATTT GGATTTTAAA AAAGAGCGCT TTAAGAGCGA TACGGAACTC     840
TTTTTAGAAT GTCTTAAGGA AAGT                                            864
```

(2) INFORMATION FOR SEQ ID NO:142:

(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:142

```
ATGGCCGCTC CACTACTTGC TCTGCCCTTT CTTTCTAACC CTTTAGTGCT TGGTGCTTTA      60
GCTGTCATAG GAGTGGGTGC TTACTTGTAT CCCAATAAGC AAGATTCTTT AGTTGTGCAA     120
GCAGATGGGC TTTATAGTGA AATTCTTGGG TTTTTCATTT CGTTTTCTAG CAAGATCTTG     180
AAAGGAATTG GTGAGCCTTT AGCCAATGTT ATCCAACCTT TTGGTATGGT TTTAGGAATG     240
CTTTTAATCC TTTTGTATTC CTTTAAACGC TATCAAAACA ATGATTTATT TGAAATCAAA     300
ACCTTTTTAA TGCTTTTTGT GTTTGTAGGA TACCTTTCTT TGTACCATTA TGCTTTTAAA     360
TCTGATGGTT CTAGTAGCGG TAATGGTCGC TCCAGTTTTG CCTTTCAAAA TCATGTAACA     420
GAAATTTTTG ACACGCCTGC TAACTTGCTA AATGCTGGGA TTTCTAATGT GGTTAAGGAA     480
TATCAAACAA ATAGTGCAAG AGAACACAAG AATATAGACA CGCACCACAG TATCACTAAC     540
GCTAATATTT CATTCCATGT CAGACAAATT TTAACGAGTT TGAATAAACT ATATGAAGAC     600
TTCAAAATTA ATAATGGACT ATCGCTAAAA ACCCTTATTG CAGCTGTTTT GTTATTAGTT     660
ATTTTAGGAT TAGAATTGTT TTTATTGTTC AAAGTTTTCT GTTATGTTTT TATGACTTAT     720
TTAGAAAAAA TTATTTACTT GTCTTTGGTT ATTTTCATGC TACTGCTAGG GTTTTTTCAG     780
CAGACTAGAG GTTTTTTAGT GTCTTATGTG AAAAAAATTA TTTCATTGAC TTTTTACATG     840
CCTTTGTTGT TGCTATTAGT GTTATTCAAC TCTTTTGCAT TACAATACGC AATCAAAGTG     900
GGAGGGAGCA ATGAAATAGT GGCTAAATTT GGCATTATTG TAGCAATAGG AATTTCACTG     960
ACATTTATTC AAAAAGTCCC CGAAATGATT AACGCTATCT TTGGCACACA AGGTGGTCTA    1020
ACGGATGCTA AAAGCTTCAT ATATCAAGGT GTGCAAATGG CTAGTGCTGG AGCTGGAGCC    1080
ATAGCTGGAA GTCTTAAGAG TGTGGGTCGT TCAGCATTTG GTAGAACGCT AGAAGCTTAT    1140
AAAGACGCAA AATCTACGAT AAACAGCACT ACGGCTAACA TGAGAGACAT GCCAGGACAT    1200
CCTGGTGTTA GAGTGGGTGT GGAGACGATT GAACTTCCCA AGTCTCATAG AGCTAGCAAA    1260
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:143:

(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:143

GTGTTAAAAT TTCAAAAATT ACCCTTATTG TTTGTTTCCA TTCTTTATAA TCAAAGCCCT 60
TTATTGGCTT TTGATTATAA GTTTAGTGGG GTAGCGGAAT CTGTTTCTAA AGTGGGGTTT 120
AACCATTCCA AACTCAATTC CAAAGAAGGG ATTTTCCCTA CAGCCACCTT TGTAACCGCC 180
ACGATCAAGC TTCAAGTGRA TTYCAAATCT GCTCCC 216

(2) INFORMATION FOR SEQ ID NO:144:

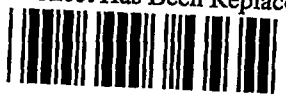
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 615 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144

ATGGGTAATC ATTTTTCTAA ATTAGGATTT GTTTTAGCGG CTTTAGGGAG CGCGATAGGT
TTAGGGCATA TCTGGCGCTT CCCCTATATG ACTGGGGTGA GTGGTGGGGG TGCTTTTGTT
TTATTGTTTT TATTTTTATC CTTAAGCGTT GGTGCGGCGA TGTTTATCGC TGAAATGCTA
TTAGGACAAA GCACGCAAAA AAATGTAACA GAAGCTTTTA AAGAGCTTGA CATTAACCCT
AAAAAACGCT GGAAATACGC AGGGATCATG CTTATTTCTG GACCTTTAAT ACTGACTTTT
TATGGCACTA TTTTAGGTTG GGTGCTTTAT TATTTGGTGA GTATTAGTTT TAATTTGCCT
AGCAGTATCC AAGAATCTGA ACAAATTTTT ACTCAAACTT TGCAGTCTAT AGGGTTACAA
TCCATAGGGC TTTTTAGCGT TTTATTCATA ACCGGATGGA TTGTTTCTAG GGGGATTAAA
GAAGGCATTG AAAAACTCAA TTTGGTTTTA ATGCCCTTAC TCTTTGCCAC TTTTTTTGGT
TTGCTTTTTT ATGCGATGAG CATGGATTCT TTTTCTAAAG CTTTCCATTT CATGTTGATT
TCAAGCCAAA AGATT

(2) INFORMATION FOR SEQ ID NO:145:

(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:145

```
ATGGAAAAAG TTTGCGTGAG CGCATGGGGG TTGCCTAAGA TTTTAGAAGA AAGATTAAAA      60
GAAAAATATG GCGATGATTG GGAAAAACAT GTTAAGGCTA AAGCAATAAA CGAAGAAGAG     120
CTTGAAGAAC AAGTCAAAGC TAAAGCCAAA GAGCAACAAA AGACACAAAG AGAAAAAACA     180
CTCAATGGAT TTTTAAAAAA AGTTGGTTTA AAAAAGCGTG ATATGTTACA AAGCACTATG     240
TTATTTGATG AAGTCAAAGA AGCTGATGTG CTTTTTCAAG CAGAGCGTAA AATTGGCGAT     300
TGGATTTTTA GCAGTGCGGT GTTCTTTTTT GCTCTAGCCC TTATAGAAGC CATTATTATT     360
GTATGCTTAT TGCCGTTAAA AGAAAAAGTG CCTTATTTAG TAACCTTTTC AAACGCTACA     420
CAAAATTTTG CCATAGTCCA AAGAGCAGAC AAGAGCATCC GTGCTAATCA AGCGCTTGTG     480
AGACAATTGG TAGCGTCTTA TGTTAATAAT AGAGAAAATA TTTCAAGTAT AAAAGAGCAA     540
AACGAAATAG CCCACGAAAC CATTAGGTTG CAAAGCGCAT TTGAAGTGTG GGATTTTTTT     600
GAAAAACTGG TTTCTTATGA GCATAGCATT TACACTAATA TAAATCTAAC ACGAAAAATT     660
AGCATTATCA ATATCGCTTT AATCAGTAAA ACCCAAGCCA ATATTGAAAT ATCCGCACAA     720
CTTTTTCATA AAGAAAAGTT AGAAAGCGAA AAGCGTTATA GAATAATTAT GACCTTTGAA     780
TTTGAACCTA TTGAAATTGA TACAAAATCT GTTCCCCTAA ACCCTACAGG CTTTATTGTT     840
ACAGGTTATG ATGTAACTGA AATTGCGATT TTAAAAGATT TAGATGAGAA AAATAAAGTC     900
AAAGATGATG GTGTGAAATC TAGGATTATC CATGTCGAGA AAAAAGACCC TCATATGAGC     960
CAGTATAAAG ATGTTAAGGA GCAA                                            984
```

(2) INFORMATION FOR SEQ ID NO:146:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146

ATGCTGCATA AGGCTAAGGT GGGCATCGTG TTTCAGGCGC TTTTAGGGAT TTTTTGCGTG 60
TTTTTATTGT TGTTTTACTT GAGCGCGTTT TTAATGGTGG CTTTTAAAGA CACTAAACGC 120
ATGTTTATAA GCGTTTTAAT AGGGAGCGTG GTGTTCCTTT GGAGCGATCT ATTGGTCTTT 180
GTAGGGTTTA AAAATATCAG CTTTGTTTTG GATATTGGTT ATGAAATC 228

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147

ATGCCGTTTT TGAAAAACTG GATCTGGAGT TTAAAGATGG CTTTGAGCGC GATTAGTGGG 60
GCTAGTGGGG TGGGGAAAAG CGTCCTTATT GCGAGCCTTT TAGGGGCGTT TGGGCTTAAA 120
GAGAGCAACG CTTCAAACAT TGAAGTGGAA TTGATCGCGC CTTTTTTAGA CACGGAAGAA 180
TACGGCATTT TTAGAGAAGA TGAGCATGAA CCCTTAGTTA TTAGCGTGAT TAAAAAAGAA 240
AAAACACGCT ATTTTTTAAA CCAAACAAGC CTATCTAAAA ACACGCTCAA AGCGTTATTA 300
AAGGGGCTTA TTAAACGCTT ATCTAACGAC AGATTCAGCC AGAATGAACT CAACGATATT 360
TTAATGCTCT CCTTATTAGA TGGCTATATC CAAAATAAAA ATARGCGTTT AGCCCCCTTT 420

(2) INFORMATION FOR SEQ ID NO:148:

(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:148

ATGCCACAAA ACCAGCTTGT GATCACCATC ATTGATGAAT CAGGCTCTAA GCAACTCAAA 60
TTTTCTAAAA ATTTAAAACG CAACCTCATC ATTTCTGTTG TCATTCTTTT ATTGATCGTG 120

This Sheet Has Been Replaced

GGGCTTGGCG TGGGGTTTTT AAAATTTTTA ATCGCTAAAA TGGATACGAT GACAAGCGAG 180
AGGAATGCGG TTTTAAGGGA TTTTAGGGGT TTGTATCAAA AAAATTACGC CCTAGCGAAA 240
GAGATTAAAA ACAAGCGAGA AGAGCTTTTT ATTGTGGGGC AAAAGATCCG TGGGCTAGAA 300
TCCTTGATTG AAATCAAAAA GGGGGCTAAT GGGGGAGGGC ATCTCTATGA TGAAGTGGAT 360
TTAGAAAATT TGAGCTTAAA TCAAAAACAT TTAGCACTCA TGCTCATTCC TAATGGCATG 420
CCCCTAAAAA CTTATAGCGC TATCAAACCC ACTAAAGAAA GGAACCACCC CATTAAAAAG 480
ATTAAGGGCG TTGAATCCGG GATCGATTTT ATCGCGCCAT TGAACACGCC TGTGTATGCG 540
AGCGCTGATG GGATTGTGGA TTTTGTGAAG ACTCGTTCTA ATGCGGGGTA TGGGAACTTG 600
GTGCGCATTG AACATGCGTT TGGTTTCAGC TCCATTTATA CGCACTTAGA TCATGTCAAT 660
GTGCAGCCTA AAAGCTTCAT CCAAAAAGGG CAGTTGATTG GCTATAGCGG GAAGAGCGGT 720
AATAGCGGCG GCGAAAAATT GCATTATGAA GTGCGGTTTT TGGGTAAAAT TTTAGACGCA 780
GAAAAATTCC TAGCATGGGA TTTGGATCAT TTTCAAAGCG CTTTAGAAGA AAATAAATTT 840
ATTGAATGGA AGAATCTGTT TTGGGTTTTA GAAGACATCG TCCAGCTCCA AGAGCATGTG 900
GATAAAGACA CCTTAAAAGG TCAG 924

(2) INFORMATION FOR SEQ ID NO:149:

(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:149

ATGATCACTG GCTCTCACAA CCCCAAAGAA TACAACGGCT TTAAAATCAC GCTCAATCAA 60
AACCCGTTTT ATGGCAAGGA CATTCAGGCT TTAAAAAACA CGCTTTTAAA CGCAAAGCAT 120
GAAATAAAGC CCCTAAAAGA AACGCCAGAG AAAGTCAATG CCCTAGAAGC GTATCATCGC 180
TATTTGATCA AGGATTTTAA GCATTTAAAA AATCTTAAAT ACAAAATCGC CCTGGATTTT 240
GGTAATGGCG TGGGGGCGTT AGGATTAGAG CCGATTTTAA AGGCTTTAAA CATTGATTTT 300
AGCAGCCTTT ATAGCGATCC TGATGGGGAT TTTCCTAACC ACCACCCAGA CCCTAGCGAA 360
GCGAAAAACT TAAAAGACTT AGAAAAACAC ATGCGAGAAA ACGCTATTTT AATAGGCTTT 420
GCTTTTGATG GCGATGCGGA TAGGATTGCG ATGCTAAGCT CTCATCATAT CTATGCGGGC 480
GATGAATTAG CGATTTTATT CGCTAAACGC TTGCATGCTC AAGGCATCAC CCCTTTTGTG 540
ATCGGCGAAG TCAAATGCTC TCAAGTGATG TATAACGCAA TCAATACTTT TGGTAAGACG 600
CTCATGTATA AAACCGGGCA TAGCAATTTA AAAATCAAGC TCAAAGAAAC TAATGCGCAT 660
TTTGCGGCTG AAATGAGCGG GCATATCTTT TTTAAAGAAC GCTATTTTGG CTATGATGAC 720
GCTCTTTACG CATGTTTAAG GGCTTTGGAG TTATTGCTTG AACAAAGTCC AAGCGACTTG 780
GAAAACACCA TTAAAAACCT CCCCTATTCC TACACCACGC CTGAAGAAAA AATCGCCGTG 840
AGCGAAGAAG AAAAATTTGA AATCATTCGC AACTTACAAG AAGCGCTTAA AAACCCGCCA 900
AGCCATTTCC CTACAATCAA AGAAATCATC AGCATTGATG GCGTGAGAGT GGTTTTTGAA 960
CATGGCTTTG GGCTTATTCG CGCAAGCAAC ACCCACCCCC TATTTAGTCA GCCGCTT 1017

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 621 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:150

```
ATGTCCAAGA ACCTTCAAAA GAAGAATCCA AAGAAGAGTT TYCCACAAGC CCAGAAAGCC      60
ATAAGGGAGA TGAAAATGTT TGAAACCATT GCYTTTTTATT TCTTTGCGAT CCTTACTTTA     120
AGCATGGCGT TAGTGGTGAT CACAACCACA AATATCCTCT ATGCCATTAC CGCTCTCGCT      180
AGTAGCATGG TTTTTATTTC TGCTTTTTTC TTTTTACTGG ACGCTGAGTT TTTGGGCGTG      240
GTGCAAATCA CGGTGTATGT GGGTGCGGTC ATTGTGATGT ATGCGTTTGG CATGATGTTT      300
TTCAACTCCG CTGCAGAAGT AGTTGAACGC AAGCAAAGCC CTAAAATCTT GTGCGTTCTT      360
TCATTTGGCG TGGCGCTGTT GCTCACCTTG ATTTTAAGCG CTCCTAGCAT TGSSGAAAAC      420
CTTTCTAAGC AAGTCAATTC CAACGCTATT GATGCGCAAA TYCCYAACAT TAAAGCGATT      480
GGTTATGTGC TTTTCACCAA TTACCTCATT CCCTTTGAAG CGGCGGCTTT AATGCTTTTA      540
GTCGCTATGG TTGGAGGCAT CGCTACAGGG ATTCAAAAAA TCCATGGGAA AAATCACACG      600
CAATTTATAA AGGAATCTCT A                                                621
```

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

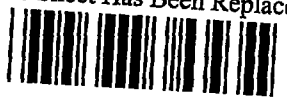
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151

```
ATGGGTGCAA TTTTATCTAT TTTAAAACTT GAAATCAAAT CTTATCTCAC CAATACAAGC      60
GCGCTATTTT GGACTTTTAT TTATCCTATT TTAATGCTCC TATTACTAAT TTTTGTTTTT     120
TCAAAAAATA CCACTGAAAT TTTTTACTTT AATAACATTA TAGGTCTAAT GGGACTTCTT     180
ATTATTTCTA GCGCGATCTT TGGTCTCACA CAAGCTATAA CAAGCTCTAG ATCGCATAAT     240
ATATTCTTAT TCTACATGCT ATCACCAGCA ACTTTCAAAC AAATAACTCT AGCATTAATC     300
GCTTCAAGAC TAATCGTTGT AATCCTATAT GCTTTTATCT TTATTGTTCT CTCTTTTTAT     360
GCGCTCAATA TCATCACTAT TCTTAATTTT AAAGCGCTTA TTTTGGGGTT TATTAGCATT     420
TTTTCAAGCG CATTGTTTTG TTTTTGCTTG GCAATTTTTG TAGCTAGAAT TTTTCAAAAC     480
GAACAAAGCA TCTTAGGATT TTGTAATATC ATCAATCTCT ATGCGCTAAT GTCTTGTAAT     540
GTTTTTGTTC CTTTAGAATA CCTACCTAAT ATTGGTCAAT TATTTATCAA AACATCTATT     600
TTTTACTACC TTAATCAACT TCTAATCAAA GCTTTTCAAG GGATTGATAC TATACTGGTT     660
TTAGCAACTT CAACATTTTT CATTATTGGT GGCATTATTT TATTTTTACT AAGCGCTAAT     720
CGCATGTTAC TAACACCAAA AGAACGCATG CGT                                  753
```

(2) INFORMATION FOR SEQ ID NO:152:

(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:152

```
ATGGCAGGCA CACAAGCTAT ATATGAATCA TCTTCTGCAG GATTCTTATC GCAAGTCTCC      60
TCAATCATCT CAAGCACAAG TGGTGTCGCA GGGCCATTTG CAGGAATAGT AGCGGGCGCT     120
ATGACAGCAG CGATTATTCC TATTGTTGTG GGATTTACTA ATCCGCAAAT GACCGYTATY     180
ATTRACCCAA TAYAATCAAA GCATCGC                                         207
```

(2) INFORMATION FOR SEQ ID NO:153:

(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

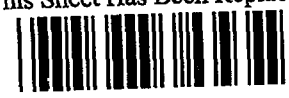
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153

```
GTGAGCCGTA TTTTAGGCTT GAGCGATGAT TTAGCGATGA CTTTATGCGC TGAATCCATC      60
CGCATTCAAG CCCCTATCAA AGGTAAAGAT GTCGTTGGTA TTGAAATCCC TAACAGCCAA     120
AGCCAAATTA TTTATTTAAG AGAAATTTTA GAAAGCGAAT TGTTTCAAAA ATCCAGCTCG     180
CCTCTAACCC TAGCTTTAGG CAAAGACATT GTGGGTAACC CTTTCATCAC GGATTTAAAA     240
AAGCTCCCCC ACTTGCTCAT CGCCGGCACG ACAGGGAGCG GTAAGAGCGT GGGCGTGAAT     300
GCGATGATTT TATCCTTACT TTATAAAAAA CCCCCC                               336
```

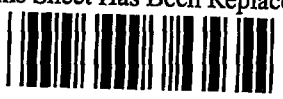
(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(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:154

```
ATGGATGAAA GSCTCGTTTA TGGGGTGATT TGCATGCCCA GTCAGGTTTT TGCCAACACC      60
GGCACTAACG TGAGCATCAT CTTTTTTCAA AAAACGCCAA GCGCAAAGGA AGTGATCTTG     120
ATTGACGCTT CCAAACTCGG CGAAGAATAC ACCGAAAACA AAAACAAAAA AACGCGCTTA     180
AGGCCAAGCG ATATGGATTT GATTTTAGAA ACTTTCCAAA ATAAAGCCCC AAAATCGGAT     240
TTTTGCGCTC TGGTTTCTTT TGATGAAATT ACAGAAAAAA ATTATTCTCT AAACCCCGGG     300
CAGTATTTCA CTATAGAAGA CACGAGCGAG ACAATCAGCC AAGCGGAGTT TGAAAACTTG     360
ATGCAACAAT ATTCAAGCGA ACTAGCGAGC CTTTTTGATG AAAGCCAAAA TTTGCAACAA     420
GAGATTTTAG AAACTTTAAA AGGGGTTAGG TTTGAG                               456
```

(2) INFORMATION FOR SEQ ID NO:155:

(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:155

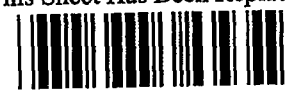
```
ATGAGAAGAA TTATTAAAAA CACACTTTCA CGCTTAGGCT ATGAAGATGT TTTAGAAGCT      60
GAGCATGGGG TGGAAGCTTG GGAAAAACTA GACGCTAATG CGGACACTAA GGTGCTTATT     120
ACGGATTGGA ACATGCCTGA AATGAACGGG TTGGATCTCG TTAAAAAGGT GCGTGCGGAT     180
AACCGATTTA AGGAAATCCC TATCATTATG ATCACCACAG AGGGCGGTAA AGCTGAGGTC     240
ATTACGACTT TAAAAGCGGG CGTGAATAAC TACATTGTGA AACCTTTTAC CCCCCAAGTT     300
TTGAAAGAAA AATTAGAGGT TGTTTTAGGG ACAAACGAT                            339
```

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 549 base pairs

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

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156

ATGGCAGAAG AACAAGAAAA TACCGCGCAA CAACCCCAAA AAAAAAGCAA AGCCCTTTTA 60
TTTGTCATTA TTGGAAGCGT GCTAGTGATG CTTTTATTGG TGGGGGTGAT TATCATGCTG 120
CTTATGGGGA ATAAGGAAGA ATCTAAAGAA AACGCTTCTA AAAACACCCA AGAAGTCCAA 180
GCTAATCCTA TGGCGAACAA GAATCAAGAA GCCAAAGAAG GCTCTAATAT CCAGCAATAT 240
TTGGTGCTTG GGCCTTTGTA TGCGATTGAT GCGCCTTTTG CGGTGAATTT GGTCTCTCAA 300
AATGGCAGAC GCTACCTTAA GGCTTCTATT TCGCTAGAAT TGAGCAATGA AAAGCTTTTG 360
AATGAAGTCA AGGTTAAAGA CACGGCGATT AAGGACACGA TTATAGAAAT TCTATCGTCT 420
AAAAGCGTGG AAGAAGTGGT TACTAACAAA GGCAAAAACA AGCTTAAAGA TGAAATTAAG 480
AGCCATTTGA ATTCGTTTTT GATTGATGGC TTTATTAAAA ATGTCTTTTT CACTGATTTC 540
ATTATCCAA 549

(2) INFORMATION FOR SEQ ID NO:157:

(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:157

ATGGGGTGTT TTAGCACCAT TTGTTGTAAG GGTTTAACGC TTAGCGTTGG TGGATTTTTG 60
GTGATGATGA GATTCTTAAT ATTCAAAGAT TTTTGCAAAG ATTTT 105

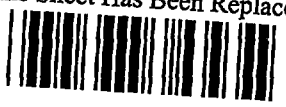
(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

This Sheet Has Been Replaced



(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158

```
GTGGCGCGTC TTGTGGTTAA AAGGCGTAAA ATTGATTATA AACAAAGCAT TCAATCTGAC      60
TCTCAATACT TGCAAGCGAS CTTGAATCAG TTTGAAAATA AAGAAGTGTA TGAGAATCAG     120
TATTTTTTAG TTTTAGAAAG CACTCACTCT TTGCATGGCG TTTTGGAGCA TAAGAAAAAA     180
TCTTTCATGC ACGCTAATAG AGAAAATTTT AAGGATATTC TCTCTTATAA AGCGCATTTT     240
TTGCAAGAAA CTTTAAAAAG CTTAGAAATC CAGCTCAAAA ACTATGCCCC CAAACTCTTA     300
AACTCTAAAG AGGTTTTGAA TTTTTATGCA GAATATATTA ATGGGTTTGA ACTCCCTTTA     360
AAACCCCTAG TAGGGGGGTA TTTGAGCGAT AGCTATATCG CTAGTTCTAT CACTTTTGAA     420
AAAGATTATT TCATTCAAGA AAGCTTTAAT CAAAAAACCT ATAACCGCTT GATTGGCATT     480
AAAGCTTATG AGAGCGAAAG GATCACTTCT ATAGCGGTGG GAGCGCTTTT ATACCAAGAG     540
ACGCCTTTGG ATATTATCTT TTCCATAGAG CCTATGAGCG TCAATAAAAC GCTGAGTTTT     600
TTAAAAGAGA GGGCCAAGTT TAGCATGTCT AATCTTGTTA AAAACGAGCT ATTAGAATAC     660
CAAGAATTAG TCAAAACCAA ACGATTATCC ATGCAAAAAT TCGCCCTAAA CGTTCTTATC     720
AAAGCCCCCA GTTTGGAGGA TTTAGACGCT CAAACCAGCT TAATTTTAGG GCTTTTATTT     780
AAAGAAAACT TAGTGGGCGT TATAGAAACT TTTGGCTTGA AAGGGGGGTA TTTTTCCTTT     840
TTCCCTGAAC GCATCCATTT AAACCACCGC TTGCGTTTTT TAACCTCTAA AGCCCTAGCG     900
TGTTTGATGG TGTTTGAAAG GCAAAATTTA GGTTTTAAGG CTAATTCATG GGGGAATAGC     960
CCTTTGAGCG TGTTTAAAAA TTTGGATTAT TCCCCTTTTT TATTCAATTT CCACAACCAA    1020
GAAGTGAGCC ATAATAACGC TAAAGAAATT GCCAGAGTGA ATGGGCATAC TTTAGTTATA    1080
GGGGCAACCG GAAGCGGTAA AAGCACGCTG ATTAGCTATT TAATGATGAG CGCTTTAAAA    1140
TACCAAAACA TGCGCCTTTT AGCTTTTGAC AGGATGCAAG GGTTGTATTC TTTCACCGAA    1200
TTTTTTAAAG GGCATTACCA TGACGGCCAA TCTTTTAGTA TCAACCCCTT TTGTTTAGAG    1260
CCTAATTTGC AGAATTTAGA ATTTTTGCAA TCCTTTTTTT TGAGCATGTT GGATCTTGCC    1320
CCTTCAAGGG ATAAAGAAGC CTTAGAAGAC ATGAATGCGA TTTCTGGCGC GATTAAGAGC    1380
CTTTATGAGA CCTTATACCC CAAAGATTTT AGTTTGCTGG ATTTTAAAGA AACGCTTAAA    1440
AGAACCTCAT CTAACCAATT GGGCTTGAGT TTAGAGCCGT ATTTGAATAA CCCCCTTTTT    1500
AACGCTTTGA ATGACGCGTT CAACTCCAAC GCTTTTTTAA ATGTGATAAA CCTAGATGCG    1560
ATCACCCAAA ACCCTAAAGA CTTAGGGCTT TTAGCCTATT ACTTGTTTTA TAAGATCTTA    1620
GAAGAGTCTA GGAAAAACGA CAGCGGCTTT TTGGTTTTTT TAGACGAATT TAAATCCTAT    1680
GTGGAAAACG ATTTGTTAAA CACTAAAATC AACGCTTTAA TCACGCAAGC CAGGAAAGCT    1740
AATGGCGTGG TGGTGTTGGC CTTGCAAGAC ATTTACCAAC TTAGCGGGGT TAAAAACGCC    1800
CATAGTTTTT TAAGCAACAT GGGGACTCTC ATTTTGTATC CGCAAAAAAA CGCTAGGGAA    1860
TTGAAACACA ATTTCAATGT GCCTTTGAGC GAAACTGAAA TTTCTTTTTT AGAAAACACC    1920
CCTCTGTATG CCAGGCAGGT TTTAGTCAAA AATCTGGGTA ACGGGAGTTC CAACATGATT    1980
GATGTGAGTT TGGAGGGCTT GGGGTGTTAT TTGAAAATCT TTAATTCAGA TTCCAGTCAT    2040
GTCAATAAAG TGAAAGCGTT ACAAAAAGAC TACCCTACAG AGTGGCGTGA GAAACTTTTG    2100
AAGAGT                                                               2106
```

(2) INFORMATION FOR SEQ ID NO:159:

(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

This Sheet Has Been Replaced



(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:159

```
ATGCAAGAAG ACTGGCAAGC CGTCCAAGAC ACCATTAAAG TGGTTTCAGA TGTGAAAGCG      60
GGGAATTTTG CGGTGCGCAT CACGGCTGAA CCCGCAAGCC CTGATTTGAA AGAATTGAGA     120
GACGCGCTAA ATGGGATCAT GSAYTATTTG CAAGAAAGCG TAGGGACTCA CATGCCAAGC     180
ATTTTCAAAA TCTTTGAAAG CTATTCTGGC TTGGATTTTA GAGGGCGGAT CCAAAACGCT     240
TCGGGTAGGG TGGAATTGGT TACTAACGCT TTAGGGCAAG AAATCCAAAA AATGCTAGAA     300
ACTTCGTCTA ATTTTGCCAA AGATCTAGCG AACGATAGCG CGAATTTAAA AGAATGCGTG     360
CAAAATTTAG AAAAGGCTTC AAACTCCCAA CACAAAAGCC TGATGGAAAC TTCCAAAACG     420
ATAGAAAATA TCACCACTTC CATTCAAGGC GTGAGCTCTC AAAGTGAAGC CATGATTGAA     480
CAAGGGAAAG ACATTAAAAG CATTGTAGAA ATCATTAGAG ATATTGCCGA TCAAACGAAT     540
CTATTAGCCC TAAACGCTGC TATTGAAGCC GCACGAGCCG GCGAGCATGG CAGAGGCTTT     600
GCGGTGGTGG CTGATGAGGT GAGGAAGCTC GCTGAAAGGA CGCAAAAATC CCTCAGTGAG     660
ATTGAAGCCA ATATTAATAT TCTCGTTCAA AGCATTTCAG ACACGAGCGA AAGCATTAAA     720
AACCAGGTTA AAGAAGTAGA AGAGATCAAC GCTTCTATTG AAGCCTTAAG ATCGGTTACT     780
GAGGGCAATC TAAAAATCGC TAGCGATTCT TTAGAAATCA GTCAAGAAAT TGACAAAGTC     840
TCTAACGATA TTTTAGAAGA TGTGAATAAA AAGCAGTTT                            879
```

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160

```
ATGCCTAAAA GTTTCACCTT ACCGACTTTC GTGTGGTGTT TGTTTGTGGG GGTTATCTTA      60
AGGAACGCTT TGTCGTTTTT TAAAATCCAT AGCGTGTTTG ACAGAGAGGT TTCAGTTATA     120
GGGAATGTGA GCTTGAGCCT GTTTTTAGCT TACGCT                               156
```

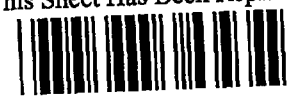
(2) INFORMATION FOR SEQ ID NO:161:

(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

This Sheet Has Been Replaced



(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:161

```
GTGGGGCTTT TAAATTCTAA GGCGTTCAAA CCCTACCGCA AGATTTTGCA AATGGTGTTT     60
CAAGACCCCT ACGCATCATT AAACCCTCGC TTAAGCATTC AAAGCATTTT AATAGAAGCT    120
TTGCGCTTTG CTTACCCTAA AGCTTCACAA CAAGAATGGC ACCATTTAGC TGAACTTTGC    180
TTAGAAGAAG TGTGTTTAAA CCCTGAATTG CTTAACTTTT ACGCTTATGA GCTCAGCGGA    240
GGGGAGCGCC AAAGAGTGGC GATCGCTAGA GCGATTGCCT TAAAACCTAG AATCATTCTT    300
TTAGATGAGC CAACCTCTGC TTTAGACAAA AGCATTCAAA AAAGCGTGTT GGAATTATTG    360
TTGAATTTAC AAGAAAAGCA GGATTTGAGC TATTTGTTTA TCAGCCATGA TTTAGATGTG    420
ATCAAAGCTT TTTGCGATAG GGTGTTAGTG GTGAGTGAGG GGAAAATCGT GGAAACAGGC    480
GCTATTGAAG AGGTGTTTGA CAACCCCAAA CACGCTTATA CCAAGCGTTT GTTGGAATCC    540
AGGCTT                                                               546
```

(2) INFORMATION FOR SEQ ID NO:162:

(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:162

```
GTGAGTTTGA TTAAAGTTAG TGGTGATAAA AAAGTGATTG AGGTTTCTAT TCCTTTAACT     60
TCCATTTCAG GCAAAGCGCG TGTGAAAATC AGACATGCCT TTAGCGATTA TGGTATTTCA    120
ACAGCGACTA GAAAAATCCC TTTTAGTTTA AAGCATTATG TAGAGTGGCA GATCGGTTAT    180
GATGTCCCCA TTAAAGATAA AGAAAAATTT GAACTCACTA CTTTAAAAGA TGAAAAATAT    240
CATTTTTTAG GGGCTAATAA TAAAGTAAAA ACTCTTTATG AATTGAGCGA AATGATTTAT    300
TACGCTAAGC GATTGGGTTT AATCAGTTTA GAAAATTTAG AAAATACTTT AAAATTTTTA    360
GAAAAACAAA AACAATTTAT AGAAGATAAT TTTATGATTA CAAGAGAAAG ATTTAGATCG    420
CATCAATTTG GTGGCATGGA TTTTGAACTC TCACGCATTT CTTATCCTTT GCTCATTCAT    480
TCTTTTGATG ATAATGAGTT GAGCGAAATA GTTATTAAGG AACAACAATA TGGCTCTAAA    540
ACCCAAGCCA TGCTGTATTT TTGCTTTTCT ATTTTGGAGT TAAAAACCGC TACCCCCTTA    600
TTAAACAGAA CCGCTATGCC CAAAGAACAT GCCCTTTTGA TTATCCATGA AACCAACGCT    660
CTTGTGTTTT TAGAAATGCT TAAAATTTTT GGACTTTTAA GCCAAGTGCA CCATAACGAT    720
GTGTTWAAGA TTTTWGAAAA AATACTTCAA AAT                                  753
```

This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163

GTGATCACGG CGTGTTTTAA TAGYGAAAAA ACCATTGAAG ACACCATTCT TTCCGTGCTT 60
AATCAAACTT ATAAAAACAT TGAATACATC ATTATAGATG GGGCTAGCGC GATAGCACTT 120

(2) INFORMATION FOR SEQ ID NO:164:

(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:164

GTGTTTGTAG GGCTTTATCA TGGGGCAAGC ATCTTTGATT TAAAATTTGA AGTCTATCTT
ACTATGCTAA TCTCTTTAAT GCCCTTTGTG GCTACGATTT ATATCAATTT CCCAAAAACC
ACAGAAACTT CGCATGGCTA TGCGAGATGG GCTAATGTTA AAGATATAGA ATGCTTTAAA
ATTTTTAGCA AAGAGGGCTT TTGTAAAGTG GTGCATAGAT TAGGGGTGCA ATTTGATAAT
GGCTTTATTC TAGGTAAATT TGGTTTTCCA AAGCTTAGAA ATGTGTGCTA TGACAAGCCC
TTAGGAACGA TGATTGTTGC ACCCCCTGGT GCGGAAAAAC TGCATGTGTG GCTTTGCCAA
ATTTAT

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

This Sheet Has Been Replaced



(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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:165

```
ATGAAACGCC TTGCTGTTGC GCTTATTTTG GTGTTGGGAG TGGTGTGGGG GAAATCCTTG      60
CCTAAGTGGG CAAAAGATTG CTCAAAAGAG ATGCGGATTG AAAAGACCCA AACCAAAGAT     120
GAAAAAATTT TAGTGTGTGG GATGAGCGAT ATATTGCTTT CAGATATGGA TTATAGCTTG     180
TCCTCAGCCA GACAAAACGC CTTAGAGAAA GTGATGGAAG CTTTCAAGGG GGATAGAATA     240
GAGATTAAGG CTGGTGAGCT AAAGGCCACT TTTATTGATA CGGATAAAGT TTATGTGCTT     300
CTAAGAATCA CTAAGAAGCA TGTCGCTTTA ATGAATGAG                             339
```

(2) INFORMATION FOR SEQ ID NO:166:

(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:166

```
ATGAACCCCC AGATTCAACC CGCCACTAAA AAACCCTTAA AATCCCTTTT AGCCGCTAGT      60
TCAGGCAATT TAGTGGAATG GTATGATTTT TACGCTTATG CGTTCCTTGC TCCTTATTTC     120
GCTAAGGAAT TTACCCACAC CAATGACCCT ACTCTAGCGC TCATCTCAGC TTTTTTAGTT     180
TTTATGCTAG GGTTTTTCAT GCGCCCTTTG GGGAGTTTGT TTTTTGGTAA ATTGGGGGAT     240
AAAAAGGGGC GTAAAACTTC CATGGTGTAT TCCATTATCC TTATGGCGCT AGGCTCTTTC     300
ATGCTCGCAT TGCTCCCCAC TAAAGAAATC GTAGGGGAAT GGGCGTTCTT GTTTTTATTG     360
TTAGCCAGGC TTTTACAGGG CTTTAGCGTG GGAGGAGAAT ATGGCGTGGT CGCCACTTAT     420
CTCTCTGAAT TAGGCAAGAA TGGTAAAAAA GGTTTTTATG GCTCTTTCCA ATATGTAACT     480
TTAGTGGGAG GGCAACTCTT AGCTATTTTT TCGCTCTTTA TCGTTGAAAA CGTTTACACG     540
CATGAGCAAA TCAGCGCGTT TGCTTGGCGT TATTTATTCG CTTTAGAGGG TATATTAGCC     600
CTACTCTCGC TCTTTTTGAG AAATATCATG GAAGAAACTA TGGATAATGA AGCGACTCCT     660
CAAAAAAAGA CTAATGTAAA TAATACAAAA GAAACCCATA TCAAAGAAAC CCAAAGAGGC     720
AGTTTAAAGG AATTGCTCAA CCATAAAAAA GCCTTAATGA TAGTCTTTGG GCTAACTATG     780
GGAGGGAGTT TGTGCTTTTA CACTTTTACG GTGTATTTAA AAATCTTTTT AACCAACAGC     840
TCATCGTTTA GCCCTAAAGA AAGCAGTTTT ATCATGCTTT TAGCGCTCTC TTATTTCATC     900
TTCTTACAAC CCTTATGCGG GATGCTTGCG GATAAAATCA AACGCACCCA AATGCTGATG     960
GTTTTTGCGA TCACAGGGCT TATTGTAACG CCTATTGTCT TTTATGGTAT CAAGCATGCC    1020
```

```
ACTAGCGTGT ATGAAGCCCT ATTTTATGAA ATACTCGCAT TGAGCAGCAT GAGTTTTTAC    1080
ACTTGCATTG CTGGGGTTAT TAAGGCGGAA TTATTCCCTG AACATGTGCG AGCGCTTGGC    1140
GTGGGTTTAG CCTATGCGAT CGCCAATGCG CTTTTTGGAG GGAGCGCGAG TTATATAGCG    1200
TTAGAGTTCA AACAGCATGG TTTTGAAGAG GGGTTTGTGG GCTATGTCAT GTTGAGTATT    1260
GTTATCTTTA TGGTTATGGT TATCATATTC CCTAAAAAAA CCTATTTGGA G              1311
```

(2) INFORMATION FOR SEQ ID NO:167:

(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:167

```
ATGGACATTA GCATTTTTAG AGAATACGAT ATTAGAGGCA TTTACCCCAC CACTTTAGAT      60
GAAAATACGG CTTTTAGTAT CGGCGTGGAG TTGGGAAAAA TCATGCGAGA ATACGATAAA     120
AGCGTGTTTG TAGGGCATGA CGCAAGGGTG CATGGGCGTT TTTTGTTTGA AGTTTTGAGC     180
GCGGGGCTGC AATCAAGCGG CTTGAAAGTG TATGATTTAG GGCTAATCCC CACACCGGTA     240
GCGTATTTTG CGGCCTTTAA TGAAATAGAC AATATCCAAT GGCCC                      285
```

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

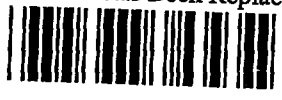
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168

```
GTGTGCGACA TTTTTTCTGA TGGCGTTTTA TTGGACAAAG CGTTAGTGAT TTATTTCAAA      60
GCCCCCTATA GTTTCACCGG TGAAGATGTG TGCGAAATCC AATGCCATGG AAGCCCCCTT     120
TTAGCGCAAR ATATCCTTCA AGCTTGCTTG AATTTAGGGG CTAGGCTCGC TAAAGCGGGG     180
GAATTTAGCA AAAAAGCCTT TTTAAACCAT AAAATGGATT TGAGCGAGAT TGAAGCGAGC     240
GTTCARCTCA TCCTTTGTGA AGRTGAAAGC GTTTTAAACG CTCTAGCCAG GCAGCTTCAA     300
```

This Sheet Has Been Replaced



GGGGGA 306

(2) INFORMATION FOR SEQ ID NO:169:

(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:169

ATGTTTAAAA AAATGTGTTT GAGCCTGCTA ATGATAAGCG GTGTTTGTGT GGGGGCAAAG 60
GATTTGGATT TCAAGCTGGA TTATCGCGCG ACTGGGGGGA AATTCATGGG GAAAATGACG 120
GACTCTAGTC TTTTAAGTAT CACTTCTATG AACGATGAAC CGGTGGTGAT TAAAAACCTT 180
ATTGTCAATA GGGGAAATTC AGTCGAAGCG ACTAAAAAAG TAGAACCCAA ATTTGGCGAT 240
AAGTTTAAAA AAGAAAAACT CTTTGATCAT GAATTAAAAT ACTCGCAACA GATATTTTAC 300
CGCCTGGATT GCAAGCCTAA CCAATTGTTA GAAGTTAAAA TCATCACGGA CAAGGGCGAA 360
TATTACCATA AATTTTCCAA A 381

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

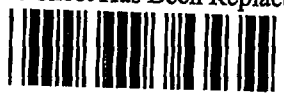
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170

ATGACCTTGA AGCCATATCC AACCAAAGAG ACTGGTCTTG CTAGCCAATT ATCTGGGCAA
TGGTTTTTTC AGCTTTCGTT ATTTAATAAA ACAAACTTTA ATCCTAATAA AATTTGGATT
CCTTTAGAGT TCAATAAAAG ATCAAAAATA AAGTTTGATA AAGATTTAGA AATCTATTTT
GATAGTCATG AATCGTTCAA TATCTCTAAA AAATACTTGC AAGAAATAGA TCAAGAATCA
CTAAAAAAGA TCAAACAATC AAAAGATTTT TTTTCAATTC AAAAAATAGA GAGTAAGCAT
GATAATAACG ATATACTGCA ACTTGAATTT TTTGAGAATG ATACAAGTTT TCTTTTTGCT
AAAGGAAGTT TTGCAGAAAT TTTAGAATAC AACATGCAAT TAAAAATAGA TTCTTTAATT

This Sheet Has Been Replaced



ACAAAAGAAT TTAATAAGCT TTTAGCGATC GTTCAAGATA GTCCCCAAGA TAGTTACCAA 480
TTAAAAATTC GTGTCCGACA TAACAATAAG CTTCCTAGAG AGAAATATAC GGAACATGAA 540
ATAAAACTTG AAGTTTATGA TTGCAGAAAA TCCCACGATC ACAATGAGCC AATCATCTTA 600
AGCCAGCAAA GCACCGGCTT CCAATGGGCG TTTAATTTCA TGTTTGGCTT TCTTTATAAT 660
GTGGGATCAC ATTTTAGTTT TAACCATAAT ATTATCTATG TCATGGACGA GCCAGCCACT 720
CATTTGAGCG TGCCAGCCAG AAAGGAGTTT AGGAAATTTT TAAAAGAATA CGCTCATAAA 780
AATCATGTTA CTTTTGTTTT AGCCACCCAT GACCCCTTTT TAGTGGATAC GGATCATTTA 840
GATGAAATAA CTATTGTGGA AAAGGAAACA GAAGGCTCTG TAATTAAGAA TCACTTTAAC 900
TATCCCCTAA AAAATGCAAG CAAAGACTCC GACGCTTTGG ACAAAATCAA ACGCTCTTTA 960
GGAGTGGGCC AGCATGTTTT TCATAACCCC CAAAAACACC GAATCATTTT TGTAGAAGGC 1020
ATCACGGATT ATTGTTATTT GAGCGCTTTT AAATTGTATT TGCGTTACAA AGAATACAAG 1080
GACAACCCCA TTCCTTTCAC TTTCTTACCC ATTTCAGGGC TTAAAAACGA TTCAAACGAT 1140
ATGAAAGAAA CCATTGAAAA ACTTTGCGAG TTAGACAATC ACCCTATTGT TTTGACAGAC 1200
GATGACAGAA AATGCGTTTT TAACCAACAA GCAACGAGCG AACGATTTAA AAGAGCTAAT 1260
GAAGAAATGC ATGATCCCAT CACCATCCTA CAACTCTCAG ACTGCGATAG GCATTTCAAA 1320
CAAATTGAAG ATTGTTTCAG CGCAAACGAT AGAAACAAAT ACGCTAAAAA TAAGCAAATG 1380
GAATTGAGCA TGGCTTTTAA AACAAGGCTT TTGTATGGCG GAGAAGATGC GATAGAAAAA 1440
CAAACAAAAA GAAATTTTTT AAAATTATTC AAATGGATTG CATGGGCTAC AAACTTGATC 1500
AAAAAC 1506

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171

GTGTATTTTT TTCTGGCATT GAGCGGGGAA AAAGTCTTAC TGCCCGTCAT TGGCGGTTTA 60
GAAAAAAACG CGCTAGAAGC CGGGCTGTTA AAGGGGGATA GAATCCTTCT ATCAACCATC 120
AAAAAA 126

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1050 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172

```
ATGGAAAATT TTAAACTCAT CAACTTTTTT ACCGGTCAAA ACGATGCGGG TAAAACCAAT      60
CTTTTAGAAG CTCTTTATAC CAACACAGGC CTTTGTGATC CTACTGCCAA TCAAGTCAGT     120
CTTCCTCCTG AACATGCCGT GAATATTAGT GAATTCAGAA AAATCAAACT CGATGCCGAC     180
AACCTAAAAA CCTTTTTTTA TCAAGGAAAC ACCGCTAATC CCATTAGTAT CCGCACTGAA     240
TTTGAACATG CTACTATCCC TCTTACTATC CAATACCCCA CACAAACCAG TTACAGCAAA     300
GACATCAATT TGAATAGCGA TGATGCTCAT ATGACAAACC TTATAAACAC AACAATAACG     360
AAGCCACAGC TCCAATTTTC CTACAATCCA TCCCTTTCCC CCATGACAAT GACTTATGAA     420
TTTGAAAGGC AAAACCTAGG TTTAATCCAT TCTAATTTAG ATAAAATCGC TCAAACCTAT     480
AAAGAAAATG CGATGTTTAT TCCTATAGAA TTATCTATTG TTAATTCTCT TAAAGCATTG     540
GAAAATTTAC AATTAGCAAG CAAAGAAAAA GAATTGATTG AAATCCTACA ATGTTTCAAC     600
CCTAATATTT TAAATGCTAA TACAATAAGA AAGTCTGTCT ATATCCAAAT CAAAGATGAA     660
AACACACCGC TAGAAGAAAG TCCCAAAAGG CTTTTAAATT TGTTTGGTTG GGGTTTTATC     720
AAATTCTTTA TTATGGTGAG CATTCTTATA GACAATCGTG TCAAGTATCT TTTTATTGAT     780
GAAATAGAAA GCGGTTTGCA CCATACAAAA ATGCAAGAGT TTTTAAAAGC TCTGTTTAAG     840
TTAGCTCAAA AATTACAGAT TCAAATTTTT GCCACCACGC ACAATAAGGA ATTTTTATTA     900
AACGCCATCA ACACGATATC CGATAATGAA ACGGGAGTTT TTAAAGACAT AGCCTTGTTT     960
GAGCTTGAAA AAGAAAGCGC TTCTGRCTTT ATCAGACACA GCTATTCTAT GCTAGAAAAA    1020
GCGCTTTATA GGGGTATGGA GGTTAGAGGC                                     1050
```

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173

```
ATGGATTTTA AAAAATGCCC TAATTTTGAA AAAAAATGTG CGTTTCTTTG TTTCTCAAAT      60
TTGGTTTTAC TTATTGAAAT CCACTCTAAA GGACTACACA TGCAAAAAAA GAAACCCAAG     120
AACCCGCAAC CGAATTTATT TAGCATCTTA GATAAGGGCG ATGTTGCAAC AAACAATCCT     180
GTTGAAGAGT CAGACAAGGC CAATAAAATA CAAGAGCCAC TCCCTTATGT CGTGAAAACG     240
CAAATCAATA AAGCAAGCAT GATTTCTAGA GATCCTATTG AATGGGCAAA GTATTTAAGC     300
TTTGAAAAAC GAGTCTATAA GGATAATAGT AAAGAAGATG TCAATTTCTT TGCCAATGGT     360
GAGATAAAAG AAAGTTCTCG TGTTTATGAA GCGAATAAAG AAGGGTTTGA AAGGCGCATC     420
ACTAAAAGAT ACGATCTGAT TGATAGAAAT ATTGATAGAA ATAGAGAATT TTTTATAAAA     480
GAAATTGAAA TTCTAACCCA CACAAACAGC TTAAAAGAAT TGAAAGAGCA AGGGTTAGAA     540
ATCCAATTGA CCCACCATAA TGAAACGCAT AAGAAAGCCT TAGAAAATGG CAATGAAATC     600
GTTAAAGAAT ACGACCATCT TAAAGATATT TACCAAGAAG TAGAAAGAAC AAAAGATGGT     660
GGATTGGTAA GAGAAATAAT CCCCAGTATT TCTAGCGCTG AGTATTTCAA GCTTTACAAC     720
AAACTGCCTT TTGAATCAAT AAACAATGAA AATACCAAAC TGAATACTAA CGACAATGAA     780
GAAGTTAAAA AACTAGAATT TGAATTAGCT AAAGAAGTGC ATATTTTAAT CCTAGAGCAA     840
CAATTGCTTT CAGCAACAAA TTATTATTCT TGGATAGATA AAGATGATAA TGCGAATTTT     900
```

This Sheet Has Been Replaced



```
GCTTGGAAAA TGCATAGGCT TATCAATGAA AATAAACTCA AAGAAAACCA TCTCAGCGCC     960
AATAACGCTA ATAAGATTAA GCAATTTTTC TTTAATAATG GTTCTATTTT AGGCTGGACT    1020
AAAGAAGAAC AAAGCGCTAT ACAAGAAAAC AGAGATTATT CTTTAAGAAG CGCTCTTTTA    1080
AGTTTAGAAG AAATCGCTCA AGCAAAAATT GAATTGCAAA AATACTATGA AAGCGTTTAT    1140
GTTAATGGTG ATGGGAATAA AAGAGAAATC AAGCCTTTTA AAGAAATTTT AAGAGACACC    1200
AACAATTTTG AAAAAGCTTA TAAGGAGCGT TATGACAAAT TGGTAAGCTT GAGTGCAGCA    1260
ATCATTCAAG CTAAAGAGGG TGGTAATGAG CGACAAAATT CTAGTGCAAA TAACAATAAC    1320
CCTATTAAAA ATACAATAGA GACTAATACT TCTAACAATA TTATTCAAAA TAATGATAAT    1380
ATAATCATCC AAATT                                                     1395
```

(2) INFORMATION FOR SEQ ID NO:174:

(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:174

```
ATGGCGCTTG AAGTGGTTTT ATGGGATTTT GATGGCGTGA TTTTTGACAG CATGCATTTA      60
AAATATGAAG GGTTTAAGGC GTTGTTTCAA AAGCATGGCA ACGATAGTAA AGAGGGTTTG     120
AAACAATTTG AAGTTTATCA CTATCAAAGT GGGGGGATTT CAAGGAATGA AAAGATCCAA     180
TATTTTTATA ACGAGATTTT AAAAACCCCT ATCGCTCAAG AAGAAATAGA TGCATTAGCC     240
CTAGAGTTTG GCGCTATCAT AGAGCAAAAG CTTTTTGATA GGGGGCATTT GAATAGCGAR     300
GTGATGGCGT TTATTGATAA GCATTATCAA AATTATATTT TCCATATCGC TTCAGCGGCC     360
TTGCATAGCG AATTGCAAGT GTTGTGCGAG TTTTTAGGGA TTACTAAGTA TTTTAAGAGC     420
GTTGAAGGGA GTCCGCCTGA TAAACCCAAG ATTATCGCTA ATATCATTCA AAAATACGCC     480
TATGACCCAA GCCGTATGCT AATGATAGCG ATAGCGTCAA TGATTATGAA AGCGCTAAGG     540
CTAATAAAGT GGCGTTTTTG GGCTATAACA GCAAGGTTT                            579
```

(2) INFORMATION FOR SEQ ID NO:175:

(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

This Sheet Has Been Replaced



(B) LOCATION 1...423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175

```
ATGCTCAAAA AAAAGATTGA TTTGCATAAA GATTCTATTA GGAAGCTCTT TTTTTATTAC      60
TTCATCCCTT TAGTTTTTTC TATGATCTCA CTTTCTACTT ACTCTATGGT AGATGACATG     120
TTTGTGGGCA AAAAACTGGG TAAAGAAGCT ATCGCTGCGG TCAATATCGC ATGGCCTATT     180
TTTCCAGGAC TCATTGCGTA TGAATTGCTT TTTGGTTTTG GGGCAGCGAG CATTGTGGGG     240
TATTTTTTAG GTCAAAATAA AACCCATAGG GCTAGGCTTG TGTTTAGCAG CGTGTTTTAT     300
TTTGTCGCTC TAAGCGCCTT TATTTTGAGC ATGGCGTTAT TGCCTTTTAG CGAAAATATC     360
GCGCAGTTTT TTGGGAGCAA TGACGCTTTA TTGAACATGT CAAACGCTAT ATTGAAATCA     420
TTT                                                                  423
```

(2) INFORMATION FOR SEQ ID NO:176:

(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:176

```
GTGAAATGTT TATTAATAAA AAAATCACTT CTATTTGCAC TGAAACCATT GCCGGACCTA      60
AAAACGACTA CCCCTATTTT AGCGCCTATG AGCGTGGTGG CTGGGAGGTT GRCTSCSCAT     120
TTAGTCCAGC ATTATTTACT GGCTTTAGAG CATGTTAAAG GGTTTATGGG TAAGGGGGTC     180
ATACTAGGGG GTTTGTCGGG TGCSCAAAGG GCTAAAATCG TCGTAATTGG AGGCGGTGTG     240
GTTGGCATGG AGAGCGCGAA AGTCTTAARC CAAATGGGGR CTAAAGTAAC GATTTTAGAA     300
TTAGACTACG CTAAATTACA AAACCACCCT TATTATCATT TGTATGATTT AGAAGTCTTA     360
AGCGTGAATG AAGCCAATAT CATTCAAGCC TTAAACGGGR CGGTGGGGCT AGTGGGAGCG     420
GTRCTGGTTA CARCGAGCCA AACCCCTAAA GTGRTCTTAA GAAGGCATTT AAAATAC        477
```

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

This Sheet Has Been Replaced



(A) NAME/KEY: misc_feature
(B) LOCATION 1...1128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177

```
ATGCTTGCAA AAATCGTTTT TAGCTCATTG GTTGCGTTTG GAGTTTTGTC GGCTAATGTG      60
GAGCAGTTTG GTTCATTTTT CAACGAGATA AAAAAAGAAC AAGAAGAAGT GGCCGCAAAA     120
GAAGACGCTC TTAAAGCTCG CAAGAAGCTC TTAAACAATA CGCATGATTT CTTAGAAGAC     180
TTGGTTTTTA GAAAACAAAA AATCAAAGAG CTTGTGGATT ACAGAGCTAA AGTTCTTTTA     240
GATTTAGAAA ACAAGTACAA AAAAGAAAAA GAGGCTCTAG AGAAAGAGAC AAGAGGTAAA     300
ATCCTTACTG CTAAGTCAAA GGCTTATGGT GATCTAGAGC AAGCCTTAAA AGATAACCCT     360
CTTTATAAGA AACTTCTTCC TAACCCTTAT GCTTATGTTT TAAACCAAGA AACATTCACG     420
CAAGAAGATA AGGAGCGTTT GAGTTATTAC TACCCCCAAG TGAAAACGAG CAGTATTTTT     480
AAAAAAACTA CCGCTACCAC TAAAGATAAG GCTCAGGCTT TGCTTCAAAT GGGTGTGTTT     540
TCTTTAGATG AAGAGCAAAA CAAAAAAGCG AGCCGATTAG CTTTATCTTA CAAGCAAGCG     600
ATTGAAGAAT ATTCCAATAA CATTTCTAAT TTATTGAGCA GAAAAGAATT GGATAATATA     660
GATTATTACT TGCAGCTTGA AAGAAACAAA TTTGACTCCA AAGCAAAAGA TATTGCTCAA     720
AAAGCCACCA ACACGCTTAT TTTTAACTCG GAACGCTTGG CGTTTAGCAT GGCGATTGAT     780
AAGATCAATG AGAAATACTT AAGGGGCTAT GAAGCTTTTT CTAACTTGTT GAAAAATGTC     840
AAAGATGATG TGGAGTTGAA TACTTTGACT AAAAACTTCA CCAATCAAAA ATTGAGTTTC     900
GCACAAAAAC AAAAATTGTG TTTGTTGGTT TTAGACAGCT TCAATTTTGA TACCCAATCC     960
AAAAAATCTA TATTAAAAAA GACTAATGAA TACAATATCT TCGTAGATAG CGATCCTATG    1020
ATGAGCGACA AAACAACTAT GCAAAAAGAA CACTACAAGA TATTTAATTT CTTCAAAACA    1080
GTGGTTTCTG CATACCGGAA CAATGTTGCC AAGAATAACC CCTTTGAA                 1128
```

(2) INFORMATION FOR SEQ ID NO:178:

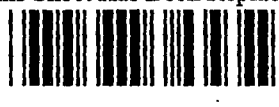
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1056 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178

```
ATGGATTTCG TAGGGTTTGA AGATTTAAAA TGCAAAGACA AAGAAAACTC TCAAAAAGTT      60
TTTGTGATCC GTAACGATAA GTTAGGCGAT TTTATTTTAG YGATTCCCGC TTTAATCGCT     120
CTCAAGCATG CTTTTTTAGA AAAAGGCGTA GAAGTGTATT TGGGCGTGGT TGTGCCTAGC     180
TATACCACCC CAATTGCTTT AGAATTCCCT TTCATTGATG AAGTTATCAT AGAAGACAAC     240
CATTTAGCCA CCACCCYCAA AAACCGCTCC ATTGACGCTC TTATCTTTTT ATTTTCTAAT     300
TTTAAAAACG CCAAACTCGC TTTCAGTTTG AGAAAATCCA TCCCTTATAT CCTAGCCCCA     360
AAGACCAAAA TCTATTCTTG GCTTTATCAA AAGAGAGTGC GCCAAAACCG CTCTTTATGC     420
TTAAAAACCG AATACGAATA CAATTTGGAC TTAATCCATG CGTTTTGTAA AGACTACGAT     480
CTCCCTAACG CTCAACTTAA AAAAATCGCA TGGAAGCTTA AAGACAAATC CAAAGAGCGA     540
TCCATCATCG CTTCAAAACT CAACGCTAAT GTTGATCTAT TGTGGATTGG CGTGCATATG     600
CATAGCGGAG GCAGTTCGCC CGTATTGCCC GCTTCGCATT TCATTGAGTT GATTGCAATC     660
TTGCATGAAA AATTAAGTTG TGAGATCATT CTTATTTGCG GGCCAGGCGA GAGAAAAGCC     720
ACAGAAGAAC TCCTTAAAGA AGTCCCTTTC GCTCACCTCT ATGATACGAG CCATAGTTTA     780
GTGGATTTAG CCAAATTGTG CGCGAATTTA AGCGTCTGTA TCGGGAACGC TTCAGGCCCT     840
TTGCATGTGA ACGCTTTATT TGACAACCAA TCTATCGGGT TTTACCCTAA CGAACTCACC     900
GCCTCTATTG CCAGATGGCG GCCTTTCAAC GAACAATTTT TAGGCATCAC CCCGCCTAAT     960
```

GGCTCAAACG ATATGGGTTT GATTGACATT CAAAAAGAAA GCGAAAAGAT TATGGGATTT 1020
ATCACAAAAA ATCTTTCTCA TCACATGCAA GAAAGA 1056

(2) INFORMATION FOR SEQ ID NO:179:

(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:179

GTGGGTGTCT TATCCCTCAA AATAGAGGCA ATTTCTAATT TTTATGGGTT ATGCGTTTTA 60
GGGGTGTTGT TAGCATGTTT TTATCTTTTA GACGCTTATT ATCTCATGCA AGAAAGGCTG 120
TTTAGGGAGC AATACCAATG GCTAATAAAA AACCGACTTA AAACCGATGA AAGGCTGTTT 180
GAAGTCTTCC CTATTCATCA AACTTGCCAA TCAACGCAAT TCTTATCGCC ATGCGTTCGT 240
TTAGTCTTTT CCCCTATTGG GCGT 264

(2) INFORMATION FOR SEQ ID NO:180:

(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

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180

ATGTCTTTAG GGGCAGTGGT CAGCTCACTC CTTTGCCATA AGTTAGAGGG GGCAATATTA 60
GATCTGAGAG CGTATCGTTS RARAGCTTAT TATCACGAAA ATAAAGATAC YTTGCTTATT 120
AAAGGCAAAA AACGCCTTCT TTACAATTAT ATTAAAGCCC ATATTGYTTT AAACTTGCTA 180
TGGACAATTA GAAATCGCAC GTRATCATTG GGAAAATTTA CTCAAAATCC AACCGAACAA 240
CCGCCCACGA ATAACCACAC CATTCAATGG AAAAACRGAA AACATTCTAA TGGACAGAAT 300
TTTAGTGATT GGTAT 315

(2) INFORMATION FOR SEQ ID NO:181:

(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:181

ATGAAAAAAA CAACCCTCTT TGTATTGGGC TTATTATTCA ATAGCTCTTT AAGCGCTGTT 60
GATGGGATTT CTCAAACCGA GCCTTCTTCT TTGAATTTGG CTGAAGATAG CCTGCCTTTG 120
AACCATTCTA ACGCCCAAAA ACTCTCTTTA AAAAACGCAT GGAATAGGGT GTTGTCTAAT 180
CATGAAGGCT TGCATGCGCA GAATACGCCA TTAAGCGAGC GAGTAAAA 228

(2) INFORMATION FOR SEQ ID NO:182:

(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:182

GTGAAAAAAG TAGAATCCAT GAATGTGGTG CCTTTCATTG ACATCATGCT TGTGTTGTTA
GTGATCGTGC TCACAACGGC GTCTTTTGTG CAAACTTCAA AGCTTCCTAT TAGCATTCCT
CAAGTGGATA AGGATAGCAC TGATTCTAAA GATGTGTTGG ACAAAAAACA AGTTACGATC
GCTATTTCTA ATAAGGGTTC TTTTTATTTT GACGATAAAG AAATCAGCTT TGAAAATTTA
AAACACAAGG TTTCCACTTT GGCTAAAGAC ACCCCTATTG TCTTTGCAAG GCGA

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

This Sheet Has Been Replaced



(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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:183

```
ATGGGATCTT ACACATTCCC TCTCATTTTG AAGCCAATAT TTATAAACAA AGTGCCTGTA      60
ACGATAGATT TTTATGCGAA CGCCAATTAC TTTTTGATTT ATGGTGCGTT AGCGAATGCG     120
GTGGTGGGGA GCATCAACGC CTTAAACGAT GAAATCAGGT TCAAACGCAA CGCCCAAATA     180
GAAGAAGCTG AATTAGGGAC AGACGGGATT AAGATTAAGC CTATCGCTTT GTATAACCCT     240
AGTGAGGGGT ATTTGAATTA CGCGCTCTCT AGCGTGTTTA TTTTCATCTT ACACCAGGTG     300
ATGCTCATTG CAAGCAGCAT GTTTACTAGC TCCAGGCGTT TGGAATTGGC CCTTTTAGAC     360
AAGAAACAAA TCGCTTTAAG GCTGTGCGCA AGACTCTTGG TGTTCATGGG GGCGTTTAGC     420
GTTTTTGTTT TATGGTATTT TGGGGCGCTG TTTTCTTTTT ATGGGATCGA ACGGCATGGA     480
AGCGCT                                                                486
```

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184

```
GTGATTATGA CTAAGCTTGA TGGCACTTCT AAGGGCGGAG CGATTTTARG CGTGCTGTAT      60
GAGTTGAAAT TACCCATTCT TTATTTAGGA ATGGGCGAAA AAGAAGACGA TTTGATCGCT     120
TTTGATGAAG AACGCTTTAT AGAAGATTTG GTTGATGCGG TGTTTGTGGA ACAA           174
```

(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)

This Sheet Has Been Replaced



(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

```
GTGTGTGGGG CTCATGGAAA GAGCAGTATC ACGGYCATGT TGAGCGCGAT TTGCCCCGCT      60
TTTGGASSGA TTATTGGGCG GCATTCTAAA GAGTTTGATT CCAATGTSSG AGAGAGCGCG     120
GATATGAGTT TGGTTTTTGA ASCCGATGAA AGTGATTCAA GTTTTTTTAT TTTCCAACCC     180
TTTTTGCGCG ATTGTGCC                                                  198
```

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186

```
GTGAATGAGT TAAAAAACTC TAAGCAAGTT TTAGGGAATG GGAAAGCCGA TCTGAGCAAC      60
GAAAACACCA AGGTAAGGCA GACTAAAACA RATCTGACTG AAAAAAATCA AAGGCTAACC     120
ACAGAAAAAA CAGAATTAAA TAACAAGATT ACTGGGTTAG CCACAGAAAA AGAAAGGTTA     180
GCCGCAGACA AAGAAAACCT AACTAAAGAA AGCAGACAAA GAAAACCTAA C              231
```

(2) INFORMATION FOR SEQ ID NO:187:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187

ATGGATTTAC AACAAATTGA TGAGCTAGAA AATAAGTTTG AAGAACAAGA AGAACAAGCC 60
CAAGATACCC CCCTAAAACA AGAGCCTAGC ACAAAGGAAG TAAAAATCCC TAAAAAAAGG 120
GGGCGTAAAA AAAGCTTGTT AGATGAAGAT AAGAAAAAGA GCTTTAACAT TGCCTTTAGT 180
CCTTGTGTGA TAAAAGAACT TAATGAATTT TTGCTAGAAT TTGGCTCATT TAAAGAGACA 240
CGAAGCACTT TTATTGAAGA AGCGCTTATT AGGCATTTAA AACACAGAAA AAACACCCAA 300
GAGCAAAAGC TTTTAAAGCA ACTAGAAAGA TTACAAAACA AAGAAAAGGG AATAATGAAA 360
ACAATGAACT TGAATGAATT TTTTACGCAT AAGATAATCT ATAAAGACAC CCCTTTAAAG 420
TTTAAGGATA CACTAGAACA AGAAATCAGC CAAGCTAGTT TAGTAGAGAA GTTAATCTTA 480
GCTAATATCT TAGCCAATAT GGTGTTTGCT AAGATAAGCA ATGAGAATGC CCCTAAAATT 540
CTTATTTTCA CGGCT 555

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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:188

ATGGGGTGCT ATGGGATAGG CATTAGCCGG TTGCTCAGCG TGATTTTAGA GCAAAAAAGC
GATGATCTAG RCTGTGTGTG GACGAAAAAT ACCGCTCCTT TTGATGTGGT GATCGTGGTT
TCTAACCTGA AAGATGAAGC GCAAAAAAAA CTCGCTTTTG AAGTGTATGA AAGACTGCTC
CAAAAGGGCG TTGATGCGCT GTTAGATGAC AGAGACGCTC GTTTTGGGGC GAAGATGAGC
GATTTTGAAT TGATTGGGGA ACGATTAGCC TTGATTGTTG GGAAGCAAAC TTTAGAGAGT
AAGGAATTTG AATGCATCAA ACGCGCTAAT TTAGAAAAGC AAACGATCAA AGACATAGGA
ATTAGAAGAA AAAATTTTAG AAATGTTAGC GAGCGAATAA GGGGAGGGAA TGGAAAAATT
AGTGATTGGC TC

(2) INFORMATION FOR SEQ ID NO:189:

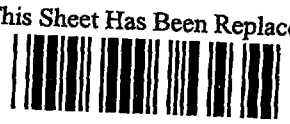
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189

```
ATGGAAATAC AACAAACACA CCGCAAAATC AATCGCCCTT TAGTTTCTCT CGTTTTAGCA      60
GGAGCGTTGA TTAGCGCCAT ACCGCAAGAG AGTCATGCCG CCTTTTTCAC GACCGTGATC     120
ATTCCAGCCA TTGTTGGGGG TATCGCCACA GGCACTGCTG TAGGAACGGT CTCAGGGCTT     180
CTTAGTTGGG GACTCAAACA AGCCGAAGAA GCGAATAAAA CCCCAGATAA ACCCGATAAA     240
GTTTGGCGCA TTCAAGCAGG AAAAGGGCTT                                      270
```

(2) INFORMATION FOR SEQ ID NO:190:

(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:190

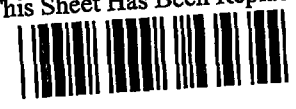
```
ATGTCAGAAA AAGAAAGACT GAATGAAGTG ATCTTAGAAG AAGAGAATAA TGGGAGTGGT      60
ACTAAAAAGG TGTTTTTGAT CGTGGCCATA GCCATTATCA TTTTGGCGGT GCTTTTAATG     120
GTGTTTTGGA AAAGCACCAG AGTCGCTCCT AAAGAGACTT TTTTACAAAC CGATAGTGGC     180
ATGCAAAAAA TAGGCAACAC TAAAGATGAG AAAAAAGACG ATGAGTTTGA AAGCTTGAAT     240
ATGGATTCTC CCAAACAAGA AGACAAGTTA GACAAAGTGG TGGATAATAT TAAAAAACAA     300
GAGAGTGAAA ATTCTATGCC CATTCAAACC GATCAAGCTC AAATGGAGAT GAAAACAACA     360
GAAGAAAAAC AAGAATCTCA AAAAGAATTA AAAGCTGTTG AGCCTATTCC CATGAGCACT     420
CAAAAAGAAT CTCAGGCTGT GGCTAAAAAA GAAACCCCCC ATAAAAAGCC TAAAGTAGCG     480
CCAAAAGATA AAGAAGCGCA TAAAGRTAAA GCTAAGCATG CAGCTAARGA GCCAAAAGTC     540
AAAAAAGAAG CTCGTAAAGA AGTTTCTAAG AAAGCTAATT CTAAAACCAA TCTTACTAAA     600
GGGCATTATT TGCAAGTGGG GGTTTTTGCG CACACGCCCA ACAAAGCCTT TTTACAAGAG     660
TTTAATCAAT TCCCCCATAA AATTGAAGAT AGGGGGGCTA CTAAACGCTA CCTYATAGGY     720
CCTTATAAGA GCAAGCAAGA AGCCTTAATG CATGCCGATG AAGTCAGCAA GAAGATGACT     780
AAACCGGTTG TCATAGAAGT GCGG                                            804
```

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(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:191

```
GTGGAATATT ATGCGTTTAA TTTCAGCGTG TTGGATTTTG TCTTAATGGG GAAAGCGACG      60
CATTTGAATC TGTTCGCTAT GCCTAAAGCT AAGCACATTA AAGAAGCCAC GAGCGTTTTA     120
GAGCGCTTGG ATTTAGAGTC CTTAAAAGAT CAAGGCATTA ACGATTTGTC CGGCGGTCAA     180
AGGCAGATGG TACTTTTAGC CAGAAGCTTG TTGCAAAGAA CGCCCTTATT GTTACTGGAT     240
GAGCCTACGA GTGCGTTAGA TTTAAAAAAC CAAGCCCTTT TTTTTGATGC GATTAAAGAT     300
GAGATGAAAA AACGAGAATT GAGCGTTTTA GTCAATATCC ATGATCCCAA TTTGGTTGCC     360
AGGCACTCCA CGCATGTGGT CATGCTCAAA GATAAAAAAC TTTTTTTGCA AGCTTCCACG     420
CCAATCGCTA TGACTTCACA CAATTTAAGC GCGCTTTATG ACACGCCCCT ARAAGCGATC     480
TGGCATGATG ATAAGCTTGT GGTGTATGCG TTG                                  513
```

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192

```
ATGATGGCAC ATTCACTTAT TTTGGTTTCA AAAACATCAC TCTCCAACCT GCTTATTTTT      60
GTGGTTCAAC CTGATGGGAA ATTGAGCATG ACTGATGCCG CCATTGATCC TAACATGACT     120
AATTCAGGAT TGAGATGGTA TAGAGTTAAT GAAATTGCAG AGAAGTTTAA GCTCATTAAA     180
GACAAAGCCC TTGTAACAGT GATCAATAAA GGCTATGGGA AAAATCCATT GACAAAAAAT     240
TACAATATCA AAAACTATGG TGAATTGGAG CGTGTGATTA AAAAGCTCCC TCTTGTCAGA     300
GATAAA                                                                306
```

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 711 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193

```
GTGCTGAATG AAGAGCAAAA TTCATTAGAA GAAAAAGGGG GCGAAAACAA AAACGAAAAA      60
GAAACCCCCC TAAAGGGCAT TCATTCTAAA ATCCCCTCTT TGAAGCAGGC TTTGGAGCAG     120
ACGATTAGTA AAATCAAAAG CTCTAAAGAG TTTTTCAAAC AGCTTCTACA CAATAAAAAA     180
AAGCTTTATA TCGCGCTTGG AATATTGCTT TCACTCATCG CGCTCATTGT GGCTTTGAGT     240
TTGTTACTAG GGCATAAAAA AGAAAATAAA CAAACTTCTT TACAAACTAA TACCGCCACC     300
ACCAATAACG AAACGCCTAA CGACACCAAT AACGCAGAAG CCGAAGGGCA AATAGAAAAT     360
TTAGACTTGC CTGATTTAAT CGGCAAAGAC TCTTTGAAAA GAAACGATGA AAGCCAAGTG     420
GATGCGATGA TGCAAAAAGC GAGCCTTTTG TATGAGCAAG GGCAAAAAGA TGAAGCCTTG     480
CATTTGTTTG ATAAGATCGC TTCTTTCTCG CAAGGGATTG CGAGCCATAA TCTAGGGGTG     540
ATTAAATTCA AAGAAAAGGA TTTTAATGGG GCGTTGGATT TGTTTGATTC CAGTATCGCT     600
TCTAAAGAAA ACGCGAGCGT GRGCGCGATT GATGCGTTAG TTACGGCTTA TCATTTGCAA     660
GATGCGGATT TGTATTATCA TTATCTAAAA ATTGTRAAGA GACACTTTGT A               711
```

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 675 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

This Sheet Has Been Replaced



(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194

```
ATGAATACAA GCTTATTGAC CCAAGCACAG GTTTTAAGCT CTAAAGAAAA TCAAATCCAT      60
CGCCTTTTGT TAGAGCTTTT AGAAGAGGCT AAGCTTCATT TTGAGCCTAA GCTTTATATC     120
ATTAACGCCC CTTACATGAA CGCTTTTGCG AGCGGGTGGG ATGAATCTAA TTCCCTTATC     180
GCTCTTACAA GCGCTTTAAT AGAGAGGTTA GATAGAGACG AATTAAAAGC CGTGATCGCT     240
CATGAGCTCA GCCACATACG GCACAACGAC ATCCGCTTGA CCATGTGCGT GGGGATTTTG     300
AGCAATATCA TGCTATTGGT GGCTAATTTT AGCGTGTATT TTTTCATGGG GAATCGCAAG     360
AATAGCGGGG CGAATTTAGC CCGAATGATT TTATGGGTTT TACAGATCAT CTTGCCTTTT     420
TTAACGCTCC TTTTGCAAAT GTATTTGAGC CGCACACGAG AATACATGGC CGATAGCGGG     480
GCGGCGTTTT TAATGCATGA CAATAAGCCC ATGATCAGAG CCTTACAAAA GATTTCTAAC     540
GATTACACCA ACAACGATTA TAAAGAAATA GATAAAAATA GCACCCGATC AGCGGCCTAT     600
CTTTTTAACG CTGAAATGTT TAGCACCCAC CCTAGTATTA AAAATCGTAT CCAATCCTTA     660
AGAAAGCGTG TGATC                                                      675
```

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1605 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195

```
ATGTTTAATA TTAAAAGGAC TTTTTTAATA ACGATCATAA GTTTTTTTCT CATTGTTCCT      60
AATTGGTTGA AAGCTATTGA TTTGCCCATT GTTTCAAATC TCAAAATTTA CCAAACAGTT     120
TATTGCATGC TGATACCGAG TTATGTTTTA ACCAACAAAA GTTTTGCAGA TATTTTGACA     180
GGCTATACAT CTATTGGTGC ATCAGGGAGT GGAAAGAGTT CAGGGCAGGG TGTGATCGAA     240
GCGCTTAGCA CACCATTAGC CACAAGTTTA GCCGCTAGCA ATCTGGTGAA ATATTTGAAT     300
ACTTTAGGTC CTTTATGGGG ATCGGCGTGG GCAAGTGTTG CTACAGCTAT ACAAGGTTTT     360
GCTCTAACGC CATCAAGTGG CTGTAATTTT GGTTGGAACG CATTGATAAA TAAAAACATA     420
GATGTATCCA TGGATAGCGT ACTAGACAAT TTGAGCAACA AGATTCAGAA TTTTACCAAA     480
GGCGGTGTTG AGGACAATGT GAAAGGCAAT ATTCTTTTAC AAATAATTGG CTCAATAACC     540
GCTCAAGCTT CTACGAATAT TACAGCTGAT GGTTTAATTT GGCTGATTGG TAAAGAATTC     600
ACTGCAAATA AACTGCAAAA CAACACTATA GCCATGCTTG CTTTTGCCGC ATTAGAATCT     660
GTTGTCAAAG GAGCGGACGC TGCTGTTCTT CCTGCATATG GTGTAGTCAA TCTGCCTGAT     720
ATTATCATAG GGCAAGGGTC ATATCTTGAT TTTGTTTCTT ACCTAATTTA TATTGTTTTT     780
GGGATTTTTG TTTTTATTTC TTTTATGAAA TTGAGAGATA TTTCAAACGG CATTCAGATT     840
AACATAGGTT TTGAATACAT GCGATTTGTT GGGGGGACAT TATTCAAAAT GGCGATGGTC     900
TCTTTTATCG CCTATGCAGG TTTTGGTTAT CTTTATAAAA TCTCTTATTC TATTTATTTT     960
GGTTTAGCAG GTGCTTTTGG GCTGAATCAA GTTCTTTTTT GGGCTTTAGA TTTAGTGCTG    1020
AATTACACTG TTAATTCAAT TTTACCTGCG GTAAGAGCTG TTTTTTCTAA TGTTGGCAAC    1080
AACGCTCCTA GTTTGTTACA AGGCTTGCAA GTGGCAGGTA TTTCTTTATT CGCTATTTTT    1140
ATGCAAGTAA CTATCATTAT GAGAATAAGC ACTGTTGTTG TGAAACCTTT GATAGCGGGG    1200
GCTTTTAGCG GTATTGTTTT CCCTATTGCA GTATGTTTGA TCGTGCTAGA TTGGTTCAAA    1260
GATTCTATGA AAAACATATT GATATGGTTT ATTAATAATC TGTTTATCTT GGTTCTAGCT    1320
ATTCCTATTT TGCTCTTTGG TGTTTTGGCA TTATTGGCAT TCAATTTGAC CATAACGCCC    1380
TCTGTTGCTA TACAAAACAT CAATCAAGGG GGATTGGGTA TCGATTCAAC TATTGCGAGT    1440
TTGATCACTC TATTTATTTT AAAAGGTTTC ATAGAGACGA TTATTGAGAG CGTCAATGCG    1500
ATCGTTAACA CCATTTTCAG CTCTGTCTCT ATGGATGGTA GCAGAATGGA TAGAGAAAGA    1560
GATGCCTTAA TGGTGGGAAG AGTTGGTGGA TCTATGTTTA AAGGA                     1605
```

(2) INFORMATION FOR SEQ ID NO:196:

(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

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196

```
ATGGCGTTTT GGCAGGCTAT CCGGTGGTGG ATTTTAAAGT TACCCTTTAT GATGGGAGCT      60
ACCATGATGT GGATTCTTTC AGAAATGGCG TTTAAAATCG CTGGYTYTAT GGCGTTTAAA     120
GAAGCGAGTC GTGCGGCTAA CCCGGTTTTA CTAGAGCCTA TGATGAAAGT GGAAGTGGAA     180
GTCCCTGAAG AATACATGGG CGATGTGATT GGCGATTTAA ACAGAAGAAG AGGGCAAATC     240
AATTCTATGG ACGATAGATT AGGTTTGAAA ATCGTGAATG CTTTCGTGCC GTTAGTGGAA     300
ATGTTTGGTT ATTCTACGGA TTTGCGATCA GCCACTCAAG GGCGTGGGAC TTACTCTATG     360
GAGTTTGACC ACTATGGCGA AGTGCCTAGC AATATCGCTA AGGAAATCGT GGAAAAACGC     420
AAAGGC                                                                426
```

(2) INFORMATION FOR SEQ ID NO:197:

(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:197

```
ATGCAGAATT TGCCGGGTAT GGCGAGAGCG GCGATGCTAA CCACATCATC AGCCCCAGCC      60
CCTGAGGGTG AAGGGGCTTT TAGAGCCATG AAAATGGCTT CAGAAATGGC GAAAGTGGAA     120
GTAGGCTATG TGAACGCCCA TGGGACAAGC ACGCATTATA ACGATTGGTA TGAAAGCATT     180
GCGTTAAAAA ATGTGTTGGC TCTAAAGAAA AAGTCCCTCC TGTTAGCTCC ACTAAAGGGC     240
AGATTGGGCT TGCTTGGGTG CTGCGGGGTT AGAAGCCGTT ATTCTATCAT GGCCATGAAY     300
CAAGGGATCT TACCTCCTAC CATTAATCAA GAAACGCCTG ACCCAGAATG CGAYCTGGAT     360
TATATCCCTA ATACAGCCAG AGAAAAGCAA GTGAATGCGG TGATGAGTAA CTCATTTGGT     420
TTTGGTGGCA CTAATGGTGT TGTGATTTTC AAAAAAGCC                             459
```

(2) INFORMATION FOR SEQ ID NO:198:

(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

This Sheet Has Been Replaced



(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:198

ATGATACTAA AAAATTTGAT TTTGTTATTT TTAGCAAAGA GAAAACTTAT TTTCATAGAA 60
GCTAATTTTT ATACCATTAG TGGGAGCAAG CTTAATGAAG TCGCAAGATC CTATCAAGAC 120
TTAGCTTTAA AATTTGAAGC ATTTCCTAAT TACGAATTTA TTTGGATAAC TGATGGCATA 180
GGTTGGCTAG ACGCTAAAAG CAAGCTCCAA GAAGCTTACA AATCTGTAGA AATCTATAAC 240
TTAAGCTATG TGAATGATTT TATATCAAAG GTGCAAAAA 279

(2) INFORMATION FOR SEQ ID NO:199:

(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:199

ATGGAATCAC AACTCATGAA ACTCGCCATT GAAACTTATA AAATCACTTT GATGATTTCT 60
TTACCGGTAT TATTAGCGGG CTTAGTGGTG GGGCTGTTAG TCAGTATTTT TCAAGCGACC 120
ACCCAAATCA ATGAAATGAC TTTGTCTTTT GTGCCTAAGA TTTTAGCCGT GATTGGGGTG 180
CTGATTTTAA CCATGCCGTG GATGACGAAC ATGCTTTTAG ATTACACCAA AACCTTAATC 240
AAGCTCATTC CTAAAATCAT AGGC 264

(2) INFORMATION FOR SEQ ID NO:200:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200

```
ATGAAATTTT TTACAAGAAT CACTGACAGC TACAAGAAAG TTGTAGTAAC TTTAGGGCTA      60
GTGGTAACAA CCAATCCTTT AATGGCGGTC ACCAGTCCTG CAACAGGCGT TACTGAGACT     120
AAAAGTTTGG TTATTCAGAT CATTTCTGTT CTAGCGATCG TAGGTGGTTG CGCTTTAGGG     180
GTCAAAGGCA TAGCAGATAT TTGGAAAATC TCTGATGACA TCAAAAGAGG TCAGGCGACT     240
GTTTTTGCTT ACGCGCAACC CATAGCTATG TTAGCGGTGG CAGGTGGCAT TATCTATTTG     300
AGCACTAAGT TTGGCTTCAA TATTGGCGAG AGTGGAGGAG CTAGC                     345
```

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201

```
ATGAAAAATC CCCAAGCTAA TGTTTTAAAA CTCTTTTTAA ATCAAGTGGC TGACCAAAAA      60
TACATAGATA TGAATGATGA AAAAAACTAT GACCCAAGAG AACCTGAACC CCCTTATGGA     120
ACAAAAGGGG CGTTAGATGA GATTATAAGG ACAGATGCTA GGAGTTGGGC AAACACTCCT     180
GATGATGAAT TTGGGAGCAT TATGTCTTCT TTTAAGCGTT TTATGTATGT CTATAAAGAC     240
CCAAAAGTGC GTGAAGCTAC TTCTAAAATG AGCTTTGATT ATGAAGAATT AAGAACGGGC     300
AATATCAGTA TTTACATTGT AATCGCTCAA ATTGATATAG GCACACTTTC TTCTTTAGTA     360
AGAGCCTTTT TAGAGAGTAT TGCTAAAAAC CTTATGGTCA AAGAAAGCTC TAAACCTGAA     420
GAGCGTATTT TTATCATTGC TGATGAATTT GTTAGATTTG GTAAGTTGCC TTTCTTGTTA     480
GAAATGCCAG CACTTTGTCG CTCTTATAAT GTTGTCCCCT TATTCATCAC GCAAGATTAT     540
GCTATGATTA GAAATACTAT AGCGATGATG ATT                                  573
```

(2) INFORMATION FOR SEQ ID NO:202:

(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:202

```
ATGATAAGTG AGATTATTAA GTTTCAATTA AAAGGAATAA AAATGATTAG ATTAAAAGGT      60
TTGAATAAAA CTTTAAAAAC AAGCTTATTA GCTGGGGTTT TACTAGGTGC TACTGCTCCC     120
TTAATGGCAA AGCCTTTATT AAGCGATGAA GACTTATTGA AACGAGTAAA ACTACACAAT     180
ATCAAAGAAG ATACGCTGAC TAGCTGTAAT GCTAAGGTGG ACGGCTCTCA ATACTTGAAT     240
AGTGGTTGGA ATTTATCTAA AGAATTTCCG CAAGAATATA GAGAAAAGAT TTTTGAATGC     300
GTAGAAGAAG AAAAACATAA ACAAGCCCTT AATTTAATCA ATAAAGAAGA CACTGAAGAT     360
AAAGAAGAAC TTGCAAAAAA AATCAAAGAA ATTAAAGAAA AAGCTAAAGT TTTAAGGCAA     420
AAATTTATGG CTTTTGAAAT GAAAGAACAC TCTAAAGAAT TCCCAAATAA AAAGCAACTT     480
CAAACCATGC TTGAGAACGC TTTTGATAAT GGAGCTGAAA GTTTTATTGA TGATTGGCAC     540
GAACGCTTTG GGGGTATAAG TAGAGAGAAT ACTTATAAAG CACTTGGCAT TAAAGAATAT     600
AGTGATGAAG GAAAGATATT AGCCTTTGGC GAAAGAAGTT ATATTAGACA ATATAAAAAA     660
GATTTTGAAG AAAGCACTTA TGATACTAGA CAAACCTTAT CTGCTATGGC TAATATGAGT     720
GGCGAAAACG ATTATAAAAT TACTTGGTTA AAACCCAAAT ATCAGCTCCA TAGTTCAAAT     780
AATATTAAAC CCTTAATGTC AAACACAGAG TTGTTAAATA TGATAGAGCT AACCAATATC     840
AAAAAAGAAT ATGTTATGGG CTGTAATATG GAAATAGATG GTTCTAAATA TCCCATTCAT     900
AAAGATTGGG GATTTTTTGG TAAGGCAAAA GTCCCAGAAA CTTGGAGAAA TAAGATTTGG     960
GAATGTATTA AGAATAAAGT AAAGTCCTAT GACAACACTA CCGCTGAAAT AGGAATAGTT    1020
TGGAAAAAAA ATACTTATTC TATCTCTCAT CAC                                 1053
```

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1053 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:203

```
ATGGCTGATA TTTTAAGCCA AGAAGAAATT GATGCGCTTT TAGAAGTCGT TGATGAGAAT      60
GTGGATATTC AAAATGTCCA AAAAAAAGAT ATTATCCCCC AACGCAGCGT AACCCTCTAT     120
GATTTCAAGC GCCCTAATCG TGTGAGTAAG GAGCAATTGC GCTCTTTTAG GAGCATCCAT     180
GATAAAATGG CTAGGAATCT TTCCAGTCAA GTCTCTTCTA TCATGCGTTC TATTGTAGAA     240
ATCCAGCTTC ATAGCGTGGA TCAAATGACT TATGGCGAAT TTTTGATGAG TTTGCCTAGC     300
CCTACGAGTT TTAATGTCTT TTCCATGAAG CCTATGGGGG GAACGGGGGT TTTAGAGATT     360
AATCCTAGCA TCGCTTTCCC TATGATTGAC AGACTATTAG GGGGTAAGGG GAGCGCGTAT     420
GATCAAAACA GGGAGTTTAG CGATATTGAA TTGAATTTAT TGGATACGAT TTTACGCCAG     480
GTGATGCAAA TTTTAAAAGA AGTGTGGTCG CCTGTGGTGG AGATGTATCC TACCATTGAC     540
GCTAAAGAAT CCAGCGCGAA TGTGGTCCAA ATCGTCGCTC AAAATGAAAT TTCTATCATG     600
GTGGTTTTAG AGATTATCAT TGGGCATAGC CGTGGGATGA TGAATATTTG TTACCCGGTG     660
ATTTCCATTG AGAGCATTCT TTCTAAAATG GGGAGTAGGG ATTTCATGCT TTCAGAAACG     720
AACTCCAAAA AGAGCCGTAA TAAGGAATTG CAAGCACTAT TGAGCGGGGT GAGCGTGGAT     780
ATGATGGTGT TTTTGGGCGC GGTGGAATTG AGTTTGAAAG AAATGTTGGA TTTAGATGTG     840
GGGGATACTA TCCGGTTGAA TAAAGTCGCT AACGATGAAG TGAGCGTGTA TGTACATAAG     900
```

AAAAAGCGTT ATTTAGCGAG CGTGGGGTTT CAAGGGTATA GGAAAACCAT TCAAATTAAA 960
GAAGTGGTTT ATAGCGAAAA AGAACGCACT AAAGAAATTT TAGAAWTGCT WGAAGAACAG 1020
CGCAGGAGGC AAAGTTGGGC GRTGTTATGG AGC 1053

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 570 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204

ATGCCCACGA TGTTAGCGGT TGGTTTTTGG GTGTTGGTTT TTTTATCCAC GAGCAATGCG 60
GTGAATTTAA CCGACGGGTT AGACGGATTA GCGAGTGTGC CTAGCATTTT CACCCTCTTA 120
AGCCTTTCTA TCTTTGTGTA TGTGGCAGGG AATGCGGAAT TTTCTAAATA CTTGCTCTAT 180
CCTAAAGTCA TAGATGTGGG GGAATTGTTT GTGATTTCGC TAGCATTAGT GGGATCGCTC 240
TTTGGCTTTT TGTGGTATAA CTGCAACCCG GCAAGCGTGT TTATGGGCGA TAGCGGGAGT 300
TTGGCAATAG GAGGGTTTAT CGCTTATAAC GCTATTGTTT CGCATAATGA AATCTTGCTC 360
GTTTTAATGG GGTCTATTTT TGTAATAGAA ACTCTGTCTG TGATCTTGCA AGTAGGGAGC 420
TATAAAACCC GTAAAAAACG CCTTTTTTTA ATGGCACCCA TCCATCATCA TTTTGAACAA 480
AAGGGTTGGG CAGAAAATAA GGTGATCGTG CGTTTTTGGA TCATTTCTAT GCTGAGTAAT 540
TTAGTCGCTC TTTTGAGCTT GAAGGTGTGT 570

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1467 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205

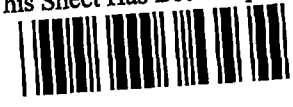
GTGCGTTTTG AAAATTTCAT CAACCGCCTA GCCTTTTACA TGGCCACAGG GAGCGGTAAA 60
ACGATCGTCA TTATCAAACT GGTAGAGCTT TTAAGCGTGG CTATGGGAAT GGGTTTGATC 120

```
CCTAAGAAAA ATATCATGTT TTTTAGCGCG AACGAGCATT TAATCAAGCA ATTTGAAAAA     180
GAAATTGAAA AATACAACCG CAATAAGGAC TATTCCAAAC AAATTGATTT CAAAAACCTT     240
AAAAGCGTTA AGAATAAGGA TTTTTATCGT GCTCCAAAAG ATTCTTTAAT GAAAGAAATC     300
GCTCTTTTTT ATTACCGCGC AGATTTAATG AGCGATGAAG AAAGCAAGGA AAACCTTTTA     360
AATTATAAGG ATTGTTGGGA TAATGGGGAA AATTATGTGA TTTTAGATGA AGCGCATAAG     420
GGGAATAAGA CTGAAAGCAA AAGACAGGCG ATTTTTAGCC TGCTGTCTTT AAAAGGGTTT     480
TTATTCAATT TCAGCGCCAC TTTCACTGAA GAAAGCGATC TCATCACTGC GGTGTATAAT     540
TTGAGCGTGG GCGAGTGGGT GAAACTTGGC TATGGTAAAG AGTCTGTTTT ATTGAAGAAA     600
AACAACTTAA ACGCTTTTAA GGAATTGAAA GATTTAAACG ACAGGGAAAA AGAAATCGCT     660
CTTTTAAAGG CGTTATTGCT TTTAGGCATG CAAAAACGCT ATAAAGTAGA AGGCTATTTT     720
CATGACCCTT TAATGCTCGT GTTCACGCAT TCTGTGAACA TGGAAAACAG CGATGCGRAA     780
ATCTTTTTTA AAACTTTAGC GCGCGTGATT GAAAATGATG ATGAGAGCGA TTTTTCAAAA     840
GCTAAAGACG ATTTATTAGA GGAATTAAAG AATCCGGAAT TCCTTTTTAG CGATGGCAAA     900
GATAAAGAAA AAGACTATAA AATTGAGGTC TTTAAAGAGA GTTTAAAGGG CATGGATTTT     960
AAAGGCTTAA AAGAAGCAGT TTTTTATGCC AGTAATGGGC ATATTGAAGT CATCATTAAC    1020
CCTAAAAACA ACCAAGAAAT CGCTTTCAAG CTCAACACGA GCGATAAAGT CTTTTGCCTG    1080
ATTAGAATAG GCGATATTAC AGAATGGATC CGTGAAAAAT TAAAGAGCGT GAAGGTGGTG    1140
AGTAAGAATT TGAGCTTCAA AGAAGAGAGC TATTTCAGCC AGATTGATAA GAGCAGTATC    1200
AATATCTTAG TGGGGTCTCG TGCTTTTGAC ACTGGGTGGG ATAGCACAAG GCCTAGCGTG    1260
ATTTTATTTT TAAATATAGG GCTTGATGAT GACGCTAAAA AGCTGGTGAA ACAATCTTTT    1320
GGCAGGGGCG TAAGGATTGA AAGCGTCAAA AACCAACGCC AAAGGTTAGC GTATTTAGAG    1380
ATAGATGAAG CCATTAAAGA ACAAGCTGAA ACCAAACGCT GCAATGCTGG AAATGCTTTT    1440
TGTGATACCT ACCAACCATG CAAGCCT                                        1467
```

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 639 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206

```
GTGTTTAAAA ATTCCCTCTT TGGTATATCA ATCTCCATGC TTATCACTTG GGTTTTAACC
GCTTGTATTT TGATTTTTAT CCTTTTTGTC CCGAATTTTA CCCTTACGCA TCCCAATTTT
CATTTCACTC CGTTTGAAAA AACCTATTTT CAAATTCTAG GACTTGTTGG TATTGTAAGT
TCTATTATTT TCACCGGGTT TTTGGCTGAT AAAATCAAAC CGCACAAAGT TTGCATGGCT
TTTAGCSCGA CCTTTGGGTT TTTTGGCTTT TTATTCTTTA AGGAATTTTA TTCTAACGCC
CCAAGTTTAG TCAATACTAT AATTTTATAC TTTTTAGCTT GCTTTTGCGC GGGCATTATC
AATTTTTGCC CCATTTTCAT GAGCGATGTG TTTAGCGCTA RAATCCGTTT TAGCGGGATT
TCCTTTGCTT ATAACATAGC CTATGCTATA ACCGCTGGCT TTACCCCTCA ACTTTCAAGC
TGGTTAAACG CAAAAGCTAT AGCAGTGCCT GAAAGTTTGC AAAGTTATGG TTTAAGCTTT
TATATCCTTA TAGTTTCTTT AATTGCTTTT ATTACATCGC TTTTAATGGC GCCAATTTAT
CACAAATCTA ATACCCAACA CGAAGTGTCG CCCACGGCA
```

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 936 base pairs

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

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207

```
ATGAAAAGCG ATAAACCCTT TTTAGAACGC TATTTTTATG ACCCCACTCT TTTGCAAAAG      60
GGGTTGATTT TCGCGCTCTA TCCTTTTTCT TTAATCTATC AATGTATTGC CACAATTAAA     120
CGAAAAACCG CTAAAAAGCA TGATTTTAAA ATCCCCATTA TCAGCATAGG CAACTTGATC     180
GCTGGGGGAA GCGGTAAAAC GCCCTTCATT TTAGAAATCG CTCCAAGATA CCAAGAAGTG     240
GCGGTTGTTT CTAGAGGGTA TCAACGGGAT TCTAAAGGTT TAGTGGTGGT GAGCGTTAAA     300
GGAAACATTT TAGTTCCTCA AAAAACAGCG GGCGATGAAG CCTATCTTTT AGCCTTAAAT     360
CTAAAACAAG CGAGCGTGAT TGTGAGCGAA AAAAGGGAGC TAGGCGTTTT AAAAGCCCTT     420
GAATTAGGAT CAAAGATCGT GTTTTTAGAC GATGGTTTTA GGTTTAATTT CAACCAATTC     480
AATGCGCTTT TAAAACCCAA AGTCCCCCCC TACTACCCTT TTTGTTTGCC TAGCGGGTTG     540
TATAGAGAAA ATATTAAAAG CTATAAAGAA GCCCATTTAG TCATTACAGA AGATAAGGAT     600
TATCAAAGAA TCACCTCTAT CACTAACCCC ACCAAACGCA TGCTTTTAGT AACGGCTATC     660
GCTAACCCTA GCAGGCTTGA TGCGTTTTTA CCCAAAGAAG TGGTTAAAAA ATTGTATTTT     720
AGAGACCATG CCCCTTTTGA TTTGAAGCTT TTAGAAAAAG AGTTTTATCA AAATAACGCC     780
ACCTCCTTAT TGGTTACTTC AAAAGATCTC GTCAAATTAC AAGATTGCAA ATTGCCTTTA     840
AGCGTATTGG ATTTAAAACT AGAAATTTGC CCTAAAGTTT TAGAGGAGAT TGATCGTTAT     900
ATCCTTTCTT ATCCTTGTAA TATAAAAGAA CATCTA                               936
```

(2) INFORMATION FOR SEQ ID NO:208:

(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:208

```
ATGTCTTTAG GGGCAGTGAT CAGGCTTATT TTTTGTTATA AGTTAGAGGG GGTAATATTA      60
GATTTAAAGC GCATCAATTT CAAATCCTAT TACCCCAATA ATAAAAATGC ATTATTTATC     120
AACAATAAGA AAAATCCATT ATCTAGTRCT TCAAAGTTCA TATTGCTT                  168
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 684 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:209

```
ATGCTAGAAA CCACTATTGA TTTTTCTCGT TACAGCAGCG TGAAAATCGG TGCGCCTTTA      60
AAAGTGAGCG TTTTAGAAAA CGATAATGAA ATCTCTCAAG AACACCAGAT CATAGGATTA     120
GCGAACAACC TTTTAATCGC TCCTGACGTG AAAAATCTCG CTTTATTAGG AAAAAACTAC     180
GATTATATTT GCGATAAGGG TGAGTGGGTG GAGGTAGGGG GAGCGGCCAA TGCGTCTAAA     240
ATTTTTAATT ATTTTAGGGC GAATGATTTA GAGGGTTTAG AGTTTTTAGG GCAATTGCCT     300
GGCACTTTAG GGGCGTTAGT TAAAATGAAT GCTGGCATGA AAGAATTTGA AATAAAAAAT     360
GTTTTAGAAA GCGCTTGCGT TAATGGCGAA TGGCTAGAAA AAGAAGCTTT GGGGCTAGAT     420
TATCGCAGCA GCGGGTTTAA TGGCGTTGTT TTGAGGGCTA GGTTTAAAAA GACGCATGGT     480
TTTAGAGAAG GGGTTTTAAA AGCGTGTAAA AGCATGCGCA AAAGCCACCC CAAATTGCCT     540
AATTTTGGGA GCTGTTTCAA AAACCCGCCT AACGATTATG CGGGCAGGCT TTTAGAGGGC     600
GTGGGCTTAA GGGGTTATTG TCTAAAAGAG TGGGCTTTGC CAAAGAACAT GCGAATTTTT     660
GGTGAATTTG GGGGGCGCAG AATT                                            684
```

(2) INFORMATION FOR SEQ ID NO:210:

(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

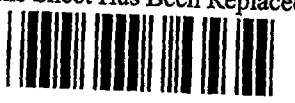
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210

```
ATGCTCAAAA ATGGCGATAA GATTCCGGAC GCTATTTTAG TGGATATTGA GATGCCTAAA      60
ATGGATGGCT ACACTTTCGC CTCTGAAGTG CGTAAATACA ATAAATTCAA AAACCTGCCC     120
TTGATCGCCG TTACCAGTCG GGTAACTAAA ACGGACAGAA TGCGCGGCGT TGAATCCGGC     180
ATGACTGAAT ACATCACCAA ACCTTATAGC GGTGAATATT TAACCACCGT AGTGAAGCGC     240
AGCATTAAAT TAGAAGGAGA CCAATCG                                         267
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:211:

(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:211

GTGTTTGAGC CGGTTATCGC TTACAAGCTT TTCCATTCCT TTGTGATTTT AGGGTGCGCG 60
ATTGAAACTT TAACGACTAA ATGCGTGGAA GGCATCACGG CTAATGAAAA GATTTGCCAC 120
GATTATGTTT TTAACAGCAT TGGCATTGTT ACCGCGCTCA ACCCTCATAT CGGCTATGAA 180
AAATCCGCTA TGATCGCCAA AGAAGCCTTA AAAAGCGATC GCTCTATCTA TGATATCGCT 240
TTAGAAAAGA AAATCTTAAC CAAAGAGCAA CTGGACGATA TTTTCAAGCC AGAAAACATG 300
CTAAGYYCTC ACGCTTTCAA AAAGCATAAA GAC 333

(2) INFORMATION FOR SEQ ID NO:212:

(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:212

ATGTTGCGTT TATTAGCCCA AAAAAGCGCT ATTAAACTCA TTCTTATCCC CCCAAGCGCG 60
AACGCTTTAG GCATCGCTTC TATTTGCGAA TTGAGCGAAG AAGTTTTTGA ACATGAAAAA 120
ATCGTAGGCA TTCGCGCTCA AGGGGATTTC ACTATCAATA GCGACGATAG GGGTTTTTGG 180
GAAAGACGCT GTCAG 195

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

This Sheet Has Been Replaced



(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:213

```
ATGAAAAAAC TTCTTTTACT CTTAGAGCAT AAGATCGTAA AAATTGGCTT AATTATTGTG      60
ATTGTGTTAG TGGGTTTTTT TCTTTTTTAT GAACAAGAAA TCAAAGAAAA AGCTGTTAAT     120
GTTTCTCAAG GTAAATTCCC CACTTCATCT TATTTGTTTC AAGCTTACGA AGGCATTAAG     180
AATAAAATAG ATACTATCAA TCAAGTGAAG CCAAACGATG AAACTAAAAG CGTTAATGAG     240
AATATAGAAA AAACACAAAA AGATTTAGAT GATTTTAATG CGCTAGTGCA AAAGTTACCA     300
AATTTGCCTA AGGACTTTAA TAAAACACTT ATTAAACCAC AAAGTCCATT TTTCAACTAC     360
AATACCGCTA ACGAAGATGA AAAAAACCGC CTGGTGATTT TAGCGTCTCG TATTAGCAGC     420
CAAAAAGAAA CGCAACCTCC CATTTCTATA AAAAATAGCG TTTCTCACAT AAAATCCAAA     480
GAAAAACGAG AACTTGAAAA AGAATGGGCA AAACCTAGTG TTTCTTTTGG TTCTTTTTCC     540
TTGCTTTCCA GTTCTTCTTC TTTTTCTTCT TTTGAAGTTT CTTTTTTATC AAGGGGAATA     600
GGATTGGATT GTGAGAAGCT CAAATCCTTT TTAAAAGCTT TTTCAAGTTC GCTATTTTCC     660
TTATTATCTT CATTGTTTTG CCATCCACTT TCTCTTTTTT GCTCTCTAAT AGGATTAATC     720
TTTTGTTTTT CTAAGTTTTC TAGAGAGCTA GTGAATGCGT CTAACAATTC GCTTGAGTTT     780
TCATCATTGT CAAGGCTAGG ATCA                                            804
```

(2) INFORMATION FOR SEQ ID NO:214:

(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:214

```
ATGGGAGCGA TAGCGAGTTG TTACGCGCAT CAAATCATCT TAACTTCAGA CAATCCTAGA      60
AGCGAAAACG AAGAAGACAT CATTAAGGAT ATTTTAAAAG GCATCAATAA TTCTTCTAAA     120
GTCATTGTAG AAAAAGACCG AAAAAAGGCC ATTTTAAACG CTTTAGAAAA TTTAAAAGAC     180
GATGAGGTGT TGTTGATTTT AGGCAAGGGC GATGAAAACA TTCAAATCTT TAAAGACAAA     240
ACGATTTTTT TTAGCGACCA GGAAGTCGTT AAAGATTATT ATCTCAATTT AAAACAAGGA     300
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:215:

(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:215

```
GTGATGGACA AACTCACTAA AAGCTTGCAA ACGCAAAAAA ACTTCGCTTA TTTAGGCAAA      60
ATCAAGCCCC AACAACTCGC TGATTTCATC ATTAACGAAC ACCCTCAAAC CATCGCCTTG     120
ATTTTGGCCC ACATGGAARC CCCTAATGCG GCTGAAACTT TGAGCTATTT CCCTGATGAA     180
ATGAAAGCCG AGATTTCCAT TAGAATGGCG AATTTTAGGC GAAATATCGC CCCAAGTGGT     240
```

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 615 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216

```
ATGCGGTATT TTAGAAGCGC TTTTTTATTA TTTTTCATGA CGCTTTTTTT TGTTTCTTGC      60
TCTAAGCACC CTTTTTCTAA GCAAACCCCT AAGACTAAGG AGCGGATCCG ACAAGAAGAA     120
GCCAATAAAA AAAGAGAAGA GACTTTGAAT GCCTTGCGCC AATTCAGACT CATTTACATT     180
AACACGCCGG TTTTTCGCTT TTATGATTAC GGCACGATCA AAACCGATAA AGACCACAAT     240
ACTGAAGTAA CCCTTTATAA GCTCAGCCAA AAAGTGGGCG ATATTTACAT GACTAAACGG     300
AGCATTTGTT TTAGCCAAAA ATGTTCGGCC AAATGGATTG CTGCAAGGGA TTTGTTTGGC     360
AAGGTGAGCT ATGGGGATTT GTTTGATGAT ATTGTTTTAG GGAGGGATAT TTTTAAAGGT     420
TTAGGGAAAC GCCACCTAAC CCCTGAATAT GTGATCCAAA GGTTTCAAAA AAGCGGGGAA     480
ATTATCCTTT ATGAAAGAAA AAATGGCCTG ATTTCTTTCC AAAACTTGAC TCAAAAAATT     540
GCTATTAGGA TTGAACCCTA TGAGCCTTCT TTGCAAGATT TAGAAGACAA TGAAAACGCT     600
GATAGCGAGC TTCAA                                                     615
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:217:

(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:217

```
ATGCGCATTG AAGAAAATGG CGTGATTTCT CTAGCCTTTA GTAACGGGGT GGTAGAGCCG      60
GTCGCTCGCA TCGGTATTTW AGCTTTCACT AACGATCAAG GCTTAAGGAA AATCGGCGGT     120
AACCTCTATG AAATGCAAGA AGGCACCATT AATGGCGAAA ACAGACCCCT AAGSGGTAAC     180
CCCATTTTAG GGTGGGACGA AGAGGGCAAG CTCAAGTTTG GGAAAATCAG GCACAAATAT     240
TTAGAAACGA GCAACGTGAA TGCCGGGAAC GCCCTAACCA ATCTCATTTT AATGCAAAGA     300
GGCTATTCTA TGAACGCTAG AGCCTTTGGC GCGGGCGATG ACATGATCAA AGAAGCCATT     360
AGCTTGAAAA AA                                                         372
```

(2) INFORMATION FOR SEQ ID NO:218:

(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

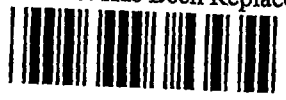
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218

```
GTGGAAGCGC GTTATTATTA TGGGGACACT TCATACTTTT ATTTGCATGT GGGAGTTTTA      60
CAAGAGTTCG CTCACTTTGG ATCGAATGAT GTGGCGTCTT TAAACACCTT TAAAATCAAT     120
GCCGCTCGCA GTCCTTTAAG CACCTATGCA AGAGCGATGA TGGGTGGGGA ATTGCAATTG     180
GCTAAAGAAG TGTTTTTGAA TTTGGGCGTG GTTTATTTGC ACAATTTGAT TTCCAACGCA     240
AGCCATTTCG CTTCCAATTT AGGAATGAGG TATAGTTTC                             279
```

(2) INFORMATION FOR SEQ ID NO:219:

This Sheet Has Been Replaced



(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:219

GTGGAGGAGC TAGCTAAATT GATCAACAAT AATAATAACA ATAAAAAACT GAGAGGCTTT 60
TTTTTGAAAG TTCTCTTAAG TCTCGTTGTT TTCAGTTCGT ATGGGTCAGC AAATGACGAT 120
AAAGAAGCCA AAAAAGAAGC GCTAGAAAAA GAAAAAAACA CTCCCAATGG GCTTGTTTAT 180
ACGAATTTAG ATTTTGATAG TTTTAAAGCG ACTATCAAAA ATTTGAAAGA CAAGAAAGTA 240
ACTTTCAAAG AAGTCAATCC CGATATTATC AAAGATGAAG TTTTTGACTT CGTGATTGTC 300
AATAGAGTCC TTAAAAAAAT AAAGGATTTG AAGCATTACG ATCCAGTTAT TGAAAAAATC 360
TTTGATGAAA AGGGTAAAGA AATGGGATTG AATGTAGAAT TACAGATCAA TCCTGAAGTG 420
AAAGACTTTT TTACTTTCAA AAGCATCAGC ACGACCAACA AACAACGCTG CTTTCTATCA 480
TTGCACGGAG AAACAAGAGA AATTTTATGC GATGATAAGC TATATAATGT TTTATTGGCC 540
GTATTCAATT CTTATGATCC TAATGATCTT TTGAAACACA TTAGCACCAT AGAGTCTCTC 600
AAAAAAATCT TTTATACGAT TACATGTGAA GCGGTATATC TA 642

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

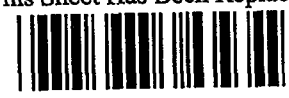
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220

GTGGGGGGCA TTGTGGCAAA CATGAACGAT CTTTCAACTT ACATGGTTGA GAATTTACTT
ATGGGTTTGT ATCTTTTTTC TAGCGCTTTA GATTTGGGCG TGAAAAAAGC CATTAATCTA
GCGAGCTCTT GCGCTTATCC TAAATACGCC CCTAACCCTT TAAAAGAGAG CGATTTATTC
AACGGCTCTT TAGAACCAAC GAATGAAGGC TACGCTTTGC CAAACTCTCT GTRR

(2) INFORMATION FOR SEQ ID NO:221:

This Sheet Has Been Replaced



(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:221

```
ATGAAGAAAA GAAAACATGT ATCCAAGAAA GTGTTTAATG TCATTATCTT GTTTGTGGCA     60
GTATTCACTC TTTTAGTCGT CATTCACAAA ACCCTTTCAA ACGGCATTCA CATACAAAAT    120
TTAAAAATTG GAAAACTTGG CATTTCTGAA TTATACTTAA AACTCAATAA CAAGCTTTCT    180
TTGGAAGTTG AGCGGGTTGA TCTCTCTTCT TTCTTCCATC AAAAACCCAC TAAAAAGCGT    240
TTAGAAGTTT CTGATTTGAT TAAAAATATC CGTTATGGCA TTTGGGCGGT GTCTTATTTT    300
GAAAAACTTA AAGTCAAAGA AATCATTTTA GACGATAAAA ATAAAGCCAA TATCTTTTTT    360
GATGGGAATA AATACGAGTT WAGAATTTCC AGGAATCAAA GGGGAATTTT CCCTAGAAGA    420
CGATTAAAAA TATCAAGCTT AAAATCATCA ATTTGCTTTT TAAAGATGTT AAAGTCCAAG    480
TGGATGGCAA CGCCCACTAT TCRCCCAAAG CCAGGAAAAT GGCGTTCAAT T             531
```

(2) INFORMATION FOR SEQ ID NO:222:

(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:222

```
GTGTCATGTT GGGGAGCGTC AAAAAAGCGG TTTTTAGGGT TTTGTGTTTG GGGGCGTTGT     60
GTTTATGCGG GGGGGTTAAT GGCAGAGCAA GATCCTAAAG AGCTTATATT TTCAGGTATA    120
ACTATTTACA CGGATAAAAA TTTCACTAGA GCTAAGAAAT ATTTTGAAAA AGCTTGCAAA    180
TCAAACGATG CTGATGGCTG TGCAATCTTA AGAGAGGTTT ATTCTAGTGG TAAAGCCATA    240
GCGAGAGAAA ACGCAAGAGA GAGCATTGAA AAAGCTCTTG AACACACCGC TACTGCTAAA    300
GTTTGTAAAT TAAACGATGC TGAAAAATGC AAGGACTTAG CAGAGTTTTA TTTTAATGTA    360
AACGATCTTA AAAATGCTTT AGAATATTAC TCTAAATCTT GTAAGTTAAA TAATGTTGAA    420
GGGTGTATGC TGTCAGCAAC TTTTTATAAC GATATGATAA AGGGTTTGAA AAAAGATAAA    480
AAAGATCTAG AATATTATTC TAAAGCTTGC GAGTTAAATA ACGGTGGAGG GTGTTCTAAA    540
TTAGGAGGGG ATTATTTTTT TGGTGAAGGC GTAACAAAAG ATTTCAAAAA AGCTTTTGAA    600
```

TATTCTGCCA AAGCTTGTGA GTTGAACGAT GCTAAAGGGT GTTACGCTCT AGCAGCGTTT 660
TATAATGAGG GTAAAGGCGT GGCAAAGGAT GAAAAGCAAA CGACAGAAAA CCTTGAAAAG 720
AGTTGCAAGC TAGGATTAAA AGAAGCATGC GATATTCTCA AAGAACAAAA ACAA 774

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223

GTGGCTCTCA CTTTGGGGGC TAGAGGGGGG GTGTATTTGT GTGGGGGGAT TATCCCACGA 60
TTCATTGATT ATTTTAAAAC TTCGCCCTTT AGAGCGCGTT TTGAAACGAA AGGGCGCATG 120
GGAGCGTTTC TCGCTTCCAT CCCTGTGCAT GTCGTGATGA AAAAAACTCC CGGACTTGAT 180
GGGGCGGGCA TTGCGTTAGA AAATTATTTA CTGCATGATA GAATA 225

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

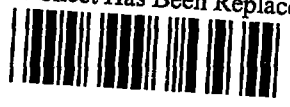
ATGAAAGGTT TAACAATGAA AAAATTAGTT TTTAGCATGC TTTTATGTTG TAAAAGCGTG 60
TTTGCAGAGG GGGAAACTCC TTTGATTGTC AATGACCCAG AAACCCATGT AAGTCAAGCC 120
ACTATCATAG GCAAAATGGT AGATAGTATC AAAAGATACG AAGAGATTAT TTCTAAGGCT 180
CAAGCTCAAG TCAATCAGTT ACAAAAAGTC AATAACATGA TAAATACGAC TAATTCTTTG 240
ATTAGTAGTA GTGCTATCAC TTTAGCCAAT CCTATGCAAG TTTTACAAAA CGCTCAGTAT 300
CAAATAGAGA GCATTAGATA CAACTATGAG AATTTAAAGC AAAGCATAGA AAATTGGAAC 360
GCACAAAATT TGTTAAGAAA CAAATACTTA CAGCAACAAT GCCCTTGGCT TAATGTCAAT 420
GCTCTTACTA ACAATAAGAT TGTCAATCTT AAAGATCTCA ATAACCTAAT CACCAAAAAT 480

```
GGCGAACAAA CCCAAACCGC AAGAGATGTG CAAAATCTCA TTCAGTCCAT TAGTGGCAGT     540
GGCTATGGAA ACATGCAATC ACTTGCTGGG GAATTGAGTG GTAGAGCGTG GGGGGAAATG     600
TTGTGTAAAA TGGTAAACGA TAGTAATTAT GAAAGCGAGC AAGCTCTTTT AGCAACAGGC     660
AATAACCCAG AAGAGCAAAA ACGAAGATTT TTGCTTAGAG TAAAGAAAAA GGTTAATGAT     720
AATAAGCAGT TAAAAGATAA ACTTGACCCA TTTCTAAAAA GACTTGATGT CCTACAAACT     780
GAGTTTGGTG TAACTGACCC TACAGCTAAC CATAATAAGC AAGGGATACA TTATTGCACA     840
GAAAATAAAG AGACAGGTAA ATGCGACCCT ATTAAAAATG TATTTAGGAC AACTCGCTTA     900
GATAACGAAT TAGAACAAGA AATCCAAACG CTCACACTTG ATTTAATCAA AGCCTCCAAT     960
AAAGACGCTC AAAGCCAAGC CTACGCAAAT TTCAATCAAA GGATTAAATT ACTTACTCTA    1020
AAATATTTAA AAGAAATTAC CAATCAAATG CTCTTTTTAA ATCAAACAAT GGCAATGCAA    1080
AGCGAGATTA TGACAGATGA TTATTTTAGG CAAAATAATG ATGGCTTTGG GGAAAAAGAA    1140
AACCATATAG ACGAACAATT AACGCAAAAA AGAATAAACG AAAGAGAAAG AGCTAGAATA    1200
TACTTTCAAA ACCCTAATGT TAAATTTGAC CAATTTGGCT TTCCCATTTT TAGTATATGG    1260
GAT                                                                  1263
```

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:225

```
ATGAGCGTGA ATTTATTGGA ATTGTTAAAA CTCGCTGTGC CTTTAGCGGT TATTTTGAGC      :
GTTCAAGTGG CGGTTATGAT CCTTTATGTG GTGCTTGTAA CCTTTAGGGT ATGCGGGAAG      :
GATTATGATG CGGCGGTGTT GTGCGCGGGG CATTGCGGTT TTGGGCTTGG AGCGACCCCA      :
ACGGCTATGG TGAATATGCA AACCATCACC AACCACTATG GGCCATCGCA TGTGGCGTTT      :
ATCGTCGTGC CTTTAGTGGG AGCGTTTTTT GTTGATATTA TTAACGCTTT AGCGATTAAA      :
GGCTTTTTGC TTTTGCCTTT TTTCCCTAGT                                       :
```

(2) INFORMATION FOR SEQ ID NO:226:

(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

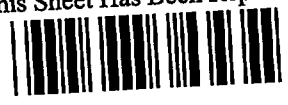
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226

```
ATGCAACTAA GCCCCTTACA AAGCGCGCTG TTATATTTCC GTTACTTTAT TTATCCGGAA     60
AAAAAAACAA GGAGCTTTGA TTTAAGCGAT TTAATTTTTA TTGTCATGGT TTTTTTAGTC    120
CTAGCTTTGG GGCTGTTGAT GAGCGAAGAA ATTTCTATCA GCTACAATGA AGCGAAAGAC    180
TTTTTTTATA GCGATGCGTG GTTTGTCAAA ATCGCTCAAA AAAGCGTAGC CATTTTAAGG    240
CCAAAACGAT TTGGCTTTAA GATTGCCTTT TTTGATCGCT CACGTCATCA ACATGTTTTT    300
ATTCTACCTC ATAGGGCGAA AGATTTTAAA AAAGCC                               336
```

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:227

```
GTGTATGCGC TCATGGTGGC GTTTTTTGCT TACATGAGTT ATTGCTTGGG GTATCAATTC     60
TCCAAATTCG TTTCTAAAAA CAACATTTCA TCGCTCTCAT CGCTTTTATC AAGCTGTGTG    120
CGCGTGGTCT CTGTGCTAAT CTTGTCGCTC AGTAGCCTAG AGTTGCGTTA CTTCTCACCC    180
CTAACTATCA TAACCATGCA TTTTGCCCTA ACGCTTATCA TCCTCTTTTT CTTTTTGTAT    240
AAGGCTAAGC CGTTTGATGA G                                               261
```

(2) INFORMATION FOR SEQ ID NO:228:

(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

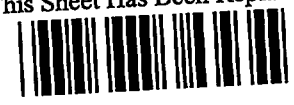
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228

```
ATGAGGTCTT GGATGAAGAA AAAATACTTC ACGCTTTTAT TGCAAAGTAG TGTGGTATTA      60
GCGGTTTTTA TAGGGTGTTC TTCTACCAGG AATCATACTT TTTCAGCCCT TAGTAATCAA     120
GAAAATACAG ACGATAAGCT CCCAGTGGTC CATTCCATTA AAACGATTAA CGATGTGAGT     180
TCAGTGGGCT TTGAATGGTC TAAAGTCGCT GACACTTATG ACATTGACGG GTTTGTTTTG     240
TATCGTTTGA AAAAAGACTC CAAGCTTAAA AGAATCGCCA CCATTAAAAA CCCTTATGCG     300
ACCCACTATT ATGATGAGGG GTTAGAAACA GAGAGTTCCT ACACTTACCA ATTAGCCACC     360
TACAAGGGCG ATAAAATTTC CAAACTTTCA GAACCCATTT TAGTAAAAAC CTCCTTTATC     420
AATCCTGTAG AAAGCGTGTT TGCAAGCCTT GAATACCCTA AAAGCGTGAA AGTCTTTTGG     480
AGCCCGCACC CAAATCCCAG CGTTTCTAAA TACATCATTC AAAGGCAGAA TAAAGACGGC     540
AAATTTTTAA ATGTGGGGGC TGTAAAAAAC CGCTTATTCG TGGAGTTTTT TGATAAAGAT     600
TTAGAAGATG GGCAAAAATA CCGCTACCAA ATCATCGCCG AAAATTTCAT GGGGGATAAA     660
TCCAGGCCTA GCGTGATAGT GGAGGGGAAA ACCAAAGACT TGCCCAAAGA AATCGCTAAT     720
GTTAGAGTGA GTCAAAACCT CACACGACAA ATTGAATTGA GTTGGGATAA ATCCCCAGAA     780
GAAGATGTGA TAGCTTATCG CATTTACGCT TCCAATAACC GCAACGATAA ATACAAATTC     840
ATCGCTCAAA CCACCAACAC TTCCTATGTG GATAAGATAG AAAAAGACAA TCTCACTCGT     900
TATTATAAAG TCGTCGCCGT AGATAAAACG CATCTTGAAG GGGCGTTACC CAAAGAGCCT     960
GCCATGGGTG AGACCTCTGA TAGGCCTGAA GCCCCTATCA TCACTAAAGG GACTATTCAA    1020
GACTCTTCGG CCTTGATCCA ATGGGAAAAC AACCCAAGCC CTAAAATAGC CACTTATGCG    1080
GTGTATCGTT TTGAAGCCAA CTCCAAAACC CCTTTGCGTT TTGGGAATAT CACACAAAAC    1140
CAGTTCGTGG ATAAGGACAT GAAAGTGGGC GTGGCTTATC GCTATCAGGT GGTGAGCGTG    1200
GATAAAGATG GTTTAGAGTC GCACCCAAGC AAAGAAGTGC GTTTGTTTTT AGAGCGC       1257
```

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:229

```
ATGCTTCCTA CTAAAACACG CATTAGAGAT CCGAACAAGC AAGAACTTAC ACAACCAAAA      60
ATAAAAGGAT TGAGTATGGG AAAAATTTTA GCTTCTTTGT TGGGTGGCGG AACAAATCTT     120
TTTACAGGTT TATCCAGTGA TTTGTTTTCT ATGATATTAA ATTTTTTGTT CTTCCTGATG     180
TTAATGATGG GACTTAATGA AGCATTAGGG AAAAAATTTA ACTTGCCTAT GGACAATATC     240
AAGAATTTTA TGGCAGAAGT GCTGAAGAAT GGATTCGATA GTATCAAAAA CATGGGATCT     300
GCTTTGGTTG GTAATGGTTT TGGTAGCAGC AAATCAGACA AAACCACTAA TAAAATGAGT     360
GTCCCACAAG TAAGACTC                                                  378
```

(2) INFORMATION FOR SEQ ID NO:230:

(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:230

```
ATGGCGAACA TGATGATGGC AGCGGCCATG TTAGGGATTG ATTCTTGCCC GATTGAAGGG      60
TATGATCAAG AAAAAGTGGA GGCTTATTTA GAGGAAAAAG GCTATCTAAA CACGGCAGAA     120
TTTGGCGTGT CGGTAATGGC CAGTTTTGGT TATCGTAACC AAGAGATTAC CCCTAAAACC     180
CGCTGGAAGA CAGAAGTTAT TTATGAAGTG ATTGAA                               216
```

(2) INFORMATION FOR SEQ ID NO:231:

(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:231

```
ATGGCCGGGC TTGTTTTGAT GGTGCTGCTC GCCAGTTATG AAAGCTTTGT TTCTAAATTA      60
GACAAGGTGG ATGCTAGCGA AATCACTTGG CTAAAACACA CAGATTTTAA CGCTTTAAAA     120
TTAAAGGTTT CCCTCTCCAT TGTAGCCATT TCGGCGATTT TCTTGCTCAA ACGCTACATG     180
AGTTTAGAAG ACGTTTTATC CAGTATTCCT AAAGACACGC CCCTATCGCA TAACCCTATT     240
TTTTGGCAAG TGGTGATCCA TTTGGTGTTT GTGTGTTCAG CGCTGTTAAC CGCTGTTACC     300
AATAACATCG CTTTTTCGCA GAAAGAAAGG CAT                                  333
```

(2) INFORMATION FOR SEQ ID NO:232:

(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

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232

```
ATGATTACGA TCGTTATTGC AAAAGCGGGG AATATAGTCA AAGYCGATAT TTTTACGCAC      60
ATTAGCGATA TTAAAATGGG GCTTATTAAA GGAGGTCAAT GGGGGGTTAT TGGTTTAGGC     120
AATATCGGTA AAAGAGTCGC CAAGCTCGCT CAAGCTTTCG GGGCAAAGGT GGTGTATTTT     180
TCCCCTAAAG ATAAAAAAGA AGAATACGAG CGCTTGAGTT TAGAGGAATT GCTTAAAACA     240
AGCGGTATTA TCAGCATTCA TGCCCCCTTA AATGAAAGCA CGCGCGATTT AATCGCTCTG     300
AAAGAATTGC AAAGCTTAAA AGATGGGGCG ATTTTAATCA ATGTGGGGCG TGGGGGCATT     360
GTGAATGAAA AGGRTTTGGC TTTRRTTTTA GAAACCACAG ATTTGTATTA CGCGAGCGAT     420
GTGTTT                                                                426
```

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:
(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:233

```
GTGAATTTCA ACGCTAAAAA TATTTCAATT GATAATTTGG TAGAAATCAA TAATCGTGTG      60
GGTTCTGGAG CCGGGAGAAA AGCCAGCTCT ACGGTTTTGA CTTTGCAAGC TTCAGAAGGG     120
ATCACTAGYA GTAAAAATGC GGAAATTTCT CTTTATGATG GCGCCACGYC AATTTGGCTT     180
CAAACAGMG                                                             189
```

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 930 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234

```
ATGCGAACGC TCATTCTGTC GCTTCTAAAA CATGCGATTT TAATGGGCAT GCTTTTAAAA      60
GAATGCCAAG AAAAGTTAAA GCGTTCTTTA AATTTGAGTG CTAATCATTG CGTCTTGAGC     120
GCGGGGTATG GGGCGAGTTC AGCGATTAAG AAATTTCAAG AAATTTTAGG GGTGTGTATC     180
CCTTCAAAAA CGAAGAAAAA TTTAGAGCCG TATTTGAAAG ATATGGCTTT AAAGCGTGTG     240
ATTGTAGGGC CTTATGAGCA TCATTCTAAT GAAGTTAGCT GGCGTGAAGG CTTGTGTGAA     300
GTGGTGCGTA TCCCTTTAAA TGAACATGGT TTATTGGATT TAGAAATTTT AGAGCAAACT     360
TTAAAAAAAA CCCCTAACAG CTTGGTTTCT GTGAGCGCGG CTTCTAATGT AACGGGAATT     420
CTTACGCCTT TAAAAGAAGT TTCATCATTG TGTAAGGAAT ATAGGGCTAT TTTAGCTTTG     480
GATTTAGCGA ATTTTAGCGC GCATGCTAAC CCTAAAGATT GCGAATACCA AACCGGTTTT     540
TATGCGCCTC ATAAGCTTTT AGGGGGCGTT GGAGGGTGCG GTCTTTTAGG CATTTCTAAA     600
GATTTGATTG ACACGCAAAT YCCTYCGAGT TTTAGCGCAG GGGGCGTGAT TAAATACGCT     660
AATCGCACAC GGCATGAATT TATTGATGAA TTGCCTTTAA GAGAAGAATT TGGCACGCCA     720
GGATTGTTGC AATTTTACAG GAGCGCTCTA GCGTATCAAT TAAGAGATGA ATGCGGTTTG     780
GATTTTATCC ATAAGAAAGA AAACAACCTT TTAAGGGTGC TTGTGTATGG CTTAAAAGAC     840
TTGCCCGCTA TTAATATTTA TGGGAATTTA ACGGCGAGTC GTGTGGGGGT AGTGRCTTTT     900
AATATTGGAG GGATTTCRCC CTATGATTTA                                      930
```

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 564 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:235

```
GTGGCATGCA ACACCGCGAG CGCTCTGGCT TTAGAAGAGA TGCAAAAGTA TTCTAAAATC      60
CCTATTGTGG GCGTGATTGA GCCAAGCATT TTAGCGATCA AGCGGCAAGT GGAAGATAAA     120
AACGCCCCTA TTTTAGTGCT AGGGACAAAA GCGACGATTC AATCCAACGC CTATGACAAC     180
GCCCTGAAAC AACAAGGCTA TTTGAACATT TCGCATTTAG CTACTTCTCT TTTTGTGCCT     240
TTGATTGAAG AAAGTATTTT AGAGGGCGAA TTGTTAGAAA CTTGCATGCA TTATTATTTC     300
ACTCCCTTAG AGATTTTACC CGAAGTGATC ATTTTAGGTT GCACGCATTT TCCCTTAATC     360
GCTCAAAAAA TTGAGGGCTA TTTCATGGGG CATTTTGCCC TTCCAACGCC CCCCCTACTC     420
ATCCATTCGG GCGATGCTAT TGTAGAATAT TTGCAACAAA AATACGCCCT TAAAAACAAT     480
GCATGCACAT TCCCTAAAGT GGAATTTCAT GCGAGCGGCG ATGTGATCTG GCTAGAAAGA     540
CAAGCTAAAG AATGGCTCAA ATTG                                            564
```

(2) INFORMATION FOR SEQ ID NO:236:

(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:236

```
GTGTTGTGGG TGCTATATTT TTTAACCAGT TTATTTATTT GCTCTTTGAT TGTTTTGTGG     60
TCTAAAAAAT CCATGCTCTT TGTGGATAAC GCTAATAAAA TCCAAGGCTT CCATCATGCA    120
AGAACCCCAC GAGCCGGGGG GCTTGGGATC TTTCTTTCTT TTGCGTTGGC TTGTTATCTT    180
GAACCTTTTG AGATGCCTTT TAAGGGGCCT TTTGTTTTCT TAGGGCTATC GCTAGTGTTT    240
TTGAGCGGTT TTTTAGAAGA CATTAACCTT TCATTAAGCC CCAAAATACG CCTTATTTTG    300
CAAGCTGTAG GGGTCGTTTG CATCATTTCA TCAACGCCTT TAGTGGTGAG CGATTTTTCG    360
CCCCTTTTTA GCTTGCCTTA TTTCATCGCT TTTTTATTCG CTATTTTTTA TGCTGGTGGG    420
TATCAG                                                               426
```

(2) INFORMATION FOR SEQ ID NO:237:

(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

This Sheet Has Been Replaced



(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:237

```
ATGGCGTGTA AATTTTGCCC TAAGATCAGA AAAACAGATT GGATTTTTAT TTTAATCGCC     60
GCTTTAGGCT TTTATTCAGT TAATAAGCTA GGGTATGCGC CCAAATTCAA TACCCCCACT    120
CCAAAATCTT CACGCCCTCT TTCACGCCCT ATTGAAAAGC CTAACAATAT GACTGAAGAA    180
GAAAGGAAAA AGCGTTTTAT AGAGTTGCAA AAAGCATGCT TACTTCATAA AGACAAAAAG    240
GCATGCGAAG AGGTTTTT                                                  258
```

(2) INFORMATION FOR SEQ ID NO:238:

(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:238

```
GTGGATTCCA TTTTAATTGA TGAAGCGAGA SCTCCTTTAA TCATTTCAGG GCCTGTGGAT      60
AGGCGCATGG AAAATTACAA CAAGGCTGAT GAAGTCGCTA AAAGCATGCA AGTGGAAGTG     120
GATTTCACCA TAGACGAAAA AAACCGCGCG ATTTTAATCA CTGAAGAGGG GATTAAAAAA     180
GCCGAAAATC TCTTTGGCGT GGATAATTTA TACAAAATTG AAAACGCCGC CCTATCGCAC     240
CATTTAGACC AAGCCTTGAA AGCGAATTAC CTCTTTTTTA TTGRTAAAGA TTATATTGTA     300
GCCAATAATG AAGTGGTGAT TGTAGATRRA TTTACCGRCC GTTTGYYTGA AGGGGAGGCG     360
CTT                                                                  363
```

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239

```
ATGACGATCA CCACCCTATC TTTTTTATTC ACAACGCCAG AAGTGTTTGT CAATCAGGAT
TTCCCATGGC TTTCTGGGGC TGGAAGGCTA GTGGTTAAAG ACTTGGCGTT ATTTGCTGGA
GGCTTGTTTG TGGCCGGATT TGATCGAAAC GCTATTTGGA GGGTAAAGGG TTTTGCT
```

(2) INFORMATION FOR SEQ ID NO:240:

(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:240

```
GTGTTTTCTG GCAATAAAAG GGCTATAAAT TATCGCACGA TTGTCAGCGC CTTTGTGATT      60
CAAGTGGCTT TAGGGGCGTT GGCTTTATAT GTGCCTTTGG GCAGAGAAAT ACTGCAGGGT     120
TTAGCTAGCG GCATACAAAG CGTGATTGGT TACGGCTATG AGGGGGTACG CTTTTTATTT     180
GGCAATCTCG CTCCAAACGC TAAGGGCGAT CAAGGGATAG GAGGCTTTAT CTTTGCGATC     240
AACGTTTTAG CGATCATTAT CTTTTTTGCT AGCTTGATTT CACTTCTATA TTATTTAAAA     300
ATCATGCCTT TAGTAATCAA CCTCATCGGS GGGGCGTTGC AAAAATGCTT AGGCACTTCT     360
AAAGCAGAAA GCATGAGCGC AGCGGCTAAT AYTYTTGTGG CGCACACCGA AGACRCCCTT     420
AGTCAT                                                                426
```

(2) INFORMATION FOR SEQ ID NO:241:

(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

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241

```
ATGCTGGTGG GTATCAGTAA CGCTATTAAT ATCATTGACG GGTTTAACGG GCTTGCATCT      60
GGGATTTGCG CGATCGCGCT TTTAGTCATT CATTATATAG ACCSTAGCAG TTTGTCTTGT     120
TTGCTCGCTT ACATGGTGCT TGGGGTTTAT GGTGTTAAAW TTCCCTTCAG GAAAGATTTT     180
TTAGGWCGAT CGGGGGGGCG TATTTTTTGG GTTTGGTGWR CGGRATTTCT CTCTTGCATT     240
```

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242

```
ATGCTACATA AAAAATATCG TCCTAATGTT GCGGCCATTA TCATGTCGCC AGACTACCCT      60
AACACATGCG AAGTTTTTAT CGCTGAGCGC ATAGACATTG AAGGGGCGTG GCAGTTCCCC     120
CAAGGAGGCA TTGATGAGGG AGAGACCCCT TTAGAAGCAC TCTATAGAGA ATTACTAGAA     180
GAAATTGGCA CGAATGAAAT AGAGATTTTG GCGCAATACC CTAGA                     225
```

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243

```
GTGATGCTAA TGGCAATTTT TACCCCTTAT ATTCTTATTT TGAAAATGAT GAAAAAGTCT      60
ATGAGTTTAT TCGCCAATAT GGGGTTGGAG CAAATTTTTT GCAACAGAGA CATTAAAGAT     120
TTAAATGATT TTGTTTTTGG TATAGAAGTG GGGCTTGATA GCAATGCGAG AAAAAATCGT     180
AGCAGAAAGG CTATGGAAAA TCATCTTATC GGTCTTTTTG TCCAAGCTCA ATTAAATTTT     240
AAAGAACAAG TAGATATTAG AGAATTTGAG GATTTACGCC AGGCTTTTGG AAATGATACT     300
AAAAAATTTG ATTTTGTTAT TTTTAGCAAA GAGAAAACTT ATTTTCATAG AAGC           354
```

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 627 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:244

```
ATGATCCGTC TAGCCGCGTT TTTTTTAGCT CTCGCTTGCG CGATTACGCC AAAAAGCCGC      60
CTTCTTTTAA AAAATGTCTT GCTCAACCCC ACTCGCATAG AAGCTTTTGA GGTTTTGAAA     120
AAAATGGGCG CTCATATAGA ATATGTTATC CAATCCAAAG ATTTAGAAGT TATTGGCGAT     180
ATTTACATAG AGCATGCCCC TTTAAAAGCG ATCAGTATTG ATCAGAATAT CGCCAGCCTT     240
ATTGATGAAA TCCCCGCTTT AAGCATCGCT ATGCTTTTTG CAAAAGGCAA AAGCATGGTG     300
AGAAACGCTA AAGATTTACG AGCCAAAGAA AGCGATAGGA TTAAAGCGGT TGTTTCTAAT     360
TTCAAAGCTT TAGGGATTGA GTGCGAAGAA TTTGAAGACG GGTTTTATAT AGAGGGATTA     420
GGAGATGCGA GTCAATTAAA GCAGCATTTT TCTAAGATTA AACCCCCTAT TATCAAGAGT     480
TTCAATGATC ACAGGATTGC GATGAGTTTC GCTGTTTTAA CTTTAGCGTT GCCTTTAGAA     540
ATTGATAATT TAGAATGCGC GAACATTTCT TTCCCAACCT TTCAGCTTTG GCTCAATCTA     600
TTCAAAAAAA GGAGTCTCAA TGGAAAT                                         627
```

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245

```
GTGGGGAGTT TGAAATTTTT AAACGCTATG GGGGTTGATT TAAAGGTTAA AGAGAGCGCT      60
AATATCATGG TAGGCTTTGC GAAAAATAAG ACCTTATGCG CGTTATTCAT TTTAGAAGAG     120
CGTTTGAAAG CTAACGCTAA AGAAGTCATT CAGGCTTTAC AAAATCAAGG CTTGGAATTA     180
GAAATTTTAA GCGGGGATAA TGAAAGCTCG GTTAAGGAGT GCGCG                     225
```

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:246

```
ATGGAGGCTT TAAACGCTTT GAACGCGCAA AGTGATGAGC AAATTTTATG CGAGGGTTAT      60
TTTGTGTTGT TGCAAATCTT AGAGCCTATG ATCCCGCACA CGGCATGGGA ATTGAGCGAG     120
AGGCTTTTTA AAAGAGAGAA TTTCAAGCCT ATAGAAGTAG ATGAAAGCGC TTTGATAGAA     180
GACTTTATGA CTTTAGGGCT TACCATTAAT GGCAAAAGGC GCGCGGAATT GAAAGTCAAT     240
ATTAACGCTA GCAAAGAAGA GATTATTATT TTGGCTAAAA AAGAATTAGA GAAATATTTA     300
GAAAACGCGA GCGTTAAAAA AGAAATTTAT GTGCCTAATA AACTTGTTAA TTTTGTTACC     360
GCA                                                                  363
```

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247

```
ATGAAAGAAA GTATTAAATA CTTGCTAGAA AGCGTGGGGC TAGTGCTTTT AATGAGCGTG      60
AATCCGGGCT TTGGCGGGCA GAAGTTTTTA GATCTAGTGC TAGAAAAGTG CTTGAAAGTT     120
AAAGAACTGA TCAAACGCTA CAACCCTAGC TGTCTTTTAG AAGTGGATGG GGGCGTGAAT     180
GATAAAAATA TCTTTGAACT CCAACAAGCG GGCGTGGATG TGGTGGTTTC AGGGAGTTAT     240
ATTTTTGAAT CCAAAGATYG TAAGCTGGCT ATTGAAGGCT TACAGAATGT CAGACAACCT     300
CTTGCA                                                               306
```

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248

```
GTGCATGACG GCGTGCTTGG GTGGGTAGGC TTCACTTTGA TTGCGAGCAT GTATCACATG      60
ACCCCTAGGC TTTTCAAAAG AGAGATCTAT TCAGGAAGAC TTGTGGATTT CCAATTTTGG     120
ATCATGACTT TAGGGATTGT GCTTTACTTT TCGTCCATGT GGATTGCAGG GATCACGCAA     180
GGGATGATGT GGAGGGATGT GGATCAATAC GGGAATCTCA CTTACCAATT CATTGACACG     240
GTTAAGGCGC TAATCCCTTA TTACAATATT AGAGGCGTTG GGGGTCTTAT GTATTTTATT     300
GGATTTATTA TTTTTGCTTA CAATATCTTT ATGACAATCA CGGCAGGCAA AAAATTAGAG     360
CGTGAGCCCA ATTACGCCAC SCCTATGGCA RRA                                  393
```

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249

```
ATGATAACGC TCTTTAGTTT TGGAGCGTTC GCTTACTATT TCGTGTCTTC TCAAATCAGT      60
CACGAAAACT ATCAAAACGA AATGCGCCAT TACCAGTTTG TTACCACTAT CAATGAAATT     120
TTAAATAACT ACTCTGATTA TAGAGCCATA GAAGATTACC TCTATAAAAT TGGCTTTAGA     180
GAAACCACAA TAGAAAATTT AGAAAAGGTT TTAGCCAAAA GACGCCACCA GTTGCACCAC     240
AGAAATATTT GGTATGCTGA AGTGTTTAAA TTCAGCGATA TGGTTTTTAT CCTTTTAAAA     300
AAGGATGAGC ATTTTGTGCT TTATAAAGAT TTGCATTCGG TTTCTTATAG GAATTATTTC     360
TTAGCCATTA CGGTGGGTTT ATTATTGATT TTATTCCTCT TTTTATTTGT TTTGCAGAGT     420
TTATTGCCTT TAAGAGAGTT AAGATCTCAA GTGAAACGCT TCGCTCAAGG GGATAAAAGC     480
GTGAGTTGTA AAAGCAAGCA AAAAGATGAA ATAGGGGATT TGGCTAACGA ATTTGACAAT     540
TGCATCCAAA AAATCAATGC GATGAATGAA TCTCGGGTTT TATTTTTGCG CTCTATCATG     600
CATGAATTAC GCACCCCTAT CACTAAGGGC AAGATACTAA GCTCTATGCT CAAAGAAGAG     660
CTGTCTTGCA AACGCTTTTC ATCTATATTT GATCACTTGA ACATGTTGAT TGAGCAATTT     720
GCCCGCATTG AGCAGCTCGC TTCCAAAAAT TATGGGAGCA ATAAAGAAAA ATTTTTAATG     780
AGCGATTTGA TAGATAAGAT TGAAAAAATG CTTTTAATTG ATGAAGATAA AAAAAGCCCT     840
ATCCATGTAT CCTCTTCAAA TTACATCATT GAAGCGGATT TTGAATTGTT TGCTATAGCG     900
TTAAAAAACA TGATAGACAA TGCGATCAAA TACAGCGATG ACAAACAGGT GTTTTTGGAT     960
TTCATAGGGA ATAATTTAGT GGTGTCCAAT AAAAGCAAAC CTTTAAAAGA AGATTTTGAA    1020
AAGTATTTGC AACCCTACTT TAAATCTTCT AACCCCAGCC AAGCCCATGG GTTTGGGTTA    1080
GGCATGTATA TCATTAAAAA CGCTTTAGAG GCTATGGGAT TGAATTTGAG CTATCATTAT    1140
AGCAATGGAA GAATCTGTTT CACTATCCAT GATTGCGTTT TTAATAGTTT TTACGATTTA    1200
GAAGCGGATA ATGAAGAGCT ACCCCCCCCC GAAAATTTGA GAGAGGTGAA GGGAATGAAG    1260
GGAACAGAAA AAGCCAATTG TGGGGTTAAA GAAAAACAAA AAGAGAGAAC ATGTTCAAAC    1320
GAT                                                                  1323
```

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:250

```
GTGCTTCTCC TTTCTCGTAT GGGTATCGCT TTTGCCCACT CTATTTTTTG GTCCATCACG      60
GCTTCTTTAG TCATTCGTGT CGCGCCAAGA AACAAAAAAC AACAGGCCTT AGGGCTGTTA     120
GCGTTAGGGA GTTCGTTAGC GATGATTTTA GGGTTGCCGC TTGGGAGGAT CATTGGGCAA     180
ATTTTGGATT GGCGATCCAC TTTTGGCGTG ATTGGGGGCG TTGCGACTCT TATAATGCTG     240
CTTATGTGGA AATTGCTCCC GCATCTACCG AGTAGAAACG CCGGCACGCT CGCAAGTGTT     300
CCTATATTAA TGAAACGCCC GCTTTTAGTG GGGATTTATT TGCYTGTGAA TCATGGTTAT     360
TTCTGGGCAT TTCACCACTT A                                               381
```

(2) INFORMATION FOR SEQ ID NO:251:

(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:251

```
ATGCGCATTA TCATAAGGTT ACTTTCATTT AAAATGAACG CTTTTTTAAA ACTCGCGCTC      60
GCTTCTTTGA TGGGGGGGCT TTGGTATGCT TTCAATGGCG AAGGCTCTGA GATTGTCGCT     120
ATAGGGATTT TTGTGTTGAT CTTGTTTGTT TTTTTTATCC GCCCTGTGAG TTTCCAAGAC     180
CCAGAAAAAC GAGAAGAATA CATAGAACGG CTTAAAAAAA ACCATGAGAG GAAAATGATC     240
TTACAAGACA AGCAAAAAGA AGAGCAAATG CGCCTCTATC AAGCCAAAAA AGAGCGAGAG     300
AGCAGGCAAA AACAAGACCT TAAAGAACAA ATGAAAAAAT ACTCA                     345
```

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(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:252

GTGCGATCTT GCAAACAGAT TTTTGATAAG GGTTTAAAGC CCTATTATAA ACATTCTGTT 60
TGCTTAAAGC CTTTTTTTAG GTTTTGTTTT CTCAAAATTC ATGCTTATCA ACAGCGTTAT 120
AGAGCGTTTG CTCTAACGCT CTTTTCTTGT AAGTTTTTTA ACGCTTGTAA GATTTTTATT 180
CCCATAATTG ATTTTAAAAT CGTTTTTATC CCTATTCTAA AACACCAAGC CAAGCTAAAA 240
AGAGTCTCTA ATGCCTAT 258

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253

ATGTGTGGAA TGGGGTTTAT TGGCTTCAAA ACAAAACTTA CTCAAACAAA GGCATTTATT 60
ATATTGATCC CAATCTTTCA GGACAGAGCG GTCAAAGCGG CAACACGCTC AGCACCTATA 120
CAGCTAATTT GT 132

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1680 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254

```
ATGGGGAATT TTAATAGCTA TGGCGATTTG GTGTTTAACC TCAGTCATTC AGTTAGTCAT      60
GCTATTATCA ATACTCAAGG CACAGCGACG ATCATGGCCA ATAATAACCC TTTGATCCAA     120
TTCAACGCTT CTTCAAAAGA AGTGGGTACT TACACGCTGA TTGATAGCGC TAAAGCCATT     180
TATTACGGGT ATAACAACCA AATCACAGGA GGCAGTAGCC TGGATAATTA CCTTAAGCTT     240
TATGCGCTCA TTGATATTAA TGGCAAGCAC ATGGTGATGA CTGACAACGG CTTAACCTAT     300
AACGGGCAAG CCGTGAGCGT TAAAGATGGC GGTTTAGTTG TAGGCTTTAA GGACTCTCAA     360
AATCAATACA TTTACACTTC CATTCTTTAT AATAAAGTGA AAATCGCTGT TTCTAATGAT     420
CCTATCAATA ACCCACAAGC CCCCACTTTA AAACAATATA TCGCTCAAAT TCAGGGCGTT     480
CAAAGCGTGG ATAGCATCRA TCAAGCTGGG GGAAATCAAG CGATTAATTG GCTCAATAAA     540
ATCTTTGAAA CTAAAGGAAG CCCTTTATTC GCTCCCTATT ATCTAGAGAG CCACTCCACA     600
AAAGATTTAA CCACGATCGC TGGAGATATT GCTAACACTT TAGAAGTCAT CGCTAACCCT     660
AATTTTAAAA ATGACGCCAC TAATATTTTA CAGATCAACA CCTACACGCA GCAAATGAGT     720
CGTTTAGCCA AGCTCTCTGA CACTTCAACT TTCGCCCGTT CTGATTTCTT AGAACGCTTA     780
GAAGCCCTTA AAAACAAGCG ATTCGCTGAT GCGATCCCTA ACGCTATGGA TGTGATTTTA     840
AAATACTCTC AAAGGAATAG AGTTAAAAAT AATGTGTGGG CGACAGGAGT TGGAGGGGCT     900
AGTTTCATTA GTGGAGGTAC TGRAACTTTA TATGGTATCA ATGWAGGGTA TGATAGGTTT     960
ATTAAGGGCG TGATTGTGGG AGGTTATGCC GCTTATGGGT ATAGCGGGTT CCATGCAAAC    1020
ATCACTCAAT CAGGCTCTAG CAATGTCAAT GTGGGCGTTT ATAGCCGAGC GTTTATCAAA    1080
AGAAGCGAGC TAACCATGAG CTTGAATGAG ACTTGGGGAT ACAATAAAAC TTTCATCAAC    1140
TCCTATGACC CCCTACTCTC AATCATCAAT CAGTCTTACA GATACGACAC TTGGACGACT    1200
GACGCTAAAA TCAATTATGG CTATGATTTC ATGTTTAAAG ATAAAAGCGT TATTTTTAAA    1260
CCCCAAGTAG GCTTAAGCTA TTATTACATT GGTTTGTCTG GTTTAAGGGG CATTATGGAT    1320
GATCCTATTT ACAACCAATT CAGAGCCAAT GCTGACCCTA ATAAAAAATC CGTTCTAACG    1380
ATCAATTTTG CCCTAGAAAG TCGGCATTAT TTCAATAAAA ACTCTTATTA TTTTGTGATT    1440
GCGGATGTGG GCAGAGACTT ATTCATTAAT TCTATGGGGG ATAAAATGGT GCGTTTCATC    1500
GGTAATAACA CCCTAAGCTA TAGAGATGGT GGCAGATACA ACACTTTTGC TAGCATTATC    1560
ACAGGCGGGG AGATAAGATT GTTCAAAACC TTTTATGTGA ATGCGGGCAT AGGGGCTAGG    1620
TTTGGGCTTG ATTATAAAGA TATTAATATT ACCGGAAATA TTGGTATGCW SYATRCTTTT    1680
```

(2) INFORMATION FOR SEQ ID NO:255:

(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:255

```
ATGGAGTCGA ATCAWTCACT CCCCATGGCA TTAATATCAT GCTCACCTAA CGCTAAAGGG      60
GCGGACATTA AAGGCTATAA CGGCTTAGTG GGGGAATTGA TTGAAAGGAA TTTCCAACGC     120
TATGGCGTGC CGTTACTGCT TTCTACGCTC ACTAACGGCC TATTGATTGG GATCACTTCG     180
GCTTTAAACA ACAGAGGCAA TAAAGAAGAG GTGACTAATT TCTTTGGGGA TTATCTTTTA     240
TTGCAATTGA TGAGGCAAAG CGGCATGGGG ATCAATCAAG TGGTCAATCA AATTTTAAGA     300
GACAAGAGCA AGATCGCCCC CATTGTGGTG ATTAGAGAGG GGAGTAGGGT CTTCATTTCG     360
```

This Sheet Has Been Replaced



CCCAATACTG ACATCTTCTT CCCTATACCC AGAGAGAATG AAGTCATCGC TGAGTTTTTG 420
AAG 423

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256

GTGAATTTTT ACCTTTCGCC CAAAGATTAC CACCACTACC ACGCCCCTTG CGATTTAGAA 60
ATTTTAGAGG CTCGTTATTT TGCGGGGAAA TTACTACCAG TCAATAAGCC CTCATTACAC 120
AAAAAACAAA ATCTGTTTGT GGGCAATGAA AGG 153

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 699 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:257

ATGGATATTT TAAAAGCAGA GCATTTAAAC AAACAGATTA AAAAAACCAA AATCGTTTCA 60
GATGTTTCTT TAGAAGTGAA AAGCGGCGAA GTGGTGGGGC TTTTAGGGCC TAATGGGGCG 120
GGTAAAACCA CCACCTTTTA CATGATATGC GGGCTTTTAG AGCCTAGTGG GGGGAGCGTT 180
TATTTAAACG ATGTGGATTT AGCTAAATAC CCCTTACACA AGCGTTCTAA CTTGGGCATA 240
GGCTACTTGC CCCAAGAATC CAGTATTTTT AAAGAATTGA GCGTGGAAGA GAATTTGGCC 300
CTAGCAGGGG AGAGCACTTT TAAAAACTCT AAAGAGAGCG AAGAAAAAAT GGAAAGCTTG 360
CTTGATGCTT TTAATATCCA AGCCATAAGA GAGCGCAAGG GCATGAGCTT GAGTGGGGGA 420
GAAAGAAGGC GCGTAGAAAT CGCTAGGGCT TTAATGAAAA ACCCTAAATT CGTGCTGTTA 480
GATGAGCCTT TTGCGGGCGT GGATCCGATT GCGGTGATTG ACATTCAAAG AATCATTGAA 540
AGCTTGATTG GATTAAACAT TGGCGTGTTG ATTACTGATC ACAATGTGCG AGAGACCTTG 600

AGCGTGTGCC ATAGGGCGTA TGTGATCAAA AGCGGCACGC TTTTAGCGGC GGGAACGCTA 660
ATGAAATTTA TGAAAACGCT TTGGTGCGTA AGTATTATT 699

(2) INFORMATION FOR SEQ ID NO:258:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258

ATGAAAGAAA TCGTTACAAT AGAGAATGTG TCTTTTAACT ACCACAATCG CGCTATTTTT 60
AAGGATTTTA ATTTAAGCAT TCAAGAAGGG GATTTTTTAT GCGTTTTAGG GGAGAGCGGG 120
AGCGGTAAAA GCACGCTTTT AGGCTTGATT TTAGGGCTTT TAAAACCCAG TCTGGGGAGC 180
GTTAAAATCT TTAATGAGAC CCTTTCAAAC AACGCTTTTT TACGCCAAAA AATAGGCTAT 240
ATCGCTCAGG GCAATTCCTT ATTCCCTCAT TTAAACGCCT TACAAAACAT GACTTTTTGC 300
CTTAATTTAC AAGGCATAAA CAAACAAGCC GCTCAAAAAG AAGCCAAAGC CTTAGCGTTA 360
AAAATGGGGT TAGACGAGAG CCTTATGGAT AAATTCCCTA ATGAATTGAG TGGGGGGCAA 420
GCCAAAGAGT GGGCATTATT AGGGGGATTA TCCACAGGCC AGAACTCATT TTAT 474

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259

ATGATTTTCC CCGAGCGCTT TCAAAACGCC TTTTTAGGGT TAAGCGAATT GTTTTACTAC
GCTTCCAGCT TGAGTTTTTA TACGATTTTG TCTTTATCGC CTATTTTGTT GTTCGTGTTC
AGTCTTTTTG TGTCTCATTA CTTGCAAGCG CACAGCGGTG AAATGGAAGC CTTGATTTTC
CCTAACGCTC CTAAACTCAT TGGCGCGATT AAGGATTTTT TAGAAAATTT TAAAAAAACA
GACATGACCT TAGGCACGCT TGAAGAGGTG TCTATTGTGG TGGCGTTGGT GCTTTTTTGT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261

GTGAGTGAGG TCGCGAGCGT GGGGGGCTTT GTGAAGGATT ATGAAGTAAC GCTTCAAAAC 60
GATTCTTTGA TCCGTTATAA CTTGAGTTTA GAACAAGTCG CTAACGCGAT TAAAAATTCC 120
AATAACGATA CCGGTGGGGG CGTTATTTTA GAAAACGGGT TTGAAAAAAT TATAAGATCG 180
CATGGCTATA TCCAATCTTT AAACGATTTA GAAGAAATTG TGGTTAAAAA AGAAGGGGCT 240
ATCCCTTTAA AAATCAAAGA TATAGCGAGC GTTAGGCTAG CGCCCAAACC GCGCAGAGGG 300
GCGGCTAATC TCAACGGCGA TAAGGAAGTG GTGGGCGGGA TTGTTATGGT GCGCTATCAC 360
GCTGACACTT ATAAGGTGCT TAAAGCCATT AAAGAAAAAA TCGCCACCTT ACAAGCGAGT 420
AACCCTGATG TGAAAATCAC CAGCGTGTAT GACAGGAGCG AATTGATTGA AAAAGGCATT 480
GACAATTTGA TTCACACGCT CATAGAAGAA AGCGTCATTG TGCTAGTCAT TATTGCGATT 540
TTCTTACTGC ATTTCAGGAG CGCTTTAGTG GTGATTATCA CTCTGCCTTT AAGYGTGTGC 600
ATCAGTTTCT TGCTCATGSG TTATTTCRAT ATTGAAGCGA GCATCATGAG TTTGGGGGGC 660
ATTGCAATCG CTATAGGGGC GATGGTGAAT GCGGCGATTG TGATGGTG 708

(2) INFORMATION FOR SEQ ID NO:262:

(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:262

GTGGAAACTT TTCTTAGAAT TTTTGAAAAA GATATTTTTA ACACGCCCTA TAAATTAGAA 60
GTCATTAACG CTACTGAGGG GGGGGCTAGG ATTAAAGGGA CTAAAGAAAT GCCCTTTAAA 120
GAAGTGTGCG AAAAAWTAGA CAAATCCAAG CCAAAGCCTC CTATCAATCT TATTTATCCC 180
ACCCAATCAG AACAGGCTAA AAATTTAAAG ATCGCCAAGA AAAAATGCGA AGAGATCATC 240
AAATACGCCA ATGAGAAAAA AACGCAAGTT GAAGAAGCGT TTTTAAAGGT GGCAGAGTTT 300
TTAGAAAAAG TGGAAAAGCT TCATGAAAAA AACAAATTAG AAGAGTTGGA TTTTGAAGAA 360
TTAGAAAATT TGAGCGCTGA AATTGATAAC GTTAAAGAGC TTTTTGATGA CAAACGATTC 420
AATTCGTATT TTATGGATGC GATACAATCT TACATTTTCC ACCAGGAATT GCATATCGCT 480
GAAATCGTGT GTAAAAAAAC GAGTAATGAA GACGGGATTA AGGGC 525

(2) INFORMATION FOR SEQ ID NO:263:

(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

This Sheet Has Been Replaced

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265

```
ATGTTTGTGG TTTTTATAGA AGGTTTTGGT TTAGCGATTT CTTTGTGCGC GGCGGTGGGG      60
GCGCAATCCT TGTTTATTGT GGAAAGGGGG ATGGCTAGGA ATTATGTGTT TTTGATTTGC     120
GCCTTGTGTT TTATGTGCGA TATTGTCTTA ATGAGCATGG GCGTGTTTGG CGTGGGGGCT     180
TATTTCGCTA AAAACCTTTA TTTGAGCTTG TTTTTGAATT TATTTGGGGC AGTTTTTACC     240
GGATTTTACG CTTTTTTGGC TTTAAAAACC CTTTTTCAAA CCTTTAAAAA AAAGCAAGTC     300
CAAACCCCTA AAAAATTATC CTTAAAAAAG ACCTTATTAT TCACTTTAGG CGTTACCTTA     360
CTCAATCCTC AAGTGTATTT GGAAATGGTG TTTTTAATTG GCGCGAGCGC TATGTCTTTT     420
AACCTAGTGC AAAAATTCGT CTTTCTAGCT GGCACTTTAT CGGCTGCCTT TTCTTGGCTT     480
TTATTGTTAT GCACCATGTC CTTACGCTAT GGCTCTAAAC TTTTGAACAA CCAAAAAATC     540
TTTATGGGCG TGAATCTCTT TGTAACCGCT ATCATGGGAA CGCTCAGCGT TACTTTATTC     600
AGGGATTTTT TAGCGTTATT GAGCAAAACC                                      630
```

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266

```
GTGAAGCCAA AGAGCATGAA AGAGAAGCTA AGAGGCGCTA TGGTGAATAT CTTAAGGATA      60
AAAATGATTG AAATAAGCGA ATGGTTGCAA AAACTAGACG ATGCCTTAGA TAAAGTTGTT     120
GCTAAAAAAG AGCCAGAGAG TTTTCTCAAG CCGATCATTT CACCAATAGA GGACTACCAA     180
AAGAGTGTCA GGCAAATTCA AGCGCAATTC ACAGACGCGC CGAAGTTCAA TGAAGAGGGT     240
GCTTACCCTC AATTTTTAAG CTGTGGTTTA TTGCAAGTTA GGGGCAAAAA TGGTGCTAAC     300
ATGGAATTTT TATTGCCTAA AGTTTATCCT TTCCCCCCTA AAAGCTTGTA TATAGAGCAT     360
GAAAAAGACG GGCAGTTTTT GAGAGAAATG CTCATGCGCT TACTCTCCAG CGCGCCTTTA     420
GTGCAATTGG AAGTGATCTT AATTGATGCG TTGAGCTTGG GGGGCATTTT CAATCTGGCC     480
AGAAGGCTTT TAGATAAAAA CAATGACTTT ATTTACCAGC AAAGGATTTT GACCGAAAGC     540
AAGGAAATAG AAGAAGCCCT AAAGCATTTG CATGAATATT TAAAGGTTAA TTTGCAAGAA     600
AAATTAGCCG GTTTTAGAGA TTTTGTGCAT TATAATGAAA ACGCCAAAGA CTCCTTGCCT     660
TTAAAAGCGC TTTTTTTAAG CGGGGTGGAT GCTTTGAGTA AAGACGCGCT TTATTATCTA     720
GAAAAGATCA TGCGTTTTGG CTCTAAAAAT GGGGTTTTGA GCTTTGTCAA TTTGGAGAGC     780
GAAAAAAACA ATCAATCCGC AGAAGATTTG AAACGCTATG CGGAGTTTTT TAAAGACAGG     840
ACAAGTTTTG AGTGSTTAAA ATACCTTAAT GTAGAAATCA TCAGCGAT                  888
```

(2) INFORMATION FOR SEQ ID NO:267:

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269

```
ATGCAAGCTT GGGTGGATAA GCCGGTATTG TTAGAGCCAG ATAGTAACGC CCAATACGCC      60
GCTGTCATTG AAATTGATGT GGCAGAAATC ACGGAGCCTA TTTTGGCATG CCCTAATGAC     120
CCTGATGACG TCGCTACTTT GAGCGAAGTT TTAGCGGATA CGACCGGCAA AAGACCCCAC     180
GCTATTGATG AAGTGTTTAT TGGCTCTTGC ATGACGAATA TTGGGCATTT CAGAGCCTTT     240
GGTGAAATCG TTAAAAACGC CCCTCCCAGT CAAGCACGCC TTTGGGTAGT GCCACCCAGT     300
AAAATGGACG AACAAGAGCT TATTAATGAG GGCTATTATG CGATTTTTGG GGCTGCCGGG     360
GCAAGGACTG AAGTACCAGG CTGTAGCTTG TGCATGGGCA ATCAAGCGAG GGTTAGGGAT     420
AATGCGGTCG TTTTTTCTAC TTCCACACGG AATTTTGATA ATCGTATGGG TAGAGGGGCT     480
AAAGTGTATT TGGGCAGTGC GGAGCTTGGG GCGGCGTGCG CTTTACTAGG GAGGATCCCC     540
ACTAAAGAAG AATACATGAA TTTAGTGAGT GAAAAGCTAG AGAGCCAAAA AGACAAGATC     600
TATCGCTMC                                                             609
```

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 660 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:270

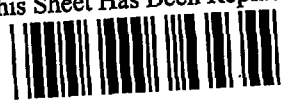
```
GTGGGCAATG CCGGGGTGGC TTTAGCGGGT TTGATGAGCG ATGAAATTTA TTTGTGCGCT      60
TTAGATTGCG CTTATATCAA AGGGTTTAAA AAGCACGCTC AAAATTCCTA TTATGGAGAT     120
GAAAAAGAGA TTGACACCTC ATCTTTAATC AGCGTAGAGG GTAATGTTGA AGGTTATGAA     180
ACTTTTAGCG ACTCGCTTTT TTTGCTCTCT AAAGAAAGGA TTGAAGAAGC CCTTCATTAT     240
TACCAGCCTA AAAAAGTCTA TAATTTAAGC TATGGGGCGA AAATCAAGCA CGCCGTTAGC     300
CTCAATCACT CTCAAGTGAA ATTGAAACAA ATCAACAAAC AAGACGCTAT CGTTCGCATT     360
AAAAGCATGT TTAGCCCTAG AAGTAATCAT GCTAAGGATT TAAAAAATTT ACAAAAAAAT     420
CTGATTCGTT TTAAAGAGGA TTTTTTCACG CATTTAAACA CGCCTTGTAA AACCAAGCAA     480
GAAGCATTTG AATGGGTGGA TAGCTTGAGT GGATTTTGCC AAACAGCCAG CGCTAAAACC     540
CCCACTATAG GCATTTTATT TGAAGGGAGT GTCGCCCATA TCTTACAAAG CGTTCTAATC     600
GTTTCATTGC ATCTTAAAGA AAATGAGCTG ACGCTTTTAT CAAATTCTCT CAAAACGCCT     660
```

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 744 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271

```
ATGCAAAAAA GTATATTCAA AATAACTCTG TTGTTGGTTT TCCTCTTTTT AAGGAATGCT      60
GTTGGTTTAG ACGATAAAAA AGCAGCTCCT AAAAGCGTTC AAAATACCCC TAAAAATTTA     120
CCCCCTATCC AGTTAAGGCT CGATCAAGCC TATGAAGACC TTATCAAAAT GTTAGACAAT     180
ATGGGAAAAA GCACGCAGTA TGAGTTCCCT AAAATTAAAG AAATCCTAGA ACAAAGCGAA     240
GAGGAATGGC TAGGAGTCGC CCATGAAGAA TGTGTGGCGT TAGTCATGTT AATAAGCCCT     300
AAGGCTTCTA TTGAAAACAG CCCGATTTAT AAGAATTGCT ATGAAGCTTA TGTGAAACAA     360
AGAATCCATG ATTTATATGA TTTTTATATA GAGGGCAAAA AAGTGAAAAG AAAAATCAAG     420
AAAGCCCATG AGCATGAAAT GGCCCTCAAC AAATCCCAAC CCTTAAAAAA GGAACCGCCT     480
AAAAGCGAGA ATAAAAAGGG CTTAACAAAA CCTAGCTTGA AAGACGCAAA GATCCCTAAA     540
GGGTATTACT TGCAAATTGG GGCTTTTTTA AATTCGCCCA GTAAGGATTT TTTGCAAACG     600
CTCAAAACTT TCCCTCACCA AATGGAGGAA AAAGACTCCC TCACGCATTA TTTGATTGGC     660
CCTTATAAAA CCAAAGAAGA AGCCCTAAAA CAGCTTGAAA ATGCGGCTAA AAGCTTTAAA     720
AATAAGCCTG CGTTGGTAGA GAAG                                            744
```

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272

```
ATGCAAGAAA TCTTAATCCC TTTAAAAGAA AAAAGCTATA AAGTGTTTTT GGGGGAACTG      60
CCTGAAATAA AATTGAAACA AAAAGCGCTC ATCATTAGCG ATAGCATCGT GGCCGGGTTG     120
CATTTGCCCT ATTTGTTAGA GCGCTTGAAC GCCTTAGAAG TCAGAGTGTG CGTGATAGAG     180
TCCGGGGAAA AATACAAAAA TTTTCATTCA TTAGAGCGGA TTTTAAACAA CGCCTTTGAA     240
```

```
ATGCAATTAA ACCGCCATTC TTTAATGATA GCCCTTGGTG GGGGAGTGAT AAGCGATATG     300
GTGGGGTTTG CGAGCAGTAT TTATTTCAGG GGGATTGATT TTATTAATAT TCCCTACGAC     360
TTTACTCGCT CAAGTGGATG CGAGCGTGGG GGGGAAAACA GGGATCAACA CGCCTTATGG     420
CAAGAACCTA ATCGGATCGT TCCACCAGCC                                      450
```

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 561 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:273

```
ATGCGAATAC TTCATTATGG AGGTGAGCTC CCATGCGATT GTCCAAAACG CATCGCTGGG      60
CTTGATTTCG CTCTTAAAAT TCTCACCAAT ATCACAAGCG ATCATTTAGA TTTCCATCAA     120
AATATAGAAA ATTACAGGGA CGCTAAAAAC AGCTTTTTTA AAGATGAGGG CTTAAAAGTC     180
ATCAACAGAG ATGAAACAAA CGCCCTTTTT AACCCCATTA ACGCGCGCAC TTACGCACTG     240
GATAAAAAAG CGCATTTGAA TGTTCAAGCC TTTTCGCTCA ACCCTTCCAT TAGCGCGTCT     300
TTATGCTACC AACACGATTT AAGAGATCCC AATCTTAAAG AAACCGCCCT GATCCATTCC     360
CCCCTTTTAG GGCGTTACAA CCTTTATAAT ATTTTAGCGG GCGTTTTAGG GGTTAAATTG     420
CTCACTCAAT TGCCTTTAGA AACGATCGCA CCGTTATTGG AAAACTTTTA TGGGGTTAAG     480
GGGCGTTTGG AAATTGTACA TTCTAAACCT TTAGTGGTCG TGGATTTTGC CCACACAACA     540
GACGGCATGC AACAAGTTTT T                                               561
```

(2) INFORMATION FOR SEQ ID NO:274:

(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:274

```
GTGAGCATTA AAGAAGAGAG CCAAACCTTA GCCGATATTA CTTTCCAAAA TTATTTCAGG      60
```

```
ATGTTTTCTA AACTTTCAGG CATGACAGGC ACGGCTCAAA CCGAAGCCAC AGAATTTTTA     120
GAAATCTACA ATTTAGAAGT GGTGTCCATC CCTACTAATC TAGCGATCAA GCGAAAAGAT     180
TTGAACGATC TGATCTATAA GAGTGAAAAA GAAAAATTTG ACGCTGTGAT CCTTAAAATT     240
AAAGAATTAC ACGATAAGGG TCAGCCCGTT TTAGTCGGCA CGGCTAGCAT TGAAAAGAGT     300
GAAACCTTGC ACGCTTTACT CAAAAAAGAG CGCATCCCTC ACACCGTTTT AAACGCCAAG     360
CAACACACTA AAGAAGCTGA AATCATCAAA GACGCCGGGC TTAAAGGGGC GGTTACGATT     420
GCGACCAACA TGGCAGGCAG GGGCGTTGAT ATTAAGCTCA CTGATGAAGT TAAAGAACTT     480
GGGGGGCTGT ATATCATTGG CACTGAAAGG CATGAGAGCC GTAGGATTGA CAATCAATTA     540
AGGGGGCGAA GCGGGCGTCA AGGCGATCCG GGAGTGAGTC AGTTTTATTT GAGC           594
```

(2) INFORMATION FOR SEQ ID NO:275:

(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:275

```
GTGGTGGCTG ATGAGGTGAG AAAGCTCGCT GAAAAAACCC AAAAAGCCAC TAAAGAAATC      60
GCTGTCGTGG TTAAAAGCAT GCAACAAGAA GCGAACGATA TTCAAACCAA CACCCACGAT     120
ATTAATTCTA TTGTAGGCTC TATTAAGGGT GATGTGGAAG AGCTTAAATC CACCGTAAAA     180
AATAACATGA TTGTCGCGCA AGCCGCAAAA TACACCATCT ACAATATCAA TAACCGGGTG     240
TTTTGCGGTY TGGCTAAACT CGATCATGTG GTCTTTAAAA ACAATCTTTA TGGCATGGTG     300
CSTTTGGTCT CAATTCCTTT GACATTACCA GCCCATAAGA GTTSCCGTTT AGGCAAATGG     360
TATTATGAGG GTGCGGGTAA AGAAAACTTT GCTAACACTT CAGGCTATAG AGCTTTAGAA     420
AGCCACCATG CGAGCGTGCA TGCTGAAGCT AATGATTTGG TTAAAGCCGT TCAAGAAGAT     480
CACGTCACCG ATTCAAAATA CCTAGAACAT AAAGTGCATT TAATGGAAGA TAGCGCTAAG     540
CATGTCAAAG AAAATATTGA TAAGATGTTT TATGAAAAAC AAGATGAACT CAATAAAATC     600
ATTGAAAAAA TTCAAAAAGG CGAA                                            624
```

(2) INFORMATION FOR SEQ ID NO:276:

(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

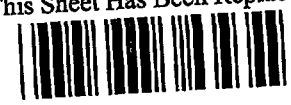
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(A) NAME/KEY: misc_feature
(B) LOCATION 1...603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276

ATGAATACAT CAAAAAAATT AGGTAACCCC TTGCTTTTTT TGCATGATAA TAAAATTTTG 60
TTGTTTGTCG TAGGGGTGAG CATGGGCGGG TGGGCCACTT CTAAAATCTA TCAATTTGAA 120
AGCGCTTTAG AGCCGATTCA TTTTAAGTTT GCGCGAAAAC TCTCTTTAAG CCCTTTTTTA 180
AATTTGAGCC ATTTAGTAAG GAATAAGCCT TTAAACACCA CTGATGGCGG GTTTATGCTA 240
CCACTCTATC ACGAATTAGC CACCCAATAC CCCTTGTTGT TGAAATTTGA CCAACAAAAT 300
AACCCAAGAG AGCTTTTAAG GCCTAATACC TTAAACCACC AGCTCCAACC AAGCTTAACC 360
CCCTTTAAAG ACTGCGCTGT CATGGCGTTT AGAAACCATT CTTTTAAAGA TAGCCTCATG 420
CTAGAAACCT GTAAAACCCC CACTGATTGG CAAAAACCCA TTTCTACAAA TCTTAAAAAC 480
TTAGATGATT CTTTAAATTT ACTCAATTTA AATGGAATAT TGTATTTGAT CCACAACCCT 540
AGCGATTTAT CACTGCGTCG TAAAGAACTT TGGCTTTCTA AATTAGAAAA CCYYCAACTC 600
RTT 603

(2) INFORMATION FOR SEQ ID NO:277:

(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:277

ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT TTGCCTTCCT
GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA
CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC
GAAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC
CGTATTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG
GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAGAATTA
YGCWGGTGGT GCCATAACCA T

(2) INFORMATION FOR SEQ ID NO:278:

(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:

This Sheet Has Been Replaced



(A) ORGANISM: Helicobacter pylori

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278

GTGAACGTGG GCGTGCCTTT TAGCTATCAA GTGAGCGCGA CCTTTCAAAA CTCACGCCTT 60
TCTAGTTTGC TAGAAACTTT AAAAAAGAGT TTTTTAGAAA AGCCCTTAAT TGAGAGCAGC 120
GCGAATAAAA TCGCGGATAT TTTTTCTAAA GCGGTGTTGT TTTTAGCCTT TGTGAGCTTT 180
TTATTGTGGC AATTTGGTTT GGGGGGTAAT TTTGAAAAAS GCTTTAATGG TGTGTAT 237

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279

ATGCTAATGG TTAATGGCTA TCAAATCACG ATGCATAAGG GTTATAAGGT AGGGTTTTTT 60
ACAAGCGGTT ACAACCCTGA TTTCGCTCAA ACCATTCAAA ATAGAAGCTA TTTGATGAGC 120
TCTTATGAGT TATCGTTTTT AAGAAAT 147

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1236 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280

```
ATGGTGCAAT TTCAAAACAC GCTTATAAAA TTCCATGCCC TATCCTTTAA AAACGCAAAT      60
TTAATTTATA ATGCAAAATT AAACAAAACA TGCTATAAAG AAAATTCAAA TACTATCATT     120
TTAAGGATTA AAATGCTCAC CCAAGAAGAT GTCTTAAACG CGTTAAAAAC GATCATCTAC     180
CCTAATTTTG AAAAGGATAT TGTCAGCTTT GGTTTTGTTA AAAACATCAC CTTGCATGAC     240
AACCAATTAG GGCTTTTAAT AGAAATCCCC TCAAGCTCTG AGGAAACGAG TGCGATTTTA     300
AGGGAAAATA TCTCCAAAGC GATGCAAGAA AAAGGCGTGA AAGCTTTGAA TTTGGATATT     360
AAAACCCCGC CTAAACCGCA AGCTCCAAAG CCCACCACTA AAAATCTGGC TAAAAACATC     420
AAGCATGTGG TCATGATAAG CTCAGGCAAG GGCGGTGTGG GTAAAAGCAC CACCAGCGTG     480
AATTTAAGCA TCGCTTTAGC GAATTTAAAC CAAAAAGTGG GGCTACTAGA CGCTGATGTG     540
TATGGCCCTA ATATCCCTAG AATGATGGGC TTGCAAAACG CTGATGTGAT CATGGATCCT     600
AGCGGTAAAA AACTCATTCC TTTAAAAGCT TTTGGCGTTT CTGTGATGAG CATGGGGCTT     660
TTGTATGATG AGGGGCAGAG TCTCATTTGG AGAGGACCCA TGCTCATGCG AGCGATTGAG     720
CAGATGCTAA GCGATATTAT TTGGGGGGAT TTAGACGTGC TGGTGGTGGA TATGCCCCCA     780
AGGAACAGGC GATGCGCAGC TCACGCAGCC CAAGCCGTGC CACTCAGCGC AGGAATCACC     840
GTTACTACGC CTCAAATCGT GAGTTTAGAT GACGCTAAAC GGAGTTTGGA CATGTTTAAG     900
AAACTACACA TTCCTATTGC GGGCATTGTA GAAAATATGG GGAGTTTTGT GTGCGAGCAT     960
TGCAAGAAAG AGAGCGAGAT TTTTGGCTCA AATTCCATGA GTGGATTATT AGAGGCTTAT    1020
AACACGCAGA TTTTAGCCAA GCTCCCTTTA GAGCCTAAAG TGCGTCTAGG GGGGGATAAG    1080
GGTGAACCGA TTGTGATTTC TCATCCCACT AGCGTGAGTG CTAAAATTTT TGAAAAAATG    1140
GCAAAGGATT TGAGTGCTTT TTTAGACAAG GTGGAAAGGG AAAAACTAGC CGATAATAAG    1200
GACATCCAGC CCACACAAAC GCATGCTTAT TCGCAT                               1236
```

(2) INFORMATION FOR SEQ ID NO:281:

(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:281

```
ATGGGTGTGG TGATTGGCGA GACCACAGAG ATTGGAGATG ATGTTACCAT TTATCATGGC      60
GTAACTCTGG GGGGTACGGG CAAGTTTAAG GGCAAACGCC ACCCTACTTT AGGCAACCGA     120
GTGGTAGTTG GGGCAGGGGC TAAGGTCTTG GGCGCGATTT GCGTGGGCGA TGATGTGAGG     180
ATTGGGGCTA ATGCGGTGGT GCTTTCAGAT TTACCCACGG GTTCTACGGC TGTAGGTGCT     240
AAAGCCAAAA CCATCACAAA GGATCGT                                         267
```

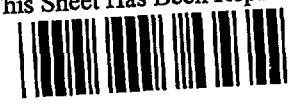
(2) INFORMATION FOR SEQ ID NO:282:

(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

This Sheet Has Been Replaced



(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:282

```
ATGCTATCTT TTATAAGCGC GTTTGATAAA AGGGGCGTTT CAATACGCCT TCTAACAGCC      60
TTGTTACTGC TTTTTAGTTT GGGTTTGGCT AAAGATTTAG AAATCCAAAC TTTTGTGGCT     120
AAATACCTTT CTAAAAATCA AAAAATACAA GCCCTACAGG AGCAAATTGA CGCTTTAGAT     180
TCTCAAGAAA AAGTCGTTAG CAAATGGGAT AACCCTATTT TGTATTTAGG CTATAACAAC     240
GCTAACGTGA GCGATTTTTT CAGGCTGGAT AGCACCTTAA TGCAAAACAT GAGCTTGGGT     300
TTGTCTCAAA AAGTGGATTT AAATGGTAAA AAACTCACGC AGTCTAAAAT GATCAATTTA     360
GAAAAACAAA AAAAAATATT AGAGCTTAAA AAAACCAAGC AGCAATTGGT GATTAATTTA     420
ATGATAAACG GCATTGAAAA CTATAAAAAC CAACAAGAAA TAGAGCTTTT AAACACAGCG     480
ATTAAAAATT TAGAAAACAC CCTCTATCAA GCCAACCATT CCAGTTCGCC CGATTTAATA     540
GYGATYGYCA AGTTRGAAAW TTTAAAAATC GCCAWT                               576
```

(2) INFORMATION FOR SEQ ID NO:283:

(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:283

```
GTGCCGGCTG TTGGGGGGGC TTTGATTTGG ATYCYTATAG YGATTTATGA GCTTTATCAT      60
GGGYATGTGA ATGAGGYTAT TTTTAYYGTT TTGTATTCCA TTTTGTTAAT TGGTGTGTTG     120
ATTGATAGCG TGATCAAGCC AATTTTAATC GTTTTTATCA AAAAAAGAAT CTTTAAAACC     180
ACCCTTAAAA TCAATGAAAT ATTGATTTTC TTTTCTATGA TTGCTGGGAT TTCTCAATTT     240
GGTTTTTGGG GGATTATCGT AGGGCCTACC ATCACGGCGT TTTTTATCGC GTTACTGCGA     300
TTGTATGAAA ATTACTTTAT TCAAAAGGAG CAAAAAACAT GCGAATGT                  348
```

(2) INFORMATION FOR SEQ ID NO:284:

(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

This Sheet Has Been Replaced



(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:284

GTGGTTGTCA TTATTTTAGT GGTCGTTATC ATTCAAAACA GCTCTTCTTT AAAAGAAGAG 60
AGAGAGCAAG AACGCGCTAT TAAGCCCGAC ACCAAAAATA ATTCTTTCAA TGAAACTAAT 120
CCTACAGAAG AAAAAAAGTT AGAGCCAACG CCTAAATTAG AAGAAAAACA CAAAGAACAA 180
GACAAGCAAG GCAAAGAAGC GATCAAAGAA AATCCTAATA CCATTTACAT TATCCCTAAA 240
CGAGATATTT GGGTAGAAGT GATTGATTTA GATGAGAAAA AAAACTCTTT TCAAAAGGTT 300
TTTAAAAAAA GTTATCCTTT AGAGGCTAAA AACCACCGCT TGTTGTTACG CTTTGGGCAT 360
GGGCATCTTA TTCTTAAAAA CAACCATCAA GAACAAGATT ATAACGACAG CAAAACTAGG 420
CGGTTTTTAT ACGAGCCAAA TAAAGGTTTA ACGCTCATCA ATGAGGCCCA ATACAAAGCG 480
CTCCAGCAA 489

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285

ATGGATGAAA TCTATCAAAT CGCTAAAAAT AAAACCCTAA TCGTTATCGC CCACCGCTTA 60
AGCACGATTG AACGCTGTGA AGTCATCATT GACATGAGCC AACACAAAGA CAATCTCGGC 120

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

This Sheet Has Been Replaced



(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286

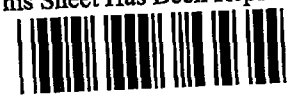
GTGGCGGGCA GCTTTATTAT TGCTCTTTTT AGCGTTTTAG CGGATCAATT TGTGAGCGTG 60
TTTCAGCATG AAAACGCCTT GCAACGCCTA TTTTCTCAAA ACGCCACCCA AAAACAAAAA 120
AAGAAGAGTT TATGT 135

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287

ATGGTAGCTT TAAGCAACGC TCTTTCAAGG GTTTTTGGTT CTGTGGCTGG CTATAAATTC 60
CCTTCTTTTA TCCAAAAAAG CATCAACGCT CTTTATGTTA AGATCTTTAA AATTGATTTG 120
AGCGAGTTTG AGCCTTTAGA AAATTATAAG AGTTTGAACG CTCTTTTCAT GCGCTCTTTA 180
AAAAAAGAAC GCCCCTTTGA CAAAGCCCCT ATATTTGCAT TGCGCCTTGC GATGGCTTTA 240
ATCACTGAAT GCGCTTTTTT AGACAACGAT AGCGCTTTAC AAATTAAAGG CATGCCCTAT 300
AAAGCGCATG AATTAGTGGG CGAAATCAAC CCCTTAAGCC CTCTTTTTTC TATG 354

(2) INFORMATION FOR SEQ ID NO:288:

(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:288

```
ATGGCAGTGT TAAAAAAGAT GATAGGTTTG GTGGCGGTTT TAAGCGTTTT ATTAGCCAGA      60
GACAACCCTT TTGAGCCTGA AATCAATTCC AAGAATTTGC AAGGGGGCTT TAGCGGGATC     120
TATGATGACT ACCTCAAAGA AATCCATGTG GATTTGCCCA CGAGCGCTAG GATCTTAAAA     180
AAAATCACGC TCACTTACCA AGATATTGAT GGCTCTATCC ATTCTAAAGT CGTGGGTATT     240
GATAAAAGCA TTGATTGGCA CTACCCCTTA AAACTTTCCC AACACACCCT TAATCAAGAC     300
GCCTTTGAAA AACGCTACCA GATCCAAGAT TTTGATTTTT TAATGGCAAA CAACACGATG     360
ATTTTGCGTT CCCCTTATAA AATTTTGCGC TCTTTTGTGT TAGTCAATCC TTATAGAATC     420
GTGTTAGACA CGCAAAAAGG CCCTTTGGAT ATTTATCAAA ACATGGATTT AAACCAGAAG     480
TTTTTTTCTC ACATTAAAGT CGGCACGCAC AAAGATTATT ACCGCATCAC GCTCATTTTA     540
GACGGGAAAT ACCGCTATCT TTTGGAAGAA AAAAACGGGG CGTATGAATT AAAACTGAAA     600
```

(2) INFORMATION FOR SEQ ID NO:289:

(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:289

```
ATGGGCGGAT TCACAAGCAT ATGGCATTGG GTCATTGTTT TATTAGTGAT TGTGTTGTTA      60
TTTGGGGCTA AAAAGATCCC AGAATTGGCT AAAGGTTTAG GCAGTGGGAT TAAGAATTTC     120
AAAAAAGCCG TGAAAGACGA TGAAGAAGAG GCTAAAAAAC GAGCTAAAAAC CCTAGACGCT     180
CAAGCAACAC AAACCAAAGT GCATGAAACT AGCGAAATTA AAAGCAAACA AGAAAGT          237
```

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 618 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:290

```
GTGCGTTTGA ATGCGGCGGT TGTGGTGGAT GGCAAGTATA AAATCGCGCT CGAAGACGGG      60
GCAAACGCTT TAGAATACGA GCCTTTAAGC GATGAATSGS TTAAAAAAAT CAACGYCCTA     120
GTCAAACAAG CCATTGGTGA TAACCAAAAT AGAGGCGATG ACGTGGCGGT GAGTAATTTT     180
GAGTTTAACC CTATGGTGCC TATGATTGAC AACGCCACCT TGAGTGAAAA AATCATCTAT     240
AAAACCCAAA AAATTTTAGG TTTATTTATG TTTTTAATCA AGGTATATTT GGTGTTTATA     300
GTGTTATTCA TTTTCTATAA AAAAGTGATC GTGCCTTTCA GCGAACGCAT GCTGGAAGTG     360
GTGCCTGATG AAGATAAGGA AGTGAAATCC ATGTTTGAAG AAATGAACGA AGAAGAAGAT     420
GAGTTGAACA AACTCGGCGA TTTGAGGAAA AAAGTAGAAG ATCAATTAGG GCTTAATGCA     480
AGCTTTAGCG AAGAAGAAGT AAGATATGAA ATTATTTTAG AAAAGATTAG AGGAACCCTT     540
AAAGAGCGTC CTGATGAAAT CGCCACGCTC TTTAAACTCT TAATCAAAGA TGAAATCTCT     600
TCAGACAGCG CGAAAGGT                                                  618
```

(2) INFORMATION FOR SEQ ID NO:291:

(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:291

```
GTGTGTTTTA TATTGCCTTT TTGTTTAGGG GTTTTAGGCA CGCAAATCTT TAAACAAGAG      60
ACCCCAAGAC AGCTCCCTAT CGTGGTGGTG GATTTGGATA AGACCACTAC AAGCCATCAA     120
GTGGCGTTTG AATTAGGCGC AACGAGTGCG GTTGAAATCA AATACCAAGT GACTAGCCTT     180
TCAGAAGCTA AACGCTTTTT AAACTCCGCT GAAGTGTATG GGGCGTTAAT TTTGCCTAAG     240
GATTTGGAGA GAAAAATCAA AATGGGGCGA AAAGTGGSAT TTGCCCTTTT ATTA           294
```

(2) INFORMATION FOR SEQ ID NO:292:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292

```
ATGAAAGGCT TATGGCTTGT AATCTCTTTA GTTTTTGTTG GTTTTTTGTG GGCTAATGAA      60
TCTTATGTTT TTAACAATTC TAAGGGGCGT TTAACAGAAA AAAGCGTTGC GTTTATAGAG     120
GGCGTTTCTA AAGAGCTTTA TCTTAAAACC GGCGTGCGTT TTGCGATTGA TATGACGGAT     180
TTTGAAAAAA ATCCTATCGC TCTAGCGAAT AAAAAAGAGC GCCAAAGCTA TCAAGAGGGC     240
TTTTTAAAGC AGCTCAAACC CCCTTTTGTG GTATTCTTTT TCTACCATGA CGCTCAAAAA     300
ATAGAATTAG TGGCTAACCC TAAAGATTTG CTAGACACTG ATAAAATCTT TTTTGAAAAA     360
ATCGCTCCCT TACTCCCCAC AAACGCTAAA GAATACACGC CCCAAAGAAT TTCAGCCATG     420
CTCATTAACG GCTATTCGGT CGCAGTAGAT GCTTTAGCGG AAAAATATCA TGTGAATATC     480
ACGCAAAATT TTAGCGCTCC TAAGGGAGTA ACTTTTGTAA AGGTGGTTAT TTATATTTTG     540
TTATTGACGC TTTTGGGCGC GTTTTTGGGG CTTTATTTTT TTAAAAAATC T               591
```

(2) INFORMATION FOR SEQ ID NO:293:

(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:293

```
ATGTGTTCTA AAAAAATAAG AAATCTCATT TTATGCTTTG GTTTTATTTT AAGCTTGTGC      60
GCTGAAGAAA ATATCACCAA AGAAAACATG ACTGAAACGA ACACGACTGA AGAAAACACC     120
CCTAAAGACG CTCCCATTCT TTTGGAAGAA AAACGCGCCC AAACTCTAGA GCTTAAAGAA     180
GAAAATGAAG TGGCAAAAAA GATT                                            204
```

(2) INFORMATION FOR SEQ ID NO:294:

(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:294

This Sheet Has Been Replaced



GTGCTAAAGA CATTATCCAT ACGATTAGTC ATACTTTTAA ATTGCTCCCT AGCGACAAAC 60
GCTTGCAGTG GGGTGCAAAA ATTGCGCGAT GAAAGCCACC GGTATGCGAT AAACTTCCAT 120
AGATCCACTA AACTTAAAAA CATGAAACAA ATCGCTCTTT TAAAAGAAAA GGGCATAGGA 180
GAAGCCAGCG TGAAAAAATT GTTGGATTAT TTTGGGAGTT TTGAAGCGAT AGAAAAAGCG 240
AGCGATCAGG AAAAAAACGC CGTTTTAAAA AAACGAAAA 279

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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:295

GTGGGCATTA TTAGGGGGAT TATCCACAGG CCAGAACTCA TTTTATTAGA TGAGCCTTTT 60
AGCGCTTTAG ATAGTTTGAA TCGTAAGAAT TTACAGGATC TCATCAAAGA AATACACCAA 120
AATTCTTGCG CTACTTTCAT TATGGTAACG CATGATGAAA ACGAGGCGCA AAAGTTAGCC 180
ACAAAAACCC TAGAAATCAA AGCCCTTAAA CAAGAGCAG 219

(2) INFORMATION FOR SEQ ID NO:296:

(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:296

GTGATTTTTA TCGCTACCGC TAATAATATT GACAGGATCC CAGCTCCTTT AAGAGACAGA 60
ATGGAATTTA TCAGCGTGTC CAGCTACACG CCTAGCGAAA AAGAAGAGAT CGCTAAAAAC 120
TACCTCATCC CCCAAGAATT AGAAAAGCAC GCCTTAAAGC CTAGCGAAGT GGATATTAGC 180
CATGAATGTT TGAAACTCAT TATTGAAAAA TACACCAGAG AAGCGGGCGT TAGGGATTTA 240
CGAAGACAGA TCGCAACGAT TATGCGTAAA GCGGCTTTAA AATACCTAGA AGATAACCCG 300

This Sheet Has Been Replaced

```
CACAAAAAAG GGCGGACCAA AAAAAGCGAA GACAAAGATA AAAAAGGCGG AAATGAAGAA     360
AACGAAAAAA GAGGTGAGAG TAAAGATTTT TGCGTCTCTA TCACGCCTGA TAACCTTAAA     420
GAGTATTTAG AACGCATGGT GTTTGAAATT GRCCCCATAG ATGAAGAAAA TAAAATCGGT     480
ATCGTCAATG GCTTGGCATG GACTCCAGTG GGCGGTGATG TGCTTAAAAT TGAAGCGGTT     540
AAGATTAGAG GCAAGGGGGA ATTGAAACTC ACCGGGAGTT TGGGCGACGT GATGAAAGAA     600
TCCGCCATTA TTGCCTTTTC TGTTGTCAAA GTCTTGTTGG ATAACGAAAC CTTAAAAGTG     660
CCTAAAATCC CTAGCGAGAC CGATGCAGAG AATWAGAAAA AGAAAAAAGT GCTGAAAGTT     720
TWWAACGCTT ACGATTTGCA CTTGCATGTC CCTAAGGGGC TACGCCTAAA GACGGCCCGA     780
GCGCTGGGAT CGCTATGGCG AGCG                                            804
```

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 498 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297

```
ATGGGGTGTT CGTTTATCTT TAAAAAAGTT AGGGTTTATT CTAAAATGTT GGTTGCTTTG      60
GGGCTTTCAA GCGTGTTGAT CGGTTGCGCG ATGAATCCAA GCGCTGAGAC AAAAAAACCA     120
AATGACGCCA AAAACCAACA ACCAGTTCAA ACTCATGAAA GAATGACAAC AAGTTCTGAA     180
CATGTTACGC CACTAGATTT TAATTACCCG GTGCATATTG TTCAAGCCCC ACAAAACCAT     240
CATGTTGTAG GTATTTTAAT GCCACGCATT CAAGTGAGCG ATAATCTAAA ACCCTATATT     300
GATAAGTTTC AAGACGCTTT AATTAATCAA ATCCAAACTA TTTTTGAAAA AAGAGGCTAT     360
CAAGTGTTGC GTTTTCAAGA TGAAAAAGCT TTGAATGTGC AAGATAAGAA AAAGATTTTT     420
TCCGTTTTGG ATTTGAAAGG GTGGGTAGGA ATCTTAGAAG ATTTGAAAAT GAATTTAAAA     480
GATTCCCATA GTCCCATT                                                  498
```

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298

ATGGATAGAA AACTCTTAAG ATTATACCAG CCCTTAAACG CTTATTCTTA CAATAGCGAT 60
TCGCTTTTTT TATACGATTT TTCACGCCCT TTTATCAAAA ATAGCGGCGC GATTTTAGAC 120
ATAGGCTCAG GGTGTGGGGT TCTAGGCTTG CTCTGCGCTA GAGACAACCC GCTAGCGAGC 180
GTTCATTTAG TGGAAAAGGA TAGCAAAATG GCGTTTTGCT CCCAAAAAAA CGCCCTTAAA 240
TTCCCTAACG CTCAAGTGTT TGAGAGCGAT TTTTTAGATT TTAACCCTCC GATTTTGTAT 300
GATGCGATTG TGTGCAACCC TCCTTTTTAT GCTTTAGGAT CTATTAAATC TCAAATTAAA 360
GGGCATGCGA GGCACCAGAG CGAATTAGAC TTCGCTTCTT TGGTGGCTAA AGTGAAAAAA 420
TGCCTGAAAC CC 432

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299

ATGTTGAGTG CGTTGGTGAT GCTGCCTTTT ATGGAGGTTT TTTATTATTT CAATTTTCCG 60
TTGTGGCTCA ATCTTTTCTT AGGGCAAACC ATTGGAGCGG TGATTTTTTT CAAGTTGGAT 120
AAGTTGATTT TTTCTAAAAA A 141

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300

ATGAATACTA TTATAAGATA TGCGAGTTTA TGGGGCTTGT GTATTACTCT AACTCTAGCG 60

This Sheet Has Been Replaced



```
CAAACCCCCT CTAAAACCCC TGATGAAATC AAGCAAATCC TTAACAATTA TAGCCATAAG      120
AATTTAAAGC TCATTGATYC GCCGACAAGT TCTTTARRAG CGACACCGGG TTTTTWWCCC      180
TCGCCTAAAG AAACAGCGAC CACGATCAAT CAAGAGATCG CTAAATACCA TGAAAAAAGC      240
GATAAAGCCG CTTTGGGGCT TTATGAATTG CTAAAGGGGG CTACCACCAA TCTCAGTTTG      300
CAAGCGCAAG AACTCAGTGT CAAGCAAGCG ATGGAAGAAC CACACCATCG CCAAAGCGAT      360
GTTTTTGCCT ACTTTGAACG CGAGTTA                                          387
```

(2) INFORMATION FOR SEQ ID NO:301:

(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:301

```
ATGGTTTTGT TTCTATCCAT TTTTAAAAAA AGCTTTAATG ATTTTTTAAG CGCTAGAATG       60
CTTTTAATCA ATCTTGGCCC TATCCTTTTG AGTTTGGCGT TTTTTGGAGC TATCTTTTAT      120
TACAATGGCG GGAGTATTGT GAATTATTGC CAAACTTTAT TACCGCAATC TTTGAATGAT      180
TACGCTCATT CTCAAGGCTT TTTTGCCGGT GTGTTCGCAT GGGTTTTTAA AGCGTTAGTG      240
TATTTTCTTA TTTTTTGGAT CGTAATTCTT TTGAGTTTAG TCATCAATAT TTTTGCGTCT      300
ATTTTTTACA CCCCTTTAGT GGTCTCTTAT TTGCACCAAA AATATTATCC CCATGTCGTT      360
TTAGAAGAAT TTGGCTCTAT CCTTTTTTCT ATTAAATATT TTTTAAAATC GCTCACTTTT      420
ATGCTTTTAT TCTTAGCGGT TTTAACGCCC CTTTATTTCA TTCCCTTTAT AGGGGTCTTT      480
GGGGTCTTTT TTTCTATAGT CCCGCATTTC CYCTTTTTCA AAAACACCAT GAGTTTGGAT      540
ATAGCCAGCA TGATTTTCAA CCATCAAAGC TATCAAAATT TACTCAAACA GCACCGATTG      600
AAGCATTATC GTTTTTCGTT TTTTTGCTAT CTTTTTTCCT TGATTCCTTT TTTTAATTTT      660
TTTGCCACCT TGTTGCAAAC CCTAAYGCTA ACGCACTACY TTTTTATCTT TAAAGAGAAA      720
GAATGC                                                                 726
```

(2) INFORMATION FOR SEQ ID NO:302:

(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

This Sheet Has Been Replaced



(B) LOCATION 1...378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302

```
ATGCAATACG CTAACGCTTA TCAAGCCTAC CAGCATAACC GAGTGAGTGT GGAATCCCCG      60
GCAAAACTCA TTGAAATGCT TTATGAAGGG ATTTTAAGAT TTTCTTCGCA AGCCAAACGC     120
TGTATTGAGA ATGAAGACAT TGAAAAGAAG ATCTATTATA TTAATAGGGT TACGGATATT     180
TTCACGGAGT TGTTGAATAT TTTAGACTAT GAAAAAGGGG GGRAAGTGGC GGTGTATCTT     240
ACAGGCTTAT ACACCCATCA AATCAAAGTT TTAACGCAAG CCAATGTGGA AAATGACGCG     300
AGTAAGATTG ATTTGGTGTT GAATGTGGCT AGGGGGTTGT TAGAGGCATG GAGGGAAATC     360
CATTCAGATG AACTCGCC                                                   378
```

(2) INFORMATION FOR SEQ ID NO:303:

(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:303

```
ATGATGTTTG ATAACACGCT TATCAATTTA TTTGAGACAG CGCCTCTTTT AACYTCGCTT      60
TTAGCTGGGA TTTTAACTTT TTTAAGCCCT TGCGTGTTGC CTTTGATCCC GGCGTATATG     120
TCTTATATTT CGCAAATTTC TTTAGAGGAT ATTAAAGATG GTAAGGCTAA AAGGGTTTCG     180
GTTTTTTTAA AATCCTTGAT GTTTGTGGTG GGGTTTTCGC TCGTGTTTTT GGGCGTGGGC     240
ATGTCTATGG CCAAGCTTAT CCATAGCTTT TCGTTTTCCT GGGTGAATTA TATCGCTGGG     300
GGGATTGTGA TCCTTTTTGG TTTGCATTTT TTAGGCGTGT TTCGTTTTGC ATTTTTGTAT     360
AAAACCCAAA GCGTTGGTTT AGCGAGCAAA TCTAACAGCA TGCAGCGCTT TACCCCTTTC     420
TTTTTGGCA                                                             429
```

(2) INFORMATION FOR SEQ ID NO:304:

(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

This Sheet Has Been Replaced



(B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304

GTGCTGGTGG TGGGCAAACC CAACGAAAGC TATGCAGATA CCCACGCCCG CATTGAGCAT 60
TTTATCAAGC TTGTAGATTT TAAGGGCGAA ATCGTTTTTA TCAATGAAGA TAATTCTAGC 120
GTAGAAGCTT ATGAAAATTT AGAGCATTTG GGTAAGAAAA ATAAGCGGAT CGCTACCAAA 180
GATGGCCGGT TAGACTCTTT GAGCGCTTGT AGGATTTTAG AGCGCTATTG CCAGCAGGTT 240
TTAAAAAAGG GC 252

(2) INFORMATION FOR SEQ ID NO:305:

(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:305

ATGCGGATAT TAATTCTCAA AAACAAGCCA CCAACGCTAC GATCAAAGGC TTTGACGCGC 60
TCTTGGGGTA TCAATTTTTC TTTGAAAAAC ACTTTGGCTT ACGCCTTTAT GGGGTTTTTT 120
GACTACGCTC ATGCCAATTC TATTAAGCTT AAAAACCCTA ACTATAATAG CGAAGCGGCG 180
CAAGTGGCTA GTCAAATTCT TGGGAAACAA GAAATCAATC GTTTAACAAA CATTGCCGAT 240
CCCAGAACTT TTGAGCCGAA CATGCTCACT TATGGGGGGG CTATGGACGT GATGGTTAAT 300
GTCATCAATA ACGGCATCAT GAGTTTGGGG GCTTTTGGCG GGATACAATT GGCCGGCAAT 360
TCATGGCTTA TGGCGASACC GAGCTTTGAG GGCATTTTAG GGGAACAAGC CCTTGTGAGC 420
AGAAAGCCAC TTCTTTCCAA TTTTTATTCA ATGTGGGGGC TCGCM 465

(2) INFORMATION FOR SEQ ID NO:306:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306

```
ATGAATGTCA AAAAAAAGGA AAAGCCACAA AGTGGAAAGA TTGATAGGGT GGATTGTTTG      60
GAGAAACTTG GGAAAGAAAA CACTACTTTT TTAAGCAGTA TAGCTATGGG GAGCATTGGT     120
CAATTAGCGA TCCCCATTCC TGGAGTTGGA GTGCTCATTG GGGGCTTTGT GGGTGGGGTG     180
ATGAGTAAAA CTTTTTATGA TGTCTCGCTA ACGATTTTCA AAGAGGCTAA ATTAGCGCGT     240
CAAAGGCGTA TTGAGATTGA AAAAGAATGC CGTGAGAGTA TCAGACAGTT AGAGATGTAT     300
CAAAATCAAT TTAATGAAGT GTTTGAGCGG TATTTTCATG GGACTATAAA ATTCTTTAAT     360
GAAAGTTTTG ATGAGCTGGR GAGGGCGCTT TGTGCGGGCG ATGCGGATTT GGCTATAGCA     420
GTCAATAACA AGATCCAAGA GGGGATGGGT CAAGAGTTGC TGTTTGACAA TAAGCAAGAG     480
TGCTGGGAAT TTATCACTAG CCGTAAAGAG GGT                                  513
```

(2) INFORMATION FOR SEQ ID NO:307:

(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

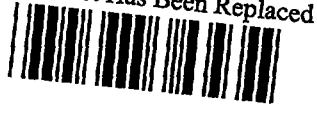
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307

```
ATGTGGCCGT RAAAGCTTTT TCTAAAACCC CTAAAAGAAA CGAGCCTTGC CCTTGTGGGA      60
GTGGCAAAAA ATATAAAGAT TGTTGCGCTA AAAGCGGGCC TAAAAAGGGC TTATTTGCCA     120
AATAGATCCT TAATCTTTTT CCTTATCAAG CGTTATTTGC GTTTTGATAA AAGCCAGCCT     180
TTCATTAGTA TCACTGCTTT GTTAGCCTTT TTTGGCGTGG CGGTTGGCGT GATGGTTTTA     240
ATTGTGGCTA TGGCGATCAT GAACGGCATG AGTAAGGAAT TTGAAAAAAA GCTTTTTGTG     300
ATGAACTACC CCTTAACGCT CTATACCACA AGCCCTTATG GGATCAGCGA AGAAGTGGTT     360
CAAGCTTTAG AAAAAAAGTT CCCTAATTTG CCTTTTTCAG YCCCTATTTG CAAACCCAAA     420
GCC                                                                  423
```

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:308

```
ATGGTATCGT TGCTTGGCGC GCTTAAACGC ACCCCTTGCA CTAATCGCTT TTATCTTAAA      60
GCACTACTAT TTGCTATATT CTATCATGCA GTAAATAATT TTCTAACGCA ATGCCCGCCC     120
CATCAAGTCC GGGAGTTTTT TTCATCACGA CATGCACAGG GATGGAAGCG AGAAACGCTC     180
CCATGCGCCC TTTCGTTTCA AAACGCGCTC                                      210
```

(2) INFORMATION FOR SEQ ID NO:309:

(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:309

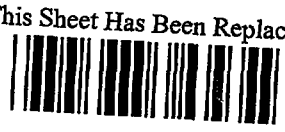
```
GTGCATCATT TGYAACGGCT TTTAGACTCA GGCTCTGAAA GGTGTATAGG CTGTGGGCTG      60
TGCGAAAAGA TTTGCACGAG CAACTGCATA AGGATCATCA CGCATAAGGG CGAAGACAAC     120
CGCAAAAAGA TCGATTCTTA CACGATCAAT TTGGGGCGTT GCATTTATTG CGGGTTGTGT     180
GCGGAAGTTT GCCCAGAATT GGCGATCGTT ATGGGGAATC GGTTTGAAAA CGCCAGCACC     240
CAACGCTCCC AATACGGCTC TAAAAGCGAG TTTCTAACGA GCGAACAAGA CGCTAAAAAC     300
TGCTCGCATG CCGAATTTTT AGGCTTTGGT GCGGTAAGCC CTAATTATAA CGAACGCATG     360
CAAGCCACCC CTTTAGATTA TGTCCAAGAA CCTTCAAAAG AAGAATCCAA AGAAGAGTTT     420
YCCACAAGCC CAGAAAGCCA TAAGGGAGAT GAAAATGTT                            459
```

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 549 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310

```
ATGGCTATTT GGGGGTGGTG TTTTTTATTT TTATCGTCCT TGATGTGGGG TTCAAGCATG      60
CATGAGTTGG TTTTAAGATC CCAAGCTTTA GGGTTTGAAA CGCGCTTAGT CCAGTGCGAT     120
TTATCGTTTT CTTATGAAAG GTTTATTTCT AAAACCAAAC GCTCTTTAGC GGTGTTAGAA     180
GAATTTGATT GGTTAAATTC TGGCTTTGAT TTTTCACGCT TGAACGTTGA AAATGACACT     240
CTGGAATTAC TCAAAGCGCT GTATTTTAAA TTAGAAAAAT TAGAGAGCCT GCTTTTAAAA     300
GAAAATTTAC TTGAATTGGA GCAAAAGGAT CGCATCATCG CTTTAGGGCA TGGGCTAGTT     360
TGCCTAAAAA AACAAAGCCT GATAGCGCCT CAAACTTACT ATGGGCGTTG CGTGTTAGAG     420
GGGAAAATCC TAGCCTTTTT TGGCGTGGCA AGGGATAAAG ATTTTTTAGA AATCACTCGC     480
ATGCACGCCT TAGACATTAA GCGTTATGAT TCCTTCATTG TTGATAGCGA AAGAAAAGGC     540
TTGAAATTA                                                             549
```

(2) INFORMATION FOR SEQ ID NO:311:

(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:311

```
ATGCCGGAAA ATTCTAAACT ACAACCTGCT AAGTTAGGGA AAAATTTTGA CCCTGTGGAT      60
CATTCTAACA GGAATTTTTT CTTTTCTCTC ATTCTGTCTG TATTGTTACA CTGGTTGATT     120
TATTTTTTAT TTGAACACAG AGAAGATTTT TTTCCTTCAA AACCCAAGCT CGTTAAATTA     180
AATCCTGAAA ATTTATTGGT Y                                               201
```

(2) INFORMATION FOR SEQ ID NO:312:

(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

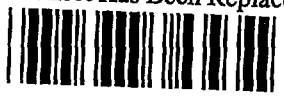
(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312

This Sheet Has Been Replaced



```
GTGTTTTTAG TTCAATCGTG GGCTTTGAGC TTGAAAATAG ACAGCCTGTT TTCTCTTTTT      60
AGCGTGGGTA AAATCCCTAG CGGATCTAAA GATCCCTTTG CGTTAAGGCG TTTGAGTTTT     120
GGGCTATTGA AAATCATCGC GCATTACGGG TTAGAATTTG ATTTGAAAGC GGATTTAAAA     180
AACCTCTTTG AAAAAGTGGG CGTTTATCAA AGCTTTGATT TAGAGGTTTT AGAAAAGTTT     240
TTACTGGAGC GCTTTCATAA TTTAATAGAT TGTAACCTCT CTATTATAAG AAGTGTGTTA     300
AACACCAACG AGCGAGACAT TGTTAAAATC ATTCAAAAAG TCAAAGCCTT AAAACGCTTT     360
TTAGACAATC CTAAGAACGC TCAAAAAAAA GAGTTGCTTT TTAGCGCTTT CAAACGATTA     420
GCTAATATCA ATAAAGACAG AAACCCTAAC GAATCAAGCG GGTTTTCTAC GAGTCTTTTC     480
AAAGAATTAC AAGAGCATGC CCTTTTTGAA GCGTTCAAC                            519
```

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 777 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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:313

```
ATGAGTCTTG CTCCAAGCGT TATGGCGGGC TTCTTGTTTT GTGCCGGCTC TTGCTCGCTT      60
CGCTTCCCTA ATTATTCTAA AATCATTTCC ATAGATGTGG ATACGGTGTT TTTAGGCGAT     120
GTTGCAAGCG CTTATTTTGC GCTGGATAAT GAACCCACTA AATTGCTTGG CATGGTGAGA     180
GACACTTTTT CCCACCTTCC TTTTGAAGCC TTTTGTGATT TTTGCGAACG CACATGCAAG     240
AATTTTAAAA TTGATCTTTT GCGCTTTAGC CAAAACGAAT TAAAACGCAT CCATCAGGGC     300
TTTAACATGG GCTTTTTGGT GGCGAATTTA GATTTATGGC GCGAAAATGG GTTTGAAAAA     360
ATCGCTTTAG AGTTTTTGAA AACTAGGGGA AAGGATCTTT TCTACCCTGA GCAGTGTTTA     420
ATCAATATGG TGTTTTTAGA GCGTATTTTA GAATTGCCTA TTCATTATAA TTGCTATTCT     480
GATTTTTTCA AAGAGCACTA CCCTAAAAGT ATCATCATGC TCCATTTCAT CAAATACAAG     540
CCGTGGCGTT CTGTCAGTTC TTTGAACGGG CGTTTGATTT GCTATGAAGC TGAAGCGAGT     600
TTTTGGCTCG CCAACCTTTT TTGCACCCCT TTTAAAAACG ATTTTTTTAA AGAACGCCTT     660
GAAATGGCTA AAGACCAACA AATGCAATCT TTTAAAACCC ACATCCGATC AAAAACGATT     720
AGGGATTATT TTTATTTTAG GATAAAAAAT ATTTTGAAAA AAGTTTTCGA ACTCTCT        777
```

(2) INFORMATION FOR SEQ ID NO:314:

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

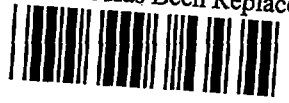
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



This Sheet Has Been Replaced



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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314

```
GTGATTGTTT GCAGCGCGGC GGGGTTGAGC CATTTTTTTG GGTTTTCTAT GTCTTTGGGG      60
GCGTTCATTG TGGGCATGGC GATTTCTAAA TCGCGCTATA AAATCAATGT CCAAGAAGAA     120
TTCGCGCAAT TAAAAAACCT CTTTTTGGCC CTTTTTTTCA TTACGATAGG GATGCAGATT     180
AATGTGAGTT TCTTCATGGA GAAATTCTTT GTCGTCATCT TTTTACTCAT TTTAGTGATG     240
AGTTTTAAGA CTTTTATCAT TTATGCGCTA TTGCGTTTTT TTAGAGACGC TAAAACCGCC     300
ATCAAAACCG CTCTTTCTTT GGCGCAAATT GGGGAGTTTT CTTTCGTGAT CTTTTTAAAT     360
TCAGGCTCGC ACCAGCTCTT TAATTTGCAA GAAAAAAAAG GGATTCTTGG TTTTTTACAC     420
CAAAAAAATA TCTTAAATAT TGCTCAAAAT GACATCCACC AGCTCCTTAT TCTCATGGTG     480
GTCTTTTCTA TGTTAGCAAC CCCTTTTATT TTAAAATACC TAGAATCTAT CGCTCAATTT     540
ATTTTGCACC AAAAGAGCCA AGAAAACGAG CCGGCTAAAA AA                        582
```

(2) INFORMATION FOR SEQ ID NO:315:

(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:315

```
ATGTTCTATC TTATCAATAC AGGAGTGCCT CATTTAGTGG GATTTGTGAA AAATAAAGGG      60
TTATTAAATT CTCTTAACAC ACTGGAATTA AGGGCTTTAA GGCATGAATT TAACGCTAAT     120
ATTAACATCG CTTTTATAGA AAATAAAGAG ACGATTTTTT TACAAACTTA TGAGAGAGGG     180
GTTGAAGATT TCACGCTAGC TTGCGGGACA GGCATGGCAG CGGTTTTTAT CGCCGCGCGC     240
CTTTTTCATA ACACCCCTAA AAAAGCCACT CTCATCCCTA AAAGCAACGA ATTTTTAGAG     300
CTTTCTTTAA AAAATGATGG AATTTTTTAT AAAGGAGTCG CGCGTTATAT CGGCATGAGC     360
GTTTTAGGCA TGGGTGTTTT TAAAAATGGG TGTTTT                               396
```

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 639 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316

```
ATGATTAAAG CGATTGATAT TTCTCATGST TTTGAAAARC CTCTTTRTRA TGGCGTGAAT     60
TTGCGCATTA AACCCAAAGA AAGCYTGGYG ATTTTAGGCG TGAGCGGGAG CGGTAAAAGC    120
ACGCTTYTAA GCCATTTGGC CACCATGCTA AAACCGGATA GCGGAACAGT CAGTTTGTTA    180
GAACACCAAG ATATTTATGC CCTAAATTCC AAAAAGCTTT TGGAATTGCG GCGCTTAAAA    240
GTGGGCATCG TTTTTCAATC GCATTACCTT TTTAAGGGTT TTAGCGCTTT AGAAAACTTG    300
CAAGTCGCTT CAATCCTAGC CAAGCAAGAA ATAAATCATT CCCTTTTAGA ACAATTAGGC    360
ATAGCCCACA CCCTAAAACA AGGCGTGGGC GAATTGAGCG GCGGCCAGCA ACAACGCTTA    420
AGCATCGCCA GAGTGCTTTC TAAAAAACCC CAAATCATTA TCGCTGATGA ACCCACCGGG    480
AATTTAGACA CCACTAGCGC TAATCAAGTC ATCAGCATGC TGCAAAATTA CATTACAGAA    540
AACGAAGGGG CGTTAGTCTT AGCCACGCAT GATGAGCATT TAGCCTTCAC TTGCTCTCAA    600
GTCTATCGCC TAGAAAAAGA ATCTTTGATT AAGGAAAAA                           639
```

(2) INFORMATION FOR SEQ ID NO:317:

(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:317

```
ATGCTTGATA AACGCATTAA AACGCTTTTA CTTTTTTTTG GTCTTAATAT GGTGTGTTTG     60
AGCGTGAGTT TTACCAATAA GCCTCATTTG TGTTTTTGGT TTTTAGTGTT AGGTTGTTAT    120
TTAGTTTATG AGTGGCAAAA GAAACAAAAA AAAGATTTTC AAAGCGCTAA AAGTTTGAAA    180
TTTGACAGCG TTAGCGAATT AGAAAAGGAT TTTGAACATG GAAGTAAC                 228
```

(2) INFORMATION FOR SEQ ID NO:318:

(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

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318

```
ATGAAAACAA TTAAAAATGG TATTATGATC GGCACACTCG GTGCGTTGTT ATTGAGCGGT      60
TGTTCTAGCT TTGATGCTCA GCGTTTCGCT TGTCTCCCTA AAGACCATTC TTCAAAAGAC     120
GCTTCTACCA AAAAAGAAGC GCAATACATT CCTAAGGGCT TTTTTGACCC TTATTCTTCT     180
AACTTAAACC ATTGGGATTC TACATTC                                         207
```

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 570 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319

```
ATGGAGCTTA TTTTAGGCTC TCAATCCAGC GCTAGGGCGA ATCTTTTAAA AGAGCATGGG      60
ATTAAGTTTG AACAAAAAGC GCTCTATTTT GATGAAGAAA GCCTAAAAAC CACAGACCCT     120
AGGGAGTTTG TCTATTTGGC GTGCAAGGGG AAATTAGAAA AAGCTAAAGA GTTACTTGCG     180
AATAATTGCG CTATCGTGGT GGCTGATAGC GTGGTGAGCG TGGGTAATCG CATGCAACGA     240
AAAGCTAAAA ACAAGCGAGA AGCCCTTGAA TTTTTAAAAC GCCAAAATGG CAATGAAATA     300
GAGGTTTTAA CTTGCTCTGC ATTGATTTCT CCTGTGTTGG AATGGCTGGA TCTATCGGTT     360
TTTAGAGCGC GTTTAAAGGC GTTTGATTGC AGCGAAATAG AAAAATATTT AGAGAGCGGT     420
TTATGGCAAG GAAGTGCGGG CTGTGTGCGT TTAGAGGACT TTCATAAGCC TTATATTAAA     480
AGCTCAAGCA AGAATTTAAG CGTGGGGTTG GGGCTGAATG TGGAAGGCTT GTTAGGGGCA     540
CTAAAATTAG GGGTTAAACT TTCATTATTA                                      570
```

(2) INFORMATION FOR SEQ ID NO:320:

(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:

This Sheet Has Been Replaced



(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320

ATGCTTATTT TAGGACACCC TTTAATCCCT AGCGCTCGTT TTGTTTTCAT TAAAAACACC 60
GATGCTATTC ATTCCAGCGC CAATAACGAT ATAGTGTGTT TTGAAGCAAA CCCAAAAAAT 120
TTGGAATTAG CCCAATATTG CTGTGAAAAT GGCGTCCATT TTAGCGTGAT CTTTTTATCG 180
CACAAGATAG AGACGGACAC CTTTTTTTTA TTCAACGCTT TCAAACCGCT CTATTGTATT 240
TTTAAGGATA TTAAGCAAGC CATACTCGCC CAACAACACG CCACTAATTA CTTGTTAGAT 300
AGCAAAATCT TGTTTTCTAT GGATTTTAAC GATACAGAGT CATGGGAGAT TTGCGCTAAA 360
AATCAAATAG ATGGTGTCAT TTCTAAAGAT TCACTCCTTT TGAAA 405

(2) INFORMATION FOR SEQ ID NO:321:

(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:321

ATGAAAAAAA GATTGAATAT AGGGCTTGTG GGTTTAGGGT GCGTGGGGAG CACGGTCGCT 60
AAAATCTTAC AAGAAAATCA AGAAATCATT AAAGACAGAG CCGGCGTGGA AATTAAAATT 120
AAAAAAGCGG TGGTGCGAGA CGTGAAAAAA CACAAGGGCT ATGCTTTTGA AATCAGTGAT 180
GATTTAGAAA GCGTGATAGA AGATAAAGGG ATTGATATTG TCGTGGAGCT TATGGGTGGG 240
GTGGAAGCGC CTTATCTTTT AGCTAAAAAA ACTTTAGCCA AACAAAARGC CTTCGTTACA 300
GCCAATAAAG CCATGTTAGC GTACCACCGC TATGAATTAG AACAAATCGC TAAAAACACC 360
CCCATAGGCT TTGAAGCGAG CGTGTGTGGG GGTATCCCCA TTATCAAGGC TTTAAAAGAC 420
GGCTTGAGCG CTAATCACAT CCTTTCTTTT AAAGGGATTT TAAACGGCAC GAGCAATTAC 480
ATTTTAAGCC AGATGTTTAA AAATCAAGCG AGCTTTAAGG ACGCTTTGAA AGACGCGCAG 540
CATTTAGGCT ATGCGGAATT GAACCCTGAA TTTGACATTA AGGGCATTGA TGCGGCGCAC 600
AAATTATTGA TTTTAGCGTC TTTAGCGTAT GGCATTGATG CGAAATTAGA AGAAATCTTG 660
ATTGAAGGCA TTGAAAAGAT AGAGCCAGAT GACATGGAAT TTGCAAAAGA GTTTGGTTAT 720
AGCATCAAAC TTTTAGGCAT CGCTAAAAAA CACCAGGGAT TGCAT 765

(2) INFORMATION FOR SEQ ID NO:322:

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

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(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:322

```
ATGCAAGAAA AACGACTTAA AGCCATTCAA AACAAAATCG CTTCTTGGAT CAAGGAAATT      60
GAAAGCGGCT TTATAGATGC ATTGTTTTCT AAGATTGGCC CTTCAAAGAT GCTGCGCTCC     120
AAACTCATGC TCGCTTTGTT AGACGAAAAA ACAGACGCTA TTTTATTAGA TAAAGCGCTC     180
AATTTGTGTG CGATTGTGGA AATGATACAG ACCGCTTCTT TATTGCATGA TGATGTGATT     240
GACAAGGCGA CCATGCGCCG AAAGCTCCCT AGCATTAACG CTCTTTTTGG GAATTTTAAC     300
GCCGTGATGC TTGGGGATGT GTTTTATTCT AAAGCCTTTT TTGAGTTGTC TAAAATGGGC     360
GAATCCATCG CTCAAGCCCT CTCTAATGCG GTTTTAAGGC TCTCTAGGGG CGAGATTGAA     420
GACGTGTTTG TGGGGGAATG TTTTAATAGC GACAAACAAA AATACTGGCG TATTTTAGAA     480
GACAAGACCG CCCATTTCAT AGAAGCGAGC TTAAAAAGCA TGGCGATTCT TTTAAATAAA     540
GACGCCAAAA TGTATGCGGA TTTTGGGTTG CATTTTGGCA TGGCGTTTCA AATCATTGAT     600
GATTTGTTAG ACATCACTCA AGACGCCAAC ACTCTAGGTA AGCCCAATTT TAGCGATTTT     660
AAAGAGGGCA AGACCACTCT ACCCTACTTG CTTTTATATG AAAAATTGAA TCAGCATGAA     720
CAGGGCTTT                                                            729
```

(2) INFORMATION FOR SEQ ID NO:323:

(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:323

```
ATGTTAGGGA AAAAAAACGA AGAAGTCTTG ATTGATGAAA ATTTGGTTGG GGGTGTGATA
GCCCTTGATA GATTGGCAAA ACTCAATAAG GCCAATAGGA CTTTCAAAAG GGCTTTTTAT
CTCTCTATGG TGCTCAATGT CGCCGCTGTA ACGAGTATTG TGATGATGAT GCCTTTGAAG
AAAACAGATA TATTTGTTTA TGGCATTGAT CGATACACAG GAGAATTTAA AATCGTCAAA
CGCTCCGATG CTAGGCAAAT CGTCAATTCT GAAGCCGTTG TGGATAGTGC AACTTCAAAA
TTTGTCTCAT TGCTGTTTGG TTATAGCAAA AATTCTTTGA GGGATCGCAA GGATCAACTA
ATGCAGTATT GCGATGTGAG TTTCCAAACC CAAGCAATGA GAATGTTCAA TGAAAATATT
AGACAATTCG TAGATAAAGT CCGAGCAGAA GCTATCATTA GCTCCAACAT ACAAAGAGAA
AAAGTCAAAA ATAGTCCCTT AACGAGATTA ACATTTTTCA TTACCATCAA AATCACGCCT
GATACAATGG AAAATTATGA ATATATCACT AAAAAACAAG TAACTATTTA TTATGATTTT
GCTAGAGGTA ACTCTTCTCA AGAAAATCTT ATCATCAACC CTTTTGGCTT CAAAGTGTTT
GACATTCAAA TCACGGATTT ACAAAACGAA CAGACAGTAA GCGAAATTTT GAGAAAGATT
AAAGAAGTGG AATCAAAAAA TAAGGCATTA AATAAA
```

This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:324:

(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:324

```
ATGAGAGCGA TCGCTATTGT TTTAGCCAGA AGTTCCAGTA AAAGGATTAA GAATAAAAAT      60
ATGATTGATT TTTTCAATAA ACCCATGCTC GCTTACCCTA TTGAAACAGC ACTAAATTCC     120
AAGCTCTTTG AAAAAGTGTT TATCTCTAGC GATAGCATGG AGTATGTCAA TTTAGCCAAA     180
AATTATGGGG CGAGTTTTTT GAATTTACGC CCTAAAAATT TAGCAGACGA CAGGGCCACG     240
ACTTTAGAAG TGATGGCCTA TCACATGAAA GAATTAGAAT TAAAAGATGA AGACATTGCG     300
TGTTGTTTGT ATGGCGTTTC AGTATTTTTA CAAGAAAAGC ATTTACAAAA CGCTTTTGAA     360
ACTTTAAAAC AAAATCAAAA TACGGATTAT GTTTTCACAT GCTCTCCCTT TAGCGCTTCG     420
CCTATCGTTC TTTTAGCCTT GAAAACGGCG TTCAAATGGC TTTTAAAGAG CATTCAAACA     480
CGCGCACGCA AGATC                                                      495
```

(2) INFORMATION FOR SEQ ID NO:325:

(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:325

```
ATGAGTAATC AAGCGAGCCA TTTGGATAAT TTTATGAACG CTAAAAATCC CAAAAGTTTT      60
TTTGATAATA AGGGGAATAC CAAATTCATC GCTATCACAA GCGGTAAGGG GGGCGTGGGG     120
AAATCCAACA TTAGCGCTAA TTTAGCTTAC TCTTTATACA AGAAAGGTTA TAAGGTAGGG     180
GTATTTGATG CGRATATTGG TTTAGCGAAT TTAGATGTCA TTTTTGGGGT GAAAACCCAY     240
AAAAATATCT TGCATGYCTT AAAAGGCGAA GYCAAATTGY AAGAAATCAT TTGCGAGATT     300
GAACCCGGGC TTTGCTTAAT CCCTGGGGAT AGCGGCGAAG AAATTTTAAA ATACATCAGC     360
GSSGCGGAAG YTTTCGATTC ATTCTTAGAT GAAGAGGGGG TTCTAAGCGC TTTAATTTAT     420
```

ATTTTAATTA ATACATTTTC TAAAAATTTG GGTCCACTAT CTCAAACTTT TCTTAATTTT 480
CAGTCATTTC TTTTTATTTT TATTCAATCT CCC 513

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326

ATGCAGCATT TAGTCTTAAT CGGTTTTATG GGGAGCGGTA AAAGCTCTCT AGCACAAGAA 60
TTGGGGCTGG CTTTGAAATT AGAAGTGCTG GATACGGATA TGATCATTAG CGAGAGGGTG 120
GGCTTGAGCG TGAGAGGGAT TTTTGAAGAG CTTGGCGAAG ACAATTTCAG GATGTTTGAA 180
AAAATT 186

(2) INFORMATION FOR SEQ ID NO:327:

(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:327

ATGAGCATTA AGGAAAATTT AGAGCAAGTT AGAAACGAAT TTAAAAGCGA TGAAAAGCTT 60
TTAGAAGGAG CGTTTAGATT AGAAAAGTTT TTCAAACGCT ACAAGTGGGT GTTGTTGTTT 120
ATCGTGGTGG CTTTTATCGC TTATTTAGGG GATACAAAAT TACAAGATTA TAAGCATGAG 180
CAAACGAGAG AGCGGATCAC TCAAATTTAT AATGAAGTGC TAGAGAGTCC TAATAATATA 240
GCCTTGCAAA AAAGATTGAA AGAAGTCGCC CCAGAGTTGT ATGACTTGTA TCAGTTCGCC 300
AGAGCGAGTG AGAGGAACGA TGCAAACGAG TTTAAAAGGC TTTCGCAATC TTCTAATGAA 360
ATCGTTAAAG CGTTCGCCAA ATATTCTTAC GCATCGCTCT CTAGAGATAA AAACCTGCTT 420
GAAAAAAGCC CCATTCTTAA AGAAATGAGC GCTTTACAAG AAGTGAACTT GTTGTATGAA 480
GAAAATTCTA AAGACGCAAT CAAAAAAGCG CATCAAAGTT TATCAACTAT CCCTCTAAGT 540

This Sheet Has Been Replaced



TCTTCACTCT ATGCTATAAT CTCTGTTTTA AAACATTATG GAATGTTAGA AGATATTCAG 600
CAAAACCCTT CCAAACCAAC CAATCTAAAG AAAGAAACCA TTCAAGGAAC GCAT 654

(2) INFORMATION FOR SEQ ID NO:328:

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

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:328

GTGCATTTCA ATCAGGTTGT TCTCCCAAAA GGCGTGGGCG CGATTTTAGT CGCACCAAAA 60
GGGCCCGGGA GCGCTTTAAG AGAAGAATAC CTTAAAAATA GGGGTTTATA CCATCTAATC 120
GCCATAGAGC AAGAAAGCTC AATTCATAAC GCTAAAGCGG TGGCTTTAAG CTATGCTAAA 180
GCGATGGGTG GGGGGAGAAT GGGGGTTTTA GAAACGAGTT TTAAAGAAGA ATGCGAGAGC 240
GATTTATTCG GCGAGCAAGC GGTCTTGTGC GGGGGGTTAG AAGTCGATCG TAAGAATGGG 300
GTT 303

(2) INFORMATION FOR SEQ ID NO:329:

(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:329

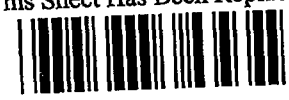
ATGAAAAAAT TTTTTTCTCA ATCTTTGTTA GCTCTTATTA TCTCTATGAA TGCGGTATCT 60
GGCATGGATG GTAATGGCGT TTTTTTAGGG GCGGGTTATT TGCAAGGACA GGCGCAAATG 120
CATGCGGATA TTAATTCTCA AAAACAAGCC ACCAACGCTA CGATCAAAGG CTTTGACGCG 180
CTCTTGGGGT ATCAATTTTT CTTTGAAAAA CACTTTGGCT TACGCCTTTA TGGGGTTTTT 240

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330

```
ATGCTAAAAA AGATTTTTTA TGGTTTTATC GTTTTATTTT TGATTATCGT AGGGTTGTTG      60
GCCGTTCTTG TCGCTCAAGT TTGGGTAACT ACGGATAAGG ATATTGCTAA AATTAAAGAT     120
TATCGCCCCA GTGTCGCTTC ACAGATTTTA GACAGAAAAG GGCGTTTGAT CGCTAATATT     180
TATGATAAGG AATTTCGTTT TTATGCGCGT TTTGAAGAAA TCCCCCCACG ATTTGTTGAA     240
AGCCTTCTAG CGGTAGAAGA CACCCTCTTT TTTGAGCATG GGGGGATCAA TTTAGACGCT     300
GTCATGCGCG CTATGATTAA AAACGCTAAA AGTGGTCGTT ACACTGAAGG GGGTAGCACT     360
CTAACCCAAC AACTCGTTAA AAACATGGTG CTCACACGGG AAAAAACCCT 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 TTCACTCTCT     660
AGGGCTAATG ATATTTTAAG GCGGTTGTAT TCTTTAGGCY 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 TGGGAGCGCR ATCAAGCCTT TTGTGTATCA AATCGCTTTT    1140
GATAATGGCT ATTCCACCAC TTCCAAAATC CCTGATACCG CGCGAAATTT TGAAAATGGC    1200
AATTATAGTA AAAACAGCGT GCAAAACCAC GCATGGCACC CTAGCAATTA TRCTCGCAAA    1260
TTTTTAGGGC TTGTAACCTT GCAAGAAGCC TTGAGCCATT CGTTAAATCT GGCTACGATT    1320
AATTTAGCGA TCGCTTGGCT A                                              1341
```

(2) INFORMATION FOR SEQ ID NO:331:

(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:331

```
ATGAACGATA CAACAGAGCA CCATGGATCC AATCCGCTAA ACGCCCCACC ACCTAGCAAC      60
TCACAGAGCA ACGATCTCTT AAATTTGCTA GACTCGTTAT ATCCTAAAGG GAGTTTAGGG     120
GAACAAAGAT TTCACGAAGC TTTAAAGAAT CAAGAAGAGT TGAAAAATAT CCTAATAGAA     180
ATAGAAAAGC TACCGCAAGA AAAAAGGTAT GAACTTCTGA TGCAGATAGG ACAAGCCAAA     240
CAGAGAATAA TGGAAGCATA CGCTCATTCA TTCTTAGGAT ATATAGGGGG ACTAGAGCAT     300
CTGTTAGGAT TGTGTATGGG TGGGATATTT GTTTTGTTTG CAATCTATTT TGTATTTTTA     360
AGAACTAGCA AAAACACAGA GCTAGTGGAA AGTCTAAAAA CAAAATTAAA ACTTCAGTAT     420
TTTTACTATG CCTTTGGTGT GGGTGCGGTT TTGTTTTTTG GATTAGAAAC AATTAGATCG     480
ATTTATGAAC TATATATCTT AGGAATTGGT AGCACTAACG ACAAGGTGCT CTTTGTTTTG     540
AAAAACATTT GCTTCATAGG TATGGGCTAT TTGATTTATA AAGTTATTAA AGTTATTGGT     600
ATAAAAAATT TTATCAATGG TCTTTTCGCT TCAAAGAAAC AAGGCGGTGC AGAA           654
```

(2) INFORMATION FOR SEQ ID NO:332:

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

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:332

```
ATGATGGATA AGGTGGGTTT TAAATCTCAA GGCATCTTTG TGATGGACGC TAGCAAGAGG      60
GATGGGCGTT TGAACGCGTA TTTTGGAGGC TTGGGTAAAA ACAAGCGGGT GGTGTTGTTT     120
GACACTTTGA TCTCTAAAGT TGGGACAGAA GGGCTTTTAG CCATTTTAGG GCATGAGTTA     180
GGGCATTTTA AAAATAAGGA TTTGTTGAAA AATTTAGGGA TTATGGGAGG CTTGCTCGCT     240
CTTGTTTTTG CTTTGATCGC TCATTTGCCG CCGTTGGTTT TTGAAGGCTT TAATGTCTCG     300
CAAACGCCAG CGAGTTTGAT CACGATTCTA CTCTTGTTTT TGCCGGTGTT TTCCTTTTAC     360
GCCATGCCTT TGATTGGGTT TTTTAGCCGC AAGAACGAAT ACAATGCGGA CAAGTTTGGG     420
GCGAGTTTAA GCTCTAAAGA GACTTTAGCC AAAGCGTTAG TGTCCATTGT GAATGAAAAT     480
AAAGCGTTCC CCTATTCGCA CCCTTTTTAT GTTTTCTTGC ATTTCACGCA CCCGCCGCTA     540
TTAGAACGCC TAAAAGCTTT GGATTATGAA ATTGAA                               576
```

(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

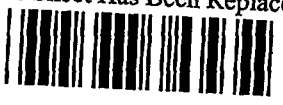
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333

```
ATGAATATTT ATCAAAAAAA CTTGCAAGCT CTTTTCAAAA AAGACCCTCT TTTGTTCGCA      60
AAGCTCAAAG CCATTAAAGA AAACAAAAAA TACGAAGTGT TTTTAGGGAA TGATAGCGCG     120
AATTTCAACC TCTTAGATAA AGAAACAAAC ACGCCCTTAT TTGAAAAAAG CCCGCTAGAT     180
TCAAGCTTAG AGCTATATAA AAATAGCGAA ATTCACATGC TCTATCCTTA TTTGTATTAT     240
TTTGGCTTGG GTAATGGGGT GTTTTATCGC TTGCTTTTAG GCAATGAAAA TTTAAAACGC     300
TTGGTGGTCA TTGAGCCTGA AATAGAGGTG ATTTTCATTG TGCTGAATCT TTTGGATTTT     360
TCCACTGAGA TTTTAGAAAA TCGTTTGATT TTATTGCATG CAAGTTTTTG CAATTACAAC     420
ATGATTGCTT CATTATTTGA TATGGATAAA AAGTCTCGTT TATACGCAAG AATGTATGAT     480
TTAAAACTTT TTAACGCTTA TTATGAACGA TACTCTCATC AAATGATAGA AATCAACCAG     540
CATTTCACGC GCGCTTTAGA GCATGGCGCT ATTAGCGTAG GCAATGACGC TAAAGCGCAC     600
TCA                                                                  603
```

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:334

```
ATGAAAAAGA TTATTCTTGC ATGCCTTGTG GCTTTTGTGG GTGCCAATTT AAGCGCAGAG      60
CCTAAGTGGT ATAGCAAGGC CTATAACAAA ACAAACGCCC AAAAAGGCTA TCTTTATGGG     120
AGTGGTTCAG CCACTTCTAA AGAGGCTTCT AAACAAAAAG CGTTAGCGGA TTTAGTGGCG     180
TCTATTAGCG TGGTGGTCAA TTCACAAATC CACATTCAAA AAAGTCGTGT GGATAATAAG     240
TTAAAATCCA GCGATTCACA AACGATCAAC TTAAAAACCG ATGACTTGGA ATTGAATAAT     300
GTAGAAATTG TCAATCAAGA AGCGCAAAAA GGGATCTACT ACACCAGAGT GAGGAATCAA     360
TCAAAACTTG TTTTTGCAGG GTTTAAGGGA                                      390
```

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335

```
ATGAAAATCC AAACAATTTC AACACTTGTC CTTACAATAA TAATGGTAAT ACAAAAAATG      60
ATTGTTGGCA AAATTTCACC CCACAAAACC GCAGAAGAAT TCACYAATTT AATGTTGAAC     120
ATGATCGCTG TTTTAGACTC CCAATCTTGG GGCGATGCGA TCTTAAACGC TCCTTTTGAG     180
TTCACTAACA GCCCAACAGA TTGCGATAAT GATCCTTCAA AATGCGTAAA TCCTGGGACA     240
AACGGGCTTG TCAATTCTAA AGTCGATCAA AAATATGTGT TAAACAAACA AGACATTGTC     300
AATAAATTTA AAAACAAAGC RGATCTTGAT GTAATTGTTT TAAAGGATTC AGGGGTTGTA     360
GGGTTRGSCA ATGGATATGG CAATGATGGT GAATATGGCA CATTAGGGGT AGWAGCCTAT     420
GCTTTAGGAT CC                                                        432
```

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336

```
GTGGTAATAA GGTTAGTCCT AAACATGCTA ACATGTCAAA TTAGCTATAT AAGGATAAGT      60
TATCTTGTCT CTGTTAGCGA TTTTGTGATT TGCAAGGAAA GATTTATGGA TGAAATTAAA     120
ACGCTGTTAG TGGATTTTTT CCCGCAGGCA AAGCATTTTG GGATAATCTT AATCAAGGCT     180
ATTGTTGTCT TTTGTATAGG TTTTTATTTT TCGTTTTTCT TACGGAACAA AACCATGAAA     240
CTCTTATCCA AAAAGGATGA GATTTTGGCG AATTTTGTCG CGCAGGTTAC TTTTATCTTA     300
ATCCTTATCA TTACTACAAT CATCGCGCTC AGCACGCTAG GCGTCCAAAC CACCTCTATT     360
ATCACTGTTT TAGGAACGGT GGGGATTGCG GTGGCGTTGG CTTTAAAAGA TTATCTTTCA     420
AGCATTGCTG GAGGGATAAT CCTTATTATT TTACACCCTT TCAAAAAAGG AGACATCATT     480
GAAATCTCTG GCCTAGAGGG CAAAGTAGAA GCGCTTAATT TTTTTAATAC TTCTTTACGC     540
TTGCATGACG GGCGCTTGGC GGTTTTGCCT AATAGAAGTG TCGCTAATTC TAATATTATC     600
AATAGCAATA ACACTGCGTG TCGGCGCATT GAATGGGTCT GTGGGGTAGG GTATGGGAGC     660
GATATTGAAC TGGTGCATAA GACTATAAAA GATGTTATTG ACGGGATGGA AAAAATTGAT     720
AAAAACATGC CCACTTTCAT TGGAATCACG GATTTTGGAC AAAGTTCGCT GAACTTCACC     780
ATTAGGGTTT GGGCAAAGAT TGAAGACGGG ATCTTTAATG TGAGGAGCGA ACTCATTGAA     840
CGCATCAAAA ACGCCCTGGA CGCTAATCGT ATTGAAATCC CTTTCAACAA GCTAGATATT     900
TCTATCAACA AACAAGACTC TTCTAAG                                         927
```

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 491 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

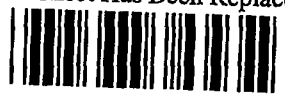
(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337

This Sheet Has Been Replaced



```
ATGAAAAACT TTTCCCCACT CTATTGTCTT AAAARGCTCA AAAAACGCCA TTTAATCGCT      60
CTGAGTCTGC CCTTGCTTTC TTATGCGAAT GGCTTTAAAA TCCAAGAGCA AAGCTTGAAT     120
GGCACGGCTT TAGGCTCGGC GTATGTCGCT GGGGCTAGGG GTGCTGACGC TTCTTTTTAC     180
AACCCGGCTA ACATGGGCTT TACTAACGAT TGGGGCGAAA ACAGAAGCGA ATTTGAAATG     240
ACCACCACCG TGATCAATAT CCCGACCTTT AGCTTTAAAG TCCCTACGAC CAATCAAGRC     300
TTATATTCGG TAACAAGTTT AGAAATTGAT AAAAGCCAAC AAAATATTTT AGGCATCATC     360
AACACTATAG GGTTAGGCAA TATCCTTAAA GCGCTTGGCA ATACGGCCGC TACCAATGGC     420
TTATCACAAG CTATCAATCG TGTTCAAGGG CTTATGAACT TAACCAATCA AAAAGTCGTA     480
ACCCTCGCTT C                                                          491
```

(2) INFORMATION FOR SEQ ID NO:338:

(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:338

```
ATGTGTTTAG CGATCCCCTC TAAAGTCATA GCCATTAACG ATAATGTGGC ACTCTTAGAG      60
ACTTTGGGCG TTCAAAGAGA AGCGAGCTTG GATTTAATGG GCGAGTCCGT TAAAGTGGGC     120
GATTATGTGC TACTACACAT CGGCTATGTG ATGAGTAAAG AT                        162
```

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 606 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339

```
ATGAAATATT TATGGCTTTT TTTAATATAC GCTATAGGGC TTTTTGCAAC AGATAAAACG      60
CTAGATATTA TTAAAACCAT TCAAAAACTT 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 TGACTACCCC     360
ATTGTAAGTT TAGATCTATA CCCTTTTGCA GCGCACAACA TGGCCATTGT GGTGAATGAT     420
TATTTAAAAG CCCCTTCTAT CGCTTGGATG AAGCGCCTGA TTGTTTTTTC TAAATACATT     480
GGACCAGGAA TCACAAACAT CGCACTAGCG AATTATACGA TGCGTTATCA AAAAGAAATC     540
ATCAAAAACA ACCGACTCAA TATTTTCCCC AAATGGGCGA ACGCTGAGCA AACGGAGTTT     600
TATTAC                                                               606
```

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 615 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340

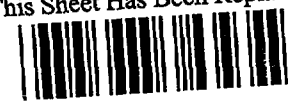
```
GTGGTGAGCG GGGTGGTGAT CATTATTGTG TTTTTTGTGC CGATTCTAAC CTTACAGGGG      60
TTAGAGGGCA AGATGTTTAG GCCTTTAGCG CAAAGCATTG TGTATGCGCT TTTAGGCACT     120
TTAGTTCTAT CCATCACTAT CATTCCTGTA GTGAGCTCTC TTGTCTTAAA AGCCACGCCC     180
CATAGCGAAA CCTTTTTAAC GAGGTTTTTA AACAGAATCT ACGCCCCTTT ATTGGAATTT     240
TTTGTGCATA ACCCTAAAAA AGTGATTTTA GGAGCGTTTG TTTTTTTAAT CGCAAGCCTT     300
TCTTTATTCC CTTTTGTGGG GAAGAATTTC ATGCCTGCTT TAGATGAGGG CGATGTGGTT     360
TTGAGCGTGG AAACCACCCC CTCTATTTCC TTAGATCAAT CTAAAGATCT CATGTTAAAC     420
ATTGAAAGCG CGATTAAAAA GCATGTCAAA GAAGTTAAAA GCATTGTCGC GCGCACAGGG     480
AGCGATGAAT TGGGGCTGGA TTTAGGGGGT TTGAATCAAA CCGATACTTT TATTTCTTTC     540
```

ATCCCTAAAA AAGAATGGAG CGTTAAAACC AAAGATGAAT TGGTTAGAAA AAATCATGGA 600
TTCTTTAAAA GACTT 615

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:341

GTGGGATATA TCCCTARGGA AAAGATTGTA GGCATTAGCG CGATCGCTAA ACTCATTGAA 60
ATTTATAGCA AACGCCTGCA AATCCAAGAA AGGCTGACCA CTCAAATTGC AGAAACTTTT 120
GATGAAATCA TAGAGCCAAG GGGCGTGATC GTGGTTTGTG AAGCCAAGCC ACTTGTGCAT 180
GAGCATGCAA GGGGTGCAAA AGCAAAATGC GATCAT 216

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342

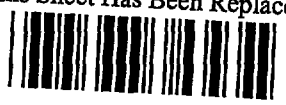
GTGGCTCTTG TGTTTGATAG TTTGATAGAG AACAAGAAG

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:343

```
ATGAAAAAAA TTGGTTTGAG CTTGTGTTTG GTTTTGAGTT TGGGTTTTTT AAAAGCCCAT      60
GAAGTGAGCG CTGAAGAGAT TGCGGATATT TTCTACAAAC TCAACGCCAA AGAGCCTAAA     120
ATGAAAATCA ACCACACGAA GGGGTTTTGC GCTAAAGGCG TGTTCCTCCC TAACCCGCAA     180
GCAAGAGAGG ATTTAGAGGT GCCACTACTC AATGAAAAAG AAATCCCTGC GTCTGTAAGG     240
TATTCTTTAG GGGGCGTGGT CGATTGGACG ATAAAAGCAA GGTTAGGGGA ATGGCGT        297
```

(2) INFORMATION FOR SEQ ID NO:344:

(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:344

```
GTGATCAAAC CTCATAGCGT GGGATTGGTA AGGATTGGGA TTTGTTTGTC TTTAGAAGTG      60
GGGTATGAAC TGCAGGTACG CACCCGTAGC GGCTTGGCTT TGAATCATCA GGTGATGGTG     120
TTAAATTYCC CTGGCACGGT GGATAATGAT TATAGGGGCG AAATTAAGGT CATTTTAGCG     180
AATTTGAGCG ATAAAGATTT TAAAGTTCAA GTAGGGGATA GGATCGCTCA AGGGGTGGTT     240
CAAAAAACTT ATAAAGCCGA ATTTATAGAA TGCGAACAAT TAGATGAAAC CTTCAAGGGG     300
```

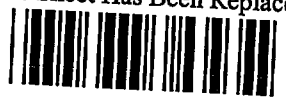
(2) INFORMATION FOR SEQ ID NO:345:

(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

This Sheet Has Been Replaced



(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:345

```
ATGGAAATCA TTTTATTAAT TGTTGCGGCG GTTGTGTTGT TTTATTTTTA CAACACCCTC      60
AAAGAATATT TGAAAAACCC CCTAAACCCT AAAACCAAAA CCGAAGAATA CGACTTGAAA     120
AATGACCCCT ATTTGCTGGT GCAATCTAGC CCCCTAGACA AATTCAAGCA AACCCAAATA     180
GGCGCGTATA TGCGTCTTTT AAAATTTTTA GACATTCAAA AAAACGCCTT GGATAACGCT     240
TTAAGAACGC TTTTTATCCA TGAATTGGAG CAGCCCTTAA ACAGCGAACA GCAAAATTTA     300
GCCAAAGAGC TTCTCAATGA GCCSGTGGAT AAAAAAGAAA ATTTTGAATC CTTATGCCAA     360
GAAATCGCCG ACCACACGCA TGGAGAATAC ACCAAACGCC TGAAATTAGT GGAATTTCTT     420
ATGCTATTAG CCTATGCTGA TGGGATTTTG GACAGCAAAG AAAAAGAATT GTTTTTAGAT     480
GTGGGGGCGT TTTTGCAGAT AGACAATCAA GATTTTAACG AGCTTTATGA CAATTTTGAA     540
CACTTCAATT CAATAGAAAT CCCTATGTCT TTAGAAGAAG CAAAAAATCT TTTTGAAATC     600
CAAACCCACA CCACCATGCA AGATTTAGAA AAAAAAGCTT TGGATTTAAG CGCCCCCTAT     660
TACCATAAAA TGAATGACAA CAAACGCTAC AGCGAACAAG ATTTTATCTC TTTGAAAAAA     720
ATCGCCCTCG CTTCCCAACT TTTAGAAAAT GATTTAAAAG ACTCA                     765
```

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346

```
ATGGAAGTAG AGCATGGCAA GATTGAAACC ACTTTAAGCT TGGGGGCGTC TCATTTGGAA      60
GTCATTAAAA TGATGCTTTT AGAGAGCCTG CCTTCTTTAG TGAATAATAT CACCATCACT     120
TTAATTTCTC TAATAGGCTA TTCGGCTAWG GCYGGAGCGT TAGGGGCTGG GGGATTGGGG     180
GATTTAGCCA TTAGGATTGG CTATCAAAGT TATAGGGGCG ATGTGCTTTT TTATGCGGTG     240
GTCGTGATCA TCGTTTTAGT GCAAATCATT CAAAGCGCGG GGGATTATGT GGTGAAACGC     300
TTGAGAAAGA ATAAGTAT                                                  318
```

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1581 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:347

```
ATGAACGAAA TTGACAAATC CGTTGATATC GGATTCTTAC GGATTCTGGA TGTTATTAAA      60
AAAGTTAAAA CCCCAAAGGG TGGTATTGAG GTTTTAAGGA CTTTAATTGA TTTCACGCCC     120
AAAATTGAAA ACGCCCTAAA TTTAGCGACC AAAAGCCATA AGGGGCAATA CAGAAAGAGC     180
GGTGAGCCTT ATATTGTCCA TCCTATTTGC GTGGCGAGCG TGGTGGCGTT TTGTGGGGGC     240
GATGAGGCGA TGGTGTGCGC CGCGCTTTTG CATGATGTGG TAGAAGACAC GCCTTGTGAG     300
ATTGAAACGA TTGAGCGAGA ATTTGGGCAA GATGTGGCTA ATTTAGTGGA TGCGCTCACC     360
AAAATCACTG AAATCAGGAA AGAAGAGTTA GGCGTGAGTT CTCAAGATCC CAGAATGGTG     420
GTTTCAGCCC TCACTTTTAG AAAGATCCTT ATTAGCGCGA TACAAGATCC AAGAGCCTTA     480
GTGGTAAAGA TTAGCGACAG GTTGCACAAC ATGCTCACCT TAGACGCCTT GCCTCATGAC     540
AAGCAGGTGC GTATTTCTAA AGAAACTCTA GCGGTGTATG CCCCCATAGC GAGTCGATTG     600
GGCATGTCTT CAATCAAAAA CGAATTAGAA GACAAGAGCT TTTATTATAT TTATCCAGAA     660
GAGTATAAAA ATATTAAGGA GTATTTGCAC AAAAACAAAC AGTCTTTACT CTTAAAACTC     720
AACGCTTTTG CGAGCAAGTT AGAAAAAAAG CTTTTTGACA GCGGGTTTAG CCATTCGGAT     780
TTTAAACTCG TTACAAGGGT GAAACGCCCT TATTCTATTT ATCTTAAGAT GCAACGAAAA     840
GGGGCGGTTA ATATTGATGA AATTTTGGAC TTGTTAGCCA TTAGGATTTT ATTGAAAAAC     900
CCGATTGATT GCTACAAGGT TTTAGGGATT ATTCATTTGA ATTTCAAACC CATTGTTTCT     960
CGTTTTAAAG ATTACATCGC TTTGCCCAAA GAAAATGGCT ATAAGACAAT ACACACGACG    1020
ATTTTTGATG AATCTTCTGT TTATGAAGTG CAGATCCGCA CTTTTGATAT GCACATGGGG    1080
GCGGAGTATG GTAATTCAGC CCATTGGAAG TATAAAGCCG GGGGCGTGGA TCATGAAGAA    1140
CATCATGAGG GCATGCGGTG GTTGCAAAAT TTTAAATACC ATGACAGCGA TTTGAAAAAC    1200
GACCCTAAGG AATTTTACGA ACTCGCTAAG AACGATTTGT ATCGTGAAGA TATTGTCGTT    1260
TTTTCGCCCC ATGGGGACAC TTACACTTTA CCGGTGGGCG CGATCGCTTT AGATTTCGCT    1320
TACATGGTGC ATAGTGATTT GGGCGATAAA GCCACGGACG CTTATATCAA TAGTAAAAAA    1380
GCCTTACTCA ATCAAGAATT AAGGAGTGGG GATGTGGTTA AAATCATTAA AGGCGATAAA    1440
GTAATACCTC GTTTCATTTG GATGGATCAG CTTAAAACTT CTAAGGCTAA AAACCATTTG    1500
CGCATCCAAA GAAGAAACCG CTTGAAAGAA ATTGACACTA AGAGCATGAT CAATATCTTA    1560
GCGACTTTTT TTTGGGCGCT C                                              1581
```

(2) INFORMATION FOR SEQ ID NO:348:

(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:348

GTGGTGGTGG TTGAGAATAT AAAAGACGCT GTGCCTTTAG CGCAAAGCCT RATARAGGGG 60
GGTATTCCAA TCATAGAAGT AACTTTGCGA TCAAACTGTG CTTTAGAGGC CATAGAGCTT 120
ATCGCTAAGA ATGTGCCAAA AATGCGCGTG GGTGCTGGCA CGATACTCAA TCTCACTCAA 180
TTAGAGCAGG CTCAAAATAG GGGGGCAGAG TTTTTGATTA GCCCGGGTCT TACGATAAAG 240
CTTTTAGAAC ACGCAAAGAA AAAAGACATG CCTTTAATAC CTGGGGTTTC TAGCAGCAGT 300
GAAGTCATGC AAGCTTTAGA ATTGGGTTAT AACGCTTTGA AATTTTTCCC GGCGGAGTAT 360
TGCGGGGGCC GT 372

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:349

GTGGAAAAAA TCAAACCCTA TGCCCCTAAA GATAGCCCTT TAATAGACTA TTCTAGCCTA 60
GTTAGAAACG TCCAATCCAC TTTAAAAGGC ACTTCTTTTG AAACGCTTAT CAATGGCGTT 120
TGGGAAAGCT TTGAAACGAA GGTTTTAGGG GAGTTTAACG CCTATAATAT CGCTTCAGCG 180
ATTTTAACCG CTAAGCATTT AGGCTTAGAG ACAGAAAGGA TCAAACGGCT TGTTTTTGAG 240
CTTAAGCCTA TTAACCATCG TTTGCAACTG TTGGAAGCGA ATCAAAAAAT CATTATAGAC 300
GATASCTTTA ATGGGAATTT AAAGGGCATG 330

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1791 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350

```
ATGTCTAATC AAGAATACAC CTTCCAAACT GAAATCAACC AGCTTTTGGA TTTGATGATC      60
CACTCTTTGT ATTCTAATAA AGAGATTTTT TTAAGGGAGT TGATTTCTAA CGCGAGCGAC     120
GCTTTGGATA AGCTGAATTA TTTGATGCTA ACCGATGAGA AATTAAAAGG GCTGAATACC     180
ACGCCTAGCA TCCATTTGAG TTTTGATAGC CAAAAAAAAA CCTTAACGAT TAAAGACAAT     240
GGTATAGGCA TGGATAAAAG CGATCTCATC GAGCATTTAG GCACGATCGC TAAATCAGGC     300
ACGAAGAGTT TTTTAAGCGC TTTGAGTGGG GATAAGAAAA AAGATAGCGC CTTAATTGGC     360
CAATTTGGCG TGGGCTTTTA TTCGGCGTTC ATGGTAGCGA GTAAGATTGT CGTTCAAACC     420
AAAAAAGTTA CCAGTCATCA AGCTTATGCA TGGGTGAGCG ATGGTAAGGG CAAGTTTGAA     480
ATCAGCGAAT GCGTCAAAGA GGAGCAAGGC ACAGAAATCA CCCTCTTTTT AAAAGAAGAA     540
GATTCTCATT TTGCGAGCCG TTGGGAGATT GATAGCGTTG TTAAAAAGTA TTCTGAGCAT     600
ATCCCTTTCC CTATTTTTTT AACTTACACC GATACGAAAT TTGAGGGCGA AGGGGATAAT     660
AAAAAAGAAG TTAAAGAAGA AAAATGCGAT CAGATCAATC AAGCGAGCGC TTTATGGAAA     720
ATGAATAAGA GCGAATTGAA AGAAAAGGAT TACAAAGACT TTTACCAATC GTTTGCGCAT     780
GATAACAGCG AGCCTTTGAG CTATATCCAT AATAAAGTGG AAGGCTCTTT AGAATACACG     840
ACGCTTTTTT ATATCCCTAG CAAAGCGCCC TTTGATTTGT TTAGGGTGGA TTATAAAAGC     900
GGGGTCAAAC TTTATGTTAA ACGGGTGTTT ATCACTGATG ATGACAAAGA ATTGTTGCCG     960
TCTTATTTGA GGTTTGTTAA AGGCGTGATT GACAGCGAAG ATTTGCCCTT GAACGTGAGT    1020
CGTGAAATCT TACAGCAGAA TAAGATTTTA GCCAATATCC GTTCGGCTTC AGTGAAAAAG    1080
ATTTTAAGCG AGATTGAAAG GCTGAGCAAG GATAACAAGA ATTACCATAA ATTCTATGAG    1140
CCTTTTGGGA AAGTGTTAAA AGAAGGCTTG TATGGGGATT TTGAAAACAA AGAAAAACTT    1200
TTAGAATTGT TGAGATTCTA TTCTAAAGAC AAAGGAGAAT GGATTTCTTT AAAAGAATAC    1260
AAAGAAAATT TAAAAGAAAA TCAAAAAAGC ATTTACTACC TTTTAGGCGA AAATTTAGAC    1320
TTATTAAAAG CGTCCCCCCT TTTAGAAAAA TACGCTCAAA AAGGCTATGA TGTTTTGTTA    1380
TTGAGCGATG AAATTGATGC GTTTGTGATG CCAGGCGTGA ATGAATACGA TAAAACGCCC    1440
TTTAGAGACG CTAGCCATAG TGAGAGTTTG AAAGAGCTTG GTTTGGCAGA AATCCATGAT    1500
GAGGTAAAAG ATCAGTTTAA AGATTTAATC AAAGCGTTTG AAGAAAATCT TAAAGATGAG    1560
ATTAAGGGCG TAGAGCTTTC TGGTCATCTC ACTTCAGCGG TGGCTTTAAT AGGCGATGAA    1620
CCAAATGCGA TGATGGCTAA TTGGATGCGT CAAATGGGGC AAAGCGTGCC TGAAAGCAAG    1680
AAAACTTTAG AATTAAACCC TAACCATGCG ATTTTGCAAA AACTCTTAAA ATGCGAAGAT    1740
AAAGAGCAGT TGAGCGCTTT TATCTGGTTG CTTTATGATG GGCGAAGCTT T             1791
```

(2) INFORMATION FOR SEQ ID NO:351:

(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

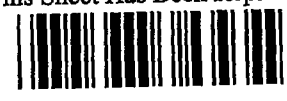
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351

```
GTGAATTTAG GGGCTTACTA CACGCCCCCT TATTTAGTGG ATTGCGCTTA CAAGCTTTTA      60
AAAAAGCATG TTGGTATTGA AAACTACACG CTTTTAGACA CCGCATGTGG TAATAAAGAG     120
TTTTTAAAGC TCCACCACCC TAAAAAAATA GGAGCGGATA TTGACCCTAA GTGTGATGCT     180
TTAATAATAA ACGCTCTAGC CAATCCTAAA AGAGAAAATT ATGGCATTAG CCAAGATGAA     240
CCTTTAATCA TCGTGGGCAA TCCCCCCTAT AACGATAGAA CTTCCTTTAT CAAACAAGAT     300
ATTAAAAATA AAGATTTCAT TTTTGAGATA GACAACGATT TGAAATCCCG AGATTTAGGG     360
ATAAGTTTTT TAAAATCTTT TGCAATTTTA AAGCCGGCGT TTATTTGCGT GCTACACCCT     420
TTATCTTATC TCATCAAAGA AGCTAATTTT AAGCAATTTA AAGCTATT                  468
```

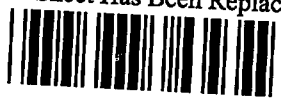
This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 471 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:352

```
ATGAAAAGCA TTTTGCTCTT TATAATTTTT GTAGTTTGTC AGTTAGAAGG CAAAAAATTT      60
TCACAAGATA ATTTTAAGGT GGATTATAAC TACTATTTGC GCAAACAGGA TTTGCACATC     120
ATTAAAACGC AAAACGATTT GTCCAATGCC TGGTATCTCC CTCCACAAAA AGCCCCCAAA     180
GAACATTCTT GGGTGGATTT TGCTAAAAAA TATTTAAACA TGATGGATTA TCTAGGCACT     240
TATTTTTTGC CTTTTTATCA TAGTTTCACC CCCATTTTTC AATGGTACCA CCCTAATATC     300
AACCCCTACY AACGCAATGA GTTTAAGTTC CAAATCAGTT TTAGAGTGCC TGTATTTAGG     360
CATATTCTTT GGACTAAAGG CACGCTTTAT CTGGYTTATA CCCAAACTAA CTGGTTTCAA     420
ATTTATAATG ACCCTCAATC CGCCCCCATG CGAATGATTA AATTTCATGC C               471
```

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353

```
ATGGGCTTGA TGGGCGTGTC GCAAGGCTTA CCAAACACCA CTAGCAAGTT TGGTATTGAA      60
TTTGACTCTT TAGCTGATGT GGTCGCTTTT GGAGTCGCCC CAAGCCTTAT TACTTACTTT     120
TATGTGGGGT ATAACTTTGG GCGTATAGGC ATGGCGGTGA GCGCGTTGTT TGTGATTTTT     180
GGAGCGATAC GATTAGCGCG ATTCAATATC AGCACCAACA CAAGCGATCC CTATTCTTTC     240
ATCGGTATCC CCATTCCTGC GGCGGCGGTA TTGGTGGTGC TTTGCGTGTT ATTAGATAAT     300
AAATACCATT TCTTAGAAGG CAATACCGAA AAGTTATTTT TAGGCTTTAT TGTCTTATTA     360
GGGGTGCTTA TGGTGAGCAA TATCCGCTAC CCTAATTTTA AAAAAGTCAA GTGGAATCTC     420
AAGCTTTTCA TCTTAGTGTT GATCTTTTTA TCGTTAGTGT TTGTGCGCCC TTTAGAGGCT     480
```

```
TTGAGCGTGT TTATGGGGTT GTATTTGATC TATGGCATCA TTCGGTGGAT CTTTTTAATG     540
GTAAAAATTA CTTTTAATAA AAATAAAAGC GCA                                  573
```

(2) INFORMATION FOR SEQ ID NO:354:

(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:354

```
ATGATAGGAG TTTACCCCAA TTATTCCAAA AAGCAACTAA AACGCCCCTT AGTCATATTT      60
GTAAGTAGGG AGTTAGCGCT GGCTAATGGT ATTCTTACAG ACGCCTATGA CATTGAAGCA     120
AATCTTTACA TGAATGCTCG TATCGTTATG AARAATAATA AAAGGAAACA TTATGAGCAG     180
CGGGTTAATT TACATTTCRT TAGAAGTCTT GGTARCGTGT TTGATCACCG CTCTAATCAT     240
GTATTATGTG ATGAAAAAGA TCTATTACGC                                      270
```

(2) INFORMATION FOR SEQ ID NO:355:

(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:355

```
GTGAAAATAA CCATAATGAT TAAAGATTTT AACCACTATT GTAGAAAAAT AACGAGAGGG      60
TTTGTAAAAA TTCCCACCAA AAAACAAGGA GCAAAAAAGA TGAAAAAAGC GGGTTTTCTT     120
TTTTTGGCGG CGATGGCTAT CATTGTTGTG AGTTTAAACG CCAAAGATCC GAATGTGTTG     180
CGTAAGATTG TTTTTGAGAA ATGTTTGCCT AATTATGAGA AAAATCAAAA TCCTTCACCA     240
TGCATAGAAG TCAAACCCGA CGCCGGCTAT GTGGTTTTAA AAGATATTAA CGGTCCGTTG     300
CAATATTTGT TGATGCCAAC GACTCACATT AGTGGCATTG AAAACCCTTT GTTGCTTGAT     360
CCTTCTACGC CTAACTTTTT TTACTTGTCA TGGCAAGCGC GCGATTTTAT GAGTWAAAAA     420
TACGGAAAAC CCATTCCTGA TTATGCGATC TCTTTGACGA TCAATTCTAA AAAAGGGCGA     480
```

This Sheet Has Been Replaced



```
TCGCAAAACC ATTTTCACAT CCATATTTCT TGCATTAGCC TTGATGTGCG CAAACAGCTG     540
GATAATAATC TAAAAAATAT CAACAGCCGT TGGTCGCCAT TATCAGGTGG CTTGAACGGG     600
CATAAATATT TGGCGCGTCG GGTAACAGAG AGCGAATTAG CGCAAAAAAG CCCGTTTGTC     660
ATGCTTGCTA AAGAAGTGCC TAACGCGCAC AAACGCATGG GAGACTATGG CTTGGCGGTG     720
GTGCAACAGA GCGATAACTC CTTTGTCTTG TTAGCGACAC AATTTAACCC ATTGACTTTA     780
AATCGCGCTT CAGCCGAAGA GATTCAAGAT CATGAATGCG CGATTTTGCG T              831
```

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356

```
GTGCTAACGA GTGGGGACAT GATCACTTGT CCGTATTGCG GGCGTATTTT RTACGCTGAG      60
AGTACGCATG AAAGTAACGC TCAACCTCCA AAAGAAAGCC AACCAAAAGA AAGCCAAGAA     120
GAAAGCCAAG AAGAAAGCCA AGAAGAAAGC CAAGAAGCCG TCCGTTTGAT TGTT           174
```

(2) INFORMATION FOR SEQ ID NO:357:

(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:357

```
ATGAAATTGA ATGACCCTTT CACAAGCCCT AATAAAGCCA AAAAAGAATT ATCGCCAAAA      60
GGCTTTAGGG GGGGGTTAGA GTCTGAAATT TTATTAGGCT TTGTCTTGCA AAAAGAAAGG     120
GTTTTTTTGC ACACGCATGA GCATTTGGAA TTAAGCCACG AAGAAGAAAC ACGCTTTTTT     180
GAATTGGTAG GAAAGCGTTT GAATGACTGC CCCATAGAGT ATTTATTAGG AAGCTGTGAT     240
TTTTATGGGC GCTCTTTTTT CGTGAATGAG CATGTTTTAA TCCCACGGCC TGAAACCGAG     300
ATTTTAGTCC AAAAAGCCCT TAATATTATT TCTCAATACC ATTTAAAAGA AATAGGCGAA     360
```

This Sheet Has Been Replaced



```
ATCGGCATAG GGAGCGGATG CGTGTCCGTG AGTTTGGCTT TAGAAAACCG TAATCTCTCT      420
ATTTATGCGA GCGATATTTC ACCAAAAGCT TTAGAAGTGG CGTTAAAAAA TATTGAACGC      480
TTTTGTCTAA AAGAGCGTGT TTTTTTAAAA CAAACGCGCC TTTGGGATCA TATGCCAACG      540
ATAGAAATGC TTGTCTCTAA CCCGCCCTAT ATCGCTAGAA ATTATCCTTT GGAAAAATCC      600
GTTCTCAAAG AACCGCACGA AGCCCTTTTT GGGGGGGTTA AAGGCGATGA AATCTTAAAA      660
GAAATCGTTT TTTTAGCCGC TAAATTAAAA ATCCCTTTTT TGGTTTGTGA AATGGGGTAT      720
GACCAGTTAA AGAGCTTGAA AGAATGCTTG GAGTTTTGCG GTTATGATGC AGAGTTTTAC      780
AAGGATTTGA GCGGCTTTGA TAGAGGGTTT GTGGGCGTTT TAAAAAGTTT TTTAAGA         837
```

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358

```
ATGATTTCTT TCATTGGGTT TGAATGCTCC GCATTAAAAG TTTTTTTAAC TTTTGGTTAC       60
ATAGTTTTTA AAAGYTGGCA CTATAGCGCT ATAAGACTAA TTGTTATA                   108
```

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

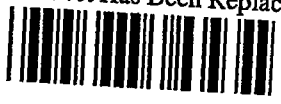
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359

```
GTGATCCAGT CTCACCCTAA ACAAACTCTA ATTGAAGATG AAAATTATTT TTATGCTAAC       60
AAGGGTCTTT ATAAAACCAA CAAAGAAGCC TTTTTAAGGG TTTATAAAAT CCCAGAGAGC      120
ATGCCCATAG AAAAACGAGA AAGTTTAAGC AAGGTTTCTA AAATCTTTTT AGCGTTGCTT      180
TTTTTCATTT CTAGCATGCT TTTTGGGATC TTTTGGCGTT TGCCCAAACG ATTGGACACT      240
AAAATGAGTT TAGAGAGCGC GCACAAAAAC GAATTAGAAA ATGCATTCCA ACGATACGAT      300
```

This Sheet Has Been Replaced



GCGCTAGGGG TGCGTTTTGA AGACATTGCA GGGGTGAATG AAGTCAAAGA AGAATTACTA 360
GAAGTGATRG ATTWTTTWAA AAAACCC 387

(2) INFORMATION FOR SEQ ID NO:360:

(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:360

ATGTTTGTAG TTAAAATGGT GTTAGGGTTT TTGATCCTTT TAAGCCCTTT GTGCGCTACT 60
GGATTGGATA TTTCACAAAC AGACATTATA GAGCGTTCTT TAAATTTCCT CTTGTTTGTG 120
GGGATTTTGT GGTATTTTTT GGCTAAAAGA TTGCGTTCAT TTTTGCATTC CAAAAGCCTT 180
GAAATCTCCA AACGCTTAGA AGAGATTCAA GCCCAACTTA AAGTGAGTAA AGAACATAAG 240
AAAAAACTCC TTAAAGAATT AGAGCAAGCC AAAGAAAAAG CTGAATTGAT TATTTCTGAT 300
GCGAATAAAG AAGCCCTACA CGATCACGCA AAAATACGAA TTACAAACCA AAATGGATGT 360
GGAAAATTTG ATCAAAAATT C 381

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 885 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361

ATGAGGGTTT TAGAGTGGAA ATATTGGTTA AATACTGATA AGTGGGATAC GCCCACCAAC 60
AAACCGCCTC AAACTTTTAA AATACAAATT TTTAAGATAC AAATAGGTAT AATCAATAAC 120
TTCAATCATT TAATCAAAGG GAGTTCTATG AAAAACGCTT TCAAAGCGTT TGCCTTGTTA 180
ATCGTATTTT TCTCAAACGC TCTATTAGCG CAGGATTTAA AAATCGCTGC TGCTGCTAAT 240
CTCACGCGCG CTTTAAAAGC CCTTGTTAAA GAATTTCAAA AAGAACACCC AAAAGACGCT 300
ATTAACATTA GCTTTAATTC TTCAGGCAAA CTCTACGCTC AAATCGCTCA AAACGCCCCT 360

This Sheet Has Been Replaced



```
TTTGATTTAT TCATTTCAGC GGATATTGCT AGACCCAAAA AACTTTATGA TGAAAAAATA     420
ACCCCTTTTA AAGAAGAAGT CTATGCTAAA GGCGTGTTGG TTTTATGGAG TGAAAATCTA     480
AAAATGGATT CTTTAGAAAT TCTTAAAGAC CCTAAAATTA AACGTATCGC TATGGCTAAT     540
CCTAAACTAG CCCCTTATGG AAAAGCCAGC ATGGAAGTCT TGGATCGTTT AAAACTCACT     600
CCTAGTCTTA AATCTAAAAT CATTTATGGC GCTTCTATTT CTCAAGCCCA TCAATTCATC     660
GCCACCAAAA ACGCTCAAAT AGGCTTTGGA GCGTTATCTT TGATCGATAA AAAAGACAAA     720
AACCTCTCTT ATTTCATCAT TGATAAAACC CTTTATAACC CTATTGAACA AGCCTTAATC     780
ATCACTAAAA ATGGGGCTAA TAACCCTTTA GCCAAAGTTT TTAAAGATTT TTTATTCAGC     840
CCTAAAGCTA GAGCTATCTT TAAAGAATAC GGCTATATTG TGGAT                     885
```

(2) INFORMATION FOR SEQ ID NO:362:

(f) 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:362

```
GTGGCTTTAT TAGAGCCAAG CGTGATGTAT CTTACCGAAA AGTATCAATA CTCTCGTTTT      60
AAGGTTACTT GGGGTCTTGT AGCGTTAATC TTTGTGGTAG GCGTGGTGTT GATTTTCTCG     120
CTCCATAAGG ATTATAAAGA CTATCTCACT TTCTTTGAAA AAAGTCTTTT TGATTGGTTG     180
GATTTTGCAT CAAGCACCAT TATCATSCCT TTAGGCGGGA TGRCAACCTT TATTTTTATG     240
GGCTGGGTTT TGAAAAAAGA AAAATTGCGT CTTTTGAGCG CGCACTTTTT AGGCCCTAAA     300
TTGTTTGCAA CTTGGTATTT CTTGCTTAAA TACATCACCC CTTTAATTGT GTTTTCCATT     360
TGGTTGAGCA AGATTTAT                                                  378
```

(2) INFORMATION FOR SEQ ID NO:363:

(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:363

This Sheet Has Been Replaced



```
GTGGGGCTTA TGAAAATAAG ATTTATGGGG CGGAGTGTTT TTGTGGGGGA TTTGGAACGC      60
ATTGAAGAAG TGGCTAGATT TGAAGAATTT TGGCTTTTAG GGGGGCAAAA AGCGATCAAA     120
GAGCCTAGAA GATTGGTTTT AGAAATCGCT TTAAAACACC AGCTCAACAA GCTTTTAAAA     180
CGCGTTCAAA AGCATTTCAA AGAAGACGAA TTAGGAATTT TTAAACAAAT GCATGACAAA     240
AAAATTCAAA GCGTCGCCAC CAATTCCATA GGGCGTTTGT TTGATATAGT GGCGTTTAGT     300
TTGGGCGTGG TGGGAACGAT TAGTTTTGAA GCCGAGAGCG GGCAGGTTTT AGAAAATCTA     360
GCCCTACAAA GCGATGAGAT CGCTTTTTAC CCTTTTGAAA TCAAAAACAG CGTGGTGCGT     420
TTGAAGGAAT TTTATCAAGC GTTTGAAAAG GATTTGGGCG TTTTAGAACC CAAACGCATC     480
GCTAAGAAAT TTTTTAACAG CTTAGTAGAA ATCATTACCG CTTTGATTGC GCCTTTTAAA     540
GGGCATGTCG TGGTGTGCAG TGGGGGCGTG TTTTGCAACC AATTGTTGTG CGAACAATTA     600
GCCAAGCGAT TGAAAAAGCT TCAAAGGGAG TATTTTTTCC ACAAGCATTT CCCCCCTAAT     660
GACAGYAGTA TCCCTGTCGG TCAAGCCTTA ATGGCGTATT TCAACCCTAC AATCATCAAA     720
AAAGGA                                                                726
```

(2) INFORMATION FOR SEQ ID NO:364:

(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

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364

```
GTGAGCGATT CTAACGCTTT AAAGGAAGTG TTTTTAAACA TCAGCGCTAA AGAAGATCAT      60
TGCGACGTTT TGATCAATTC CGCCGGTTAT GGGGTGTTTG GGAGCGTGGA AGACACGCCC     120
ATTGAAGAGG TTAAAAAGCA ATTTAGCGTG AATTTTTTCG CCCTTTGTGA AGTGGTGCAA     180
CTTTGTTTGC CCTTATTAAA AAACAAGCCT TATTCTAAGA TTTTCAATCT TTCTTCCATA     240
GCGGGGCGTG TGAGCATGCT CTTTTTAGGC CATTACAGCG CGAGTAAGCA TGCCTTAGAG     300
GCTTATAGCG ATGCCTTGCG TTTAGAGCTT AAGCCCTTTA ACGTTCAAGT GTGTTTGATT     360
GAGCCAGGCC CGGTGAAAAG CAATTGGGAA AAAACCGCTT TTGAAAATGA TGAGCGGAAA     420
GATAGCGTTT ATGCTTTGGA AGTGAATGCG GCT                                  453
```

(2) INFORMATION FOR SEQ ID NO:365:

(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:365

```
GTGATAGTGG CGTGGCTTTT TAGGTTTAAA AGCATTGCGT TTTCTATTTT AATCACTCTG      60
TTGGTTATTT TAGTGGATAT TTGGGTGTAT AGCGATGTGC GCCAGTTTTT ATTGGACACT     120
TCTAGCTCTT TTATTTGGCT TTTAATCGCT TTACTAATCA AGTGGGGCGT GATTGTTATA     180
AGTGCGCGCA AATGCTACCA ATTCAGCCAA AAAATGTTTG CGTTAATCCA AAGAAAAAGG     240
CAAATCAGAG AGAATTTAAA AAACCGCTCC AATCGCAAAG ATGCTAAAAA TTTTGAAAAA     300
CTCTCTAACA TCGCTGAAGA AATCATTTCA AAAAAACAAG AAGAGTCCCA CCACAAAGAA     360
GATTCTAATG ATGAAAACCA CAAAGACAAG CTTTCTAACA TTACCGAAGA AATGATTCTC     420
AAAAAACAAG AGGAACTGAA AGCTAGAAAG GATAAGGGGG AT                        462
```

(2) INFORMATION FOR SEQ ID NO:366:

(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

This Sheet Has Been Replaced



(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:366

```
ATGAACTACC CTAATCTACC TAACAGCGCT TTAGRGATAA GCGAACAGCC AGAAGTGAAA      60
GAAATCACTA ACGAGCTTTT AAAGCAATTA CAAAACGCTT TAAGGAGCAA CGCGCATTTT     120
AGCGAGCAAG TGGAATTAAG CCTTAAATGC ATCGTTAGGA TTTTAGAAGT GCTTTTGAGT     180
TTGGATTTTT TTAAGAATGC GAATGAGATT GATAGCAGTT TAAGAAATTC CATTGAGTGG     240
CTGACTAACG CCGGCGAGAG CTTGAAATTA AAAATGAAAG AATACGAGCG CTTTTTTAGC     300
GAGTTTAATA CGAGCATGCA TGCCAACGAG CAGGAAGTAA CCAATACCTT AAACGCTAAC     360
GCCGAGAACA TTAAAAGCGR AATTAAAARG CTAGAAAATC AATTGATAGA AACCACGACA     420
AGACTTTTAA CGAGCTATCA AATCTTTTTA AACCAAGCCA GAGATAACGC TAACAACCAA     480
ATCACAAAAA ACAAAACCCR AAGCCTTGAA GCGATTACAC AAGCTAAAAA CAACAGC        537
```

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367

GTGTTTGCCA CTGACAGCAG TAGCTTTTCT ATGGGGCTTA CCATGGCGAG TGCTTATGAY 60
CCCATTTCAG GATCGCAAAA ACCCATTGTG GGGCAAGCCC TTTTATTGTT AGCGATTTTA 120
ATTTTATTGG ATTTATCGTT CCACCATCAA ATCATTTTAT TTGTGGATCA CAGCTTAAAA 180
GCCGTCCCTT TAGGGCGATT TGTCTTTGAG CCAGAATTAG CTAAAAACAT TGTCAAAGCC 240
TTTTCACACT TGTTTGTCAT AGGGTTTTCT ATGGCGTTCC CTATTTTATG CTTGGTGTTA 300
TTGAGCGATA TTATTTTTGG CATGATCATG AAAACCCACC CTCAATTCAA CCTGCTCGCT 360
ATCGGGTTTC CGGTTAAAAT TGCGATCGGG TTTGTGGGCA TTATTTTAAT CGCTTCGGCT 420
ATCATGGGGC GTTTTAAAGA AGAAATCAGC CTGGCCTTTA GCGTTATTRG TAAAATCTTT 480

(2) INFORMATION FOR SEQ ID NO:368:

(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:368

ATGTATGGCG TGAAAGAGAT TAAAGATAAA ATTGACAAGC AACTCCACAA TAACGATCAT
TTGTTTGAAG GGCTTTTTGG GGAAAAAGAA GATTTGAAAA AATTGGTGAG CATGTTTGGG
CAGTTGCGTT TCCAAAAGCG CTGGAGCCAA ACCCCAAGAG TGCCACAAAC CAGTGTTCTA
GGGCATACTT TATGCGTGGC GATTATGGGG TATTTATTGA GTTTTGACTT GAAAGCTTGT
AAAAGCATGC GGATCAATCA TTTTTTGGGC GGGCTTTTTC CA

(2) INFORMATION FOR SEQ ID NO:369:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369

```
ATGACTTTAG ATGACTTATT AGGGGGGAGT TTGGACCCGC ATTGTTTTTG CAAACCCTTA      60
ATCAAAACCA AAAAAGACCA AGAAAGGCTC TTATCCCTTG CTTTAAAAGC CCACCCTAAA     120
ATCTCTTTTG GAWWGGACAG TGCCCCGCAT TTCATTTCTA AAAAGCATAG CGCTAACATC     180
CCGGCGGGCA TCTTTTCTGC CCCTATTTTG TTGCCTGCGT TGTGCGAACT TTTTGAAAAA     240
CACAACGCTT TAGAAAATTT GCAAGCCTTT ATCAGTGATA ACGCTAAAAA AATCTACGCG     300
CTAGACAATT TACCCAGTAA AAAAGCGCAT TTGTCTAAAA AACCCTTTAT AGTCCCTACG     360
CACACGCTTT GCTTGAATGA AAAAATCGCT ATCTTAAGAG GGGGCGAAAC GCTATCTTGG     420
AACCTTCAAG AAATCGCC                                                   438
```

(2) INFORMATION FOR SEQ ID NO:370:

(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:370

```
ATGGGCGTTT TGGGCATGTT CGCTTTTTTT TCATGGGTTT TTTTATTCAA GCACAATCTC      60
AGCCATAAAA TCCGCTTATA CCATGAAAAA AAGGATTTTG ACAAATTGCT CAAACAAATC     120
CTATCCCAAG ACACCCAAAA GACTTTTTTA AAAACAAAAT TTAAAAGCGA TCTCGCTAAA     180
AACCTCTCTC AAATCTTAGC CCGCTATGAT TTAAAAGCTG ATTTAAACAC GCCAAATAGC     240
GGGTGCGAAA AAGTGGATAA CCTTTTTAAA CATTACCACA ATATAGAAAA TAACACCCTT     300
GAGCCTAAAG ATCACGCTAA ACATTCCCTA GCTTATGAGC ATGCTTATTT TTCTAAACGC     360
TTGAAGGCTT TCATTCATAA CGATTTGAAA AACGCCTTTG AAGTTTTAAC AAACGCGCAA     420
ATCCCTTTGG AATTACGCCG CTACGCTTAT AGAAATCGCC CAAAAAGGCA GCAAAAAAGA     480
GGTTTTAAAG GCTGTGAATG CGATGCAAGA GGATTTGGA                            519
```

(2) INFORMATION FOR SEQ ID NO:371:

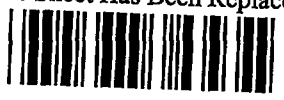
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 579 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371

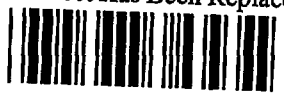
```
GTGAGTGTTC CTGCAACGAG TGCGAATTTA GGCCCCGGTT TTGATTGCTT GGGTTTGAGT      60
TTGAATTTAC GCAATCGTTT TTTTATTGAG CCTAGTAATA TCCATGCGGT GAAATTGGTT     120
GGGGAGGGTG AAGGGATCCC TAAATTTTTA ACCAACAATA TTTTCACCAA AGTGTTTTAT     180
GAGATTTTAA AAAAGCATGG GAATGACGGC TCGTTTAAAT TTTTATTGCA TAATAAAGTC     240
CCTATTACAA GGGGCATGGG GTCTAGCTCA GCGATGATTG TGGGGGCGGT CGCTTCAGCG     300
TTTGCGTTTT TAGGGTTTGC TTTTGATAGA GAAAACATTC TCAATACTGC TCTAATTTAT     360
GAAAACCACC CGGATAATAT CACCCCGGCG GTGTTTGGGG GGTATAATGC AGCGTTTGTG     420
GAAAAAAAGA AAGTGATAAG TTTAAAAACC AAAATCCCTT CTTTTTTAAA AGCGGTGATG     480
GTGATCCCTA ATAGGGTCAT TTCTACCAAG CAATCGCGCC ATCTCTGCCC AAGCGTTACA     540
GCGTGCAAGA AAGCGTGTTT AACCTTTCGC ATGCGAGTT                            579
```

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(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:372

```
GTGGCTAAAA ATTTGGTAGC GAGCGGGGTT TGCGATAAAG CGACCGTGCA GCTTGCTTAT      60
GCGATTGGGG TGATAGAGCC TGTGTCTATT TATGTGAACA CGCATAACAC GAGCAAGCAT     120
TCAAGCGCGG AGTTGGAAAA ATGCGTGAAA TCGGTTTTCA AACTCACGCC AAAAGGCATC     180
ATTGAAAGCT TGGATTTGTT AAGACCCATT TATTCGCTCA CTTCAGCTTA TGGGCATTTT     240
GGGCGCGAGT TAGAAGAATT CACTTGGGAA AAGACTAACA AGGTTGAAGA GATTAAAGCG     300
TTCTTTAAGC GT                                                        312
```

(2) INFORMATION FOR SEQ ID NO:373:

(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:373

```
GTGCGTTTGT TTAGATTTGT GGGGTGGTAT TATTTCAAAT ACTTTTTAAT CGTGCTTTTA      60
GCTTTGGAAT TGTTTTTTGT AGGCATTGAC AGCCTGAAAT ACGCCGATAA AATGCCTGAT     120
TCTGCGAACA TGATCATTTT ATTTTTCACC TATGATATTT TATTCGCTCT CAATTACACC     180
TTGCCCATTT CCTTGCTTTT AGCGATGGTT TTATTTTATA TCACCTTCAT TAAATCCAAC     240
CAATACACCG CCCTGCTCTC TATTGGATTT TCCAAATGCC AGATTTTAAG CCCTATTTTT     300
TTGATTAGCC TGTTTTTTCAC GGCTGTTTAT GTGGGGTTGA ACGCGACTCC TTTTGTGTAT     360
ATGGAAGAAA AAACGCAAAA TTTAATTTAT AAAGACAATT CTTTGAGCGT TTCAGAGCAT     420
TTGTTAGTGA AATACAACGA TGATTACGTG TATTTTGATA AGATTAATCC CTTATTGCAA     480
AAAGCCCAAA ATATCAAGGT TTTTCGCCTA AAAGATAAAA CTTTAGAATC TTATGCTGAA     540
GCTAAAGAAG CTTTTTTTGA AGACAAATAT TGGATTTTAC ATGACACTAC TATCTATGAG     600
ATGCCCTTGA GTTTTGAACT GGGCGCGAAC GCTTTAAACA CCACGCATTT AGAAACCTTT     660
AAAACGCTCA AAAATTTCCG CCCTAAAGTT TTAGACACCA TTTATCAAAA CAAGCCTGCG     720
GTTTCTATCA CAGACGCTCT TTTATCCTTG CATGCTTTAG TGCGCCAAAA CGCGGACACG     780
AAAAAAGTGC GCTCGTTTTT GTATGTGTTT GCGATTTTGC CCTTTTTTGT GCCGTTTTTA     840
AGCGTTTTAA TCGCTTATTT TTCGCCCAGT CTCGCCCGCT ATGAAAACCT GGCTCTTTTA     900
GGGCTAAAGT TTATCATTAT CACGCTCGTT GTTTGGGGGC TATTCTTTGC TTTAGGGAAG     960
TTCAGCATTT CAGGGATACT CATTCCTGAA ATAGGCGTTC TATCGCCCTT TTTCGTATTT    1020
CTAGCTCTCA GTCTTTGGTA TTTTAAAAAA CTTAATAAGA GATTG                    1065
```

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 717 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

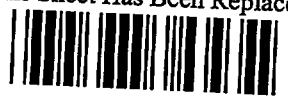
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374

```
ATGATTTATG GCGTTTTAGA CGGCTTGTTT TTGGCTATTT TACAGGCTCA AAATTACCGC      60
TTCCATTCGC TTTATTTGTT TGAAGAAAAT TTAGACTTGT TTAAAATCAG TTGCTATTTT     120
GCGCGTTATG AAGATTTGAT TAAAAAAGGG GCTAAACTTT TTATTCAAGG GTTTTTTAAC     180
CCTAATGAAT TGAAAATGGA TTTTTTGAAA CGCCCTATCA CGCATTCTTT TTTAAAGCTA     240
GAAATCATGC CCTATAAAAG CGCTTTTAAT TTGCGCATGC GAGAAAACAT TCAAAGCTAT     300
TACAAACAAG CCTTAAGGGG TTGGGGGAGT TTTGAAGACG AATTGCTAGG GTTAAAGAAC     360
ACGCTTAAAA ACTTACCCCT ATACCAAACC CTAAAAACCA AACCCAAAAA AATTAACGCC     420
CCCATTTGCG TGGTGGGTAA TGGGCCAAGC CTGGATTTAT TGTTAGATTT TTTAAAAGAA     480
AATGAAGAAA AATTCATCAT TTTTTCATGC GGAACCGCTT TAAAGCCTTT AAAAGCGCAT     540
GGCGTTAAAG TGGATTTTCA AATAGAAGTG GAGCGCATAG ACTATCTTAA GGAGGTTTTA     600
GAAAGAGCCC CCCTAGAAGA CACCCCCTTA ATGGGCGCTA ACATGCTCAA TCCTAACGCT     660
TTTGATTTAG CCAAAGAAGC GTTGATGTTT ATGCGTGGGG GGAGCGCTTG CGCAGTA       717
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 867 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...867

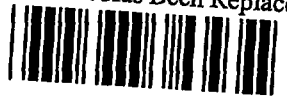
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375

```
ATGCTGGCGT TTTTAAAAAC CCCTAGAAAC AGCGCTTTTG CTTTGGGTYT TTTCGTGGGG      60
GCGTTATTGT TTTACTGGTG CGCTTTAAGG CTTTCGCATT CGGATTTCAC YTATTTATTG     120
CCCTTAATCA TTGTTTTAGT AGCGTTAGTT TATGGGGTTT TATTTTATTT GTTGCTCTAT     180
TTTGAAAACC CCTACTTCAG GCTTTTGAGT TTTTTAGGCT CTAGTTTTAT CCACCCTTTT     240
GGATTTGATT GGTTAGTCCC GGATAGCTTT TTTTCTTATA GCGTGTTTAG GGTGGATAAA     300
TTATCTTTAG GGCTTATTTT TTTAGCTTGC ATTTTTTTGA GCGCTCAAAA TCTTAAAAAA     360
TACAGAATGA TAGGGGTTTT ATTGCTGCTT GGCGCGTTGG ATTTTCATTT TTTTAAAATA     420
AGCGATTTAA AAGAGGTTGG AAATATTGAA TTAGTCTCTA CAAGAACGCC CCAAGATTTG     480
AAATTTGACT CAAATTACCT TAATAATATT GAAAACAACA TTCTTAAAGA AATCAAACTC     540
GCTCAAAGCA AGCAAAAAAC CTTGATTGTT TTTCCAGAGA CCGCTTACCC TATCGCTTTA     600
GAAAACTCCC CTTTTAAAAC CCAACTAGAA GATTTAAGCG ACAAGATCGC CATTTTAATA     660
GGGACATTGC GCGCTCARGG CTATAGCCTT TATAACAGCT CGTTTTTATT TTCTAAAAAA     720
AGCGTTCAAA TCGCTGATAA AGTGATCTTA GCCCCCTTTG GCGAGATAAT GCCTTTACCG     780
GAGTTTCTTC AAAAACCCCT TGAAAAGCTC TTTTTTGCGA GAGCGCTTAT TTATACCGCA     840
ACGCTCCCCA TTTCAGCGAT TTTACAT                                         867
```

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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

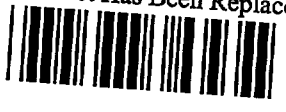
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376

```
ATGAACGATC CTAAGCATGT GGTGTATGTT TGGCTGGACG CTTTATTGAA TTATGCGAGC     60
GCGTTAGGGT ATTTGAACGG TTTAGACAAT AAAATGGCGC ATTTTGAACG CGCTAGGCAT    120
ATTGTGGGTA AGGATATTTT ACGCTTCCAT GCCATTTATT GGCCAGCCTT TTTGATGAGT    180
TTGAATTTGC CCTTATTCAA ACAGCTCTGT GTGCATGGGT GGTGGACGAT AGAGGGCGTG    240
AAAATGAGTA AGAGCTTGGG TAATGTTTTA GACGCTCAAA AGCTCGCCAT GGAGTATGGG    300
ATTGAAGAAT TACGCTATTT TTTATTGCGT GAGGTGCCTT TTGGGCAAGA TGGGGATTTT    360
TCTAAAAAAG CGTTAGTAGA ACGGATTAAT GCGAATTTGA ATAACGATTT GGGGAATTTG    420
TTGAATCGTT TGCTAGGCAT GGCTAAAAAG TATTTCAATT ATTCTCTAAA AAGCACCAAA    480
ATCACTGCGT ATTATCCTAA AGAGCTAGAA AAAGCACATC AAATTTTAGA TAACGCTAAT    540
TCTTTTGTGC CTAAAATGCA ATTGCATAAG GCTTTAGAGG AATTGTTTAA TATTTATGAT    600
TTTTTGAATA AACTCATCGC TAAAGAAGAG CCGTGGGTCT TGCACAAAAA CAACGAATCA    660
GAAAAATTAG AAGCCTTATT GAGTTTGATC GCAAACACGC TACTACAATC AAGCTTCTTG    720
CTCTATGCGT TCATGCCAAA GAGCGCTATG AAATTAGCGA GCGCTTTTCG TGTAGAAATC    780
ACGCCCAATA ATTACGAACG CTTTTTTAAG GCTAAAAAAT TACAAGATAT GGTTTTACAA    840
GACACCGAGC CTTTATTTTC CAAAATTGAG AAAATTGAAA AGATTGAAAA GATTGAAAAG    900
ATTGAAAAGA TTGAAAAAGG GGAGGAAGCC CTAGCAGAAA AAGCAGAAAA AAAAGAAAAA    960
GAAAAAGCCC CACCAACACA AGAAAATTAT ATTAGTATTG AGGATTTCAA GAAAGTAGAG   1020
ATTAAAGTGG GGCTTATCAA AGAAGCTCAA AGGATTGAAA AATCCAATAA ATTACTGCGC   1080
TTAAAAGTGG ATTTAGGCGA AAATCGTTTG AGGCAGATCA TCTCAGGGAT CGCTTTGGAT   1140
TATGAGCCTG AAAGCTTGGT GGGTCAAATG GTGTGCGTGG TGGCTAATTT AAAACCCGCA   1200
AAGCTTATGG GTGAAATGAG TGAGGGCATG ATTTTAGCGG TGCGAGATAA TGATAATCTG   1260
GCTTTAATCA GCCCTACCAG AGAAAAAATT GCAGGAAGTT TGATCAGC                1308
```

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 342 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:377

```
ATGAAACGAC CGATCAGCAA ATTGAAACAA AACTTTTTAC AATTCAAACA TTCTTTCAAC     60
AAACATTTAG ATAAGTACAG CCTTTATTAT AGGCTGTTCA ATATCAGCTC TATCGTTATA    120
GGTTTTTTAA TAGCGCTTTT TTCTTATGGG GCAGGGGTGA TTTTAGTTTA TCCAATATTA    180
TTCTTGTTTG CTCTTATAAT AAAACCTAGC TTTTTTTATT ACACTACTTA TCTTTTGCTA    240
CTCGTTTCTC TCAGCATAAT AAGCAAATAC TATCTCCTAA GCCACGCAAA TTTCACAATG    300
AAGCTAATCA TGCTTATGAC TCAATGGCAA AATTGGTTCT TA                       342
```

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378

ATGGG 5

This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:379:

(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:379

GTGTTCACTT ATTCCTTGGG GCAGGTTTTC TTTTCTCTAA GTATCGGTTT AGGGATCAAT 60
ATCACTTATG CTGCCGTTAC GGATAAAACG CAGAATTTGC TTAAAAGCAC GATTTGGGTG 120
GTTTTATCAG GRATTTTAAT TTCTCTTGTG RCAGGGCTTA TGATTTTCAC TTTTGTGTTT 180
GAATATGGGG CTAATGTCTC ACAAGGCACA GGGTTAATCT TCACTTCTTT ACCGGTGGTT 240
TTTGGCCAAA TGGGAGCGAT AGGCGTTCCT TGTTTCAATT CTTTTCTTGC TCGCGCTCGC 300
TTTTGCTGGC ATCACTTCTA CGGTGGCTTT ATTAGAGCCA AGCGTGATGT ATCTTACCGA 360
AAAGTATCAA TACTCTCGTT T 381

(2) INFORMATION FOR SEQ ID NO:380:

(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:380

```
ATGAAACCAT TGCATTTTTC ACACCTGGAC AGAGAGCAAT CAGGCGATGT GGGTTTTATC      60
ATTAAAAACC TTATTTTTTT AGGGGTTTTT TCCTTATTGG GTTGGTTGAA TACCGAGTAT     120
TTTCTATGGC CTAGCATGCT GGAATTAAAA AAAATCCTTT TAGAAGAAAA TCGTAAAAAA     180
AGCGTTTTAG AATACGCGCA AAGGCATTTT GAAACAGCCC TAGCAAACTA CCGCAATCAA     240
AAAGAAACCA GCGAATCTTT GTTAAAGATT TTTAATGATG AAGAGTCCAG GCGGATTTTA     300
GAAAAGATCT TAAAAAAATG TTTTGACGCC TATAAAATCA AACCCTTGCT CTCTCAAAAC     360
CCCTCCCAAA AAACCCAATT TTTTATCATG GCTAGAGCGA GCGAATTGGA AAAAACTTAT     420
CTTTTTTTCA CCTTAATCAA CAAGTATTTA CCGAGCGCTC AAAGCCAATT GCCCTTAAAG     480
ATTTCTAAAG ATAGCGACGG GTTGTTGGTG CAATTTGGCG TGAGTATTGA TCTCCAA        537
```

(2) INFORMATION FOR SEQ ID NO:381:

(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:381

```
ATGAATGCAT TGAAGCGTGC GTGTTTAAGA TTGATGGGCG AAACCAATAC CGATGATTTA      60
ASCCCARYGA GCGACGCTTT CACACGGAGC GATATTCCTT TACACGCCAA AGCCATGCTA     120
AAAAACCGGA TTGAAAATTA CGAACAACGC ATTGAAGCCA TTAAAACTAA AGGCGTTCCT     180
GTAGCGTATG TGGGCGATGT GGTTGGCACA GGAAGCTCTA GAAAAAGCGC GACTAACTCT     240
ATCATGTGGC ATTTTGGTAA GGACATTCCT TTTGTGCCTA ATAAAAGGAG TGGAGGCATT     300
GTGATTGGGG GGGTGATCGC TCCGATTTTC TTTGCGACTT GTGAAGATAG CGGGGCGTTA     360
CCCATTGTGG CTGATGTTAA GGATTTGAAA GAGGGCGATA TCATTAAAAT CTACCCTTAT     420
AAAGGCGAAA TCACGCTGAA CGATAAGGTG GTTAGCACCT TTAAGCTAGA GCCTGAAACT     480
TTATTAGATG AAGTCAGGGC TTCTGGGCGT ATCCCCTTAA TCATTGGTAG GGGTTTGACC     540
AATAAAGCGC GTAAATTTTT GGGCCGGCGA ATCGGAAGCG TTCAAAAAAC CTTCCGCCCC     600
TCAAGCGCGC TAAGGCTACA CTTTGCC                                         627
```

(2) INFORMATION FOR SEQ ID NO:382:

(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

This Sheet Has Been Replaced



(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

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

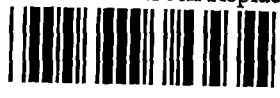
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382

```
ATGCTTTCAG CCCACCAACC TTTTAAAAAT TACCCTGATC TGATTAAAAA AGAGTTGCAA      60
GAGCATAACG CCTATGCGAG CGTCGCTAGT GGGGTGCCAG CGATGTGTGA TGGTATCACG     120
CAAGGTTATG AGGGAATGGA ATTGAGCTTG TTTAGTAGAG ATGTGATCGC ATTAAGCACC     180
SCCGTAGGGT TAAGCCATAA TGTTTTTGAC GGGGCGTTTT TTTTGGGCGT GTGCGATAAA     240
ATTGTGCCAG GCTTGCTCAT AGGAGCGTTA AGCTTTGGGA ATTTAGCGAG CGTGTTTGTG     300
CCAAGCGGGC CTATGGTGAG CGGGATAGAA AATTATAAAA AAGCCAAAGC GCGCCAAGAT     360
TTTGCAATGG GAAAGATCAA CAGAGAAGAG CTTTTAAAAG TGGAAATGCA AAGCTATCAT     420
GATGTGGGCA CTTGCACTTT TTATGGCACG GCTAATTCTA ATCAAATGAT GATGGAGTTT     480
ATGGGGTTGC ATGTGGCCAA TTCTAGCTTT ATCAACCCTA ACAACCCCTT ACGAAAGGTT     540
TTAGTAGAAG AGAGCGCTAA AAGATTAGCG AGCGGGAAAG TCCTGCCTTT AGCCAAACTC     600
ATTGATGAAA AAAGCATTCT TAACGCTCTT ATAGGCTTAA TGGCAACAGG GGGTTCTACT     660
AACCACACTT TGCATTTGAT CGCTATCGCA GATCTTGTGG GG                        702
```

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 795 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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

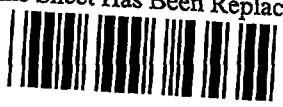
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383

```
ATGAAATTTT TAAAATTCTT TGCCAGTAGC GTAACTCTAG ATGAAAAATT TTTAATGTTC      60
CTTCTTTGCA ACGCTCTTTC TAACGCTTAC AAAAATAGCG ATTTGTTTTC TTTCTCTAAA     120
GGCTTTTTAG GCGCTTTTTT AATCGGGTTT GTGGTGTATT ATGGTTGCGC GCTAATCCCT     180
AAAAAACGCT TGAAATATTC ATTAGAATGG CTGTTTATAG GAAGCGGTAT TATTTTTAGC     240
GTGGCAGAAA TTTTTACGCT GTTTATGTTT AAAATGCCTT TTTCCAAAGG CTTGATTGAC     300
ACGCTTTTAG CCACAAACAG CTCTGAAACG ATGGCGTTTA TAAAAAGCTA TAAAAATTAT     360
TTGCTTTACT ACGCTTTGAT TTTGATCGCT TTGTTGATCG CCATTAAAAT CATTCGCTTT     420
AGAGCGCTTG TGCCTGGTGT GATAGCGAGC GTTTTAGGGC TTTCTATCCT TACAATAGGG     480
AGCGTTCGTA ACATTAAACA CCTTACAAAG AACGATGCGA TTTTAAAAAG ATCACTCTTT     540
TCTCTTTCTT TAGCTAGGGG GTTTTATTCC GCTTATTTGA GTTTGTTTGA TCGCCAACAA     600
GCCATAAAAT TTTATAGCTT TTTAAATAAT CTTTATTTAC CAAGCGATTA TCTTTCTAGC     660
ACGGGCGATA TTTCAAATGT CGTCTTAGTC ATCGCGAAAG CGCGAGCAGA AATTTCATGC     720
AACTCTATGG CTATAGCGTT CCTAATAATC CCTTATSCGA GCGAACTCGC CAACGAGAGA     780
GAGAGAGAGA GAGAG                                                      795
```

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 509 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...509

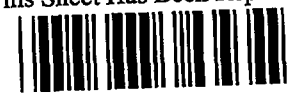
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384

```
Met Cys Ser Gln Glu Ile Leu Ser Ser Leu Gln Thr Ile Ile Ala Glu
1               5                  10                  15
Gln Phe Ser Ile Asn Ile Ile Thr Gln Leu Ala Asn Lys Leu Thr Gln
            20                  25                  30
Val Lys Asn Leu Asn Phe Phe Glu Asn Lys Asp His Thr Ile Lys Leu
        35                  40                  45
Asn Thr Ile His Asn Gly Leu His Ile Arg Pro Leu Asn Tyr Val Ser
    50                  55                  60
Asn Leu Phe Phe Asn Leu Gln Arg Ile Ile Gly Leu Ile Ser Leu Phe
65                  70                  75                  80
Gly Ile Leu Phe Ser Ile Ser Ile Tyr Leu Pro Phe Ile Met Ile Phe
                85                  90                  95
Ala Thr Val Pro Cys Ile Leu Ile Ser Asn His Ile Ala Lys Lys His
            100                 105                 110
Ser Ala Ser Ile Asp Lys Leu Gln Asp Gln Lys Glu Ser Met Gln Asn
        115                 120                 125
Tyr Leu Tyr Ser Gly Leu Asp Asn Gln Lys Asn Lys Asp Asn Leu Leu
    130                 135                 140
Phe Asn Phe Met Leu Asn Phe His His Lys Phe Ile Glu Thr Lys Glu
145                 150                 155                 160
Leu Tyr Leu Asn Asn Phe Val Lys Val Ala Gln Lys Asn Leu Ile Phe
                165                 170                 175
Thr Ile Tyr Ala Asp Val Leu Ile Thr Thr Leu Ser Ile Ala Leu Phe
            180                 185                 190
Phe Leu Met Val Phe Ile Ile Leu Ser Lys Leu Ile Gly Val Gly Ala
        195                 200                 205
Ile Ala Gly Tyr Ile Gln Ala Phe Ser Ser Thr Gln Gln Gln Leu Gln
    210                 215                 220
Asp Leu Ser Phe Tyr Gly Lys Trp Phe Phe Ala Ile Asn Lys Tyr Phe
225                 230                 235                 240
Glu Asn Tyr Phe Cys Ile Leu Asp Tyr Lys Ile Pro Lys Pro Glu Thr
                245                 250                 255
Gln Ile Lys Leu Glu Glu Lys Ile His Ser Ile Thr Phe Glu Asn Ile
            260                 265                 270
Ser Phe Ser Tyr Pro Asn Ser Lys Leu Ile Phe Glu Asn Phe Asn Leu
        275                 280                 285
Ser Leu His Ser Asn Lys Ile Tyr Ala Leu Val Gly Lys Asn Ala Ser
    290                 295                 300
Gly Lys Ser Thr Leu Ile Asn Leu Leu Leu Gly Phe Tyr Thr Pro Asn
305                 310                 315                 320
Ser Gly Gln Ile Ile Ile Asn Asn Lys Tyr Pro Leu Gln Asp Leu Glu
                325                 330                 335
Leu Asn Ser Tyr His Gln Gln Met Ser Ala Ile Phe Gln Asp Phe Ser
            340                 345                 350
Leu Tyr Ala Gly Tyr Ser Ile Asp Asp Asn Leu Phe Met Gln Asn Asn
        355                 360                 365
```

```
Ile Thr Lys Glu Gln Leu Lys Gln Lys Arg Glu Ile Leu Lys Ser Phe
    370                 375                 380
Asp Glu Asn Phe Gln Asn Cys Leu Asn Asp Cys Asn Asn Thr Leu Phe
385                 390                 395                 400
Gly Ala Gln Tyr Asn Gly Val Asp Phe Ser Leu Gly Gln Lys Gln Arg
                405                 410                 415
Ile Ala Thr Met Arg Ala Phe Leu Lys Pro Ser Asn Cys Ile Val Leu
            420                 425                 430
Asp Glu Pro Ser Ser Ala Ile Asp Pro Ile Met Glu Lys Glu Phe Leu
        435                 440                 445
Asp Phe Ile Phe Lys Lys Ser Gln Ser Lys Met Ala Leu Ile Ile Thr
    450                 455                 460
His Arg Met Asn Ser Val Lys Gln Ala Asn Glu Ile Ile Val Leu Asp
465                 470                 475                 480
Gln Gly Lys Leu Ile Glu Gln Gly Asn Phe Glu Thr Leu Met Lys Lys
                485                 490                 495
Gln Gly Leu Phe Cys Glu Leu Phe Leu Lys Gln Gln Tyr
            500                 505
```

(2) INFORMATION FOR SEQ ID NO:385:

This Sheet Has Been Replaced



(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:385

```
Met Lys Gly Pro Ile Leu Trp Pro Ala Phe Ser Gln Phe Ser Asp Gln
1               5                  10                  15
Asp Leu Ser Asp Ile Val Ala Tyr Leu Thr Ser Ile Leu Pro Lys Asn
            20                  25                  30
Leu Ser Asp Lys Glu Val Phe Ala Gln Ser Cys Gln Arg Cys His Ser
        35                  40                  45
Leu Asp Tyr Ala Lys Asp Lys Ala Phe Ser Asp Pro Lys Asp Leu Ala
    50                  55                  60
Asn Tyr Leu Gly Ser His Ala Pro Asp Leu Ser Met Met Ile Arg Ala
65                  70                  75                  80
Lys Gly Glu His Gly Leu Asn Val Phe Ile Asn Asp Pro Gln Lys Leu
                85                  90                  95
Leu Pro Gly Thr Ala Met Pro Arg Val Gly Leu Asn Glu Lys Ala Gln
            100                 105                 110
Lys Gln Val Ile Ser Tyr Leu Glu Lys Ala Gly Asp Arg Lys Lys His
        115                 120                 125
Glu Arg Asn Thr Leu Gly Ile Lys Ile Met Ile Phe Phe Ala Val Leu
    130                 135                 140
Ser Phe Leu Ala Tyr Ala Gly Lys Glu Lys Phe Gly Ala Lys Cys Ile
145                 150                 155                 160
Lys Phe Lys Lys Gly Gly Thr Trp Phe Tyr Asp Phe
                165                 170
```

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:385

```
Met Lys Gly Pro Ile Leu Trp Pro Ala Phe Ser Gln Phe Ser Asp Gln
1               5                  10                  15
Asp Leu Ser Asp Ile Val Ala Tyr Leu Thr Ser Ile Leu Pro Lys Asn
            20                  25                  30
Leu Ser Asp Lys Glu Val Phe Ala Gln Ser Cys Gln Arg Cys His Ser
        35                  40                  45
Leu Asp Tyr Ala Lys Asp Lys Ala Phe Ser Asp Pro Lys Asp Leu Ala
    50                  55                  60
Asn Tyr Leu Gly Ser His Ala Pro Asp Leu Ser Met Met Ile Arg Ala
65                  70                  75                  80
Lys Gly Glu His Gly Leu Asn Val Phe Ile Asn Asp Pro Gln Lys Leu
                85                  90                  95
Leu Pro Gly Thr Ala Met Pro Arg Val Gly Leu Asn Glu Lys Ala Gln
            100                 105                 110
Lys Gln Val Ile Ser Tyr Leu Glu Lys Ala Gly Asp Arg Lys Lys His
        115                 120                 125
Glu Arg Asn Thr Leu Gly Ile Lys Ile Met Ile Phe Phe Ala Val Leu
    130                 135                 140
Ser Phe Leu Ala Tyr Ala Gly Lys Glu Lys Phe Gly Ala Lys Cys Ile
145                 150                 155                 160
Lys Phe Lys Lys Gly Gly Thr Trp Phe Tyr Asp Phe
                165                 170
```

(2) INFORMATION FOR SEQ ID NO:386:

(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:386

```
Met Glu Arg Lys Thr Leu Gln Ser Ile Leu Cys Leu Ile Lys Lys Glu
1               5                  10                  15
```

```
Met Met Arg Pro Lys Gly Ile Leu Met Asn Cys Cys Arg Thr Trp Lys
            20                  25                  30
His Gln Val Leu Lys Gln Ser Thr Thr Gly Leu Val Val Leu Ser Ile
        35                  40                  45
Ile Ser Ser Thr Ala Pro Phe Ile Gly Leu Phe Gly Thr Val Val Glu
    50                  55                  60
Ile Leu Glu Ala Phe Asn Asn Leu Gly Ala Leu Gly Gln Ala Ser Phe
65                  70                  75                  80
Gly Val Ile Ala Pro Ile Ile Ser Lys Ala Leu Ile Ala Thr Ala Ala
                85                  90                  95
Gly Ile Leu Ala Ala Ile Pro Ala Tyr Ser Phe Tyr Leu Ile Leu Lys
            100                 105                 110
Arg Lys Val Tyr Asp Leu Ser Val Tyr Val Gln Met Gln Val Asp Ile
        115                 120                 125
Leu Ser Ser Lys Lys
    130
```

(2) INFORMATION FOR SEQ ID NO:387:

This Sheet Has Been Replaced



(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:387

```
Met His Glu Arg Ile Glu Arg Gly Ile Unk Asn Asn Glu Cys Lys Glu
1               5                   10                  15
Ile Phe Gly Asn Glu Leu Lys Gln Arg Lys Thr Lys Leu Ile Glu Asp
            20                  25                  30
Ile Glu Arg Arg Phe Lys Glu Cys Glu Glu Gln Phe Arg Gly Ser Val
        35                  40                  45
Gly Lys Asn Ile Glu Gln Leu Glu Glu Arg Val Lys Asp Ser Leu Ala
    50                  55                  60
Ile Ile Lys Arg Ile Asn Asn Leu Gly Leu Asn Pro Asn Ser Asn Phe
65                  70                  75                  80
Asn Met Asp Ser Gly Ile Asp Thr Ile Gly Leu Phe Ser Ser Ile Gly
                85                  90                  95
Gly Leu Val Leu Leu Leu Leu Thr Pro Val Val Gly Glu Phe Ala Leu
            100                 105                 110
Ile Ala Gly Val Gly Leu Ala Leu Val Gly Val Gly Lys Ser Ile Trp
        115                 120                 125
Ser Phe Phe Asp Ser Asp Tyr Lys Lys Ser Gln Gln Arg Lys Glu Val
    130                 135                 140
Asp Lys Asn Leu His Gln Ile Cys Glu Lys Leu Cys Arg Met
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388

```
Met Pro Gly Val Tyr Gln Met Ser Ile Glu Pro Leu Leu Lys Glu Cys
1               5                  10                  15
Glu Glu Leu Val Gly Leu Gly Ile Lys Ala Val Leu Leu Phe Gly Ile
            20                  25                  30
Pro Lys His Lys Asp Ala Thr Gly Ser His Ala Leu Asn Lys Asp His
        35                  40                  45
Ile Val Ala Lys Ala Thr Arg Glu Ile Lys Lys Arg Phe Lys Asp Leu
    50                  55                  60
Ile Val Ile Ala Asp Leu Cys Phe Cys Glu Tyr Thr Asp His Gly His
65                  70                  75                  80
Cys Gly Ile Leu Glu Asn Ala Ser Val Ser Asn Asp Lys Thr Leu Lys
                85                  90                  95
Ile Leu Asn Leu Gln Gly Leu Ile Leu Leu Lys Ala Val Trp Ile Phe
            100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:389:

(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:389

```
Val Glu Asn Asn Lys Ser Leu Lys His Ala Asn Glu Leu Arg Asp Lys
1               5                  10                  15
Arg Asp Glu Leu Glu Phe His Leu Arg Glu Leu Phe Gly Gly Asn Val
            20                  25                  30
Phe Lys Ser Ser Ile Lys Thr His Ser Leu Thr Asp Lys Asp Ser Ala
        35                  40                  45
Asp Phe Asp Glu Ser Tyr Asn Leu Asn Ile Gly His Gly Unk Asn Unk
    50                  55                  60
Ile
65
```

(2) INFORMATION FOR SEQ ID NO:390:

This Sheet Has Been Replaced



(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:390

```
Met Gln Glu Phe Ser Leu Trp Cys Asp Phe Ile Glu Arg Asp Phe Leu
1               5                  10                  15
Glu Asn Asp Phe Leu Lys Leu Ile Asn Lys Gly Ala Ile Cys Gly Unk
            20                  25                  30
Thr Ser Asn Pro Ser Leu Phe Cys Glu Ala Ile Thr Lys Ser Ala Phe
        35                  40                  45
Tyr Gln Asp Glu Ile Ala Lys Unk Gln Arg Gln Lys Ser
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:390:

(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:390

```
Met Gln Glu Phe Ser Leu Trp Cys Asp Phe Ile Glu Arg Asp Phe Leu
1               5                  10                  15
Glu Asn Asp Phe Leu Lys Leu Ile Asn Lys Gly Ala Ile Cys Gly Unk
            20                  25                  30
Thr Ser Asn Pro Ser Leu Phe Cys Glu Ala Ile Thr Lys Ser Ala Phe
        35                  40                  45
Tyr Gln Asp Glu Ile Ala Lys Unk Gln Arg Gln Lys Ser
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 619 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391

```
Val Phe Val Ala Ser Lys Gln Ala Asp Glu Gln Lys Lys Leu Val Ile
1               5                  10                  15
Glu Gln Glu Val Gln Lys Arg Gln Phe Gln Lys Ile Glu Glu Leu Lys
            20                  25                  30
Ala Asp Met Gln Lys Gly Val Asn Pro Phe Phe Lys Val Leu Phe Asp
        35                  40                  45
Gly Gly Asn Arg Leu Phe Gly Phe Pro Glu Thr Phe Ile Tyr Ser Ser
    50                  55                  60
Ile Phe Ile Leu Phe Val Thr Ile Val Leu Ser Val Ile Leu Phe Gln
65                  70                  75                  80
Ala Tyr Glu Pro Val Leu Ile Val Ala Ile Val Ile Val Leu Val Ala
                85                  90                  95
Leu Gly Phe Lys Lys Asp Tyr Arg Leu Tyr Gln Arg Met Glu Arg Ala
            100                 105                 110
Met Lys Phe Lys Lys Pro Phe Leu Phe Lys Gly Val Lys Asn Lys Ala
        115                 120                 125
Phe Met Ser Ile Phe Ser Met Lys Pro Ser Lys Glu Met Ala Asn Asp
    130                 135                 140
Ile His Leu Asn Pro Asn Arg Glu Asp Arg Leu Val Ser Ala Ala Asn
145                 150                 155                 160
Ser Tyr Leu Ala Asn Asn Tyr Glu Cys Phe Leu Asp Asp Gly Val Ile
                165                 170                 175
Leu Thr Asn Asn Tyr Ser Leu Leu Gly Thr Ile Lys Leu Gly Gly Ile
            180                 185                 190
Asp Phe Leu Thr Thr Ser Lys Lys Asp Leu Ile Glu Leu His Ala Ser
        195                 200                 205
Ile Tyr Ser Val Phe Arg Asn Phe Val Thr Pro Glu Phe Lys Phe Tyr
    210                 215                 220
Phe His Thr Val Lys Lys Lys Ile Val Ile Asp Glu Thr Asn Arg Asp
225                 230                 235                 240
Tyr Gly Leu Ile Phe Ser Asn Asp Phe Met Arg Ala Tyr Asn Glu Lys
                245                 250                 255
Gln Lys Arg Glu Ser Phe Tyr Asp Ile Ser Phe Tyr Leu Thr Ile Glu
            260                 265                 270
Gln Asp Leu Leu Asp Thr Leu Asn Glu Pro Val Met Asn Lys Lys His
        275                 280                 285
Phe Ala Asp Asn Asn Phe Glu Glu Phe Gln Arg Ile Ile Arg Ala Lys
    290                 295                 300
Leu Glu Asn Phe Lys Asp Arg Ile Glu Leu Ile Glu Glu Leu Leu Ser
305                 310                 315                 320
Lys Tyr His Pro Thr Arg Leu Lys Glu Tyr Thr Lys Asp Gly Ile Ile
                325                 330                 335
Tyr Ser Lys Gln Cys Glu Phe Tyr Asn Phe Leu Val Gly Met Asn Glu
            340                 345                 350
Ala Pro Phe Ile Cys Asn Arg Lys Asp Leu Tyr Leu Lys Glu Lys Met
        355                 360                 365
His Gly Gly Val Lys Glu Val Tyr Phe Ala Asn Lys His Gly Lys Ile
    370                 375                 380
Leu Asn Asp Asp Leu Ser Glu Lys Tyr Phe Ser Ala Ile Glu Ile Ser
385                 390                 395                 400
Glu Tyr Ala Pro Lys Ser Gln Ser Asp Leu Phe Asp Lys Ile Asn Ala
                405                 410                 415
```

```
Leu Asp Ser Glu Phe Ile Phe Met His Ala Tyr Ser Pro Lys Asn Ser
            420                 425                 430
Gln Val Leu Lys Asp Lys Leu Ala Phe Thr Ser Arg Arg Ile Ile Ile
        435                 440                 445
Ser Gly Gly Ser Lys Glu Gln Gly Met Thr Leu Gly Cys Leu Ser Glu
    450                 455                 460
Leu Val Gly Asn Gly Asp Ile Thr Leu Gly Ser Tyr Gly Asn Ser Leu
465                 470                 475                 480
Val Leu Phe Ala Asp Ser Phe Glu Lys Met Lys Gln Ser Val Lys Glu
                485                 490                 495
Cys Val Ser Ser Leu Asn Ala Lys Gly Phe Leu Ala Asn Ala Ala Thr
            500                 505                 510
Phe Ser Met Glu Asn Tyr Phe Phe Ala Lys His Cys Ser Phe Ile Thr
        515                 520                 525
Leu Pro Phe Ile Phe Asp Val Thr Ser Asn Asn Phe Ala Asp Phe Ile
    530                 535                 540
Ala Met Arg Ala Met Ser Phe Asp Gly Lys Glu Asp Asn Asn Ala Trp
545                 550                 555                 560
Gly Asn Ser Val Met Thr Leu Lys Ser Glu Ile Asn Ser Pro Phe Tyr
                565                 570                 575
Leu Asn Phe His Met Pro Thr Asp Phe Gly Ser Ala Ser Ala Gly His
            580                 585                 590
Thr Leu Ile Leu Gly Ser Thr Gly Ser Gly Lys Asn Ser Val Tyr Val
        595                 600                 605
His Asp Ser Lys Arg Tyr Gly Ala Ile Cys Leu
    610                 615
```

(2) INFORMATION FOR SEQ ID NO:392:

This Sheet Has Been Replaced



(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:392

```
Val Lys Thr Ser Cys Leu Val Thr Ile Gly Arg Ile Arg Gly Val Phe
1               5                   10                  15
Ile Ile Lys Ala Gln Leu Leu Leu Arg Glu Gly Gly Phe Met Asn Phe
            20                  25                  30
Thr Ala Tyr Asn Thr Lys Thr Pro Gly His Leu His Leu Tyr Val His
        35                  40                  45
Lys Gly His Thr Glu Leu Gly Glu Gly Glu Arg Leu Ile Lys Thr Leu
    50                  55                  60
Ser Met Lys Leu Ala Gln Gly Leu Pro Lys Glu Trp Arg Val Phe Pro
65                  70                  75                  80
Ser Asn Glu Trp Pro Lys Glu Phe Asn Ile Leu Ala Leu Pro Tyr Glu
                85                  90                  95
Val Phe Ala Lys Glu Arg Gly Ser Ser Trp Ala Lys His Leu
            100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:393:

(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:393

```
Val Ala Lys Asp Ile Ile Ser Glu Ser Gln Asn Leu Cys Ala Arg Lys
1               5                  10                  15
Phe Arg Arg Leu Tyr Ala Leu Leu Lys Glu Asn Glu Met Leu Ile Arg
            20                  25                  30
Ile Gly Ser Tyr Gln Met Gly Asn Asp Lys Glu Leu Asp Glu Ala Ile
        35                  40                  45
Lys Lys Lys Ala Leu Met Glu Gln Phe Leu Val Gln Asp Glu Asn Ala
    50                  55                  60
Leu Unk Ala Phe
65
```

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 446 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394

```
Met Lys Ser Arg Pro Ile Leu Ala Gln Ala Tyr Ala Leu Gln Met Met
1               5                  10                  15
Val Lys Gln Ile Ala Phe Leu Glu Thr Ile Leu Val Glu Asn Glu Gln
            20                  25                  30
Asp Ala Leu Ile Leu Glu Asn Ser Leu Ile Lys Gln Leu Lys Pro Lys
        35                  40                  45
Tyr Asn Ile Leu Leu Arg Asp Asp Lys Thr Tyr Pro Tyr Ile Tyr Met
    50                  55                  60
Asp Phe Ser Ile Asp Phe Pro Ile Pro Leu Ile Thr Arg Lys Ile Leu
65                  70                  75                  80
Lys Gln Pro Gly Val Lys Tyr Phe Gly Pro Phe Thr Ser Gly Ala Lys
                85                  90                  95
Asp Ile Leu Asp Ser Leu Tyr Glu Leu Leu Pro Leu Val Gln Lys Lys
            100                 105                 110
```

```
Asn Cys Ile Lys Asp Lys Lys Ala Cys Met Phe Tyr Gln Ile Glu Arg
        115                 120                 125
Cys Lys Ala Pro Cys Glu Asp Lys Ile Thr Lys Glu Glu Tyr Leu Lys
    130                 135                 140
Ile Ala Lys Glu Cys Leu Glu Met Ile Glu Asn Lys Asp Arg Leu Ile
145                 150                 155                 160
Lys Glu Leu Glu Leu Lys Met Glu Arg Leu Ser Ser Asn Leu Arg Phe
                165                 170                 175
Glu Glu Ala Leu Ile Tyr Arg Asp Arg Ile Ala Lys Ile Gln Lys Ile
            180                 185                 190
Ala Pro Phe Thr Cys Met Asp Leu Ala Lys Leu Tyr Asp Leu Asp Ile
        195                 200                 205
Phe Ala Phe Tyr Gly Gly Asn Asn Lys Ala Val Leu Val Lys Met Phe
    210                 215                 220
Met Arg Gly Gly Lys Ile Ile Ser Ser Ala Phe Glu Lys Ile His Ser
225                 230                 235                 240
Leu Asn Gly Phe Asp Thr Asp Glu Ala Met Lys Gln Ala Ile Ile Asn
                245                 250                 255
His Tyr Gln Ser His Leu Pro Leu Met Pro Glu Gln Ile Leu Leu Ser
            260                 265                 270
Ala Cys Ser Asn Glu Thr Leu Lys Glu Leu Gln Glu Phe Ile Ser His
        275                 280                 285
Gln Tyr Ser Lys Lys Ile Ala Leu Ser Ile Pro Lys Lys Gly Asp Lys
    290                 295                 300
Leu Ala Leu Ile Glu Ile Ala Met Lys Asn Ala Gln Glu Ile Phe Ser
305                 310                 315                 320
Gln Glu Lys Thr Ser Asn Glu Asp Arg Ile Leu Glu Glu Ala Arg Ser
                325                 330                 335
Leu Phe Asn Leu Glu Cys Val Pro Tyr Arg Val Glu Ile Phe Asp Thr
            340                 345                 350
Ser His His Ser Asn Ser Gln Cys Val Gly Gly Met Val Val Tyr Glu
        355                 360                 365
Asn Asn Ala Phe Gln Lys Asp Ser Tyr Arg Arg Tyr His Leu Lys Gly
    370                 375                 380
Ser Asn Glu Tyr Asp Gln Met Ser Glu Leu Leu Thr Arg Arg Ala Leu
385                 390                 395                 400
Asp Phe Ala Lys Glu Pro Pro Pro Asn Leu Trp Val Ile Asp Gly Gly
                405                 410                 415
Arg Ala Gln Leu Asn Ile Ala Leu Glu Ile Leu Lys Ser Ser Gly Ser
            420                 425                 430
Phe Val Glu Val Ile Ala Ile Ser Lys Glu Lys Arg Gly Phe
        435                 440                 445
```

(2) INFORMATION FOR SEQ ID NO:395:

(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:395

Val Ser Leu Gly Ala Phe Gln Gly Tyr Tyr Gly Gly Leu Val Asp Leu

This Sheet Has Been Replaced



```
1               5                   10                  15
Val Gly Gln Arg Leu Ser Glu Ile Trp Ser Ala Ile Pro Met Leu Phe
            20                  25                  30
Leu Leu Ile Val Ile Ser Ser Ala Phe Asn Ser Asn Phe Trp Ile Ile
        35                  40                  45
Leu Phe Leu Val Leu Leu Phe Ser Trp Met Gly Leu Ser Gln Val Val
    50                  55                  60
Arg Thr Glu Phe Leu Lys Ala Arg Asn Met Asp Tyr Thr Lys Ala Ala
65                  70                  75                  80
Arg Ala Leu Gly
```

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396

```
Met Ser Glu Ala Tyr Phe Leu His His Lys Asn Ala Ser Gln Val Ser
1               5                   10                  15
Leu Asn Glu Gln Val Leu Asn Val Met Lys Gln Val Gln Leu Asp Glu
            20                  25                  30
Asn Phe Trp Asn Val Ser Leu Met
        35                  40
```

(2) INFORMATION FOR SEQ ID NO:397:

(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:397

```
Val Ile Leu Ile Phe Ile Ile Val Val Glu Asp Gln Lys Gly Ile Phe
1               5                   10                  15
Pro Ile Ala Ala Ser Lys Arg Lys Ser Gln Ser Ser Val Ile Ile Glu
            20                  25                  30
```

This Sheet Has Been Replaced



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

(2) INFORMATION FOR SEQ ID NO:398:

(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:398

```
Met Lys Glu Lys Asn Phe Trp Pro Leu Gly Ile Met Ser Val Leu Ile
1               5                   10                  15
Phe Gly Leu Gly Ile Val Val Phe Leu Val Val Phe Ala Leu Lys Asn
            20                  25                  30
Ser Pro Lys Asn Asp Leu Val Tyr Phe Lys Gly His Asn Glu Val Asp
        35                  40                  45
Leu Asn Phe Asn Ala Met Leu Lys Thr Tyr Glu Asn Phe Lys Ser Asn
    50                  55                  60
Tyr Arg Phe Ser Val Gly Leu Lys Pro Leu Thr Glu Ser Pro Lys Thr
```

This Sheet Has Been Replaced



```
65                  70                  75                  80
Pro Ile Leu Pro Tyr Phe Ser Lys Gly Thr His Gly Asp Lys Lys Ile
                85                  90                  95
Gln Glu Asn Leu Leu Asn Asn Ala Leu Ile Leu Glu Lys Ser Asn Thr
            100                 105                 110
Leu Tyr Ala Gln Leu Gln Pro Leu Lys Pro Ala Leu Asp Ser Pro Asn
        115                 120                 125
Ile Gln Val Tyr Leu Ala Phe Tyr Pro Ser Gln Ser Gln Pro Arg Leu
    130                 135                 140
Leu Gly Thr Leu Asp Cys Lys Asn Ala Cys Glu Pro Leu Lys Phe Asp
145                 150                 155                 160
Leu Leu Glu Gly Asp Lys Val Gly Arg Tyr Lys Ile Leu Phe Lys Phe
                165                 170                 175
Val Phe Lys Asn Lys Glu Glu Leu Ile Leu Glu Gln Leu Leu Phe Leu
            180                 185                 190
Ser Ser Met Ala Cys Met Gly Ile Ser Ile Leu Lys Asn Ala Lys Ala
        195                 200                 205
Phe Phe Lys Tyr Lys Ile
    210
```

(2) INFORMATION FOR SEQ ID NO:399:

(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:399

```
Met Pro Ile Lys Gly Ser Phe Leu Ala Arg Asn Arg Leu Val Ile Ala
1               5                   10                  15
Leu Thr Asp Ala Val Ile Ile Pro Gln Ala Asp Leu Lys Ser Gly Ser
            20                  25                  30
Met Ser Ser Ala Arg Leu Ala Gln Lys Tyr Gln Lys Pro Leu Phe Val
        35                  40                  45
Leu Pro Gln Arg Leu Asn Glu Ser Asp Gly Thr Asn Glu Leu Leu Glu
    50                  55                  60
Lys Gly Gln Ala Gln Gly Ile Phe Asn Ile Gln Asn Phe Ile Asn Thr
65                  70                  75                  80
Leu Leu Lys Asp Tyr His Leu Lys Glu Met Pro Glu Met Lys Asp Glu
                85                  90                  95
Phe Leu Glu Tyr Cys Ala Lys Asn Pro Ser Tyr Glu Glu Ala Tyr Leu
            100                 105                 110
Lys Phe Gly Asp Lys Leu Leu Glu Tyr Glu Leu Leu Gly Lys Ile Lys
        115                 120                 125
Arg Ile Asn His Leu Val Val Leu Ala
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 272 amino acids

This Sheet Has Been Replaced



(B) TYPE: amino acid
(D) TOPOLOGY: linear

(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:400

```
Met Val Val Glu Leu Lys Asn Ile Glu Lys Ile Tyr Glu Asn Gly Phe
1               5                  10                  15
His Ala Leu Lys Gly Val Asn Leu Glu Leu Lys Lys Gly Asp Ile Leu
            20                  25                  30
Gly Val Ile Gly Tyr Ser Gly Ala Gly Lys Ser Thr Leu Ile Arg Leu
        35                  40                  45
Ile Asn Cys Leu Glu Arg Pro Ser Ser Gly Glu Val Leu Val Asn Gly
    50                  55                  60
Val Asn Leu Leu Asn Leu Lys Pro Lys Glu Leu Gln Lys Ala Arg Gln
65                  70                  75                  80
Lys Ile Gly Met Ile Phe Gln His Phe Asn Leu Leu Ser Ala Lys Asn
                85                  90                  95
Val Phe Glu Asn Val Ala Phe Ala Leu Glu Ile Ala Arg Trp Glu Lys
            100                 105                 110
Thr Lys Ile Lys Ser Arg Val His Glu Leu Leu Glu Leu Val Gly Leu
        115                 120                 125
Glu Asp Lys Val His Phe Tyr Pro Lys Gln Leu Ser Gly Gly Gln Lys
    130                 135                 140
Gln Arg Val Ala Ile Ala Arg Ser Leu Ala Asn Cys Pro Asn Leu Leu
145                 150                 155                 160
Leu Cys Asp Glu Ala Thr Ser Ala Leu Asp Ser Lys Thr Thr His Ser
                165                 170                 175
Ile Leu Thr Leu Leu Ser Gly Ile Gln Lys Lys Phe Asp Leu Ser Ile
            180                 185                 190
Val Phe Ile Thr His Gln Ile Glu Val Val Lys Glu Leu Cys Asn Gln
        195                 200                 205
Met Cys Val Ile Ser Ser Gly Glu Ile Val Glu Arg Gly Ser Val Glu
    210                 215                 220
Glu Ile Phe Ala Asn Pro Lys His Ala Val Thr Lys Glu Leu Leu Gly
225                 230                 235                 240
Ile Lys Asn Glu His Ala Asp Gln Lys Ser Gln Asp Ile Tyr Arg Ile
                245                 250                 255
Val Phe Leu Gly Glu His Leu Asp Glu Pro Ile Ile Ser Unk Phe Unk
            260                 265                 270
```

(2) INFORMATION FOR SEQ ID NO:401:

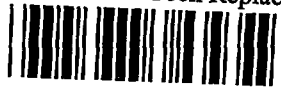
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401

```
Leu Unk Pro Met Lys Val Ile Gln Val Phe Leu Phe Ser Asn Pro Phe
1               5                  10                  15
Cys Ala Ile Val Pro Asn Thr Glu Pro Glu His Leu Glu His Tyr Asp
            20                  25                  30
His Asp Leu Glu Arg Phe Phe Phe Ala Tyr Lys Tyr Phe Leu Asp His
        35                  40                  45
Ala Gln Lys Arg Val Ile Tyr Lys Glu Asp Pro Phe Leu Lys Asn Tyr
    50                  55                  60
Ser Lys Asp Ala Ile Val Leu Glu Lys Lys Asp Ile Tyr Asn Ile Gln
65                  70                  75                  80
Tyr Ile Leu Lys Asp Gly Glu Pro Tyr Thr Ser Phe Glu Leu Lys Asn
                85                  90                  95
Leu Gly Ala Phe Leu Val Trp Gly Leu Gly Glu His Asn Ala Thr Asn
            100                 105                 110
Ala Ser Leu Ala Ile Leu Ser Ala Leu Asp Glu Leu Asn Leu Glu Glu
        115                 120                 125
Ile Arg Asn Asn Unk Leu Asn Phe Lys Gly Ile Lys Lys Arg Phe Asp
    130                 135                 140
Ile Leu Gln Lys Asn Asn Leu Ile Leu Ile Asp Asp Tyr Ala His His
145                 150                 155                 160
Pro Thr Glu Ile Gly Unk Thr Leu Lys Ser Ala Arg Ile Tyr Ala Asn
                165                 170                 175
Leu Leu Asn Thr Gln Glu Lys Ile Ile Val Ile Trp Gln Ala His Lys
            180                 185                 190
Tyr Ser Arg Leu Met Asp Asn Leu Glu Glu Phe Lys Lys Cys Phe Leu
        195                 200                 205
Glu His Cys Asp Arg Leu Ile Ile Leu Pro Val Tyr Ser Ala Ser Glu
    210                 215                 220
Val Lys Arg Asp Ile Asp Leu Lys Ala His Phe Lys His Tyr Asn Pro
225                 230                 235                 240
Thr Phe Ile Asp Arg Val Arg Lys Lys Gly Asp Phe Leu Glu Leu Leu
                245                 250                 255
Val Asn Asp Asn Val Val Glu Thr Ile Glu Lys Gly Phe Val Ile Gly
            260                 265                 270
Phe Gly Ala Gly Asp Ile Thr Tyr Gln Leu Arg Gly Glu Met
        275                 280                 285
```

(2) INFORMATION FOR SEQ ID NO:401:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401

```
Leu Unk Pro Met Lys Val Ile Gln Val Phe Leu Phe Ser Asn Pro Phe
1               5                  10                  15
Cys Ala Ile Val Pro Asn Thr Glu Pro Glu His Leu Glu His Tyr Asp
            20                  25                  30
His Asp Leu Glu Arg Phe Phe Phe Ala Tyr Lys Tyr Phe Leu Asp His
        35                  40                  45
Ala Gln Lys Arg Val Ile Tyr Lys Glu Asp Pro Phe Leu Lys Asn Tyr
    50                  55                  60
Ser Lys Asp Ala Ile Val Leu Glu Lys Lys Asp Ile Tyr Asn Ile Gln
65                  70                  75                  80
Tyr Ile Leu Lys Asp Gly Glu Pro Tyr Thr Ser Phe Glu Leu Lys Asn
                85                  90                  95
Leu Gly Ala Phe Leu Val Trp Gly Leu Gly Glu His Asn Ala Thr Asn
            100                 105                 110
Ala Ser Leu Ala Ile Leu Ser Ala Leu Asp Glu Leu Asn Leu Glu Glu
        115                 120                 125
Ile Arg Asn Asn Unk Leu Asn Phe Lys Gly Ile Lys Lys Arg Phe Asp
    130                 135                 140
Ile Leu Gln Lys Asn Asn Leu Ile Leu Ile Asp Asp Tyr Ala His His
145                 150                 155                 160
Pro Thr Glu Ile Gly Unk Thr Leu Lys Ser Ala Arg Ile Tyr Ala Asn
                165                 170                 175
Leu Leu Asn Thr Gln Glu Lys Ile Ile Val Ile Trp Gln Ala His Lys
            180                 185                 190
Tyr Ser Arg Leu Met Asp Asn Leu Glu Glu Phe Lys Lys Cys Phe Leu
        195                 200                 205
Glu His Cys Asp Arg Leu Ile Ile Leu Pro Val Tyr Ser Ala Ser Glu
    210                 215                 220
Val Lys Arg Asp Ile Asp Leu Lys Ala His Phe Lys His Tyr Asn Pro
225                 230                 235                 240
Thr Phe Ile Asp Arg Val Arg Lys Lys Gly Asp Phe Leu Glu Leu Leu
                245                 250                 255
Val Asn Asp Asn Val Val Glu Thr Ile Glu Lys Gly Phe Val Ile Gly
            260                 265                 270
Phe Gly Ala Gly Asp Ile Thr Tyr Gln Leu Arg Gly Glu Met
        275                 280                 285
```

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402

```
Met Gly Ala Leu Ile Ala Met Phe Phe Leu Met Leu Ile Lys Lys Thr
1               5                  10                  15
Ile Ala Tyr Lys Glu Asp Lys Lys Ser Ala Ala Leu Lys Val Val Pro
            20                  25                  30
Tyr Leu Val Ala Leu Met Ser Leu Ala Phe Ser Trp Tyr Leu Ile Val
        35                  40                  45
Lys Val Leu Lys Arg Leu Tyr Ala Val Ser Phe Glu Ile Gln Leu Ala
```

This Sheet Has Been Replaced



```
    50                  55                  60
Cys Gly Cys Val Leu Ala Leu Leu Ile Phe Ile Leu Phe Lys Arg Phe
65                  70                  75                  80
Val Leu Lys Lys Ala Pro Gln Leu Glu Asn Ser His Glu Ser Val Asn
                85                  90                  95
Glu Leu Phe Asn Val Pro Leu Ile Phe Ala
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:403:

(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:403

```
Met Ile Lys Arg Ile Ala Cys Ile Leu Ser Leu Ser Ala Ser Leu Ala
1               5                   10                  15
Leu Ala Gly Glu Val Asn Gly Phe Phe Met Gly Ala Gly Tyr Gln Gln
            20                  25                  30
Gly Arg Tyr Gly Pro Tyr Asn Ser Asn Tyr Ser Asp Trp Arg His Gly
        35                  40                  45
Asn Asp Leu Tyr Gly Leu Asn Phe Lys Leu Gly Phe Val Gly Phe Ala
    50                  55                  60
Asn Lys Trp Phe Gly Ala Arg Val Tyr Gly Phe Leu Asp Trp Phe Asn
65                  70                  75                  80
Thr Ser Gly Thr Glu His Thr Lys Thr Asn Leu Leu Thr Tyr Gly Gly
                85                  90                  95
Gly Gly Asp Leu Ile Val Asn Leu Ile Pro Leu Asp Lys Phe Ala Leu
            100                 105                 110
Gly Leu Ile Gly Gly Val Gln Leu Ala Gly Asn Thr Trp Met Phe Pro
        115                 120                 125
Tyr Asp Val Asn Gln Thr Arg Phe Gln Phe Leu Trp Asn Leu Gly Gly
    130                 135                 140
Arg Met Arg Val Gly Asp Thr Val Arg Leu Lys Arg Ala
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:404:

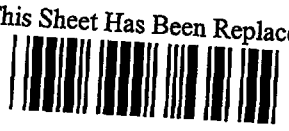
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 278 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404

```
Met Tyr Arg His Val Leu Lys Asp Phe Ser Leu Asp Phe Ser Lys Glu
1               5                  10                  15
Ser Val Gln Glu Leu Phe Asn Gln Leu Ala Lys Asp Thr Phe Leu Leu
            20                  25                  30
Leu Leu Pro Val Leu Ile Ile Leu Met Val Val Ala Phe Leu Ser Asn
        35                  40                  45
Val Leu Gln Phe Gly Trp Leu Phe Ala Pro Lys Val Ile Glu Pro Lys
    50                  55                  60
Phe Ser Lys Ile Asn Pro Ile Asn Gly Val Lys Asn Leu Phe Ser Leu
65                  70                  75                  80
Lys Lys Ile Leu Asp Gly Ser Leu Ile Thr Leu Lys Val Phe Leu Ala
                85                  90                  95
Phe Phe Leu Gly Phe Phe Ile Phe Ser Leu Phe Leu Gly Glu Leu Asn
            100                 105                 110
His Ala Ala Leu Leu Asn Leu Gln Gly Gln Leu Leu Trp Phe Lys Ser
        115                 120                 125
Lys Ala Leu Trp Leu Ile Ser Ser Leu Leu Phe Leu Phe Phe Val Leu
    130                 135                 140
Ala Phe Val Asp Leu Ile Ile Lys Arg Arg Gln Tyr Thr Asn Ser Leu
145                 150                 155                 160
Lys Met Thr Lys Gln Glu Val Lys Asp Glu Tyr Lys Gln Gln Glu Gly
                165                 170                 175
Asn Pro Glu Ile Lys Ala Lys Ile Arg Gln Met Met Val Lys Asn Ala
            180                 185                 190
Thr Asn Lys Met Met Gln Glu Ile Pro Lys Ser Asn Val Val Val Thr
        195                 200                 205
Asn Pro Thr His Tyr Ala Val Ala Leu Lys Phe Asp Glu Glu His Pro
    210                 215                 220
Val Pro Val Val Val Ala Lys Gly Thr Asp Tyr Leu Ala Ile Arg Ile
225                 230                 235                 240
Lys Gly Ile Ala Arg Glu His Asp Ile Glu Ile Ile Glu Asn Lys Thr
                245                 250                 255
Leu Ala Arg Glu Leu Tyr Arg Asp Val Lys Leu Asn Ala Thr Ile Pro
            260                 265                 270
Glu Glu Leu Phe Glu Arg
        275
```

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:405

```
Met Asn Thr Unk Pro Leu Ile Ala Thr Leu Leu Gln Ala Pro Leu His
```

```
1               5                   10                  15
Val Leu Gly Ile Arg Glu Pro Val Ser Phe Gln Pro Phe Tyr Pro Lys
            20                  25                  30
Thr Glu Lys Pro Asn Arg Pro Gln Lys Phe Ala His Val Ser Ser Met
        35                  40                  45
Pro Ser Leu Glu Phe Leu Glu Lys Leu Val Ile Arg Tyr Leu Leu Glu
    50                  55                  60
Asp Arg Ser Leu Leu Asp Leu Ala Val Gly Tyr Ile His Ser Gly Val
65                  70                  75                  80
Phe Leu His Lys Lys Gln Glu Phe Asp Ala Leu Cys Gln Glu Lys Leu
                85                  90                  95
Asp Asp Pro Lys Leu Val Ala Leu Leu Leu Asp Ala Asn Leu Pro Leu
            100                 105                 110
Lys Lys Gly Gly Phe Glu Lys Glu
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406

```
Met Gly Gln Ala Phe Phe Lys Lys Ile Val Gly Cys Phe Cys Leu Gly
1               5                   10                  15
Tyr Leu Phe Leu Ser Ser Ala Ile Glu Ala Val Ala Leu Asp Ile Lys
            20                  25                  30
Asn Phe Asn Arg Gly Arg Val Lys Val Val Asn Lys Lys Ile Ala Tyr
        35                  40                  45
Leu Gly Asp Glu Lys Pro Ile Thr Ile Trp Thr Ser Leu Asp Asn Val
    50                  55                  60
Thr Val Ile Gln Leu Glu Lys Asp Glu Thr Ile Ser Tyr Ile Thr Thr
65                  70                  75                  80
Gly Phe Asn Lys Gly Trp Ser Ile Val Pro Asn Ser Asn His Ile Phe
                85                  90                  95
Ile Gln Pro Lys Ser Val Lys Ser Asn Leu Met Phe Glu Lys Glu Ala
            100                 105                 110
Val Asn Phe Ala Leu Met Thr Arg Asp Tyr Gln Glu Phe Leu Lys Thr
        115                 120                 125
Lys Lys Leu Ile Val Asp Ala Pro Asp Pro Lys Glu Leu Glu Glu Gln
    130                 135                 140
Lys Lys Ala Leu Glu Lys Glu Lys Glu Ala Lys Glu Gln Ala Gln Lys
145                 150                 155                 160
Ala Gln Lys Asp Lys Arg Glu Lys Arg Lys Glu Glu Arg Ala Lys Asn
                165                 170                 175
Arg Ala Asn Leu Glu Asn Leu Thr Asn Ala Met Ser Asn Pro Gln Asn
            180                 185                 190
Leu Ser Asn Asn Lys Asn Leu Ser Glu Leu Ile Lys Gln Gln Arg Glu
        195                 200                 205
Asn Glu Leu Asp Gln Met Glu Arg Thr Arg Gly His Ala Arg Ala Gly
    210                 215                 220
```

Ser Ser
225

(2) INFORMATION FOR SEQ ID NO:407:

(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:407

```
Leu Leu Leu Phe Phe Leu Leu Lys Gly Val Val Phe Ser Leu Gly Phe
1               5                  10                  15
Phe Ser Phe Phe Glu Glu Val Ser Gly Ser Phe Unk Ala Val Ser Leu
            20                  25                  30
Unk Val Leu Ala Leu Val Met Gly Ser Ser Unk Gly Leu Glu Glu Phe
        35                  40                  45
Cys Val Leu Glu Glu Leu Ile Asn Ser Gly Leu Ser Val
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

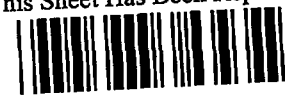
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407

```
Leu Leu Leu Phe Phe Leu Leu Lys Gly Val Val Phe Ser Leu Gly Phe
1               5                  10                  15
Phe Ser Phe Phe Glu Glu Val Ser Gly Ser Phe Unk Ala Val Ser Leu
            20                  25                  30
Unk Val Leu Ala Leu Val Met Gly Ser Ser Unk Gly Leu Glu Glu Phe
        35                  40                  45
Cys Val Leu Glu Glu Leu Ile Asn Ser Gly Leu Ser Val
    50                  55                  60
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...50

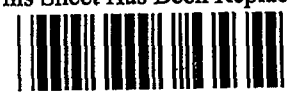
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408

```
Met Asn Thr Glu Ile Leu Thr Ile Met Leu Val Val Ser Val Leu Met
1               5                  10                  15
Gly Leu Val Gly Leu Ile Ala Phe Leu Trp Gly Val Lys Ser Gly Gln
            20                  25                  30
Phe Asp Asp Glu Lys Arg Met Leu Glu Ser Val Leu Tyr Asp Ala Arg
        35                  40                  45
Ala Thr
    50
```

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:409

```
Met Gly Phe Leu Lys Val Leu Lys His Asp Ala Leu Gly Gln Val Gly
1               5                  10                  15
Asn Ile Val Ile Gly Asn Phe Leu Ile Thr Leu Thr Val Leu Ala Val
            20                  25                  30
Cys Phe Ser Ser Gln Ser Ala Glu Glu Thr Thr Met Leu Thr Leu Ser
        35                  40                  45
Tyr Thr Leu Phe Phe Ile Leu Gly Ala Phe Leu Leu Val Ala Ile Ser
    50                  55                  60
Val Gly Ala Ile Lys Asn Leu Asn Ala Leu Phe Ser Lys Arg Gly Val
65                  70                  75                  80
Leu Ser Phe Ser Leu Pro Ile Ser Leu Glu Ser Leu Leu Leu Pro Lys
                85                  90                  95
Ile Leu Leu Pro Unk Val Phe Phe Tyr Leu Gln Phe Val Leu Val Cys
            100                 105                 110
Gly Glu Arg Ala Phe Gly Leu Leu Pro Phe
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:409:

(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:409

```
Met Gly Phe Leu Lys Val Leu Lys His Asp Ala Leu Gly Gln Val Gly
1               5                  10                  15
Asn Ile Val Ile Gly Asn Phe Leu Ile Thr Leu Thr Val Leu Ala Val
            20                  25                  30
Cys Phe Ser Ser Gln Ser Ala Glu Glu Thr Thr Met Leu Thr Leu Ser
        35                  40                  45
Tyr Thr Leu Phe Phe Ile Leu Gly Ala Phe Leu Leu Val Ala Ile Ser
    50                  55                  60
Val Gly Ala Ile Lys Asn Leu Asn Ala Leu Phe Ser Lys Arg Gly Val
65                  70                  75                  80
Leu Ser Phe Ser Leu Pro Ile Ser Leu Glu Ser Leu Leu Leu Pro Lys
                85                  90                  95
Ile Leu Leu Pro Unk Val Phe Phe Tyr Leu Gln Phe Val Leu Val Cys
            100                 105                 110
Gly Glu Arg Ala Phe Gly Leu Leu Pro Phe
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:410

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

```
        35                  40                  45
Ser Asp Glu Gly Leu Glu Lys Leu Lys Lys Unk Gly Unk Asp Met Val
    50                  55                  60
Unk Unk Pro Thr Lys Leu Met Ala Gln Arg Val Ser Ala Asn Unk Trp
65                  70                  75                  80
Cys Unk Leu Asp Met Glu Asn Ile Leu Glu Arg Phe Ile Asn Lys Lys
                85                  90                  95
Asp Thr Leu Leu Asp Leu Glu Glu Val Ile Val Pro Lys Thr Ser Trp
            100                 105                 110
Leu Val Leu Arg Lys Leu Lys Glu Ala His Phe Arg Glu Ile Ala Lys
        115                 120                 125
Ala Phe Val Ile Gly Ile Thr Gln Lys Asp Gly Lys Tyr Ile Pro Met
    130                 135                 140
Pro Asp Gly Glu Thr Ile Ile Ala Ser Glu Ser Lys Leu Leu Met Val
145                 150                 155                 160
Gly Thr Ser Glu Gly Val Ala Thr Cys Lys Gln Leu Ile Thr Ser His
                165                 170                 175
Gln Lys Pro Lys Glu Val Asp Tyr Ile Ser Leu
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

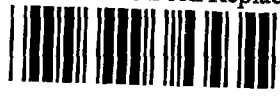
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410

```
Met Leu Lys Thr His Leu Ser Ser Ala Arg Gly Val Val Val Leu Ser
1               5                   10                  15
Lys Ile Leu Pro Val Asn Val Val Leu Met Val Ser Val Arg Leu Phe
            20                  25                  30
Glu Lys Glu Leu Lys Arg Lys Pro Tyr Tyr Ile Ile Ala Ser Ala His
        35                  40                  45
Ser Asp Glu Gly Leu Glu Lys Leu Lys Lys Unk Gly Unk Asp Met Val
    50                  55                  60
Unk Unk Pro Thr Lys Leu Met Ala Gln Arg Val Ser Ala Asn Unk Trp
65                  70                  75                  80
Cys Unk Leu Asp Met Glu Asn Ile Leu Glu Arg Phe Ile Asn Lys Lys
                85                  90                  95
Asp Thr Leu Leu Asp Leu Glu Glu Val Ile Val Pro Lys Thr Ser Trp
            100                 105                 110
Leu Val Leu Arg Lys Leu Lys Glu Ala His Phe Arg Glu Ile Ala Lys
        115                 120                 125
Ala Phe Val Ile Gly Ile Thr Gln Lys Asp Gly Lys Tyr Ile Pro Met
    130                 135                 140
Pro Asp Gly Glu Thr Ile Ile Ala Ser Glu Ser Lys Leu Leu Met Val
145                 150                 155                 160
Gly Thr Ser Glu Gly Val Ala Thr Cys Lys Gln Leu Ile Thr Ser His
                165                 170                 175
Gln Lys Pro Lys Glu Val Asp Tyr Ile Ser Leu
            180                 185
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:411:

(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:411

```
Met Phe Val Ala Ala Gly Leu Gly Ala Tyr Ala Ile Ala Leu Phe His
1               5                  10                  15
Leu Phe Thr His Ala Phe Phe Lys Ser Leu Leu Phe Leu Gly Ser Gly
            20                  25                  30
Asn Val Met His Ala Met Glu Asp Asn Leu Asp Ile Thr Lys Met Gly
        35                  40                  45
Ala Leu Tyr Lys Pro Met Arg Ile Thr Ala Val Phe Met Ile Ile Gly
    50                  55                  60
Ser Val Ala Leu Cys Gly Ile Tyr Pro Phe Ala Gly Tyr Phe Ser Lys
65                  70                  75                  80
Asp Lys Ile Leu Glu Val Ala Phe Gly Met His His His Ile Leu Trp
                85                  90                  95
Phe Val Leu Leu Ile Gly Ala Ile Phe Thr Ala Phe Tyr Ser Phe Arg
            100                 105                 110
Leu Ile Met Leu Val Phe Phe Ala Pro Lys Gln His Glu Ile Asn His
        115                 120                 125
Pro Pro
    130
```

(2) INFORMATION FOR SEQ ID NO:412:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412

```
Met Phe Ile Ser Ser Ser Tyr Thr Leu Ser Phe Val Trp Leu Phe Leu
1               5                  10                  15
Ile Phe Phe Phe Phe Lys Asn Lys Pro Leu Gly Leu Arg Phe Ser Leu
```

```
            20                  25                  30
Ser Leu Ile Ser Val Ile Leu Ser Asn Ile Ala Leu Lys Asp Ser Leu
        35                  40                  45
Ser Leu Asn Glu Phe Leu Ser Ser Phe Thr Ala Pro Leu Ser Pro Phe
    50                  55                  60
Ser Cys Leu Leu Ile Leu Ala Tyr Ala Ser Phe Ser Cys His Ile Leu
65                  70                  75                  80
Lys Lys Pro Pro Leu Glu Thr Leu Gln Ser Tyr Ser Val Met Leu Phe
                85                  90                  95
Phe Asn Leu Leu Leu Leu Thr Asp Ile Leu Gly Phe Leu Pro Phe Ser
            100                 105                 110
Ile Tyr His His Phe Met Ala Ser Leu Ile Phe Ser Ala Leu Phe Cys
        115                 120                 125
Ser Ser Leu Phe Leu Ser Ser Pro Leu Leu Gly Val Ile Ala Leu Val
    130                 135                 140
Ala Leu Ser Ser Ser Leu Leu Met Arg Ser Asn Phe Gln Ile Leu Asp
145                 150                 155                 160
Ser Leu Leu Asp Phe Pro Leu Phe Leu Phe Val Phe Phe Lys Thr Leu
                165                 170                 175
Tyr Leu Ala Lys Lys Arg Leu
            180
```

(2) INFORMATION FOR SEQ ID NO:413:

(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:413

```
Val Gly Ser Phe Leu Phe Val Gly Pro Ser Gly Val Gly Lys Thr Glu
1               5                   10                  15
Leu Ala Lys Glu Leu Ala Leu Asn Leu Unk Leu His Phe Glu Arg Phe
            20                  25                  30
Asp Met Ser Glu Tyr Lys Glu Ala His Ser Val Ala Lys Leu Ile Gly
        35                  40                  45
Ser Pro Ser Gly Tyr Val Gly Phe Glu Gln Gly Gly Leu Leu Val Asn
    50                  55                  60
Ala Ile Lys Lys His Pro His Cys Leu Leu Leu Leu Asp Glu Ile Glu
65                  70                  75                  80
Lys Ala His Pro Asn Val Tyr Asp Leu Leu Leu Gln Val Met Unk Asn
                85                  90                  95
Ala Thr Leu Ser Asp Asn Leu Gly Asn Lys Ala Ser Phe Lys His Val
            100                 105                 110
Ile Leu Ile Met Thr Unk Unk Val Gly Ser Lys Asp Lys Asp Thr Leu
        115                 120                 125
Gly Phe Phe Ser Thr Lys Asn Ala Lys Tyr Asp Arg Ala Val Lys Glu
    130                 135                 140
Leu Leu Thr Pro Glu Leu Arg Ser Arg Ile Asp Ala Ile Val Pro Phe
145                 150                 155                 160
Asn Ala Leu Ser Leu Glu Asp Phe Glu Thr His Cys Phe Cys Gly Ile
                165                 170                 175
```

This Sheet Has Been Replaced



```
Gly Arg Val Lys Ser Pro Ser Thr Arg Ala Arg Arg Asp Leu Lys Ile
            180                 185                 190
Pro
```

(2) INFORMATION FOR SEQ ID NO:413:

(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:413

```
Val Gly Ser Phe Leu Phe Val Gly Pro Ser Gly Val Gly Lys Thr Glu
1               5                  10                  15
Leu Ala Lys Glu Leu Ala Leu Asn Leu Unk Leu His Phe Glu Arg Phe
            20                  25                  30
Asp Met Ser Glu Tyr Lys Glu Ala His Ser Val Ala Lys Leu Ile Gly
        35                  40                  45
Ser Pro Ser Gly Tyr Val Gly Phe Glu Gln Gly Gly Leu Leu Val Asn
    50                  55                  60
Ala Ile Lys Lys His Pro His Cys Leu Leu Leu Leu Asp Glu Ile Glu
65                  70                  75                  80
Lys Ala His Pro Asn Val Tyr Asp Leu Leu Leu Gln Val Met Unk Asn
                85                  90                  95
Ala Thr Leu Ser Asp Asn Leu Gly Asn Lys Ala Ser Phe Lys His Val
            100                 105                 110
Ile Leu Ile Met Thr Unk Unk Val Gly Ser Lys Asp Lys Asp Thr Leu
        115                 120                 125
Gly Phe Phe Ser Thr Lys Asn Ala Lys Tyr Asp Arg Ala Val Lys Glu
    130                 135                 140
Leu Leu Thr Pro Glu Leu Arg Ser Arg Ile Asp Ala Ile Val Pro Phe
145                 150                 155                 160
Asn Ala Leu Ser Leu Glu Asp Phe Glu Thr His Cys Phe Cys Gly Ile
                165                 170                 175
Gly Arg Val Lys Ser Pro Ser Thr Arg Ala Arg Arg Asp Leu Lys Ile
            180                 185                 190
Pro
```

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414

```
Met Arg Leu Asp Tyr Ala Leu Phe Asn Gln His Leu Ala Asn Ser Arg
1               5                  10                  15
Glu Lys Ala Lys Ala Leu Val Leu Lys Lys Gln Val Leu Val Asn Lys
            20                  25                  30
Met Val Val Ser Lys Pro Ser Phe Ile Val Lys Glu Gly Asp Gln Ile
        35                  40                  45
Glu Leu Ile Ala Pro Asn Leu Phe Val Ser Arg Ala Gly Glu Lys Leu
    50                  55                  60
Gly Ala Phe Leu Glu Asp His Phe Ile Asp Phe Lys Glu Lys Val Val
65                  70                  75                  80
Leu Asp Val Gly Ala Ser Lys Gly Gly Phe Ser Gln Val Ala Leu Leu
                85                  90                  95
Lys Gly Ala Lys Lys Val Leu Cys Val Asp Val Gly Lys Met Gln Leu
            100                 105                 110
Asp Glu Ser Leu Lys Asn Asp Gln Arg Ile Glu Cys Tyr Glu Glu Cys
        115                 120                 125
Asp Ile Arg Gly Phe Lys Thr Pro Glu Lys Ile Asp Leu Ala Leu Cys
    130                 135                 140
Asp Val Ser Phe Ile Ser Leu Tyr Cys Ile Leu Glu Ala Ile Leu Pro
145                 150                 155                 160
Leu Ser Gly Glu Phe Leu Thr Leu Phe Lys Pro Gln Phe Glu Val Gly
                165                 170                 175
Arg Thr Ile Lys Arg Asn Lys Lys Gly Val Val Met Asp Lys Glu Ala
            180                 185                 190
Ile Leu Asn Ala Leu Glu Asn Phe Lys Asn His Leu Lys Thr Lys Asp
        195                 200                 205
Phe Gln Ile Leu Thr Ile Gln Glu Ser Leu Val Lys Gly Lys Asn Gly
    210                 215                 220
Asn Val Glu Phe Phe Ile His Phe Lys Arg Ala
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:415

```
Met Ser Leu Pro Pro Val Cys Ile Leu Lys Asp Val Asn His Leu Leu
1               5                  10                  15
Gln Val Leu His Ser Leu Val Ala Leu Gly Asn Ser Met Leu Val Ile
            20                  25                  30
```

```
Glu His Asn Leu Asp Ile Ile Lys Asn Ala Asp Tyr Ile Ile Asp Met
        35                  40                  45
Gly Pro Asp Gly Gly Asp Lys Gly Gly Lys Val Ile Ala Ser Gly Thr
    50                  55                  60
Pro Leu Glu Val Ala Gln Asn Cys Glu Lys Thr Gln Ser Tyr Thr Gly
65                  70                  75                  80
Lys Phe Leu Ala Leu Glu Leu Lys
                85
```

(2) INFORMATION FOR SEQ ID NO:416:

(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:416

```
Met Gln Asn Arg Ser His Glu Ile Gln Gly Val Ser His Ile Lys Asn
1               5                   10                  15
Asn Tyr Lys Phe Phe Thr Lys Glu Leu Asp Asn Tyr Ile Ser Lys Gly
            20                  25                  30
Tyr Arg Ile Glu Glu Ile Tyr Gly Ala Phe Leu Trp Leu Lys Ile Val
        35                  40                  45
Ala Ile Gly Leu Glu Leu Gly Glu Asp Asp Pro Gln Val Val Phe Glu
    50                  55                  60
Ser Ile Asn Ala Thr Gly Val Gln Leu Lys Gly Leu Asp Leu Ile Arg
65                  70                  75                  80
Asn Tyr Leu Met Met Gly Glu Asn Unk Asp Asn Gln Asn Arg Leu Tyr
                85                  90                  95
Asn Thr Tyr Trp Val Pro Leu Glu Asn Trp Leu Gly Glu
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:417:

(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:417

This Sheet Has Been Replaced



```
Met Asp Thr Ile Lys Ser Ile Pro Ile Arg Thr Phe Ile Leu Leu Tyr
1               5                  10                  15
Lys Ser Ser Pro Lys Cys Val Val Leu Ala Ser Ile Thr Val Leu Phe
            20                  25                  30
Val Gly Ile Leu Unk Ser Leu Asn Ile Leu Val Met Ile Lys Leu Ile
        35                  40                  45
Asp Ile Val Val Asn Leu Leu Gln Lys His Thr His Phe Glu Tyr Ser
    50                  55                  60
Leu Leu Leu Pro Thr Leu Leu Leu Trp Gly Ala Leu Leu Phe Leu Thr
65                  70                  75                  80
His Val Phe Ser Gly Asn Phe Ile Lys Leu Ala Asn His Tyr Cys Arg
                85                  90                  95
Thr Ile Phe Tyr Lys Tyr His His Ser Ala Cys
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:418:

(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:418

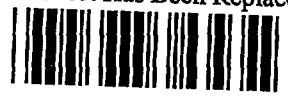
```
Met Ile Phe Tyr Thr Thr Ile Lys Glu Pro Leu Lys Asn Leu Gln Tyr
1               5                  10                  15
Arg Tyr Ala Gln Phe Phe Gly Lys Ile Lys Pro Cys Ser Phe Leu Glu
            20                  25                  30
Ser Leu Lys Ser Cys Phe Phe Gln Thr Tyr Ser Phe Ser Leu Thr Arg
        35                  40                  45
Lys Gln Asp Phe Lys Ser His Leu Arg His Phe Ile Asp Ser Ala His
    50                  55                  60
Ser Asn Ala Leu Val Gly Asn Leu Tyr Arg Ala Leu Phe Ile Gly Asp
65                  70                  75                  80
Ser Leu Asn Lys Asp Leu Arg Asp Arg Ala Asn Ala Leu Gly Ile Asn
                85                  90                  95
His Leu Leu Ala Ile Ser Gly Phe His Leu Gly Ile Leu Ser Ala Ser
            100                 105                 110
Val Tyr Phe Leu Phe Ser Leu Phe Tyr Thr Pro Leu Gln Lys Arg Tyr
        115                 120                 125
Phe Pro Tyr Arg Asn Ala Phe Unk
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...54

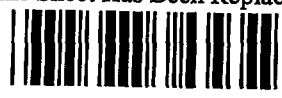
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419

```
Met Asn Lys Pro Phe Leu Ile Leu Leu Ile Ala Leu Ile Ala Phe Ser
1               5                  10                  15
Gly Cys Asn Met Arg Lys Tyr Phe Lys Pro Ala Lys His Gln Ile Lys
            20                  25                  30
Ala Lys Arg Ile Ser Leu Thr Ile Cys Lys Lys Ala Ser Phe Arg Leu
        35                  40                  45
Ile Val Met Glu Pro Phe
    50
```

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(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:420

```
Met Ala Ala Trp Asn Thr Leu Val Glu Lys Ile Ile Ala Pro Lys His
1               5                  10                  15
Lys Val Lys Ile Gly Phe Val Gly Lys Tyr Leu Ser Leu Lys Glu Ser
            20                  25                  30
Tyr Lys Ser Leu Ile Glu Ala Leu Ile His Ala Gly Ala His Leu Asp
        35                  40                  45
Thr Gln Val Asn Ile Glu Trp Leu Asp Ser Glu Asn Phe Asn Glu Lys
    50                  55                  60
Thr Asp Leu Glu Gly Val Asp Ala Ile Leu Val Pro Gly Gly Phe Gly
65                  70                  75                  80
Glu Arg Gly Ile Glu Gly Lys Ile Cys Ala Ile Gln Arg Ala Arg Leu
                85                  90                  95
Glu Lys Leu Pro Phe Leu Gly Ile Cys Leu Gly Met Gln Leu Ala Ile
            100                 105                 110
Val Glu Phe Cys Arg Lys Cys Phe Arg Leu Glu Arg Gly
        115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:421:

(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:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421

```
Met Thr Lys Ala Phe Val Pro Leu Ser Leu Leu Val Ser Ala Ile Leu
1               5                  10                  15
Leu Ala Phe Ser Leu Ile Leu Ile Pro Thr Ser Lys Ser Ala Tyr Tyr
            20                  25                  30
Gly Phe Leu Arg Gln Lys Lys Asp Lys Ile Asp Ile Asn Ile Arg Ala
        35                  40                  45
Gly Glu Phe Gly Gln Lys Leu Gly Asp Trp Leu Val Tyr Val Asp Lys
    50                  55                  60
Thr Glu Asn Asn Ser Tyr Asp Asn Leu Val Leu Phe Ser Asn Lys Ser
65                  70                  75                  80
Leu Ser Gln Glu Ser Phe Ile Leu Ala Gln Lys Gly Asn Ile Asn Asn
                85                  90                  95
Gln Asn Gly Val Phe Glu Leu Asn Leu Tyr Asn Gly His Ala Tyr Phe
            100                 105                 110
Thr Gln Gly Asp Lys Met Arg Lys Val Asp Phe Glu Glu Leu His Leu
        115                 120                 125
Arg Asn Lys Leu Lys Ser Phe Asn Ser Asn Asp Ala Ala Tyr Leu Gln
    130                 135                 140
Gly Thr Asp Tyr Leu Gly Tyr Trp Lys Lys Ala Phe Gly Lys Asn Ala
145                 150                 155                 160
Asn Lys Asn Gln Lys Arg Arg Phe Ser Gln Ala Ile Leu Val Ser Leu
                165                 170                 175
Phe Pro Leu Ala Ser Val Phe Leu Ile Pro Leu Phe Gly Ile Ala Asn
            180                 185                 190
Pro Arg Phe Lys Thr Asn Trp Ser Tyr Phe Unk Val Leu Gly Ala Val
        195                 200                 205
Gly Val Tyr Phe Leu Met Val His Val Ile Ser Thr Asp Leu Phe Leu
    210                 215                 220
Met Thr Phe Phe Phe Pro Phe Ile Trp Ala Phe Ile Ser Tyr Leu Leu
225                 230                 235                 240
Phe Arg Lys Phe Ile Leu Lys Arg Tyr
                245
```

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:422

```
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 Leu Tyr Gly Leu 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 Lys Lys Val Thr Glu Lys Gln Asp Asp Phe Leu Glu Pro Lys Arg
65                  70                  75                  80
Arg Thr Gln Arg Gly Ala
                85
```

(2) INFORMATION FOR SEQ ID NO:423:

(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:423

```
Val Met Ala Gln Ser Leu Leu Val His Ala Phe Phe Ala Ala Leu Leu
1               5                  10                  15
Ala Leu Ala Phe Met Ile Asn Leu Tyr Thr Leu Phe Lys Glu Lys Asn
            20                  25                  30
Phe Ile Gln Leu Asn Arg Lys Ile Tyr Leu Val Met Pro Ala Ile Tyr
        35                  40                  45
Ile Leu Leu Ser Ile Ala Leu Leu Ser Gly Val Phe Ile Trp Ala Met
    50                  55                  60
Gln Gln Phe Glu Phe Ser Phe Ser Ala Val Val Met Leu Leu Gly Leu
65                  70                  75                  80
Leu Leu Met Leu Ile Ala Glu Ile Lys Arg His Lys Ser Val Lys Phe
                85                  90                  95
Ala Ile Thr Lys Lys Glu Arg Met Lys Ala Tyr Ile Lys Lys Ala Lys
            100                 105                 110
Ile Leu Tyr Phe Leu Glu Thr Ile Leu Ile Ile Val Leu Met Gly Ile
        115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...93

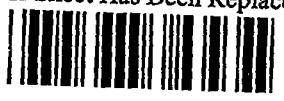
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424

```
Val Arg Asn Val Val Leu Phe Ile Leu Thr Ala Ile Phe Leu Ala Phe
1               5                  10                  15
Met Leu Leu Val Ser Tyr Cys Met Pro His Tyr Ser Val Ala Val Ile
            20                  25                  30
Ser Gly Val Glu Val Lys Arg Met Asn Glu Asn Glu Asn Thr Pro Asn
        35                  40                  45
Asn Lys Glu Val Lys Thr Leu Ala Arg Asp Val Tyr Phe Val Gln Thr
    50                  55                  60
Tyr Asp Pro Lys Asp Gln Lys Ser Val Thr Val Tyr Arg Asn Glu Asp
65                  70                  75                  80
Thr Arg Phe Gly Phe Pro Phe Tyr Phe Lys Phe Asn Ser
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:425

```
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 Unk Unk 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
65                  70                  75                  80
Lys Asp Trp Met Pro Arg Ser Ile
                85
```

(2) INFORMATION FOR SEQ ID NO:426:

(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:426

```
Val His Phe Thr Cys Ile Phe Leu Thr Leu Leu Lys Trp Ile Leu Pro
1               5                  10                  15
Ala Lys Asn Lys Gln Ala Cys Lys Lys Ala Thr Asn Gln Ile His Ser
            20                  25                  30
Arg Unk Ala Lys His Pro Ala Lys Tyr Pro Pro Ser Ser Ile Asn Pro
        35                  40                  45
Ser Ile Gln Ala Gly Ile Gln Gly Val Met Gln Gly Phe Gly Ala Leu
    50                  55                  60
Ser Ser Unk Leu Glu Unk Pro Unk Phe Val Unk Unk Ala Lys Cys Gly
65                  70                  75                  80
Trp Ile Gly Gly Phe Glu His Tyr Leu Ser Pro Leu Tyr Gly Trp Gly
                85                  90                  95
Lys Ile His Asp Gly Ala His Cys Asp Leu Met Gln Lys Asp Ala Asn
            100                 105                 110
Gly Arg Gly Ile Gly Leu Glu Lys Gly Leu Pro Pro Phe Lys Gly Leu
        115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:427

```
Met Gln Lys Phe Phe Ser Arg Phe Arg Arg Trp Ala Leu Pro Phe Tyr
1               5                  10                  15
Phe Val Ser Ala Leu Ala Ala Ile Asp Ile Asp Glu Val Thr Glu Ala
            20                  25                  30
Gln Ala Asn Ser Ile Lys Leu Ser Asp Gln Leu Val Ser Leu Ser Asp
        35                  40                  45
Lys Leu Leu Glu Lys Ala Val Asp Arg Gly Arg Asn Thr Asp His Leu
    50                  55                  60
Lys Asp Leu Asn Asp Leu His Glu Lys Ile Lys His Leu Arg Leu Ile
65                  70                  75                  80
Leu Glu Pro Lys Pro Lys Gly Lys Glu Asp Ser Pro Asn Leu Gly Gly
                85                  90                  95
Asn Lys Asp Met Lys Thr Val Glu Ile Gly Ser Gly
```

100 105

(2) INFORMATION FOR SEQ ID NO:428:

(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:428

```
Val Ile Leu Ala Phe Ala Phe Gly Met Ser Leu Leu Gly Leu Ala Gly
1               5                  10                  15
Met Phe Ile Asp Ile Pro Phe Leu Ser Thr Gly Val His Ile Pro Arg
            20                  25                  30
Lys Glu Asp Ile Leu Trp Ile Ser Leu Ile Gly Ile Ser Gly Thr Leu
        35                  40                  45
Gly Gln Tyr Phe Leu Thr Tyr Ala Tyr Met Asn Ala Pro Ala Gly Ile
    50                  55                  60
Ile Ala Pro Ile Glu Tyr Thr Arg Ile Val Trp Gly Leu Leu Phe Gly
65                  70                  75                  80
Leu Tyr Leu Gly Asp Thr Phe Leu Asp Leu Lys Ser Ser Leu Gly Val
                85                  90                  95
Ala Leu Ile Leu Cys Ser Gly Leu Leu Ile Ala Leu Pro Ala Leu Leu
            100                 105                 110
Lys Glu Leu Lys Lys Ile
        115
```

(2) INFORMATION FOR SEQ ID NO:429:

This Sheet Has Been Replaced

(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:429

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

```
Pro Val Leu Met Gly Leu Ile Trp Arg Val Val Tyr Leu Thr Phe Phe
        35                  40                  45
Pro Ile Gln Lys Ala Thr
    50
```

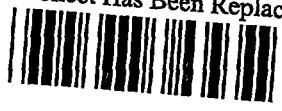
(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 288 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430

```
Met Ala Ala Lys Ser Lys Ala Unk Thr Leu Lys Val Phe Ser Lys Phe
1               5                  10                  15
Phe Ser Asn Phe Lys Ile Thr Lys Leu Lys Asp Asn His Glu Glu Ala
            20                  25                  30
His Lys Leu Phe Gly Glu Asn Ser Arg Lys Ala His Asp Thr Glu Ile
        35                  40                  45
Ile Tyr Ser Thr Leu Gln Val Val Pro Arg Tyr Ser Ile Glu Thr Val
    50                  55                  60
Gly Phe Ser Leu Leu Ile Leu Ala Val Ala Tyr Ile Leu Phe Lys Tyr
65                  70                  75                  80
Gly Glu Ala Arg Met Val Leu Pro Thr Ile Ser Met Tyr Ala Leu Ala
                85                  90                  95
Leu Tyr Arg Ile Leu Pro Ser Val Thr Gly Val Ile Ser Tyr Tyr Asn
            100                 105                 110
Glu Ile Ala Tyr Asn Gln Leu Ala Thr Asn Val Val Phe Lys Ser Leu
        115                 120                 125
Ser Lys Thr Ile Val Glu Glu Asp Leu Val Pro Leu Asp Phe Asn Glu
    130                 135                 140
Lys Ile Thr Leu Gln Asn Ile Ser Phe Ala Tyr Lys Ser Lys His Pro
145                 150                 155                 160
Val Leu Lys Asn Phe Asn Leu Thr Ile Gln Lys Gly Gln Lys Ile Ala
                165                 170                 175
Leu Ile Gly His Ser Gly Cys Gly Lys Ser Thr Leu Ala Asp Ile Ile
            180                 185                 190
Met Gly Leu Thr Tyr Pro Lys Ser Gly Glu Ile Phe Ile Asp Asn Thr
        195                 200                 205
Leu Leu Thr Ser Glu Asn Arg Arg Ser Trp Arg Lys Lys Ile Gly Tyr
    210                 215                 220
Ile Pro Gln Asn Ile Tyr Leu Phe Asp Gly Thr Val Gly Asp Asn Ile
225                 230                 235                 240
Ala Phe Gly Ser Ala Ile Asp Glu Lys Arg Leu Ile Lys Val Cys Lys
                245                 250                 255
Met Ala His Ile Tyr Asp Phe Leu Cys Glu His Glu Gly Leu Lys Thr
            260                 265                 270
Gln Val Gly Glu Gly Ala Leu Ser Leu Ala Ala Val Lys Asn Ser Ala
        275                 280                 285
```

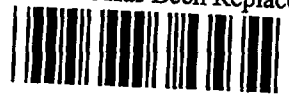
(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431

```
Met Ala Phe Gln Val Asn Thr Asn Ile Asn Ala Met Asn Ala His Val
1               5                  10                  15
Gln Ser Ala Leu Thr Gln Asn Ala Leu Lys Thr Ser Leu Glu Arg Leu
            20                  25                  30
Ser Ser Gly Leu Arg Ile Asn Lys Ala Ala Asp Asp Ala Ser Gly Met
        35                  40                  45
Thr Val Ala Asp Ser Leu Arg Ser Gln Ala Ser Ser Leu Gly Gln Ala
    50                  55                  60
Ile Ala Asn Thr Asn Asp Gly Met Gly Ile Ile Gln Val Ala Asp Lys
65                  70                  75                  80
Ala Met Asp Glu Gln Leu Lys Ile Leu Asp Thr Val Lys Val Lys Ala
                85                  90                  95
Thr Gln Ala Ala Gln Asp Gly Gln Thr Thr Glu Ser Arg Lys Ala Ile
            100                 105                 110
Gln Ser Asp Ile Val Arg Leu Ile Gln Gly Leu Asp Asn Ile Gly Asn
        115                 120                 125
Thr Thr Thr Tyr Asn Gly Gln Ala Leu Leu Ser Gly Gln Phe Thr Asn
    130                 135                 140
Lys Glu Phe Gln Val Gly Ala Tyr Ser Asn Gln Ser Ile Lys Ala Ser
145                 150                 155                 160
Ile Gly Ser Thr Thr Ser Asp Lys Ile Gly Gln Val Arg Ile Ala Thr
                165                 170                 175
Gly Ala Leu Ile Thr Ala Ser Gly Asp Ile Ser Leu Thr Phe Lys Gln
            180                 185                 190
Val Asp Gly Val Asn Asp Val Thr Leu Glu Ser Val Lys Val Ser Ser
        195                 200                 205
Ser Ala Gly Thr Gly Ile Gly Val Leu Ala Glu Val Ile Asn Lys Asn
    210                 215                 220
Ser Asn Arg Thr Gly Val Lys Ala Tyr Ala Ser Val Ile Thr Thr Ser
225                 230                 235                 240
Asp Val Ala Val Gln Ser Gly Ser Leu Ser Asn Leu Thr Leu Asn Gly
                245                 250                 255
Ile His Leu Gly Asn Ile Ala Asp Ile Lys Unk Asn Asp Ser Asp Gly
            260                 265                 270
Arg Leu Val Thr Ala Ile Asn Ala Val Thr Ser Glu Thr Gly Val Unk
        275                 280                 285
Ala Tyr Thr Asp Gln Lys Gly Arg Leu Asn Leu Arg Ser Ile Gly
    290                 295                 300
```

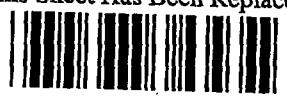
(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431

```
Met Ala Phe Gln Val Asn Thr Asn Ile Asn Ala Met Asn Ala His Val
1               5                  10                  15
Gln Ser Ala Leu Thr Gln Asn Ala Leu Lys Thr Ser Leu Glu Arg Leu
            20                  25                  30
Ser Ser Gly Leu Arg Ile Asn Lys Ala Ala Asp Asp Ala Ser Gly Met
        35                  40                  45
Thr Val Ala Asp Ser Leu Arg Ser Gln Ala Ser Ser Leu Gly Gln Ala
    50                  55                  60
Ile Ala Asn Thr Asn Asp Gly Met Gly Ile Ile Gln Val Ala Asp Lys
65                  70                  75                  80
Ala Met Asp Glu Gln Leu Lys Ile Leu Asp Thr Val Lys Val Lys Ala
                85                  90                  95
Thr Gln Ala Ala Gln Asp Gly Gln Thr Thr Glu Ser Arg Lys Ala Ile
            100                 105                 110
Gln Ser Asp Ile Val Arg Leu Ile Gln Gly Leu Asp Asn Ile Gly Asn
        115                 120                 125
Thr Thr Thr Tyr Asn Gly Gln Ala Leu Leu Ser Gly Gln Phe Thr Asn
    130                 135                 140
Lys Glu Phe Gln Val Gly Ala Tyr Ser Asn Gln Ser Ile Lys Ala Ser
145                 150                 155                 160
Ile Gly Ser Thr Thr Ser Asp Lys Ile Gly Gln Val Arg Ile Ala Thr
                165                 170                 175
Gly Ala Leu Ile Thr Ala Ser Gly Asp Ile Ser Leu Thr Phe Lys Gln
            180                 185                 190
Val Asp Gly Val Asn Asp Val Thr Leu Glu Ser Val Lys Val Ser Ser
        195                 200                 205
Ser Ala Gly Thr Gly Ile Gly Val Leu Ala Glu Val Ile Asn Lys Asn
    210                 215                 220
Ser Asn Arg Thr Gly Val Lys Ala Tyr Ala Ser Val Ile Thr Thr Ser
225                 230                 235                 240
Asp Val Ala Val Gln Ser Gly Ser Leu Ser Asn Leu Thr Leu Asn Gly
                245                 250                 255
Ile His Leu Gly Asn Ile Ala Asp Ile Lys Unk Asn Asp Ser Asp Gly
            260                 265                 270
Arg Leu Val Thr Ala Ile Asn Ala Val Thr Ser Glu Thr Gly Val Unk
        275                 280                 285
Ala Tyr Thr Asp Gln Lys Gly Arg Leu Asn Leu Arg Ser Ile Gly
    290                 295                 300
```

(2) INFORMATION FOR SEQ ID NO:432:

(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:432

```
Met Leu Asp Ile Trp Ile Asp Met Ile Ile Cys Ile Phe Tyr Leu Leu
1               5                  10                  15
Phe Phe Thr Thr Pro Tyr Ile Val Gly Asp Ile Leu Gln Leu Lys Phe
            20                  25                  30
Ile Arg Gln Lys Leu Cys Glu Lys Pro Val Leu Leu Pro Gln Lys Asp
        35                  40                  45
Tyr Glu Glu Ala Gly Asn Tyr Ala Ile Arg Lys Met Gln Leu Ser Ile
    50                  55                  60
Ile Ser Gln Ile Leu Asp Gly Val Ile Phe Ala Gly Trp Val Phe Phe
65                  70                  75                  80
Gly Leu Thr His Leu Glu Asp Leu Thr His Tyr Leu Asn Leu Pro Glu
                85                  90                  95
Thr Leu Gly Tyr Leu Val Phe Ala Leu Leu Phe Leu Ala Ile Gln Ser
            100                 105                 110
Val Leu Ala Leu Pro Ile Ser Tyr Tyr Thr Thr Met His Leu Asp Lys
        115                 120                 125
Glu Phe Gly Phe Ser Lys Val Ser Leu Ser Leu Phe Phe Lys Asp Phe
    130                 135                 140
Phe Lys Gly Leu Leu Leu Thr Leu Gly Val Gly Leu Leu Leu Ile Tyr
145                 150                 155                 160
Thr Leu Ile Met Ile Ile Glu His Val Glu His Trp Glu Ile Ser Ser
                165                 170                 175
Phe Phe Val Val Phe Val Phe Met Ile Leu Ala Asn Leu Phe Leu Pro
            180                 185                 190
```

(2) INFORMATION FOR SEQ ID NO:433:



(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:433

```
Met Leu Lys Lys Ile Phe Leu Thr Asn Ser Leu Gly Ile Leu Cys Ser
1               5                  10                  15
Arg Ile Phe Gly Phe Leu Arg Asp Leu Met Met Ala Asn Ile Leu Gly
            20                  25                  30
Ala Gly Val Tyr Ser Asp Ile Phe Phe Val Ala Phe Lys Leu Pro Asn
        35                  40                  45
Leu Phe Arg Arg Ile Phe Ala Glu Gly Ser Phe Ser Gln Ser Phe Leu
    50                  55                  60
Pro Ser Phe Ile Arg Ser Ser Ile Lys Gly Gly Phe Ala Ser Leu Val
65                  70                  75                  80
```

```
Gly Leu Ile Phe Cys Gly Val Leu Phe Met Trp Cys Leu Leu Val Ala
                85                  90                  95
Leu Asn Pro Leu Trp Leu Thr Lys Leu Leu Ala Tyr Gly Phe Asp Glu
            100                 105                 110
Glu Thr Leu Lys Leu Cys Thr Pro Ile Val Ala Ile Asn Phe Trp Tyr
        115                 120                 125
Leu Leu Leu Val Phe Ile Thr Thr Phe Leu Gly Ala Leu Leu Gln Tyr
    130                 135                 140
Lys His Ser Phe Phe Ala Ala Leu Met Arg Lys Leu Thr Gln Phe Met
145                 150                 155                 160
His Asp Phe Ser Pro Phe Asp Phe
                165
```

(2) INFORMATION FOR SEQ ID NO:434:

(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:434

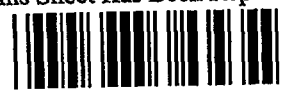
```
Met Asn Leu Glu Val Ala Leu Lys Ala Phe Glu Thr Leu Leu Pro Cys
1               5                  10                  15
Asn Lys Gln Glu Val Leu Lys Asn Leu Lys Pro Leu Asp Leu Ile Gly
            20                  25                  30
Arg Cys Glu Leu Leu Ser Pro Asn Ile Leu Ile Asp Val Gly His Asn
        35                  40                  45
Pro His Ser Ala Lys Ala Leu Lys Glu Glu Ile Lys Arg Ile Phe Asn
    50                  55                  60
Ala Pro Ile Val Leu Ile Tyr Asn Cys Tyr Gln Asp Lys Asp Ala Phe
65                  70                  75                  80
Leu Val Leu Glu Ile Leu Lys Ser Val Val Lys Lys Val Leu Ile Leu
                85                  90                  95
Glu Leu His Asn Glu Arg Ile Ile Gln Leu Glu Lys Leu Lys Gly Ile
            100                 105                 110
Leu Glu Thr Leu Gly Leu Glu His Ala Leu Phe Glu Glu Leu Lys Glu
        115                 120                 125
Asn Glu Asn Tyr Leu Val Tyr Gly Ser Phe Leu Val Ala Asn Ala Phe
    130                 135                 140
Tyr Glu Arg Tyr Pro Lys Lys Arg Asp
145                 150
```

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435

```
Met Phe Phe Lys Thr Tyr Gln Lys Leu Leu Gly Ala Ser Cys Leu Ala
1               5                  10                  15
Leu Tyr Leu Val Gly Cys Gly Asn Gly Gly Gly Gly Glu Ser Pro Val
            20                  25                  30
Glu Met Ile Unk Asn Ser Glu Gly Thr Phe Gln Ile Asp Ser Lys Ala
        35                  40                  45
Asp Ser Ile Thr Ile Gln Gly Val Lys Leu Asn Arg Gly Asn Cys Ala
    50                  55                  60
Val Asn Phe Val Pro Val Ser Glu Thr Phe Gln Met Gly Val Leu Ser
65                  70                  75                  80
Gln Val Thr Pro Ile Ser Ile Gln Asp Phe Lys Asp Met Ala Ser Thr
                85                  90                  95
Tyr Lys Ile Phe Asp Gln Lys Lys Gly Leu Ala Asn Ile Ala Asn Lys
            100                 105                 110
Ile Ser Gln Leu Glu Gln Lys Gly Val Met Met Lys Pro Unk Thr Leu
        115                 120                 125
Asn Phe Gly Glu Ser Leu Lys Gly Ile Ser Gln Gly Cys Asn Ile Ile
    130                 135                 140
Glu Ala Glu Ile Gln Thr Asp Lys Gly Ala Trp Thr Phe Asn Phe Asp
145                 150                 155                 160
Lys
```

(2) INFORMATION FOR SEQ ID NO:435:

(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

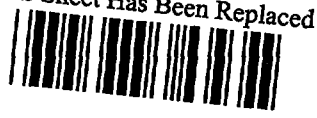
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435

```
Met Phe Phe Lys Thr Tyr Gln Lys Leu Leu Gly Ala Ser Cys Leu Ala
1               5                  10                  15
Leu Tyr Leu Val Gly Cys Gly Asn Gly Gly Gly Gly Glu Ser Pro Val
            20                  25                  30
Glu Met Ile Unk Asn Ser Glu Gly Thr Phe Gln Ile Asp Ser Lys Ala
        35                  40                  45
Asp Ser Ile Thr Ile Gln Gly Val Lys Leu Asn Arg Gly Asn Cys Ala
    50                  55                  60
Val Asn Phe Val Pro Val Ser Glu Thr Phe Gln Met Gly Val Leu Ser
65                  70                  75                  80
```

```
Gln Val Thr Pro Ile Ser Ile Gln Asp Phe Lys Asp Met Ala Ser Thr
                85                  90                  95
Tyr Lys Ile Phe Asp Gln Lys Lys Gly Leu Ala Asn Ile Ala Asn Lys
            100                 105                 110
Ile Ser Gln Leu Glu Gln Lys Gly Val Met Met Lys Pro Unk Thr Leu
        115                 120                 125
Asn Phe Gly Glu Ser Leu Lys Gly Ile Ser Gln Gly Cys Asn Ile Ile
    130                 135                 140
Glu Ala Glu Ile Gln Thr Asp Lys Gly Ala Trp Thr Phe Asn Phe Asp
145                 150                 155                 160
Lys
```

(2) INFORMATION FOR SEQ ID NO:436:

This Sheet Has Been Replaced



(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:436

```
Met Ala Ile Gly Phe Pro Leu Val Phe Gly Ile Leu Leu Thr Leu Phe
1               5                   10                  15
Ser Arg Ser Tyr Trp Arg Glu Phe Gly Gly Val Ser Gly Val Leu Trp
            20                  25                  30
Arg Ala Ser Gly Phe Ser Gly Ala Lys Val Glu Arg Asn Leu Glu Arg
        35                  40                  45
Asp Pro His Ala Phe Phe Thr His Cys Asp Phe
    50                  55
```

(2) INFORMATION FOR SEQ ID NO:437:

(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:437

```
Met Lys Lys Lys Ala Lys Val Phe Trp Cys Cys Phe Lys Met Ile Arg
```

```
1               5                   10                  15
Trp Leu Tyr Leu Ala Val Phe Phe Leu Leu Ser Val Ser Asp Ala Lys
            20                  25                  30
Glu Ile Ala Met Gln Arg Phe Asp Lys Gln Asn His Lys Ile Phe Glu
        35                  40                  45
Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn Val Ile Thr Ala Ser
    50                  55                  60
Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr Ile Leu Ala Asp Lys
65                  70                  75                  80
Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu Leu Glu Gly Asn Ile
                85                  90                  95
Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys Thr Asp Tyr Val Lys
            100                 105                 110
Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe Pro Phe Tyr Val Gln
        115                 120                 125
Asp Ser Val Ser Gly Ile Trp Val Ser Ala Asp Ile Ala Ser Gly Lys
    130                 135                 140
Asp Gln Lys Tyr Lys Ile Lys Asn Met Ser Ala Ser Gly Cys Ser Ile
145                 150                 155                 160
Asp Asn Pro Ile Trp His Val Asn Ala Thr Ser Gly Ser Phe Asn Met
                165                 170                 175
Gln Lys Ser His Leu Ser Met Trp Asn Pro Lys Ile Tyr Val Gly Asp
            180                 185                 190
Ile Pro Val Leu Tyr Leu Pro Tyr Ile Phe Met Ser Thr Ser Asn Lys
        195                 200                 205
Arg Thr Thr Gly Phe Leu Tyr Pro Glu Phe Gly Thr Ser Thr
    210                 215                 220
```

(2) INFORMATION FOR SEQ ID NO:438:

This Sheet Has Been Replaced



(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:438

```
Met Leu Asp Phe Asp Leu Val Leu Phe Gly Ala Thr Gly Asp Leu Ala
1               5                   10                  15
Met Arg Lys Leu Phe Val Ser Leu Tyr Glu Ile Tyr Ile Ser Phe Met
            20                  25                  30
Val Leu Lys Thr Ile Leu Gly Leu Ser His Arg Gly Val Arg Ser Tyr
        35                  40                  45
Pro Met Lys Ser Phe
    50
```

(2) INFORMATION FOR SEQ ID NO:439:

(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:439

```
Met Gln Asp Leu Pro Pro Cys Pro Lys Arg Asn Asp Ala Tyr Thr Tyr
1               5                  10                  15
His Asp Gly Thr Gln Phe Val Cys Ser Ser Cys Leu Tyr Glu Trp Asn
            20                  25                  30
Gly Asn Glu Ile Ser Asn Glu Glu Leu Ile Val Lys Asp Cys His Asn
        35                  40                  45
Asn Leu Leu Gln Asn Gly Asp Ser Val Ile Leu Ile Lys Asp Leu Lys
    50                  55                  60
Val Lys Gly Ser Ser Leu Val Leu Lys Lys Gly Thr Lys Ile Lys Asn
65                  70                  75                  80
Ile Lys Leu Val Asn Ser Asp His Asn Val Asp Cys Lys Val Glu Gly
                85                  90                  95
Gln Ser Leu Ser Leu Lys Ser Glu Phe Leu Lys Lys Ala
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:440

```
Val Asp Gly Ala Ile Ile Thr Gly Asn Tyr Ala Leu Gln Ala Lys Leu
1               5                  10                  15
Thr Gly Ala Leu Phe Ser Glu Asp Lys Asp Ser Pro Tyr Ala Asn Leu
            20                  25                  30
Val Ala Ser Arg Glu Asp Asn Ala Gln Asp Glu Ala Ile Lys Ala Leu
        35                  40                  45
Ile Glu Ala Leu Gln Ser Glu Lys Thr Arg Lys Phe Ile Leu Asp Thr
    50                  55                  60
Tyr Lys Gly Ala Ile Ile Pro Ala Phe
65                  70
```

(2) INFORMATION FOR SEQ ID NO:441:

(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:441

```
Val Phe Thr Met Leu Val Leu Val Leu Ser Asp Asn Phe Leu Gly Leu
1               5                  10                  15
Phe Ile Gly Trp Glu Gly Val Gly Leu Cys Ser Tyr Leu Leu Ile Gly
            20                  25                  30
Phe Trp Tyr His Lys Lys Ser Ala Asn Asn Ala Ser Ile Glu Ala Phe
        35                  40                  45
Val Met Asn Arg Ile Thr Asp Leu Gly Met Leu Met Gly Ile Ile Leu
    50                  55                  60
Ile Phe Trp Asn Phe Gly Thr Leu Gln Tyr Lys Glu Val Phe Ser Met
65                  70                  75                  80
Leu Asn Asn Ala Asp Tyr Ser Met Leu Phe Tyr Ile Ser Val Phe Leu
                85                  90                  95
Phe Ile Gly Ala Met Gly Lys Ser Ala Gln Phe Pro Met His Thr Trp
            100                 105                 110
Leu Ala Asn Ala Met Glu Gly Pro Thr Pro Val Ser Ala Leu Ile His
        115                 120                 125
Ala Thr Thr Met Val Thr Ala Gly Val Tyr Leu Ile Ile Arg Ala Asn
    130                 135                 140
Pro Leu Tyr Ser Ala Val Phe Glu Val Gly Tyr Phe Ile Ala Cys Leu
145                 150                 155                 160
Gly Ala Phe Val Ala Leu Phe Gly Ala Ser Met Ala Leu Val Asn Lys
                165                 170                 175
Asp Leu Lys Arg Ile Val Glu Tyr Ser Thr Leu Ser Gln Leu Gly Leu
            180                 185                 190
Tyr Val Cys Ser Gly Arg Ala Trp Gly Leu Cys Asp Arg Ala Phe Pro
        195                 200                 205
Pro Leu Tyr Ala Cys Val Leu Gln Ile Pro Pro Phe Leu Arg Leu Arg
    210                 215                 220
Gln Cys His Ala Cys Asp Gly Arg Gln Ser Gly Tyr Tyr
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:442:

(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

This Sheet Has Been Replaced



(B) LOCATION 1...91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442

```
Val Cys Leu Gly Leu Ala Asp Val Met Val Val Leu Ser Leu His Leu
1               5                  10                  15
Asn Leu Asn Pro Thr Asn Pro Lys Trp Leu Asn Arg Asp Arg Leu Val
            20                  25                  30
Phe Ser Gly Gly His Ala Ser Ala Leu Val Tyr Ser Leu Leu His Leu
        35                  40                  45
Trp Gly Phe Asp Leu Ser Leu Asp Asp Leu Lys Arg Phe Arg Gln Leu
    50                  55                  60
His Ser Lys Thr Pro Gly His Pro Glu Leu His His Thr Glu Gly Ile
65                  70                  75                  80
Glu Ile Thr Thr Unk Phe Arg Ala Arg Phe Cys
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:442:

(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:442

```
Val Cys Leu Gly Leu Ala Asp Val Met Val Val Leu Ser Leu His Leu
1               5                  10                  15
Asn Leu Asn Pro Thr Asn Pro Lys Trp Leu Asn Arg Asp Arg Leu Val
            20                  25                  30
Phe Ser Gly Gly His Ala Ser Ala Leu Val Tyr Ser Leu Leu His Leu
        35                  40                  45
Trp Gly Phe Asp Leu Ser Leu Asp Asp Leu Lys Arg Phe Arg Gln Leu
    50                  55                  60
His Ser Lys Thr Pro Gly His Pro Glu Leu His His Thr Glu Gly Ile
65                  70                  75                  80
Glu Ile Thr Thr Unk Phe Arg Ala Arg Phe Cys
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:443:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443

```
Met Met Ile Thr Lys Gln Ser Tyr Gln Arg Phe Ala Leu Met Arg Val
1               5                  10                  15
Phe Val Phe Ser Leu Ser Ala Phe Ile Phe Asn Thr Thr Glu Phe Val
            20                  25                  30
Pro Val Ala Leu Leu Ser Asp Ile Ala Lys Ser Phe Glu Met Glu Ser
        35                  40                  45
Ala Thr Val Gly Leu Met Ile Thr Ala Tyr Ala Trp Val Val Ser Leu
    50                  55                  60
Gly Ser Leu Pro Leu Met Leu Leu Ser Ala Lys Ile Glu Arg Lys Arg
65                  70                  75                  80
Leu Leu Leu Phe Leu Phe Ala Leu Phe Ile Phe Ser His Ile Leu Ser
                85                  90                  95
Arg
```

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444

```
Met Lys Leu Arg Ala Ser Val Leu Ile Gly Val Ala Ile Leu Cys Leu
1               5                  10                  15
Ile Leu Ser Ala Cys Ser Asn Tyr Ala Lys Lys Val Val Lys Gln Lys
            20                  25                  30
Asn His Val Tyr Thr Pro Val Tyr Asn Glu Leu Ile Glu Lys Tyr Ser
        35                  40                  45
Glu Ile Pro Leu Asn Asp Lys Leu Lys Asp Thr Pro Phe Met Val Gln
    50                  55                  60
Val Lys Leu Pro Asn Tyr Lys Asp Tyr Leu Leu Asp Asn Lys Gln Val
65                  70                  75                  80
Val Leu Thr Phe Lys Leu Val His His Ser Lys Lys Ile Thr Leu Ile
                85                  90                  95
Gly Asp Ala Asn Lys Ile Leu Gln Tyr Lys Asn Tyr Phe Gln Ala Asn
            100                 105                 110
Gly Ala Arg Ser Asp Ile Asp Phe Tyr Leu Gln Pro Thr Leu Asn Gln
        115                 120                 125
Lys Gly Val Val Met Ile Ala Ser Asn Tyr Asn Asp Asn Pro Asn Asn
    130                 135                 140
Lys Glu Lys Pro Gln Thr Phe Asp Val Leu Gln Gly Ser Gln Pro Met
145                 150                 155                 160
Leu Gly Ala Asn Thr Lys Asn Leu His Gly Tyr Asp Val Ser Gly Ala
                165                 170                 175
```

```
Asn Asn Lys Gln Val Ile Asn Glu Val Ala Arg Glu Lys Ala Gln Leu
            180                 185                 190
Glu Lys Ile Asn Gln Tyr Tyr Lys Thr Leu Leu Gln Asp Lys Glu Gln
        195                 200                 205
Glu Tyr Thr Thr Arg Lys Asn Asn Gln Arg Glu Ile Leu Glu Thr Leu
    210                 215                 220
Ser Asn Arg Ala Gly Tyr Gln Met Arg Gln Asn Val Ile Ser Ser Glu
225                 230                 235                 240
Ile Phe Lys Asn Gly Asn Leu Asn Met Gln Ala Lys Glu Glu Glu Val
                245                 250                 255
Arg Glu Lys Leu Gln Glu Glu Arg Glu Asn Glu Tyr Leu Arg Asn Gln
            260                 265                 270
Ile Arg Ser Leu Leu Ser Gly Lys
        275                 280
```

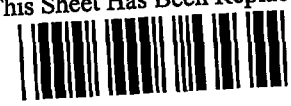
(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445

```
Met Thr Thr Pro Met Ile Ile Ile Ser Leu Glu Met Gly Leu Ser Leu
1               5                   10                  15
Val Pro Met Arg Gln Cys Leu Val Cys Gln Ala Leu Ala Arg Ser Ile
            20                  25                  30
Ser Trp Asn Gly Leu Gly Gly Asn Val Arg Asn Thr Lys Val Tyr Gly
        35                  40                  45
Lys Phe Ala Ala Tyr His His Leu Gln Lys Tyr Leu Leu Ile Asp Leu
    50                  55                  60
Ile Ala Arg Phe Lys Thr Gln Gly Gly Tyr Ile Phe Arg Tyr Asn Thr
65                  70                  75                  80
Asp Asp Tyr Leu Pro Leu Asn Ser Thr Phe Tyr Met Gly Gly Val Thr
                85                  90                  95
Thr Val Arg Gly Phe Arg Asn Gly Ser Ile Thr Pro Lys Asp Glu Phe
            100                 105                 110
Gly Leu Trp Leu Gly Gly Asp Gly Ile Phe Thr Unk Ser Thr Glu Leu
        115                 120                 125
Ser Tyr Gly Val Leu Lys Ala Ala Lys Met Arg Leu Ala Trp Phe Phe
    130                 135                 140
Asp Phe Gly Phe Leu Thr Phe Unk Thr Pro Thr Arg Gly Ser Phe Phe
145                 150                 155                 160
Tyr Asn Ala Unk Thr Thr Thr Ala Asn Phe Lys Asp Tyr Unk Val Val
                165                 170                 175
Gly Unk Unk Phe Glu Unk Ala Thr Trp Arg Ala
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:445:

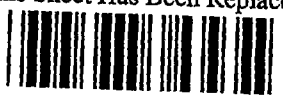
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445

```
Met Thr Thr Pro Met Ile Ile Ile Ser Leu Glu Met Gly Leu Ser Leu
1               5                  10                  15
Val Pro Met Arg Gln Cys Leu Val Cys Gln Ala Leu Ala Arg Ser Ile
            20                  25                  30
Ser Trp Asn Gly Leu Gly Gly Asn Val Arg Asn Thr Lys Val Tyr Gly
        35                  40                  45
Lys Phe Ala Ala Tyr His His Leu Gln Lys Tyr Leu Leu Ile Asp Leu
    50                  55                  60
Ile Ala Arg Phe Lys Thr Gln Gly Gly Tyr Ile Phe Arg Tyr Asn Thr
65                  70                  75                  80
Asp Asp Tyr Leu Pro Leu Asn Ser Thr Phe Tyr Met Gly Gly Val Thr
                85                  90                  95
Thr Val Arg Gly Phe Arg Asn Gly Ser Ile Thr Pro Lys Asp Glu Phe
            100                 105                 110
Gly Leu Trp Leu Gly Gly Asp Gly Ile Phe Thr Unk Ser Thr Glu Leu
        115                 120                 125
Ser Tyr Gly Val Leu Lys Ala Ala Lys Met Arg Leu Ala Trp Phe Phe
    130                 135                 140
Asp Phe Gly Phe Leu Thr Phe Unk Thr Pro Thr Arg Gly Ser Phe Phe
145                 150                 155                 160
Tyr Asn Ala Unk Thr Thr Thr Ala Asn Phe Lys Asp Tyr Unk Val Val
                165                 170                 175
Gly Unk Unk Phe Glu Unk Ala Thr Trp Arg Ala
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446

```
Met Trp Leu Asp His Ile Ala Lys Glu Ile Arg Ser Leu Val Glu Asn
1               5                  10                  15
```

```
Asp Ile Glu Val Gly Ile Val Ile Gly Gly Gly Asn Ile Ile Arg Gly
            20                  25                  30
Val Ser Ala Ala Leu Gly Gly Ile Ile Arg Arg Thr Ser Gly Asp Tyr
        35                  40                  45
Met Gly Met Leu Ala Thr Val Ile Lys Arg
    50                  55
```

(2) INFORMATION FOR SEQ ID NO:447:

(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:447

```
Val His Asn Phe His Trp Asn Val Lys Gly Thr Asp Phe Phe Asn Val
1               5                   10                  15
His Lys Ala Thr Glu Glu Ile Tyr Glu Gly Phe Ala Asp Met Phe Asp
            20                  25                  30
Asp Leu Ala Glu Arg Ile Val Gln Leu Gly His His Pro Leu Val Thr
        35                  40                  45
Leu Ser Glu Ala Ile Lys Leu Thr Arg Val Lys Glu Glu Thr Lys Thr
    50                  55                  60
Ser Phe His Ser Lys Asp Ile Phe Lys Glu Ile Leu Glu Asp Tyr Lys
65                  70                  75                  80
His Leu Glu Lys Glu
                85
```

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:
(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:448

```
Met Asn Lys Thr Ile Lys Ala Ala Ala Leu Ala Tyr Asn Met Gly Gln
1               5                   10                  15
Asp His Ala Pro Lys Val Ile Ala Ser Gly Val Gly Glu Val Ala Lys
```

This Sheet Has Been Replaced



```
            20                  25                  30
Arg Ile Ile Gln Lys Ala Lys Glu Tyr Asp Ile Ala Leu Phe Ser Asn
        35                  40                  45
Pro Met Leu Val Asp Ser Leu Leu Lys Val Glu Leu Asp Cys Ala Ile
    50                  55                  60
Pro Glu Glu Leu Tyr Glu Ser Val Val Gln Val Phe Leu Trp Leu Asn
65                  70                  75                  80
Ser Val Glu Asn Asn Ala Gln Met Ser Lys
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:449:

(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:449

```
Met Gln Ala Leu Lys Ser Leu Leu Glu Val Ile Thr Lys Leu Gln Asn
1               5                  10                  15
Leu Gly Gly Tyr Leu Met His Ile Ala Ile Phe Ile Ile Phe Ile Trp
            20                  25                  30
Ile Gly Gly Leu Lys Phe Val Pro Tyr Glu Ala Glu Gly Ile Ala Pro
        35                  40                  45
Phe Val Unk Asn Ser Pro Phe Phe Ser Phe Met Tyr Lys Phe Glu Lys
    50                  55                  60
Pro Ala Tyr Lys Gln His Lys Met Ser Glu Ser Gln Ser Met Gln Glu
65                  70                  75                  80
Glu Met Gln Asp Asn Pro Lys Ile Val Glu Asn Lys Unk Trp His Lys
                85                  90                  95
Glu Asn Arg Thr Ser Phe Ser Gly
            100
```

(2) INFORMATION FOR SEQ ID NO:449:

(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

This Sheet Has Been Replaced

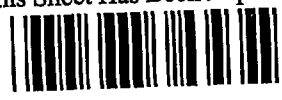


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449

```
Met Gln Ala Leu Lys Ser Leu Leu Glu Val Ile Thr Lys Leu Gln Asn
1               5                  10                  15
Leu Gly Gly Tyr Leu Met His Ile Ala Ile Phe Ile Ile Phe Ile Trp
            20                  25                  30
Ile Gly Gly Leu Lys Phe Val Pro Tyr Glu Ala Glu Gly Ile Ala Pro
        35                  40                  45
Phe Val Unk Asn Ser Pro Phe Phe Ser Phe Met Tyr Lys Phe Glu Lys
    50                  55                  60
Pro Ala Tyr Lys Gln His Lys Met Ser Glu Ser Gln Ser Met Gln Glu
65                  70                  75                  80
Glu Met Gln Asp Asn Pro Lys Ile Val Glu Asn Lys Unk Trp His Lys
                85                  90                  95
Glu Asn Arg Thr Ser Phe Ser Gly
            100
```

(2) INFORMATION FOR SEQ ID NO:450:

This Sheet Has Been Replaced



(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:450

```
Met Gly Lys Ile Ser Ala His Leu Ala His Glu Ile Arg Asn Pro Val
1               5                  10                  15
Gly Ser Ile Ser Leu Leu Ala Ser Val Leu Leu Lys His Ala Asn Glu
            20                  25                  30
Lys Thr Lys Pro Ile Val Val Glu Leu Gln Lys Ala Leu Trp Arg Val
        35                  40                  45
Glu Arg Ile Ile Lys Ala Thr Leu Leu Phe Ser Lys Gly Ile Gln Ala
    50                  55                  60
Asn Arg Thr Lys Gln Ser Leu Lys Thr Leu Glu Ser Asp Leu Lys Glu
65                  70                  75                  80
Ala Leu Asn Cys Tyr Thr Tyr Ser Lys Asp Ile Asp Phe Leu Phe Asn
                85                  90                  95
Phe Ser Asp Glu Glu Gly Phe Phe Asp Phe Asp Leu Met Gly Ile Val
            100                 105                 110
Leu Gln Asn Phe Leu Tyr Asn Ala Ile Asp Ala Ile Glu Ala Leu Glu
        115                 120                 125
Glu Ser Glu Gln Gly Gln Val Lys Ile Glu Ala Phe Ile Gln Asn Glu
    130                 135                 140
Phe Ile Val Phe Thr Ile Ile Asp Asn Gly Lys Glu Val Glu Asn Lys
145                 150                 155                 160
Ser Ala Leu Phe Glu Pro Phe Glu Thr Thr Lys Leu
                165                 170
```

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451

```
Val Ser Glu Phe His Gln Val Tyr Asp Pro Leu Gly Asn Ile Trp Leu
1               5                  10                  15
Ser Ala Leu Val Ala Leu Leu Pro Ile Leu Leu Phe Phe Leu Ser Leu
            20                  25                  30
Met Val Phe Lys Leu Lys Gly Tyr Thr Ala Ala Phe Leu Ser Val Ala
        35                  40                  45
Leu Ser Ala Ile Ile Ala Val Leu Val Tyr Lys Met Pro Val Ser Met
    50                  55                  60
Val Gly Ser Ser Phe Leu Tyr Gly Phe Leu Tyr Gly Leu Trp Leu Phe
65                  70                  75                  80
Ala Trp Ile Ile Ile Ala Ala Ile Phe Leu Tyr Lys Leu Ser Val Lys
                85                  90                  95
Ser Gly Tyr Phe Glu Ile Leu Lys Glu Ser Val Gln Ser Ile Thr Leu
            100                 105                 110
Asp His Arg Ile Leu Val Ile Leu Ile Gly Phe Cys Phe Gly Ser Phe
        115                 120                 125
Leu Glu Gly Ala Ile Gly Phe Gly Gly Pro Ile Ala Ile Thr Ala Ala
    130                 135                 140
Ile Leu Val Gly Leu Gly Leu Ser Pro Leu Tyr Ser Ala Gly Leu Cys
145                 150                 155                 160
Leu Ile Ala Asn Thr Ala Pro Val Ala Phe Gly Ala Val Gly Ile Pro
                165                 170                 175
Ile Ser Ala Met Ala Ser Ala Val Gly Val Pro Ala Ile Leu Ile Ser
            180                 185                 190
Ala Met Thr Gly Lys Ile Leu Phe Phe Val Ser Leu Leu Val Pro Phe
        195                 200                 205
Phe Ile Val Phe
    210
```

(2) INFORMATION FOR SEQ ID NO:452:

This Sheet Has Been Replaced



(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:452

```
Met Glu Ile Lys Met Ala Lys Asp Tyr Gly Phe Cys Phe Gly Val Lys
1               5                  10                  15
Arg Ala Ile Gln Ile Ala Glu Lys Asn Gln Asn Ser Leu Ile Phe Gly
            20                  25                  30
Ser Leu Ile His Asn Ala Lys Glu Ile Asn Arg Leu Glu Lys Asn Phe
        35                  40                  45
Asn Val Lys Ile Glu Glu Asp Pro Lys Lys Ile Pro Lys Asn Lys Ser
    50                  55                  60
Val Ile Ile Arg Thr His Gly Ile Pro Lys Gln Asp Leu Glu Tyr Leu
65                  70                  75                  80
Lys Asn Lys Gly Val Lys Ile Thr Asp Ala Thr Cys Pro Tyr Val Ile
                85                  90                  95
Lys Pro Gln Gln Ile Val Glu Ser Met Ser Lys Glu Gly Tyr Gln Ile
            100                 105                 110
Val Leu Phe Gly Asp Ile Asn His Pro Glu Val Lys Gly Val Ile Ser
        115                 120                 125
Tyr Ala Thr Asn Gln Ala Leu Val Gly Asn Ser Leu Glu Glu Leu Gln
    130                 135                 140
Glu Lys Lys Leu Gln Arg Lys Val Ala Leu Val Ser Gln Thr Thr Gln
145                 150                 155                 160
Ala Asn Pro Lys Thr Leu Ala Asn Arg Phe Leu Phe Gly Gly Unk Cys
                165                 170                 175
Thr Glu Val Arg Ile Phe
            180
```

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear.

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453

```
Met Asp His Glu Phe Leu Ile Thr Met Arg Leu Ser Phe Ser Leu Ala
1               5                  10                  15
Leu Ile Thr Thr Leu Ile Leu Leu Pro Ile Gly Ile Phe Leu Gly Tyr
            20                  25                  30
Phe Leu Ser Leu Lys Arg Asn Leu Leu Thr Ser Leu Thr Glu Thr Leu
        35                  40                  45
Val Tyr Met Pro Leu Val Leu Pro Pro Ser Val Leu Gly Phe Tyr Leu
    50                  55                  60
Leu Leu Ile Phe Ser Pro Ser Ser Phe Leu Gly Ala Phe Leu Gln Asp
65                  70                  75                  80
Val Leu Asn Val Lys Leu Val Phe Ser Phe Gln Gly Leu Ile Leu Gly
                85                  90                  95
Ser Val Ile Phe Ser Leu Pro Phe Met Val Ser Pro Ile Lys Ser Ala
            100                 105                 110
Leu Ile Ser Leu Pro Thr Ser Leu Lys Glu Ala Ser Tyr Ser Leu Gly
        115                 120                 125
Lys Gly Glu Tyr Tyr Thr Leu Phe Phe Val Leu Leu Pro Asn Ile Lys
```

```
    130                 135                 140
Pro Ser Val Leu Met Ala Ile Ile Thr Thr Phe Met His Thr Ile Gly
145                 150                 155                 160
Glu Phe Gly Val Val Met Met Leu Gly Gly Asp Ile Leu Gly Glu Thr
                165                 170                 175
Arg Val Ala Ser Ile Thr Ile Phe Asn Glu Ala Glu Ala Leu Asn Tyr
            180                 185                 190
Ser Lys Ala His Gln Tyr Ala Leu Thr Leu Thr Leu Ile Ser Phe Ser
        195                 200                 205
Leu Leu Phe Val Thr Leu Phe Leu Asn Lys Lys Gln Ser Ser Phe Leu
    210                 215                 220
```

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454

```
Met His Pro Ile Met Phe Ala Tyr Ile Ala Asn Ala Leu Ala Gln Ala
1               5                   10                  15
Arg Lys Ile Asn Gly Thr Leu Cys Met Ala Phe Gln Lys Ile Ser Gln
            20                  25                  30
Val Lys Glu Leu Gly Ile Asp Lys Ala Lys Ser Leu Ile Gly Asn Leu
        35                  40                  45
Ser Gln Val Ile Ile Tyr Pro Thr Lys Asp Thr Asp Glu Leu Ile Glu
    50                  55                  60
Cys Gly Val Pro Leu Ser Asp Ser Glu Ile Asn Phe Leu His Asn Thr
65                  70                  75                  80
Asp Met Arg Ala Arg Gln Val Leu Val Lys Asn Ile Val Thr Asn Ala
                85                  90                  95
Ser Ala Phe Ile Glu Ile Asp Leu Lys Lys Ile Cys Lys Asn Tyr Phe
            100                 105                 110
Ile Phe Leu Ile Ala Met Leu Val Ile Glu Lys Ser Ser Met Ile Leu
        115                 120                 125
Lys Lys Gln
    130
```

(2) INFORMATION FOR SEQ ID NO:455:

(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:

This Sheet Has Been Replaced



(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455

```
Met Cys Leu Thr Gly Gly Leu Met Arg Trp Leu Lys Ser Val Lys Pro
1               5                  10                  15
Glu Arg Ile Leu His Ser Val Val Glu Phe Val Asp Ile Ala Gly Leu
            20                  25                  30
Ile Lys Gly Ala Ser Lys Gly Glu Gly Leu Gly Asn Gln Phe Leu Ala
        35                  40                  45
Asn Ile Lys Glu Cys Glu Val Ile Leu Gln Val Val Arg Cys Phe Glu
    50                  55                  60
Asp Asp Asn Asn His Ala Cys Glu Arg
65                  70
```

(2) INFORMATION FOR SEQ ID NO:456:

(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:456

```
Met His Val Ala Cys Leu Leu Ala Leu Gly Asp Asn Leu Ile Thr Leu
1               5                  10                  15
Ser Leu Leu Lys Glu Ile Ala Ser Lys Gln Gln Gln Ser Leu Lys Ile
            20                  25                  30
Leu Gly Thr His Leu Thr Leu Lys Ile Ala Lys Leu Leu Glu Cys Glu
        35                  40                  45
Lys His Phe Glu Ile Ile Pro Val Phe Glu Asn Ile Pro Ala Phe Tyr
    50                  55                  60
Asp Leu Lys Lys Gln Gly Val Phe Trp Ala Met Lys Asp Phe Leu Trp
65                  70                  75                  80
Leu Leu Lys Gln Leu Lys Asn Ile Lys Ser Asn Val
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457

```
Met Lys Lys Lys Pro Leu Met Trp Arg Ile Cys Ala Leu Arg Arg Leu
1               5                  10                  15
Leu Leu Gly Phe Lys Arg Glu Arg Glu Leu Leu Ser Phe Ala Lys His
            20                  25                  30
Trp Asn Ile Pro Thr Ile Val Val Phe Thr His Thr Gln Ala Glu Ala
        35                  40                  45
Gly Asp Ala Phe Val Gln Glu Thr Lys Gly Ile Ile Asp Glu Glu Trp
    50                  55                  60
Gly Phe Lys Gly Phe Val Arg Ala Tyr Val Arg Val Asn Ser Val Ala
65                  70                  75                  80
Phe Ser Phe Arg Gly Leu Lys Val Pro Val Glu Gly Leu Glu Glu Leu
                85                  90                  95
Val Asp Glu Thr Lys Lys Cys Leu Ser Asp Ala Glu Lys Asn Lys Lys
            100                 105                 110
Arg His Phe Leu Ser Ile Gln Arg Val Lys Ile Gln Glu Arg Lys Gln
        115                 120                 125
Ala Met Ile Glu Glu Cys Lys Thr Ile Ile His Val Ala Ser Gly Ala
    130                 135                 140
Ala Gly Val Ala Gly Leu Ile Pro Ile Pro Phe Ser Asp Ala Leu Ala
145                 150                 155                 160
Ile Ala Pro Ile Gln Ala Gly Met Ile Tyr Lys Met Asn Asp Ala Phe
                165                 170                 175
Gly Met Asp Leu Asp Lys Ser Val Gly Ala Ser Leu Val Ala Gly Leu
            180                 185                 190
Leu Gly Val Asn Cys Arg Ala Ser Gly Glu Asp Ser Arg
        195                 200                 205
```

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...41

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458

```
Val Leu Gly Val Unk Asn Leu Arg Gly Asn Val Phe Pro Leu Ile Ser
1               5                  10                  15
Leu Arg Leu Lys Phe Gly Leu Lys Ala Glu Lys Gln Asn Lys Asp Thr
            20                  25                  30
Arg Tyr Leu Val Val Arg His Asn Asp
        35                  40
```

This Sheet Has Been Replaced

SUBSTITUTE SHEET (RULE 26)



(2) INFORMATION FOR SEQ ID NO:459:

(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:459

```
Val Lys Ser Val Phe Ser Glu Glu Lys Glu Thr Pro Val Thr Lys Glu
1               5                  10                  15
Asn Gly Ser Tyr Leu Ile Ala Tyr Asp Pro Leu Asp Gly Ser Ser Val
            20                  25                  30
Met Glu Ala Asn Phe Leu Val Gly Thr Ile Ile Gly Val Tyr Glu Lys
        35                  40                  45
Asp Tyr Lys Ala Gln Asn Leu Val Ala Ser Leu Tyr Val Val Phe Gly
    50                  55                  60
His Lys Ile Glu Leu Val Val Ala Leu Glu Glu Val Tyr Arg Tyr Ala
65                  70                  75                  80
Phe Tyr Gln Asn Lys Phe His Phe Ile Glu Thr Ile Val Leu Glu Asn
                85                  90                  95
Lys Gly Lys Ile Ile Ala Ser Gly Gly Asn Gln Lys Asp Phe Ser Leu
            100                 105                 110
Gly Leu Lys Lys Ala Leu Glu Gly Phe Phe Ala Glu Asn Tyr Arg Leu
        115                 120                 125
Arg Tyr Ser Gly Ser Met Val Ala Asp Val His His Val Leu Val Lys
    130                 135                 140
Lys Gly Gly Met Phe Ser Tyr Pro Gln Lys Lys Leu Arg Lys Leu Phe
145                 150                 155                 160
Glu Val Phe Pro Leu Ala Leu Met Val Glu Lys Ala Lys Gly Glu Ala
                165                 170                 175
Phe Tyr Phe Asp Lys Gly Val Lys Lys Arg Leu Leu Asp Gln Ser Val
            180                 185                 190
Glu Ser Tyr His Glu Lys Ser Glu Cys Tyr Leu Ala Ser Pro His Glu
        195                 200                 205
Ala Gln Ile Leu Glu Lys His Leu Lys Gly Glu
    210                 215
```

(2) INFORMATION FOR SEQ ID NO:460:

(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:

This Sheet Has Been Replaced



(A) NAME/KEY: misc_feature
(B) LOCATION 1...188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460

```
Met Lys Ser Ile Gly Glu Val Met Ala Ile Gly Gly Asn Phe Leu Glu
1               5                  10                  15
Ala Leu Gln Lys Ala Leu Cys Ser Leu Glu Asn Asn Trp Leu Gly Phe
            20                  25                  30
Glu Ser Leu Ser Lys Asp Leu Glu Ala Ile Lys Lys Glu Ile Arg Arg
        35                  40                  45
Pro Asn Pro Lys Arg Leu Leu Tyr Ile Ala Asp Ala Phe Arg Leu Gly
    50                  55                  60
Val Ser Val Asp Glu Val Phe Glu Leu Cys Gln Ile Asp Arg Trp Phe
65                  70                  75                  80
Leu Ser Gln Ile Gln Lys Leu Val Lys Ala Glu Glu Gly Ile Asn Ser
                85                  90                  95
Ser Val Leu Thr Asp Ala Lys Lys Leu Arg Gly Leu Lys Asn Leu Gly
            100                 105                 110
Phe Ser Asp Ala Arg Ile Ala Thr Lys Ile Lys Glu Asn Glu Asn Leu
        115                 120                 125
Glu Val Ser Pro Phe Glu Val Glu Leu Ala Arg Ser Asn Leu Gln Ile
    130                 135                 140
Ala Pro His Phe Glu Glu Val Asp Thr Cys Ala Ala Glu Phe Leu Ser
145                 150                 155                 160
Leu Thr Leu Ile Cys Ile Pro Pro Met Pro Leu Thr Leu Cys Pro Leu
                165                 170                 175
Leu Glu Thr Asn Lys Lys Asn Lys Lys Arg Lys Ser
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:461:

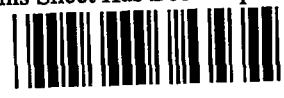
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461

```
Met Phe Gly Asn Lys Gln Leu Gln Leu Gln Ile Ser Gln Lys Asp Ser
1               5                  10                  15
Glu Ile Ala Glu Leu Lys Lys Glu Val Asn Leu Tyr Gln Ser Leu Leu
            20                  25                  30
Asn Leu Cys Leu His Glu Gly Phe Val Gly Ile Lys Asn Asn Lys Val
        35                  40                  45
Val Phe Lys Ser Gly Asn Leu Ala Ser Leu Asn Asn Leu Glu Glu Gln
    50                  55                  60
Ser Val His Phe Lys Glu Asn Ala Glu Ser Val Asn Leu Gln Gly Val
65                  70                  75                  80
Ser Tyr Ser Leu Lys Ser Gln Asn Ile Asp Gly Val Gln Tyr Phe Ser
                85                  90                  95
Leu Ala Lys Lys Thr Gly Gly Val Gly Glu Tyr His Lys Asn Asp Leu
            100                 105                 110
```

```
Phe Lys Thr Phe Cys Thr Ser Leu Lys Glu Gly Leu Glu Asn Ala Gln
        115                 120                 125
Glu Ser Met Gln Tyr Phe His Gln Glu Thr Gly Leu Leu Leu Asn Ala
    130                 135                 140
Ala Lys Asn Gly Glu Glu His Ser Asn Glu Gly Leu Ile Thr Val Asn
145                 150                 155                 160
Lys Thr Gly Gln Asp Ile Glu Ser Leu Tyr Glu Lys Met Gln Asn Ala
                165                 170                 175
Thr Ser Leu Ala Asp Ser Leu Asn Gln Arg Ser Asn Glu Ile Thr Gln
            180                 185                 190
Val Ile Ser Leu Ile Asp Asp Ile Ala Glu Gln Thr Asn Leu Leu Ala
        195                 200                 205
Leu Asn Ala Ala Ile Glu Ala Ala Arg Ala Val Asn Met Ala Glu Gly
    210                 215                 220
Leu Arg Trp Trp Leu Met Arg
225                 230
```

(2) INFORMATION FOR SEQ ID NO:462:

(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:462

```
Met Trp Ile Met Ser Ser Leu Ser Ser Ser Phe Phe His Ser Leu Phe
1               5                   10                  15
Phe Ile Lys Ser Asn Pro Gly Gln Leu Leu Lys Gly Trp Gly Ser Lys
            20                  25                  30
Ile Phe Phe Ile Asn Arg Lys Phe Val Leu Ala Gln Tyr Asn Pro Ser
        35                  40                  45
Val Ser Ile Phe Ile Leu Leu Asn Arg Val Phe Gly Val Gly Val
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:463:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463

```
Met Gln Phe Glu Glu Met Lys Glu Leu Ala His Gln Ile Gly Val Phe
1               5                  10                  15
Tyr His Val Gly Val Asp Gly Ile Ala Leu Phe Leu Leu Leu Leu Asn
            20                  25                  30
Ala Ile Val Val Leu Leu Ser Val Val Tyr Val Lys Glu Arg Arg Lys
        35                  40                  45
Asp Phe Val Ile Cys Leu Leu Leu Leu Unk Gly Ile Leu Met Gly Val
    50                  55                  60
Phe Ser Ser Leu Asn Val Ile Phe Phe Tyr Ala Phe Trp Glu Ile Ser
65                  70                  75                  80
Leu Leu Pro Val Leu Tyr Leu Ile Gly Arg Phe Gly Arg Asn Asn Lys
                85                  90                  95
Ile Tyr Ser Gly Met Lys Phe Phe Leu Tyr Thr Phe Leu Ala Ser Leu
            100                 105                 110
Cys Met Leu Leu Gly Ile Leu Tyr Ile Gly Tyr Asp Tyr Ala Asn Asn
        115                 120                 125
Tyr Gly Met Met Ser Phe Asp Ile Leu Asp Trp Tyr Gln Leu Asn Phe
    130                 135                 140
Ser Ser Gly Ile Lys Thr Trp Leu Phe Val Ala Phe Leu Ile Gly Ile
145                 150                 155                 160
Ala Val Lys Ile Pro Leu Phe Pro Phe Thr His Gly Cys Leu Met Arg
                165                 170                 175
Ile Leu Thr Pro Pro Leu
            180
```

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463

```
Met Gln Phe Glu Glu Met Lys Glu Leu Ala His Gln Ile Gly Val Phe
1               5                  10                  15
Tyr His Val Gly Val Asp Gly Ile Ala Leu Phe Leu Leu Leu Leu Asn
            20                  25                  30
Ala Ile Val Val Leu Leu Ser Val Val Tyr Val Lys Glu Arg Arg Lys
        35                  40                  45
Asp Phe Val Ile Cys Leu Leu Leu Leu Unk Gly Ile Leu Met Gly Val
    50                  55                  60
Phe Ser Ser Leu Asn Val Ile Phe Phe Tyr Ala Phe Trp Glu Ile Ser
65                  70                  75                  80
Leu Leu Pro Val Leu Tyr Leu Ile Gly Arg Phe Gly Arg Asn Asn Lys
                85                  90                  95
Ile Tyr Ser Gly Met Lys Phe Phe Leu Tyr Thr Phe Leu Ala Ser Leu
            100                 105                 110
Cys Met Leu Leu Gly Ile Leu Tyr Ile Gly Tyr Asp Tyr Ala Asn Asn
        115                 120                 125
```

```
Tyr Gly Met Met Ser Phe Asp Ile Leu Asp Trp Tyr Gln Leu Asn Phe
    130                 135                 140
Ser Ser Gly Ile Lys Thr Trp Leu Phe Val Ala Phe Leu Ile Gly Ile
145                 150                 155                 160
Ala Val Lys Ile Pro Leu Phe Pro Phe Thr His Gly Cys Leu Met Arg
                165                 170                 175
Ile Leu Thr Pro Pro Leu
            180
```

(2) INFORMATION FOR SEQ ID NO:464:

(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:464

```
Val Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val Lys Ser
1               5                   10                  15
Leu Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu Glu Ser
            20                  25                  30
Lys Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala Leu Leu
        35                  40                  45
His Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu Thr Ile
    50                  55                  60
Thr Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu Thr Glu
65                  70                  75                  80
Gln Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe Lys Ser
                85                  90                  95
Glu Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Unk Glu Gln
            100                 105                 110
Phe Unk Ala Gln
        115
```

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

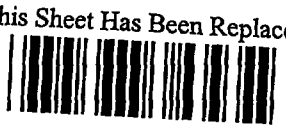
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...116

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464

```
Val Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val Lys Ser
1               5                  10                  15
Leu Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu Glu Ser
            20                  25                  30
Lys Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala Leu Leu
        35                  40                  45
His Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu Thr Ile
    50                  55                  60
Thr Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu Thr Glu
65                  70                  75                  80
Gln Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe Lys Ser
                85                  90                  95
Glu Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Unk Glu Gln
            100                 105                 110
Phe Unk Ala Gln
        115
```

(2) INFORMATION FOR SEQ ID NO:465:

(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:465

```
Val Gly Ala Asn Pro Val Pro His Ala Gln Ile Leu Gln Ser Val Val
1               5                  10                  15
Asp Asp Leu Lys Glu Lys Gly Ile Lys Leu Val Ile Val Ser Phe Thr
            20                  25                  30
Asp Tyr Val Leu Pro Asn Leu Ala Leu Asn Asp Gly Ser Leu Asp Ala
        35                  40                  45
Asn Tyr Phe Gln His Arg Pro Tyr Leu Asp Arg Phe Asn Leu Asp Arg
    50                  55                  60
Lys Met His Leu Val Gly Leu Ala Asn Ile His Val Glu Pro Leu Arg
65                  70                  75                  80
Phe Tyr Ser Gln Lys Ile Thr Asp Ile Lys Asn Leu Lys Lys Gly Ser
                85                  90                  95
Val Ile Ala Val Pro Asn Asp Pro Ala Asn Gln Gly Arg Ala Leu Ile
            100                 105                 110
Leu Leu His Lys Gln Gly Leu Ile Ala Leu Lys Asp Pro Ser Asn Leu
        115                 120                 125
Tyr Ala Thr Glu Phe Asp Ile Val Lys Asn Pro Tyr Asn Ile Lys Ile
    130                 135                 140
Lys Pro Leu Glu Ala Ala Val Ile Ala
145                 150
```

(2) INFORMATION FOR SEQ ID NO:466:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...43

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466

```
Met Gly Leu Val Ala Ser Gly Ile Asn Asp Glu Glu Leu Leu Lys Trp
1               5                  10                  15
Leu Gln Ala Phe Gly Leu Lys Met Gly Leu Cys Phe Gln Val Leu Asp
            20                  25                  30
Asp Ile Ile Asp Val Thr Gln Asp Glu Lys Glu
        35                  40
```

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467

```
Met Met Lys Asn Lys Arg Ser Gln Asn Ser Pro Tyr Val Thr Pro Asp
1               5                  10                  15
Asn Pro Tyr Leu Thr Leu Glu Lys Ala Leu Gly Tyr Ser Phe Lys Asp
            20                  25                  30
Lys Arg Leu Leu Glu Gln Ala Leu Thr His Lys Ser Cys Lys Leu Ala
        35                  40                  45
Leu Asn Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Val Leu Gly Leu
    50                  55                  60
Val Ile Gly Glu Leu Leu Tyr His Lys Phe Unk Unk Unk Asp Gly Gly
65                  70                  75                  80
Lys Leu Ser Lys Leu Arg Ala Ser Ile Val Ser Ala His Gly Phe Thr
                85                  90                  95
Lys Leu Ala Lys Ala Ile Ala Leu Gln Asp Tyr Leu Arg Val Ser Ser
            100                 105                 110
Ser Glu Glu Ile Ser Lys Gly Arg Glu Lys Pro Ser Ile Leu Ser Ser
        115                 120                 125
Ala Phe Glu Ala Leu Met Ala Gly Val Tyr Leu Glu Ala Gly Leu Ala
    130                 135                 140
Lys Val Arg Lys Ile Ile Gln Asn Leu Leu Asn Arg Ala Tyr Lys Arg
```

```
145                 150                 155                 160
Leu Asp Leu Glu His Leu Phe Met Asp Tyr Lys Thr Ala Leu Gln Glu
                165                 170                 175
Leu Thr Gln Unk Gln Phe Cys Val Ile Pro Thr Tyr Gln Leu Leu Gln
            180                 185                 190
Glu Lys Gly Pro Asp His His Lys Glu Phe Glu Met Ala Leu Tyr Ile
        195                 200                 205
Gln Asp Lys Met Tyr Ala Thr Ala Lys Gly Lys Ser Lys Lys Glu Ala
    210                 215                 220
Glu Gln Gln Cys Ala Tyr Gln Ala Leu Gln Asn Leu Arg Lys Pro Asn
225                 230                 235                 240
```

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467

```
Met Met Lys Asn Lys Arg Ser Gln Asn Ser Pro Tyr Val Thr Pro Asp
1               5                  10                  15
Asn Pro Tyr Leu Thr Leu Glu Lys Ala Leu Gly Tyr Ser Phe Lys Asp
            20                  25                  30
Lys Arg Leu Leu Glu Gln Ala Leu Thr His Lys Ser Cys Lys Leu Ala
        35                  40                  45
Leu Asn Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Val Leu Gly Leu
    50                  55                  60
Val Ile Gly Glu Leu Leu Tyr His Lys Phe Unk Unk Unk Asp Gly Gly
65                  70                  75                  80
Lys Leu Ser Lys Leu Arg Ala Ser Ile Val Ser Ala His Gly Phe Thr
                85                  90                  95
Lys Leu Ala Lys Ala Ile Ala Leu Gln Asp Tyr Leu Arg Val Ser Ser
            100                 105                 110
Ser Glu Glu Ile Ser Lys Gly Arg Glu Lys Pro Ser Ile Leu Ser Ser
        115                 120                 125
Ala Phe Glu Ala Leu Met Ala Gly Val Tyr Leu Glu Ala Gly Leu Ala
    130                 135                 140
Lys Val Arg Lys Ile Ile Gln Asn Leu Leu Asn Arg Ala Tyr Lys Arg
145                 150                 155                 160
Leu Asp Leu Glu His Leu Phe Met Asp Tyr Lys Thr Ala Leu Gln Glu
                165                 170                 175
Leu Thr Gln Unk Gln Phe Cys Val Ile Pro Thr Tyr Gln Leu Leu Gln
            180                 185                 190
Glu Lys Gly Pro Asp His His Lys Glu Phe Glu Met Ala Leu Tyr Ile
        195                 200                 205
Gln Asp Lys Met Tyr Ala Thr Ala Lys Gly Lys Ser Lys Lys Glu Ala
    210                 215                 220
Glu Gln Gln Cys Ala Tyr Gln Ala Leu Gln Asn Leu Arg Lys Pro Asn
225                 230                 235                 240
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:468:

(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:468

```
Met Gly Phe Asn Arg Leu Val Asp Arg Asp Ile Asp Lys Asp Asn Pro
1               5                  10                  15
Arg Thr Lys Asn Arg Pro Ser Val Asp Gly Arg Ile Ser Val Lys Gly
            20                  25                  30
Met Val Ile Phe Ser Val Ser Asn Ala Leu Leu Phe Val Gly Val Ser
        35                  40                  45
Tyr Phe Ile Asn Pro Leu Ala Phe Lys Leu Ser Leu Pro Phe Leu Ile
    50                  55                  60
Ile Leu Gly Gly Tyr Ser Tyr Phe Lys Arg Phe Ser Ser Leu Ala His
65                  70                  75                  80
Phe Val Val Gly Leu Ala Leu Gly Leu Ala Pro Ile Ala Gly Ser Val
                85                  90                  95
Ala Val Leu Gly Asp Ile Pro Leu Trp Asn Val Phe Leu Ala Leu Gly
            100                 105                 110
Val Met Leu Trp Val Ala Gly Phe Asp Leu Leu Tyr Ser Leu Gln Asp
        115                 120                 125
Met Glu Phe Asp Lys Glu Arg Gly Leu Phe Ser Ile Pro Ser Gln Leu
    130                 135                 140
Gly Glu Lys Trp Cys Leu Asn Leu Ser Arg Leu Ser His Leu Val Ala
145                 150                 155                 160
Leu Ile Cys Trp Leu Cys Phe Val Lys Cys Tyr His Gly Gly Leu Phe
                165                 170                 175
Ala Tyr Leu Gly Leu Gly Val Ser Ala Leu Ile Leu Leu Tyr Glu Gln
            180                 185                 190
Ile Leu Val Ala Arg Asp Tyr Lys Asn Ile Pro Lys Ser Leu Phe Cys
        195                 200                 205
Glu
```

(2) INFORMATION FOR SEQ ID NO:469:

This Sheet Has Been Replaced



(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:469

```
Val Glu Gln Asn Lys Ile Ile Lys Leu Phe Thr Val Ala Thr Met Ala
1               5                  10                  15
Met Met Pro Pro Thr Leu Ile Gly Thr Ile Asn Gly Met Asn Phe Lys
            20                  25                  30
Phe Met Pro Glu Leu Glu Trp Gln Tyr Gly Tyr Leu Phe Ala Leu Ile
        35                  40                  45
Val Met Ala Ile Ser Thr Ile Leu Pro Val Ile Tyr Phe Lys Lys Lys
    50                  55                  60
Gly Leu Val Val Ala Phe His Gly Ile Phe Ile Leu Thr Leu Arg Arg
65                  70                  75                  80
Ser Phe Tyr Thr Ala Trp His Ser Leu Leu Gly Tyr Ala Thr Leu
                85                  90                  95
```

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:470

```
Leu Leu Val Leu Leu Asn Leu Lys Unk Thr Pro Asn Leu Met Trp Pro
1               5                  10                  15
Leu Asp Ile Ile Val Val Val Ala Trp Val Leu Trp Gly Val Asn Met
            20                  25                  30
Phe Gly Ser Met Ser Val Arg Arg Glu Asn Thr Ile Tyr Val Ser Leu
        35                  40                  45
Trp Tyr Tyr Ile Ala Thr Tyr Val Gly Ile Ala Val Met Tyr Ile Phe
    50                  55                  60
Asn Asn Leu Ser Ile Pro Thr Tyr Phe Val Ala Asp Met Gly Ser Val
65                  70                  75                  80
Trp His Unk Ile Ser Met Tyr Ser Gly Ser Asn Asp Ala Leu Ile Gln
                85                  90                  95
Trp Trp Trp Gly His Asn Ala Val Ala Phe Val Phe Thr Ser Gly Val
            100                 105                 110
Ile Gly Thr Ile Tyr Tyr Phe Leu Pro Lys Glu Ser Gly Gln Pro Ile
        115                 120                 125
Phe Ser Tyr Lys Leu Thr Leu Phe Ser Phe Trp Ser Leu Met Phe Val
    130                 135                 140
Tyr Ile Trp Ala Gly Gly His His Leu Ile Tyr Ser Thr Val Unk Asp
145                 150                 155                 160
Unk Val Gln Thr Leu Ser Ser Unk Phe Ser Val Val Leu Ile Leu Pro
                165                 170                 175
Ser Unk Gly Thr Ala Ile Asn Met Leu Leu Unk Met Arg Gly Gln Trp
            180                 185                 190
His Gln Unk Lys Glu Ser Pro Leu Ile Lys Phe Leu Val Leu Ala Ser
        195                 200                 205
```

Thr Phe Tyr Met Leu Ser Thr Leu Glu Gly Ser Ile Gln Ala Ile Lys
210 215 220
Ser Val Asn Ala
225

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470

Leu Leu Val Leu Leu Asn Leu Lys Unk Thr Pro Asn Leu Met Trp Pro
1 5 10 15
Leu Asp Ile Ile Val Val Val Ala Trp Val Leu Trp Gly Val Asn Met
20 25 30
Phe Gly Ser Met Ser Val Arg Arg Glu Asn Thr Ile Tyr Val Ser Leu
35 40 45
Trp Tyr Tyr Ile Ala Thr Tyr Val Gly Ile Ala Val Met Tyr Ile Phe
50 55 60
Asn Asn Leu Ser Ile Pro Thr Tyr Phe Val Ala Asp Met Gly Ser Val
65 70 75 80
Trp His Unk Ile Ser Met Tyr Ser Gly Ser Asn Asp Ala Leu Ile Gln
85 90 95
Trp Trp Trp Gly His Asn Ala Val Ala Phe Val Phe Thr Ser Gly Val
100 105 110
Ile Gly Thr Ile Tyr Tyr Phe Leu Pro Lys Glu Ser Gly Gln Pro Ile
115 120 125
Phe Ser Tyr Lys Leu Thr Leu Phe Ser Phe Trp Ser Leu Met Phe Val
130 135 140
Tyr Ile Trp Ala Gly Gly His His Leu Ile Tyr Ser Thr Val Unk Asp
145 150 155 160
Unk Val Gln Thr Leu Ser Ser Unk Phe Ser Val Val Leu Ile Leu Pro
165 170 175
Ser Unk Gly Thr Ala Ile Asn Met Leu Leu Unk Met Arg Gly Gln Trp
180 185 190
His Gln Unk Lys Glu Ser Pro Leu Ile Lys Phe Leu Val Leu Ala Ser
195 200 205
Thr Phe Tyr Met Leu Ser Thr Leu Glu Gly Ser Ile Gln Ala Ile Lys
210 215 220
Ser Val Asn Ala
225

(2) INFORMATION FOR SEQ ID NO:471:

(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

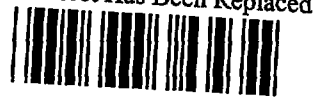
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471

```
Met Phe Asp Ser Ile Val Tyr Phe Phe Asn Lys Ser Gly Phe Val Thr
1               5                  10                  15
Thr Leu Val Leu Val Trp Ile Ser Leu Tyr Leu Val Met Thr Leu Trp
            20                  25                  30
Val Phe Leu Tyr Lys Ser Ile Val Leu Lys Ile Glu Leu Arg Arg Glu
        35                  40                  45
Met Gln Ser Leu Ser Asn Ile Leu Asn Gly Ala Gln Asp Ala Pro Glu
    50                  55                  60
His Phe Met Phe Asn Lys Lys Arg Asn Asp Glu Thr Lys Arg Tyr Ser
65                  70                  75                  80
Asn Glu Leu Leu Gln Asp Leu Glu Thr Pro Gly Ser
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:472:

This Sheet Has Been Replaced



(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:472

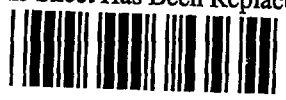
```
Met Ala Met Leu Tyr Cys Met Arg Leu Leu Met Pro Ile Leu Gly Ala
1               5                  10                  15
Ile Lys Gly Gly Asp Ile Gly Glu Trp Phe Pro Asp Asn Asp Pro Lys
            20                  25                  30
Tyr Lys Asn Ala Ser Ser Lys Glu Leu Leu Lys Ile Val Leu Asp Phe
        35                  40                  45
Ser Gln Ser Ile Gly Phe Glu Leu Leu Glu Met Gly Ala Thr Ile Phe
    50                  55                  60
Ser Glu Ile Pro Lys Ile Thr Pro Tyr Lys Pro Ala Ile Leu Glu Asn
65                  70                  75                  80
Leu Ser Gln Leu Leu Gly Leu Glu Lys Ser Gln Ile Ser Leu Lys Ala
                85                  90                  95
```

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1178 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

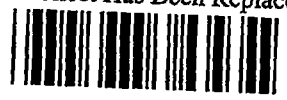
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473

```
Met Ile Pro Asn Leu Asp Ile Glu Gly Glu Thr Met Thr Asn Glu Ala
1               5                  10                  15
Ile Asn Gln Gln Pro Gln Thr Glu Ala Ala Phe Asn Pro Gln Gln Phe
            20                  25                  30
Ile Asn Asn Leu Gln Val Ala Phe Ile Lys Val Asp Asn Val Val Ala
        35                  40                  45
Ser Phe Asp Pro Asn Gln Lys Pro Ile Val Asp Lys Asn Asp Arg Asp
    50                  55                  60
Asn Arg Gln Ala Phe Glu Lys Ile Ser Gln Leu Arg Glu Glu Phe Ala
65                  70                  75                  80
Asn Lys Ala Ile Lys Asn Pro Thr Lys Lys Asn Gln Tyr Phe Ser Ser
                85                  90                  95
Phe Ile Ser Lys Ser Asn Asp Leu Ile Asp Lys Asp Asn Leu Ile Asp
            100                 105                 110
Thr Gly Ser Ser Ile Lys Ser Phe Gln Lys Phe Gly Thr Gln Arg Tyr
        115                 120                 125
Gln Ile Phe Met Asn Trp Val Ser His Gln Asn Asp Pro Ser Lys Ile
    130                 135                 140
Asn Thr Gln Lys Ile Arg Gly Phe Met Glu Asn Ile Ile Gln Pro Pro
145                 150                 155                 160
Ile Ser Asp Asp Lys Glu Lys Ala Glu Phe Leu Arg Ser Ala Lys Gln
                165                 170                 175
Ala Phe Ala Gly Ile Ile Ile Gly Asn Gln Ile Arg Ser Asp Gln Lys
            180                 185                 190
Phe Met Gly Val Phe Asp Glu Ser Leu Lys Glu Arg Gln Glu Ala Glu
        195                 200                 205
Lys Asn Gly Glu Pro Asn Gly Asp Pro Thr Gly Gly Asp Trp Leu Asp
    210                 215                 220
Ile Phe Leu Ser Phe Val Phe Asn Lys Lys Gln Ser Ser Asp Leu Lys
225                 230                 235                 240
Glu Thr Leu Asn Gln Glu Pro Val Pro His Val Gln Pro Asp Val Ala
                245                 250                 255
Thr Thr Thr Thr Asp Ile Gln Ser Leu Pro Pro Glu Ala Arg Asp Leu
            260                 265                 270
Leu Asp Glu Arg Gly Asn Phe Ser Lys Phe Thr Leu Gly Asp Met Asn
        275                 280                 285
Met Leu Asp Val Glu Gly Val Ala Asp Ile Asp Pro Asn Tyr Lys Phe
    290                 295                 300
Asn Gln Leu Leu Ile His Asn Asn Ala Leu Ser Ser Val Leu Met Gly
305                 310                 315                 320
Ser His Asn Gly Ile Glu Pro Glu Lys Val Ser Leu Leu Tyr Gly Asn
                325                 330                 335
Asn Gly Gly Pro Glu Ala Arg His Asp Trp Asn Ala Thr Val Gly Tyr
            340                 345                 350
Lys Asn Gln Arg Gly Asp Asn Val Ala Thr Leu Ile Asn Val His Met
        355                 360                 365
Lys Asn Gly Ser Gly Leu Val Ile Ala Gly Gly Glu Lys Gly Ile Asn
    370                 375                 380
Asn Pro Ser Phe Tyr Leu Tyr Lys Glu Asp Gln Leu Thr Gly Ser Gln
```

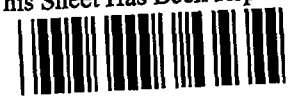
This Sheet Has Been Replaced



385 390 395 400
Arg Ala Leu Ser Gln Glu Glu Ile Gln Asn Lys Val Asp Phe Met Glu
405 410 415
Phe Leu Ala Gln Asn Asn Ala Lys Leu Asp Asn Leu Ser Lys Lys Glu
420 425 430
Lys Glu Lys Phe Gln Asn Glu Ile Glu Asp Phe Gln Lys Asp Ser Lys
435 440 445
Ala Tyr Leu Asp Ala Leu Gly Asn Asp His Ile Ala Phe Val Ser Lys
450 455 460
Lys Asp Lys Lys His Leu Ala Leu Val Ala Glu Phe Gly Asn Gly Glu
465 470 475 480
Leu Ser Tyr Thr Leu Lys Asp Tyr Gly Lys Lys Ala Asp Lys Ala Leu
485 490 495
Asp Arg Glu Ala Lys Thr Thr Leu Gln Gly Ser Leu Lys His Asp Gly
500 505 510
Val Met Phe Val Asp Tyr Ser Asn Phe Lys Tyr Thr Asn Ala Ser Lys
515 520 525
Ser Pro Asp Lys Gly Val Gly Ala Thr Asn Gly Val Ser His Leu Glu
530 535 540
Ala Gly Phe Ser Lys Val Ala Val Phe Asn Leu Pro Asn Leu Asn Asn
545 550 555 560
Leu Ala Ile Thr Ser Val Val Arg Gln Asp Leu Glu Asp Lys Leu Ile
565 570 575
Ala Lys Gly Leu Ser Pro Gln Glu Ala Asn Lys Leu Val Lys Asp Phe
580 585 590
Leu Ser Ser Asn Lys Glu Leu Val Gly Lys Ala Leu Asn Phe Asn Lys
595 600 605
Ala Val Ala Glu Ala Lys Asn Thr Gly Asn Tyr Asp Glu Val Lys Gln
610 615 620
Ala Gln Lys Asp Leu Glu Lys Ser Leu Lys Lys Arg Glu Arg Leu Glu
625 630 635 640
Lys Asp Val Ala Lys Asn Leu Glu Ser Lys Ser Gly Asn Lys Asn Lys
645 650 655
Met Glu Ala Lys Ser Gln Ala Asn Ser Gln Lys Asp Glu Ile Phe Ala
660 665 670
Leu Ile Asn Lys Glu Ala Asn Arg Asp Ala Arg Ala Ile Ala Tyr Ala
675 680 685
Gln Asn Leu Lys Gly Ile Lys Arg Glu Leu Ser Asp Lys Leu Glu Asn
690 695 700
Ile Asn Lys Asp Leu Lys Asp Phe Ser Lys Ser Phe Asp Glu Phe Lys
705 710 715 720
Asn Gly Lys Asn Lys Asp Phe Ser Lys Ala Glu Glu Thr Leu Lys Ala
725 730 735
Leu Lys Gly Ser Val Lys Asp Leu Gly Ile Asn Pro Glu Trp Ile Ser
740 745 750
Lys Val Glu Asn Leu Asn Ala Ala Leu Asn Glu Phe Lys Asn Gly Lys
755 760 765
Asn Lys Asp Phe Ser Lys Val Thr Gln Ala Lys Ser Asp Leu Glu Asn
770 775 780
Ser Ile Lys Asp Val Ile Ile Asn Gln Lys Ile Thr Asp Lys Val Asp
785 790 795 800
Asn Leu Asn Gln Ala Val Ser Val Ala Lys Ala Thr Gly Asp Phe Ser
805 810 815
Gly Val Glu Gln Ala Leu Ala Asp Leu Lys Asn Phe Ser Lys Glu Gln
820 825 830
Leu Ala Gln Gln Ala Gln Lys Asn Glu Asp Phe Asn Thr Gly Lys Asn
835 840 845
Ser Ala Leu Tyr Gln Ser Val Lys Asn Gly Val Asn Gly Thr Leu Val
850 855 860
Gly Asn Gly Leu Ser Lys Ala Glu Ala Thr Thr Leu Ser Lys Asn Phe
865 870 875 880
Ser Asp Ile Lys Lys Glu Leu Asn Ala Lys Leu Gly Asn Phe Asn Asn
885 890 895
Asn Asn Asn Asn Gly Leu Glu Asn Ser Thr Glu Pro Ile Tyr Thr Gln
900 905 910

```
Val Ala Lys Lys Val Lys Ala Lys Ile Asp Arg Leu Asp Gln Ile Ala
        915                 920                 925
Ser Gly Leu Gly Asp Val Gly Gln Ala Ala Ser Phe Leu Leu Lys Arg
    930                 935                 940
His Asp Lys Val Asp Asp Leu Ser Lys Val Gly Leu Ser Ala Asn His
945                 950                 955                 960
Glu Pro Ile Tyr Ala Thr Ile Asp Asp Leu Gly Gly Pro Phe Pro Leu
                965                 970                 975
Lys Arg His Asp Lys Val Asp Asp Leu Ser Lys Val Gly Leu Ser Arg
            980                 985                 990
Glu Gln Lys Leu Thr Gln Lys Ile Asp Asn Leu Asn Gln Ala Val Ser
        995                 1000                1005
Glu Ala Lys Ala Ser His Phe Asp Asn Leu Asp Gln Met Ile Asp Lys
    1010                1015                1020
Leu Lys Asp Ser Thr Lys Lys Asn Val Val Asn Leu Tyr Val Glu Ser
1025                1030                1035                1040
Ala Lys Lys Val Pro Thr Ser Leu Ser Ala Lys Leu Asp Asn Tyr Ala
                1045                1050                1055
Thr Asn Ser His Thr Arg Ile Asn Ser Asn Val Lys Asn Gly Thr Ile
            1060                1065                1070
Asn Glu Lys Ala Thr Gly Met Leu Thr Gln Lys Asn Ser Glu Trp Leu
        1075                1080                1085
Lys Leu Val Asn Asp Lys Ile Val Ala His Asn Val Gly Ser Ala Pro
    1090                1095                1100
Leu Ser Ala Tyr Asp Lys Ile Gly Phe Asn Gln Lys Asn Met Lys Asp
1105                1110                1115                1120
Tyr Ser Asp Ser Phe Lys Phe Ser Thr Arg Leu Ser Asn Ala Val Lys
                1125                1130                1135
Asp Ile Lys Ser Gly Phe Val Gln Phe Leu Thr Asn Ile Phe Ser Met
            1140                1145                1150
Gly Ser Tyr Ser Leu Met Lys Ala Ser Val Glu His Gly Val Lys Asn
        1155                1160                1165
Thr Asn Thr Lys Gly Gly Phe Gln Lys Ser
    1170                1175
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:474:

(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:474

```
Met Lys Ala Pro Ser Gln Unk Asp Leu Lys Lys Ile Leu Gly Ile Glu
1               5                   10                  15
Glu Val Ile Unk Unk Ser Thr Ser Pro Met Glu Leu Arg Leu Ala Asn
            20                  25                  30
Gln Lys Leu Gly Asn Arg Phe Ile Lys Thr Leu Gln Ala Met Asn Glu
        35                  40                  45
Leu Asp Met Gly Ala Phe Phe Asn Ala Tyr Ala Gln Thr Thr Lys Asp
    50                  55                  60
Pro Thr His Ala Thr Ser Tyr Gly Val Phe Ala Ala Ser Leu Asn Met
```

```
65                  70                  75                  80
Glu Leu Lys Lys Ala Leu Arg His Tyr Leu Tyr Ala Gln Thr Ser Asn
                85                  90                  95
Met Val Ile Asn Cys Val Lys Ser Val Pro Leu Ser Gln Asn Asp Gly
            100                 105                 110
Gln Lys Ile Leu Leu Ser Leu Gln Ser Pro Phe Asn Gln Leu Ile Glu
        115                 120                 125
Lys Thr Leu Glu Leu Asp Glu Ser His Leu Cys Ala Ala Ser Val Gln
    130                 135                 140
Asn Asp Ile Lys Ala Met Gln His Glu Ser Leu Tyr Ser Arg Leu Tyr
145                 150                 155                 160
Met Ser
```

(2) INFORMATION FOR SEQ ID NO:474:

(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

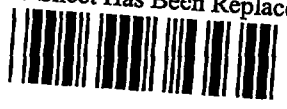
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474

```
Met Lys Ala Pro Ser Gln Unk Asp Leu Lys Lys Ile Leu Gly Ile Glu
1               5                   10                  15
Glu Val Ile Unk Unk Ser Thr Ser Pro Met Glu Leu Arg Leu Ala Asn
            20                  25                  30
Gln Lys Leu Gly Asn Arg Phe Ile Lys Thr Leu Gln Ala Met Asn Glu
        35                  40                  45
Leu Asp Met Gly Ala Phe Phe Asn Ala Tyr Ala Gln Thr Thr Lys Asp
    50                  55                  60
Pro Thr His Ala Thr Ser Tyr Gly Val Phe Ala Ala Ser Leu Asn Met
65                  70                  75                  80
Glu Leu Lys Lys Ala Leu Arg His Tyr Leu Tyr Ala Gln Thr Ser Asn
                85                  90                  95
Met Val Ile Asn Cys Val Lys Ser Val Pro Leu Ser Gln Asn Asp Gly
            100                 105                 110
Gln Lys Ile Leu Leu Ser Leu Gln Ser Pro Phe Asn Gln Leu Ile Glu
        115                 120                 125
Lys Thr Leu Glu Leu Asp Glu Ser His Leu Cys Ala Ala Ser Val Gln
    130                 135                 140
Asn Asp Ile Lys Ala Met Gln His Glu Ser Leu Tyr Ser Arg Leu Tyr
145                 150                 155                 160
Met Ser
```

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 466 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

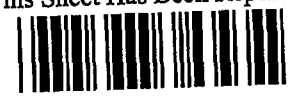
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475

```
Met Lys Ala Leu Lys Thr Phe Leu Lys Lys Ser Leu Ile Leu Leu Leu
1               5                  10                  15
Ala Ile Ala Leu Asn His Leu Asn Ala Val Ala Met Ile Val Asp Asn
            20                  25                  30
Pro Thr Gln Asn Ala Trp Asn Gly Ala Lys Arg Ala Trp Asp Glu Ser
        35                  40                  45
Lys Trp Ala Lys His Leu Ala Thr Ile Thr Glu Arg Ile Lys Leu Ala
    50                  55                  60
Gln Asp Thr Leu Asp Arg Ala Asn Gln Thr Leu Asn Ser Ile Asn Lys
65                  70                  75                  80
Val Asn Asp Val Leu Asn Lys Thr Asn Gln Phe Leu Thr Gly Ser Ile
                85                  90                  95
Leu Ser Ile Pro Asn Pro Met Gln Tyr Val Glu Lys Ile Gln Ser Phe
            100                 105                 110
Ala Lys Gln Val Gln Ala Asn Thr Glu Arg Ile Lys Glu Asn Ala Gln
        115                 120                 125
Asn Tyr Asp Ile Arg Asn Gln Ile Ala Ala Lys Arg Ile Ser Glu Lys
    130                 135                 140
Cys Pro Glu Leu Asn Trp Asp Val Ser Gln Asp Ala Ser Pro Thr Glu
145                 150                 155                 160
Lys Asn Leu His Gln Phe Phe Thr Ser Lys Gly Lys Glu Ser Ala Asn
                165                 170                 175
Thr Lys Ala Leu Lys Asp Phe Ala Asn Ala Ile Gly Asn Thr Gln Ile
            180                 185                 190
Ser Thr Ala Asn Asp Leu Gly Ala Gly Leu Arg Gly Arg Ala Leu Leu
        195                 200                 205
Glu Tyr Ile Cys Ile Gln Lys Gly Asn Leu Glu Ala Ala Lys Lys Ile
    210                 215                 220
Gln Leu Leu Asp Ser Gln Met Thr Leu Ala Leu Leu Asn Asn Asp Tyr
225                 230                 235                 240
Thr Ala Tyr Glu Lys Leu Arg Ala Glu Lys Glu Glu Leu Lys Arg Gln
                245                 250                 255
Ile Ala Ser Asn Val Tyr Ala Lys Val Lys Gln Leu Val Val Ala Ser
            260                 265                 270
Gln Asp Arg Ala Phe Ser Gln Met Asp Asn Glu Leu Gly Val Lys Thr
        275                 280                 285
Phe Gly Phe Asn Asp Glu Asn Val Lys Lys Gly Tyr Cys Lys Lys Glu
    290                 295                 300
Asn Arg Asn Gly Lys Ser Glu Cys Ile Pro Asn Met Leu Asn Val Asn
305                 310                 315                 320
Arg Leu Lys Ala Gln Phe Asp Glu Leu Asn Leu Asp Tyr Ser Arg Asp
                325                 330                 335
Ile Ala Gly Lys Lys Gly Glu Ala Ala Ala Lys Val Phe Asn Asp Tyr
            340                 345                 350
Lys His Arg Phe Gln Gln Leu Ser Val Glu Thr Ala Leu Glu Ile Ala
        355                 360                 365
Gln Asn Leu Ser Phe Met Asn Lys Thr Leu Gly Leu Met Val Gln Met
    370                 375                 380
Gln Ser Tyr Ala Phe Lys Gln Gln Met Gly Tyr Phe Glu Asp Ile Ile
385                 390                 395                 400
Pro Ala Asp Ala Leu Lys Asp Asp Lys Glu His Gln Glu Asn Leu Glu
```

```
                405                 410                 415
Gln Lys Gln Gln Glu Ile Glu Lys Val Tyr Arg Ala Lys Leu Asp Ala
            420                 425                 430
Tyr Gly Phe Pro Asn Gly Ser Val Gly Lys Ala Ser Gly Val Asn Ser
        435                 440                 445
Asn Ser Asn Asn Glu Ala Pro Ser Ser Asp Asn Ile Gln Ser Phe Asn
    450                 455                 460
Pro Tyr
465
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:476:

(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:476

```
Met Ala Phe Ile Leu Thr Thr Asn Leu Phe Ile Lys Ser Phe Thr Asn
1               5                   10                  15
Ser Ile Arg Ile Thr Gly Cys Ile Ile Ser Pro Asn Val Phe Phe Ala
            20                  25                  30
Tyr Glu Phe Cys Ala Leu Gly Phe Arg Lys Gly Gly Leu Ile Leu Asp
        35                  40                  45
Asn Phe Ser Lys Phe Val Ser His Arg Leu Gln
    50                  55
```

(2) INFORMATION FOR SEQ ID NO:476:

(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:476

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

```
Tyr Glu Phe Cys Ala Leu Gly Phe Arg Lys Gly Gly Leu Ile Leu Asp
        35                  40                  45
Asn Phe Ser Lys Phe Val Ser His Arg Leu Gln
    50                  55
```

(2) INFORMATION FOR SEQ ID NO:477:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477

```
Val Arg Phe Phe Ile Phe Leu Ile Leu Ile Cys Pro Leu Ile Cys Pro
1               5                  10                  15
Leu Met Ser Ala Asp Ser Ala Leu Pro Ser Val Asn Leu Ser Leu Asn
            20                  25                  30
Ala Pro Ser Asp Pro Lys Gln Leu Val Thr Thr Leu Asn Val Ile Ala
        35                  40                  45
Leu Leu Thr Leu Leu Val Leu Ala Pro Ser Leu Ile Leu Val Met Thr
    50                  55                  60
Ser Phe Thr Arg Leu Ile Val Val Phe Ser Phe Leu Arg Thr Ala Leu
65                  70                  75                  80
Gly Thr Gln Gln Thr Pro Pro Thr Gln Ile Leu Val Ser Leu Ser Leu
                85                  90                  95
Ile Leu Thr Phe Phe Ile Met Glu Pro Ser Leu Lys Lys Ala Tyr Asp
            100                 105                 110
Thr Gly Ile Lys Pro Tyr Met Asp Lys Lys Ile Ser Tyr Thr Glu Ala
        115                 120                 125
Phe Glu Lys Ser Thr Leu Pro Phe Lys Glu Phe Met Leu Lys Asn Thr
    130                 135                 140
Arg Glu Lys Asp Leu Ala Leu Phe Phe Arg Ile Arg Asn Leu Pro Asn
145                 150                 155                 160
Pro Lys Thr Pro Asp Asp Val Ser Leu Ser Val Leu Ile Pro Ala Phe
                165                 170                 175
Met Ile Ser Glu Leu Lys Thr Ala Phe Gln Ile Gly Phe Leu Leu Tyr
            180                 185                 190
Leu Pro Phe Leu Val Ile Asp Met Val Ile Ser Ser Ile Leu Met Ala
        195                 200                 205
Met Gly Met Met Met Leu Pro Pro Val Met Ile Ser Leu Pro Phe Lys
    210                 215                 220
Ile Leu Val Phe Ile Leu Val Asp Gly Phe Asn Leu Leu Thr Glu Asn
225                 230                 235                 240
Leu Val Ala Ser Phe Lys Met Val
                245
```

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477

```
Val Arg Phe Phe Ile Phe Leu Ile Leu Ile Cys Pro Leu Ile Cys Pro
1               5                  10                  15
Leu Met Ser Ala Asp Ser Ala Leu Pro Ser Val Asn Leu Ser Leu Asn
            20                  25                  30
Ala Pro Ser Asp Pro Lys Gln Leu Val Thr Thr Leu Asn Val Ile Ala
        35                  40                  45
Leu Leu Thr Leu Leu Val Leu Ala Pro Ser Leu Ile Leu Val Met Thr
    50                  55                  60
Ser Phe Thr Arg Leu Ile Val Val Phe Ser Phe Leu Arg Thr Ala Leu
65                  70                  75                  80
Gly Thr Gln Gln Thr Pro Pro Thr Gln Ile Leu Val Ser Leu Ser Leu
                85                  90                  95
Ile Leu Thr Phe Phe Ile Met Glu Pro Ser Leu Lys Lys Ala Tyr Asp
            100                 105                 110
Thr Gly Ile Lys Pro Tyr Met Asp Lys Lys Ile Ser Tyr Thr Glu Ala
        115                 120                 125
Phe Glu Lys Ser Thr Leu Pro Phe Lys Glu Phe Met Leu Lys Asn Thr
    130                 135                 140
Arg Glu Lys Asp Leu Ala Leu Phe Phe Arg Ile Arg Asn Leu Pro Asn
145                 150                 155                 160
Pro Lys Thr Pro Asp Asp Val Ser Leu Ser Val Leu Ile Pro Ala Phe
                165                 170                 175
Met Ile Ser Glu Leu Lys Thr Ala Phe Gln Ile Gly Phe Leu Leu Tyr
            180                 185                 190
Leu Pro Phe Leu Val Ile Asp Met Val Ile Ser Ser Ile Leu Met Ala
        195                 200                 205
Met Gly Met Met Met Leu Pro Pro Val Met Ile Ser Leu Pro Phe Lys
    210                 215                 220
Ile Leu Val Phe Ile Leu Val Asp Gly Phe Asn Leu Leu Thr Glu Asn
225                 230                 235                 240
Leu Val Ala Ser Phe Lys Met Val
                245
```

(2) INFORMATION FOR SEQ ID NO:478:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature

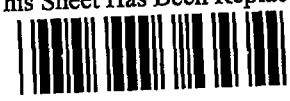
(B) LOCATION 1...44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478

```
Val Met Asp Ala Glu Asn Gly Glu Leu Leu Val Ala Gly Ser Tyr Pro
1               5                  10                  15
Glu Tyr Asn Leu Asn Asp Phe Val Gly Gly Ile Ser Gln Asp Lys Trp
            20                  25                  30
Gln Lys Leu Gln Asp Asp Ile Tyr Asn Pro Leu Leu
        35                  40
```

(2) INFORMATION FOR SEQ ID NO:479:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 421 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479

```
Met Asn Phe Phe Asp Thr Leu Met Gly Met Phe Val Glu Pro Ser Gln
1               5                  10                  15
Lys Val Ala Lys Ser Leu Ala Glu His Val Gly Ser Phe Phe His Ala
            20                  25                  30
Gln Leu Ile Leu Asn Thr Ile Ile Thr Ile Leu Phe Met Ile Trp Ala
        35                  40                  45
Tyr Lys Arg Val Lys Glu Gly Asp Met Phe Glu Phe Lys Thr Ala Met
    50                  55                  60
Gly Val Val Val Phe Ile Ala Phe Val Gly Phe Ile Asn Trp Gly Ile
65                  70                  75                  80
Lys Asn Pro Asn Asp Phe Asn Thr Tyr Phe Ile Asn Thr Ile Phe Tyr
                85                  90                  95
Pro Ser Glu Lys Leu Ala Ile Leu Ile Ala Gln Ser Leu Asn Asp Gly
            100                 105                 110
Leu Glu Ile Pro Thr Asn Thr Asn Leu Ser Pro Ser Glu Ile Phe Ser
        115                 120                 125
Ile Gly Asn Leu Ala Ser Ser Ala Tyr Ala Met Ile Val Asn Leu Trp
    130                 135                 140
Asp Asn Ala Phe Asp Gly Ile Asn Met Phe Asn Trp Leu Thr Met Ile
145                 150                 155                 160
Pro Lys Ile Ile Met Phe Phe Leu Val Ile Leu Gly Glu Leu Leu Phe
                165                 170                 175
Leu Gly Leu Leu Leu Ile Ile Val Leu Leu Val Thr Ala Glu Ile Phe
            180                 185                 190
Met Trp Ser Ala Leu Gly Leu Ile Val Leu Pro Leu Gly Leu Ile Pro
        195                 200                 205
Gln Thr Lys Gly Met Leu Phe Ser Tyr Leu Lys Lys Leu Ile Ser Leu
    210                 215                 220
Thr Leu Tyr Lys Pro Cys Met Met Leu Val Ala Phe Phe Asn Tyr Gly
225                 230                 235                 240
Ile Ile Tyr Lys Val Asn Thr Leu Ile Pro Thr Lys His Glu Val Thr
                245                 250                 255
Gln Gly Phe Tyr Gly Asn Ala Asp Lys Met Ala Asn Glu Gly Lys Ile
```

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

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(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

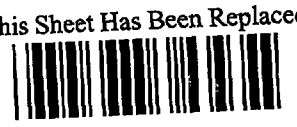
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480

```
Leu Leu Val Thr Phe Leu Asn Gly Phe Asp Pro Lys Ile Ala Asn Leu
1               5                  10                  15
Arg Lys Ala Cys Asn Val Tyr Ser Val Gly Val Ile Tyr Ile Val Thr
            20                  25                  30
Thr Asn Thr Leu Asn Ile Leu Ser Cys Glu Ser Phe Glu Ile Leu Glu
        35                  40                  45
Lys Arg Glu Leu Asp Thr Ser Gly Val Thr Lys Thr Ser Thr Pro Phe
    50                  55                  60
Phe Ser Arg Val Glu Gly Ile Asp Ala Gly Thr Leu Gly Lys Leu Phe
65                  70                  75                  80
Ser Gly Ser Gln Ser Lys Asn Tyr Phe Ala Tyr Tyr Asp Ala Leu Val
                85                  90                  95
Lys Lys Glu Lys Arg Lys Glu Val Arg Ile Glu Lys Lys Glu Glu Arg
            100                 105                 110
Ile Asp Ala Arg Glu Asn Lys Arg Glu Ile Lys Gln Glu Ala Ile Lys
        115                 120                 125
Glu Pro Lys Lys Ala Asn Gln Gly Thr Glu Asn Ala Pro Thr Leu Glu
    130                 135                 140
Glu Lys Unk Tyr Gln Lys Ala Glu Arg Lys Phe Asp Ala Lys Unk Unk
145                 150                 155                 160
Arg Arg Ser Phe Lys Unk
                165
```

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(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:480

```
Leu Leu Val Thr Phe Leu Asn Gly Phe Asp Pro Lys Ile Ala Asn Leu
1               5                  10                  15
Arg Lys Ala Cys Asn Val Tyr Ser Val Gly Val Ile Tyr Ile Val Thr
            20                  25                  30
Thr Asn Thr Leu Asn Ile Leu Ser Cys Glu Ser Phe Glu Ile Leu Glu
        35                  40                  45
Lys Arg Glu Leu Asp Thr Ser Gly Val Thr Lys Thr Ser Thr Pro Phe
    50                  55                  60
Phe Ser Arg Val Glu Gly Ile Asp Ala Gly Thr Leu Gly Lys Leu Phe
65                  70                  75                  80
Ser Gly Ser Gln Ser Lys Asn Tyr Phe Ala Tyr Tyr Asp Ala Leu Val
                85                  90                  95
Lys Lys Glu Lys Arg Lys Glu Val Arg Ile Glu Lys Lys Glu Glu Arg
            100                 105                 110
Ile Asp Ala Arg Glu Asn Lys Arg Glu Ile Lys Gln Glu Ala Ile Lys
        115                 120                 125
Glu Pro Lys Lys Ala Asn Gln Gly Thr Glu Asn Ala Pro Thr Leu Glu
    130                 135                 140
Glu Lys Unk Tyr Gln Lys Ala Glu Arg Lys Phe Asp Ala Lys Unk Unk
145                 150                 155                 160
Arg Arg Ser Phe Lys Unk
                165
```

(2) INFORMATION FOR SEQ ID NO:481:

(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:481

```
Met Asp Glu Pro Glu Thr Ser Leu Glu Gln Asn Ala Leu Ile Arg Leu
1               5                  10                  15
Ser Asn Leu Ile Ser Leu Arg Asn Thr Gln Gln Leu Thr Ser Ile Ile
            20                  25                  30
Ala Thr His Asp Pro Ile Val Leu Asp Ser Cys Glu Trp Val Leu Leu
        35                  40                  45
Leu Lys Asn Gly Asn Ile Ala Gln Tyr Lys Pro Leu Asn Ser Ile Leu
    50                  55                  60
Lys Ser Val Ala Lys Thr Phe Asn Phe Lys Glu Lys Pro Thr Thr Lys
65                  70                  75                  80
Asp Leu Leu Ala Leu Leu Lys Asp Ile
                85
```

(2) INFORMATION FOR SEQ ID NO:482:

This Sheet Has Been Replaced



(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:482

```
Val Lys Thr Leu Gly Leu Ser Ser Leu Gly Gly Thr Leu Glu Phe Tyr
1               5                  10                  15
Asp Phe Ile Ile Phe Val Phe Phe Thr Ser Ile Ile Ala Lys His Phe
            20                  25                  30
Phe Pro Asn Thr Leu Ser Pro Ile Trp Ser Glu Ile Asn Thr Tyr Gly
        35                  40                  45
Ile Phe Ala Ala Gly Tyr Leu Ala Arg Pro Leu Gly Gly Ile Val Met
    50                  55                  60
Ala His Phe Gly Asp Lys Phe Gly Arg Lys Asn Met Phe Met Leu Ser
65                  70                  75                  80
Ile Leu Leu Met Val Ile Pro Thr Phe Ala Leu Ala Leu Met Pro Thr
                85                  90                  95
Phe Asn Asp Leu Val Gly Phe Gly Val Asp Ser Met Gly Leu Thr Pro
            100                 105                 110
Lys Asn Ala His Tyr Leu Gly Tyr Ile Ala Pro Val Phe Leu Val Leu
        115                 120                 125
Val Arg Ile Cys Gln Gly Val Ala Val Gly Gly Glu Leu Pro Gly Ala
    130                 135                 140
Trp Val Phe Val His Glu His Ala Pro Gln Gly Gln Lys Asn Thr Tyr
145                 150                 155                 160
Ile Gly Phe Leu Thr Ala Ser Val Val Ser Gly Ile Leu Leu Gly Ser
                165                  70                 175
Leu Val Tyr Ile Gly Ile Tyr Met Val Phe Asp Lys Pro Val Val Glu
            180                 185                 190
Asp Trp Ala Trp Arg Val Ala Phe Gly Leu Gly Gly Ile Phe Gly Ile
        195                 200                 205
Ile Ser Val Tyr Leu Arg Arg Phe Leu Glu Glu Thr Pro Val Phe Gln
    210                 215                 220
Gln Met Lys Gln Gly Arg Cys Leu Ser Gln Ile Pro Ala
225                 230                 235
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 471 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483

```
Met Arg Lys Phe Leu Asp Gly Ala Lys Ser Glu Val Leu Lys Tyr Asp
1               5                  10                  15
Val Ile Ser Phe Asp Ile Phe Asp Thr Leu Leu Leu Arg Pro Phe Ile
            20                  25                  30
Lys Pro Thr Asp Leu Phe Leu Tyr Ile Glu Thr Lys Tyr Asn Ile Lys
        35                  40                  45
Gly Phe His Gln Ala Arg Ile Leu Ala Glu Met Gln Ser Arg Lys Leu
    50                  55                  60
Ser Lys Arg Gln Asp Ile Thr Leu Asp Glu Ile Tyr His Gln Ile Pro
65                  70                  75                  80
Lys Glu Phe His Ser Tyr Lys Gly Val Glu Ile Ala Thr Glu Lys Glu
                85                  90                  95
Val Leu Val Pro Asn Leu Glu Met Leu Glu Leu Tyr Arg Phe Ala Lys
            100                 105                 110
Glu Asn Asn Lys Arg Val Ile Ile Val Ser Asp Met Tyr Leu Pro Leu
        115                 120                 125
Glu Val Leu Glu Asp Ile Leu Ile Ser Lys Gly Phe Asp Gly Tyr Thr
    130                 135                 140
Asn Phe Tyr Leu Ser Asn His Ile Met Leu Thr Lys His Ser Lys Asp
145                 150                 155                 160
Leu Phe Lys His Val Leu Lys Gln Glu Asn Ile Thr Asn Thr Gln Ile
                165                 170                 175
Leu His Ile Gly Asp Asn Ser Trp Ala Asp Asp Ala Met Pro Lys Ser
            180                 185                 190
Leu Gly Ile Ala Thr Leu Phe Arg Lys Ser Val Leu Lys Gln Leu Glu
        195                 200                 205
Glu Val Phe Pro Lys Tyr Lys Thr Phe Asn Pro Thr Ser Val Ala Gln
    210                 215                 220
Ser Phe Ile Leu Gly Ser Leu Cys Val Phe Tyr Lys Asn Tyr Ile Gln
225                 230                 235                 240
Lys His Glu Lys Phe Asp Tyr Trp Phe Leu Leu Gly Ala Met Gln Ala
                245                 250                 255
Gly Ile Ala Ala Val Ala Tyr Cys Gln Phe Ile Tyr Lys Glu Ile His
            260                 265                 270
Lys Arg Asn Ile Asp Thr Leu Val Phe Val Ala Arg Asp Gly Tyr Leu
        275                 280                 285
Leu Gln Lys Ile Phe Asn Ile Leu Tyr Pro Asn Ser Tyr Lys Thr Thr
    290                 295                 300
Tyr Val Tyr Ala Pro Arg Ile Leu Lys Lys Ala Val Phe Leu Glu Val
305                 310                 315                 320
Val Glu Gly Glu Ser Leu Glu Ile Leu Arg Ile Leu Glu Gly Glu Glu
                325                 330                 335
Glu Val Lys Lys Lys Gln Ile Thr Thr Asn Gln Gln Ala Tyr Val Tyr
```

```
            340                 345                 350
Leu Tyr Ser Asn Phe Glu His Cys Arg His Leu Ala Leu Lys Cys Leu
        355                 360                 365
Asp Asn Tyr Arg Lys Tyr Leu Phe Ser Ser Asn Leu Glu Gly Asn Ile
    370                 375                 380
Ala Ile Val Asp Thr Ile Thr Leu Gly Tyr Ser Ser Gln Gly Leu Ile
385                 390                 395                 400
Gln Lys Ala Leu Asn Lys Glu Val Phe Gly Cys Tyr Val Asp Leu Leu
                405                 410                 415
Arg Ile Leu Asn Tyr Asp Cys Val Ser Phe Leu Pro Phe Ser His Pro
            420                 425                 430
Lys Pro Val Tyr Phe His Asn Trp Asp Phe Met Glu Phe Leu Leu Thr
        435                 440                 445
Ser Pro Glu Tyr Pro Ile Leu Asn Val Glu Asn Gly Val Pro Ile Leu
    450                 455                 460
Ser Lys Arg Arg Phe Ile Leu
465                 470
```

This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:484:

(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:484

```
Val Leu Lys Phe Phe Glu Asp Ser Lys Gln Leu Ser Thr Pro Met Gly
1               5                   10                  15
Lys Ser Ala Val Gly Ile Leu Ile Phe Gln Asp Ile Ala Ala Ile Pro
            20                  25                  30
Met Leu Leu Ile Leu Thr Ile Leu Gly Ser Lys Asp Ser His Val Asn
        35                  40                  45
Leu Leu Ile Leu Lys Thr Leu Ile Ser Ala Gly Ile Ile Leu Ile Leu
    50                  55                  60
Leu Leu Leu Pro Gly Lys Lys Gly Ala Asn Leu Ile Leu Glu Gln Ala
65                  70                  75                  80
Lys Asp Thr Arg Leu Pro Glu Ile Phe Ile Gly Thr Asp Phe Ser Asp
                85                  90                  95
Cys Leu Gln Arg Gly Gly Val Glu Pro Phe Phe Trp Val Phe Tyr Val
            100                 105                 110
Phe Gly Gly Val His Cys Gly His Gly Asp Phe
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...127

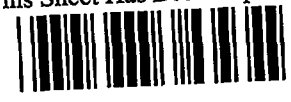
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485

```
Met Glu Asn Ser Thr Leu Tyr Ile Val Ile Ala Gly Leu Trp Leu Ala
1               5                  10                  15
Val Gly Phe Gly Ile Phe Leu Lys Lys Leu Asp Met Pro Val Ile Ile
            20                  25                  30
Gly Tyr Ile Cys Thr Gly Thr Val Leu Ala Ala Phe Phe Lys Ile Asn
        35                  40                  45
Asp Phe Asn Leu Leu Ser Asp Ile Gly Glu Phe Gly Ile Val Phe Leu
    50                  55                  60
Met Phe Met Ile Gly Ile Glu Phe Asn Phe Asp Lys Leu Lys Ser Ile
65                  70                  75                  80
Lys Gln Glu Val Leu Val Phe Gly Leu Leu Gln Val Val Leu Cys Ala
                85                  90                  95
Leu Ile Ala Phe Leu Leu Gly Tyr Phe Val Leu Gly Leu Ser Pro Ile
            100                 105                 110
Phe Ser Leu Val Leu Gly Met Gly Leu Ser Leu Ser Ser Thr Ala
        115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...127

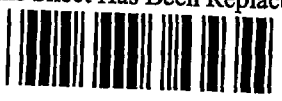
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485

```
Met Glu Asn Ser Thr Leu Tyr Ile Val Ile Ala Gly Leu Trp Leu Ala
1               5                  10                  15
Val Gly Phe Gly Ile Phe Leu Lys Lys Leu Asp Met Pro Val Ile Ile
            20                  25                  30
Gly Tyr Ile Cys Thr Gly Thr Val Leu Ala Ala Phe Phe Lys Ile Asn
        35                  40                  45
Asp Phe Asn Leu Leu Ser Asp Ile Gly Glu Phe Gly Ile Val Phe Leu
    50                  55                  60
Met Phe Met Ile Gly Ile Glu Phe Asn Phe Asp Lys Leu Lys Ser Ile
65                  70                  75                  80
Lys Gln Glu Val Leu Val Phe Gly Leu Leu Gln Val Val Leu Cys Ala
                85                  90                  95
Leu Ile Ala Phe Leu Leu Gly Tyr Phe Val Leu Gly Leu Ser Pro Ile
            100                 105                 110
Phe Ser Leu Val Leu Gly Met Gly Leu Ser Leu Ser Ser Thr Ala
```

115 120 125

(2) INFORMATION FOR SEQ ID NO:486:

This Sheet Has Been Replaced



(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:486

```
Met Ile Leu Ala Leu Leu Ile Ser Lys Glu Lys Thr His Leu Glu Ala
1               5                  10                  15
Leu Tyr Tyr Leu Ser Tyr Gly Val Leu Leu Gly Gly Val Ala Gln Ile
            20                  25                  30
Leu Leu His Phe Tyr Pro Leu Val Lys Leu Gly Leu Trp Asp Leu Leu
        35                  40                  45
Phe Lys Gly Leu Leu Gly Phe Lys Thr Lys Asn Thr Asn Lys Lys Glu
    50                  55                  60
Tyr Arg Leu Asn Arg Ala Lys Lys Asp Leu Lys Ala Phe Phe Lys Gln
65                  70                  75                  80
Phe Phe Pro Ser Val Leu Gly Asn Ser Ser Ala Gln Ile Ala Ser Phe
                85                  90                  95
Leu Asp Thr Thr Ile Ala Ser Phe Leu Ala Ser Gly Ser Val Ser Tyr
            100                 105                 110
Leu Tyr Tyr Ala Asn Arg Val Phe Gln Leu Pro Leu Ala Leu Phe Ala
        115                 120                 125
Ile Ala Ile Ser Thr Ala Leu Phe Pro Ser Ile Ala Ile Ala Leu Lys
    130                 135                 140
Asn Asn Gln Gln Asp Leu Ile Leu Gln Arg Leu Gln Lys Ala Trp Phe
145                 150                 155                 160
Phe Leu Val Gly Val Leu Leu Leu Cys Ser Ile Gly Gly Ile Met Leu
                165                 170                 175
Ser Lys Glu Ile Thr Glu Leu Leu Phe Glu Arg Gly Gln Phe Ser Pro
            180                 185                 190
Lys Asp Thr Leu Ile Thr Ser Gln Val Phe Ser Leu Tyr Leu Leu Gly
        195                 200                 205
Leu Leu Pro Phe Gly Leu Thr Lys Leu Phe Ser Leu Trp Leu Tyr Ala
    210                 215                 220
Lys Leu Glu Gln Lys Lys Ala Ala Lys Ile Ser Leu Ile Ser Leu Phe
225                 230                 235                 240
Leu Gly Leu Ala Ala Ser Leu Ser Leu Met Pro Leu Leu Gly Val Leu
                245                 250                 255
Gly Leu Arg
```

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487

```
Leu Leu Leu Met Leu Asn Lys Pro Lys Pro Leu Phe Leu Unk Leu Gly
1               5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487

```
Leu Leu Leu Met Leu Asn Lys Pro Lys Pro Leu Phe Leu Unk Leu Gly
1               5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...77

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488

```
Val Leu Lys Tyr Pro Thr Met Phe Met Cys Ala Asp Ala Val Ile Ile
1               5                   10                  15
Ser Lys Ala Asp Met Ile Glu Val Phe Asn Phe Arg Val Ser Gln Val
```

```
           20                  25                  30
Lys Glu Asp Met Gln Lys Leu Lys Pro Glu Ala Pro Ile Phe Leu Met
        35                  40                  45
Ser Ser Lys Asp Pro Lys Ser Leu Glu Asp Phe Lys Asn Phe Leu Leu
    50                  55                  60
Glu Lys Lys Arg Glu Asn Tyr Gln Ser Thr His Ser Phe
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:489:

This Sheet Has Been Replaced



(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:489

```
Met Leu Leu Cys Ala Gly Arg Asn Glu Thr Leu Lys Lys Ala Val Pro
1               5                  10                  15
Ile Gly Val Gly Leu Ile Glu Ser Ala Ile Asn Leu Thr Arg Met Cys
            20                  25                  30
Leu Lys Asn Pro Asp Thr Glu Ser Leu Ile Phe Ile Gly Ser Ala Gly
        35                  40                  45
Ser Tyr Ser Pro Glu Thr Glu Ile Leu Ser Val Phe Glu Ser Ile Glu
    50                  55                  60
Gly Tyr Gln Ile Glu Glu Ser Phe Ser His Leu Asn Ser Tyr Thr Pro
65                  70                  75                  80
Leu Asp Asn Phe Ile His Ile Glu Thr Lys Glu Gln Ala Leu Phe Glu
                85                  90                  95
Arg Val Arg Val Asn Ser Ser Asn Tyr Ile His Thr Ser Glu Met Phe
            100                 105                 110
Ala Lys Lys Met Val Gln Lys Gly Val Leu Leu Glu Asn Met Glu Phe
        115                 120                 125
Phe Ser Val Leu Ser Val Ala Lys Ile Phe Ser Leu Lys Ala Lys Gly
    130                 135                 140
Ile Phe Cys Val Ser Asn His Val Gly Leu Asn Ala His Lys Glu Phe
145                 150                 155                 160
Lys Glu Asn His Ala Lys Val Lys Gln Ile Leu Glu Asn Ile Ile Asp
                165                 170                 175
Ser Leu Ile Val
            180
```

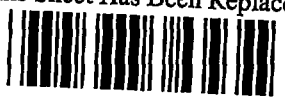
(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490

```
Val Tyr Glu Glu Arg Ile Thr Leu Ala Ser Gln Gly Ile Pro Lys Thr
1               5                  10                  15
Ser Lys Val Gly Phe Glu Ile Phe Asp Thr Lys Asp Phe Gly Ala Thr
            20                  25                  30
Asp Phe Asp Gln Asn Ile Lys Leu Ile Arg Ala Ile Glu Gly Glu Leu
        35                  40                  45
Ser Arg Thr Ile Glu Ser Leu Asn Pro Ile Leu Lys Ala Asn Val His
    50                  55                  60
Ile Ala Ile Pro Lys Asp Ser Val Phe Val Ala Lys Glu Val Pro Pro
65                  70                  75                  80
Ser Ala Ser Val Met Leu Lys Leu Lys Pro Asp Met Lys Leu Ser Pro
                85                  90                  95
Thr Gln Ile Leu Gly Ile Lys Asn Leu Ile Ala Ala Ala Val Pro Lys
            100                 105                 110
Leu Thr Ile Glu Asn Val Lys Ile Val Asn Glu Asn Gly Glu Ser Ile
        115                 120                 125
Gly Glu Gly Asp Ile Leu Glu Asn Ser Lys Glu Leu Ala Leu Glu Gln
    130                 135                 140
Leu Arg Tyr Lys Gln Asn Phe Glu Asn Ile Leu Glu Asn Lys Ile Val
145                 150                 155                 160
Asn Ile Leu Ala Pro Ile Val Gly Unk Lys Asn Unk Val Val Unk Unk
                165                 170                 175
Val Asn Unk Glu Phe Unk Phe Unk Gln Lys Lys Ser Thr Lys Glu Thr
            180                 185                 190
Phe Asp Pro Asn Asn Val Gly Lys Glu Arg Ala Lys Phe Arg Arg Lys
        195                 200                 205
Lys Arg Arg Arg Ser
    210
```

(2) INFORMATION FOR SEQ ID NO:491:

(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:491

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

```
        35                  40                  45
Tyr Lys Leu His Lys Asn His Gly Ser Glu Thr Glu Thr Lys Asn Asp
    50                  55                  60
Lys Lys Leu Tyr Asp Phe Thr Lys Asn Ser Gly Leu Glu Gly Val Asp
65                  70                  75                  80
Leu Glu Lys Ser Pro Asn Leu Lys Ser His Lys Lys Ser Asp Lys Lys
                85                  90                  95
Phe Tyr Lys Gln Leu Ala Lys Asn Asn Ile Ala Glu Gly Val Ser Met
            100                 105                 110
Pro Ile Val Asn Phe Asn Lys Ala Leu Ser Phe Gly Pro Tyr Phe Glu
        115                 120                 125
Arg Thr Lys Ser Lys Lys Thr Gln Tyr Met Asp Gly Gly Leu Met Met
    130                 135                 140
His Ile Arg Phe
145
```

(2) INFORMATION FOR SEQ ID NO:492:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 281 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...281

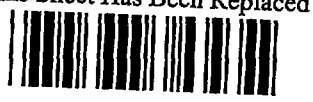
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492

```
Val Met Ile Asp Pro Lys Met Val Glu Phe Ser Ile Tyr Ala Asp Ile
1               5                  10                  15
Pro His Leu Leu Thr Pro Ile Ile Thr Asp Pro Lys Lys Ala Ile Gly
            20                  25                  30
Ala Leu Gln Ser Val Ala Lys Glu Met Glu Arg Arg Tyr Ser Leu Met
        35                  40                  45
Ser Glu Tyr Lys Val Lys Thr Ile Asp Ser Tyr Asn Glu Gln Ala Gln
    50                  55                  60
Ser Asn Asp Val Glu Ala Phe Pro Tyr Leu Ile Val Val Ile Asp Glu
65                  70                  75                  80
Leu Ala Asp Leu Met Met Thr Gly Gly Lys Glu Ala Glu Phe Pro Ile
                85                  90                  95
Ala Arg Ile Ala Gln Met Gly Arg Ala Ser Gly Leu His Leu Ile Val
            100                 105                 110
Ala Thr Gln Arg Pro Ser Val Asp Val Val Thr Gly Leu Ile Lys Thr
        115                 120                 125
Asn Leu Pro Ser Arg Val Ser Phe Arg Val Gly Thr Lys Ile Asp Ser
    130                 135                 140
Lys Val Ile Leu Asp Thr Asp Gly Ala Gln Ser Leu Leu Gly Arg Gly
145                 150                 155                 160
Asp Met Leu Phe Thr Pro Pro Gly Thr Asn Gly Leu Val Arg Leu His
                165                 170                 175
Ala Pro Phe Ala Thr Glu Asp Glu Ile Lys Lys Ile Val Asp Phe Ile
            180                 185                 190
Lys Ala Gln Lys Glu Val Glu Tyr Asp Lys Asp Phe Leu Leu Glu Glu
        195                 200                 205
Ser Arg Met Pro Leu Asp Thr Pro Asn Tyr Gln Gly Asp Asp Ile Leu
    210                 215                 220
```

```
Glu Arg Ala Lys Ala Val Ile Leu Glu Lys Lys Ile Thr Ser Thr Ser
225                 230                 235                 240
Phe Leu Gln Arg Gln Leu Lys Ile Gly Tyr Asn Gln Ala Ala Thr Ile
                245                 250                 255
Thr Asp Glu Leu Glu Ala Gln Gly Phe Leu Ser Pro Arg Asn Ala Lys
            260                 265                 270
Gly Asn Arg Glu Ile Leu Gln Asn Phe
        275                 280
```

(2) INFORMATION FOR SEQ ID NO:493:

This Sheet Has Been Replaced



(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:493

```
Met Asn Phe Phe Lys Ile Leu Leu Met Glu Leu Arg Ala Ile Val Ser
1               5                   10                  15
His Lys Gly Val Leu Leu Ile Leu Ile Gly Ala Pro Leu Ile Tyr Gly
            20                  25                  30
Leu Leu Tyr Pro Leu Pro Tyr Leu Lys Asp Ile Val Thr Gln Gln Lys
        35                  40                  45
Ile Ala Leu Val Asp Glu Asp Asn Ser Phe Leu Ser Arg Gln Leu Ala
    50                  55                  60
Phe Met Val Gln Ser Ser Asn Glu Leu Glu Ile Ala Phe Phe Ser Pro
65                  70                  75                  80
Ser Met Leu Glu Ala Lys Lys Leu Leu Lys Glu Glu Lys Ile Tyr Gly
                85                  90                  95
Ile Leu His Ile Pro Ser His Phe Glu Ala Asn Ile Tyr Lys Gln Ser
            100                 105                 110
Ala Cys Asn Asp Arg Phe Leu Cys Glu Arg Gln Leu Leu Phe Asp Leu
        115                 120                 125
Trp Cys Val Ser Glu Cys Gly Gly Gly Glu His Gln Arg Leu Lys Arg
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:494:

(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:

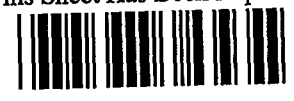
(A) NAME/KEY: misc_feature
(B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494

```
Val Gly Gly Leu Ala Met Leu Gly Phe Phe Tyr Asn Ile Glu Lys Ile
1               5                  10                  15
Ser Leu Ala Thr Ala Thr Ala Phe Ser Gln Cys Ala Pro Unk Tyr Thr
            20                  25                  30
Val Leu Leu Ser Pro Leu Leu Leu Lys Glu Lys Leu Lys Arg Ser Ala
        35                  40                  45
Leu Ile Ser Ala Cys Ile Gly Leu Val Gly Val Val Leu Ile Ser Asp
    50                  55                  60
Pro Ser Val Glu Asn Val Gly Pro Ser
65                  70
```

(2) INFORMATION FOR SEQ ID NO:495:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495

```
Val Cys Trp Thr Asp Leu Ile Gln Gly Leu Leu Met Met Ser Ala Leu
1               5                  10                  15
Ile Val Val Pro Ile Val Met Ile Ile His Leu Gly Gly Ile Gly Glu
            20                  25                  30
Gly Ile Lys Ile Ile Arg Glu Ile Lys Pro Glu Asn Leu Ser Phe Unk
        35                  40                  45
Gln Gly Ser Ser Val Val Ala Ile Ile Ser Ser Leu Ala Trp Gly Leu
    50                  55                  60
Gly Tyr Phe Gly Gln Pro His Ile Leu Val Arg Phe Met Ser Ile Arg
65                  70                  75                  80
Ser Ile Arg Asp Val Pro Lys Ala Thr Thr Ile Gly Ile Ser Trp Met
                85                  90                  95
Val Ile Ser Leu Ile Gly Ala Cys Val Met Gly Leu Leu Gly Val Ala
            100                 105                 110
Tyr Val His Lys Unk Asp Leu Ser Leu Glu Asp Pro Glu Lys Ile Phe
        115                 120                 125
Ile Val Met Ser Gln Leu Leu Phe Asn Pro Trp Ile Thr Gly Ile Leu
    130                 135                 140
Leu Ser Ala Ile Leu Ala Ala Val Met Ser Thr Ala Ser Ser Gln Leu
145                 150                 155                 160
Leu Val Ser Ser Ser Thr Ile Ala Glu Asp Phe Tyr Ala Thr Ile Phe
                165                 170                 175
Asn Lys Asn Ala Pro Gln Lys Leu Val Met Thr Ile Ser Arg Leu Ser
            180                 185                 190
Val Leu Gly Val Ala Cys Ile Ala Phe Phe Ile Ser Thr Asp Lys Asn
        195                 200                 205
Ala Ser Ile Leu Ser Ile Val Ser Tyr Ala Trp Ala Gly Phe Gly Ala
    210                 215                 220
```

```
Ser Phe Gly Ser Val Ile Leu Phe Ser Leu Phe Trp Ser Arg Met Thr
225                 230                 235                 240
Arg Ile Gly Ala Ile Ala Gly Met Leu Ser Gly Ala Ser Thr Val Ile
                245                 250                 255
Leu Tyr Asp Lys Phe Gly Lys Ser Phe Leu Asp Ile Tyr Glu Ile Val
            260                 265                 270
Pro Gly Phe Ile Val Ala Ser Val Ala Ile Val Ala Phe Ser Leu Phe
        275                 280                 285
Ser Ser Val Arg Ser Gly Thr Lys Glu Ala Phe Glu Thr Met Leu Lys
    290                 295                 300
Glu Ile Glu Ser Leu Lys His
305                 310
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:496:

(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:496

```
Val Gly Leu Phe Ile Val Leu Phe Leu Ile Ile Met Lys His Gln Thr
1               5                   10                  15
Ser Pro Tyr Ala Phe Thr His Asn Gln Ala Leu Val Thr Gln Thr Pro
            20                  25                  30
Pro Tyr Phe Thr Gln Leu Thr Ile Pro Lys Pro Asn Asp Ala Leu Ser
        35                  40                  45
Ala His Ala Ser Ser Leu Ile Ser Leu Pro Asn Asp Asn Leu Leu Ser
    50                  55                  60
Ala Tyr Phe Ser Gly Thr Lys Glu Gly Ala Arg Asp Val Lys Ile Ser
65                  70                  75                  80
Ala Asn Leu Phe Asp Ser Lys Thr Asn Arg Trp Ser Glu Ala Phe Ile
                85                  90                  95
Leu Leu Thr Lys Glu Glu Leu Ser His His Ser His Glu Tyr Ile Lys
            100                 105                 110
Lys Ile Arg
        115
```

(2) INFORMATION FOR SEQ ID NO:497:

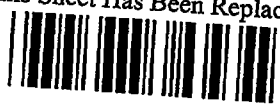
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497

```
Met Leu Val Gly Pro Thr Gly Val Gly Lys Thr Thr Thr Leu Ala Lys
1               5                  10                  15
Leu Ala Ala Arg Tyr Ser Arg Met Leu Ala Lys Lys Tyr Lys Val Gly
            20                  25                  30
Ile Ile Thr Leu Asp Asn Tyr Arg Ile Gly Ala Leu Glu Gln Leu Ser
        35                  40                  45
Trp Tyr Ala Asn Lys Met Lys Met Ser Ile Glu Ala Val Ile Asp Ala
    50                  55                  60
Lys Asp Phe Ala Lys Glu Ile Glu Ala Leu Glu Tyr Cys Asp Phe Ile
65                  70                  75                  80
Leu Val Asp Thr Thr Gly His Ser Gln Tyr Asp Lys Glu Lys Ile Ala
                85                  90                  95
Gly Leu Lys Glu Phe Ile Asp Gly Gly Tyr Asn Ile Asp Val Ser Leu
            100                 105                 110
Val Leu Ser Val Thr Thr Lys Tyr Glu Asp Met Lys Asp Ile Tyr Asp
        115                 120                 125
Ser Phe Gly Val Leu Gly Ile Asp Thr Leu Ile Phe Thr Lys Leu Asp
    130                 135                 140
Glu Ser Arg Gly Leu Gly Asn Leu Phe Ser Leu Val His Glu Ser Gln
145                 150                 155                 160
Lys Pro Ile Ser Tyr Leu Ser Val Gly Gln Glu Val Pro Met Asp Leu
                165                 170                 175
Lys Val Ala Thr Asn Glu Tyr Leu Val Asp Cys Met Leu Asp Gly Phe
            180                 185                 190
Ser Asn Pro Asn Lys Glu Gln Ala
        195                 200
```

(2) INFORMATION FOR SEQ ID NO:498:

(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:498

```
Val Gly Gly Ala Ser Phe Ile Ser Gly Gly Asn Gly Thr Leu Tyr Gly
1               5                  10                  15
Leu Asn Val Gly Tyr Asp Arg Leu Val Lys Ser Val Ile Leu Gly Gly
            20                  25                  30
Tyr Val Ala Tyr Gly Tyr Ser Gly Phe Asn Gly Asn Ile Met His Ser
        35                  40                  45
Leu Ala Asn Asn Val Asp Val Gly Met Tyr Ala Arg Ala Phe Leu Lys
    50                  55                  60
Arg Asn Glu Phe Thr Leu Ser Ala Asn Glu Thr Tyr Gly Gly Asn Ala
65                  70                  75                  80
```

```
Ser His Ile Asn Ser Ser Asn Ser Leu Leu Ser Val Leu Asn Gln Arg
                85                  90                  95
Tyr Asn Tyr Asn Thr Trp Thr Thr Ser Val Asn Gly Asn Tyr Gly Tyr
            100                 105                 110
Asp Phe Met Phe Lys Gln Lys Ser Val Val Leu Lys Pro Gln Val Gly
        115                 120                 125
Leu Ser Tyr His Phe Ile Gly Leu Ser Gly Met Lys Gly Lys Met Gln
    130                 135                 140
Asn Pro Ala Tyr Gln Gln Phe Val Met His Ser Asn Pro Ser Asn Glu
145                 150                 155                 160
Ser Val Leu Thr Leu Asn Met Gly Leu Glu Ser Arg Lys Tyr Phe Gly
                165                 170                 175
Lys Asn Ser Tyr Tyr Phe Val Thr Ala Arg Leu Gly Arg Asp Leu Leu
            180                 185                 190
Ile Lys Ala Lys Gly Asp Asn Val Val Arg Phe Val Gly Glu Asn Thr
        195                 200                 205
Leu Leu Tyr Arg Lys Gly Glu Ile Phe Asn Thr Phe Ala Ser Val Ile
    210                 215                 220
Thr Gly Gly Glu Met His Leu Trp Arg Leu Met Tyr Val Asn Ala Gly
225                 230                 235                 240
Val Gly Leu Lys Met Gly Leu Gln Tyr Gln Asp Leu Asn Ile Thr Gly
                245                 250                 255
Asn Val Gly Met Arg Val Ala Phe
            260
```

(2) INFORMATION FOR SEQ ID NO:499:

(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:499

```
Met Asp Gly Tyr Gly Phe Lys Met Gln Asp Leu Gly Gln Lys Thr Gln
1               5                  10                  15
Val Ile Gln His Ile Phe Ala Gly Asp Asp Val Ser Ala Leu Glu Val
            20                  25                  30
Lys Glu Asn Glu Cys Val Lys Ile Met Thr Gly Ala Met Val Pro Lys
        35                  40                  45
Gly Ile Glu Thr Ile Val Pro Ile Glu Cys Met Leu Glu Ser His Lys
    50                  55                  60
Asp Phe Ala Leu Ala Pro Lys Asp Phe Lys Ile His Ala Asn Ile Arg
65                  70                  75                  80
Gln Lys Gly Glu Asn Ala Ser Leu Asn Ser Val Leu Val Pro Lys Asn
                85                  90                  95
Thr Arg Leu Asn Tyr Gly His Ile Ala Leu Ile Ala Ser Gln Gly Phe
            100                 105                 110
Lys Glu Ile Lys Ala Phe Arg Lys Leu Lys Ile Ala Leu Phe Ser Ser
        115                 120                 125
Gly Asp Glu Leu Val Pro Leu Gly Gln Asn Ala Leu Glu Cys Gln Val
    130                 135                 140
Tyr Asp Val Asn Ser Val Gly Val Phe Asn Met Leu Lys Asn Tyr Asn
```

This Sheet Has Been Replaced



```
145                 150                 155                 160
Thr His Phe Leu Gly Val Leu Lys Asp Asp Lys Asn Leu Gln Leu Lys
                165                 170                 175
Ile Leu Glu Leu Gln Gly Tyr Asp Val Ile Leu Ser Ser Ala Gly Val
            180                 185                 190
Ser Val Gly Asp Lys Asp Phe Phe Lys Asp Ala Leu Lys Glu Arg Asn
        195                 200                 205
Ala Leu Phe Tyr Tyr Glu Lys Val Asn Leu Lys Pro Gly Lys Pro Val
    210                 215                 220
Thr Leu Ala Gln Leu Asn Gln Ser Ile Ile Ile Gly Leu Pro Gly Asn
225                 230                 235                 240
Pro Leu Ser Cys Leu Leu Val Leu Arg Val Leu Ile Leu Pro Leu Leu
                245                 250                 255
Glu Arg Leu Ser Leu Asn Lys Asp Phe Lys Leu Lys Pro Phe Lys Ala
            260                 265                 270
Gln Ile Asn Ala Pro Leu Lys Leu Asn Asn Lys Arg Thr His Leu Ile
        275                 280                 285
Leu Gly Asn Tyr Ser Asn His Gln Phe Ile Pro Tyr Asn Asn Arg Tyr
    290                 295                 300
Glu Ser Gly Ala Ile Gln Ala Leu Ala Gln Val Asp Ser Ile Thr Leu
305                 310                 315                 320
Ile Asp Glu Gly Val Gly Leu Val Gln Gly Glu Ile Glu Ile Leu Arg
                325                 330                 335
Phe Glu Asn
```

(2) INFORMATION FOR SEQ ID NO:500:

This Sheet Has Been Replaced



(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:500

```
Met Pro Tyr Ala Leu Arg Lys Arg Phe Phe Lys Arg Leu Leu Leu Phe
1               5                  10                  15
Phe Leu Ile Val Cys Met Ile Asn Leu His Ala Lys Ser Tyr Leu Phe
            20                  25                  30
Ser Pro Leu Pro Pro Ala His Gln Gln Ile Ile Lys Thr Glu Pro Cys
        35                  40                  45
Ser Leu Glu Cys Leu Lys Asp Leu Met Leu Gln Asn Gln Ile Phe Ser
    50                  55                  60
Phe Val Ser Gln Tyr Asp Asp Asn Asn Gln Asp Glu Ser Leu Lys Thr
65                  70                  75                  80
Tyr Tyr Lys Asp Ile Leu Asn Lys Leu Asn Pro Val Phe Ile Ala Ser
                85                  90                  95
Gln Thr Pro Ala Lys Glu Ser Tyr Glu Pro Lys Ile Glu Leu Ala Ile
            100                 105                 110
Leu Leu Pro Lys Lys Val Val Gly Arg Tyr Ala Ile Leu Val Met Asn
        115                 120                 125
Thr Leu Leu Ala Tyr Phe Glu His Gln Lys Gln Arg Phe Gln Tyr Pro
    130                 135                 140
```

Ser Leu
145

(2) INFORMATION FOR SEQ ID NO:501:

(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

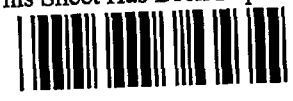
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501

```
Met Pro Ile Asn Pro Leu Tyr Leu Phe Pro Asn Leu Phe Thr Ala Ser
1               5                  10                  15
Ser Ile Phe Leu Gly Met Met Ser Ile Phe Tyr Ala Ser Ser Tyr Gln
            20                  25                  30
Phe Val Met Ala Cys Trp Leu Val Val Ala Ser Leu Ile Leu Asp Gly
        35                  40                  45
Leu Asp Gly Arg Val Ala Arg Leu Thr Lys His His
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 350 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:502

```
Met Ala Leu Arg Val Leu Leu Phe Phe Cys Phe Leu Phe Leu Gln Ala
1               5                  10                  15
Glu Asp Lys Ser Gln Glu Leu Ser Ser Ile Gln Lys Gln Met Ala Leu
            20                  25                  30
Val Asp Lys Lys Leu Ala Lys Asp Asp Asn Val Trp Leu Lys Lys Phe
        35                  40                  45
Glu Asn Tyr Lys Ile Tyr Asn Gln Ile Tyr Thr Glu Lys Glu Ser Val
    50                  55                  60
Arg Gln Glu Leu Arg Arg Leu Lys Asn Lys Lys Ser Lys Asp Leu Leu
65                  70                  75                  80
Lys Ile Ser Thr Leu Glu His Thr Leu Lys Ala Leu Glu Ser Gln Gln
```

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

(2) INFORMATION FOR SEQ ID NO:502:

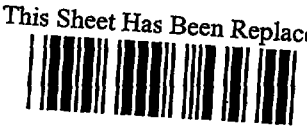
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 350 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502

```
Met Ala Leu Arg Val Leu Leu Phe Phe Cys Phe Leu Phe Leu Gln Ala
1               5                  10                  15
Glu Asp Lys Ser Gln Glu Leu Ser Ser Ile Gln Lys Gln Met Ala Leu
            20                  25                  30
Val Asp Lys Lys Leu Ala Lys Asp Asp Asn Val Trp Leu Lys Lys Phe
        35                  40                  45
Glu Asn Tyr Lys Ile Tyr Asn Gln Ile Tyr Thr Glu Lys Glu Ser Val
    50                  55                  60
Arg Gln Glu Leu Arg Arg Leu Lys Asn Lys Lys Ser Lys Asp Leu Leu
65                  70                  75                  80
```

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

(2) INFORMATION FOR SEQ ID NO:503:

(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:503

```
Met Leu Ser Ala Leu Leu Ser Lys Met Gly Thr Tyr Ala Leu Leu Arg
1               5                  10                  15
Phe Leu Leu Pro Leu Phe Pro Glu Leu Ser Glu Ile Tyr Leu Thr Pro
            20                  25                  30
Ile Ala Ile Val Ala Leu Cys Met Ile Ile Tyr Gly Gly Phe Leu Ala
        35                  40                  45
Tyr Ala Gln Lys Asp Leu Lys Thr Leu Ile Ala Tyr Ser Ser Phe Ser
    50                  55                  60
His Met Gly Val Val Val Leu Gly Val Phe Ser Phe Asn Val Glu Gly
```

This Sheet Has Been Replaced



```
65                  70                  75                  80
Val Ser Gly Ala Val Phe Met Met Phe Ala His Gly Val Ile Val Met
                85                  90                  95
Gly Leu Phe Leu Leu Ala Gly Ile Leu Glu Glu Arg Ala Ser Ser Leu
            100                 105                 110
Glu Ile Ala Arg Phe Gly Ser Ile Ala Lys Ser Ala Pro Val Phe Ala
        115                 120                 125
Ala Phe Phe Met Ile Val Leu Met Ala Asn Val Gly Met Pro Leu Ser
    130                 135                 140
Ile Gly Phe Val Gly Glu Phe Leu Asn Leu Leu Gly Phe Phe Ala Thr
145                 150                 155                 160
Tyr Pro Leu Leu Ala Ile Ile Ala Gly Thr Ser Leu Ile Leu Ser Ala
                165                 170                 175
Val Tyr Ile Leu Thr Ser Tyr Lys Asp Val Phe Phe Gly Asn Leu Lys
            180                 185                 190
Thr Gly Asn Asn Gln Ile Ser Val Phe Glu Asp Leu Asn Ala Arg Glu
        195                 200                 205
Val Gly Val Leu Ser Val Ile Leu Ala Phe Asp Leu Asn Phe Arg Asp
    210                 215                 220
Leu Tyr Lys Ser Ala Phe Lys Thr Asp
225                 230
```

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...32

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504

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

(2) INFORMATION FOR SEQ ID NO:505:

(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

This Sheet Has Been Replaced



(B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505

```
Met Lys Ile Phe Gly Thr Asp Gly Val Arg Gly Lys Ala Gly Val Lys
1               5                  10                  15
Leu Thr Pro Met Phe Val Met Arg Leu Gly Ile Ala Ala Gly Leu Tyr
            20                  25                  30
Phe Lys Lys His Ser Gln Thr Asn Lys Ile Leu Ile Gly Lys Asp Thr
        35                  40                  45
Arg Lys Ser Gly Tyr Met Val Glu Asn Ala Leu Val Ser Ala Leu Thr
    50                  55                  60
Ser Ile Gly Tyr Asn Val Ile Gln Ile Gly Pro Met Pro Thr Pro Ala
65                  70                  75                  80
Ile Ala Phe Leu Thr Glu Asp Met Arg Cys Asp Ala Gly Ile Met Ile
                85                  90                  95
Ser Ala Ser His Asn Pro Phe Glu Asp Asn Gly Ile Lys Phe Phe Asn
            100                 105                 110
Ser Tyr Gly Tyr Lys Leu Lys Glu Glu Glu Glu Arg Ala Ile Glu Glu
        115                 120                 125
Ile Phe His Asp Glu Glu Leu Leu His Ser Ser Tyr Lys Val Gly Glu
    130                 135                 140
Ser Val Gly Ser Ala Lys Arg Ile Asp Asp Val Ile Gly Pro Leu Tyr
145                 150                 155                 160
Arg Ala Phe Glu Ala Leu Tyr Thr Gln Thr Phe
                165                 170
```

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506

```
Val Arg Ala Val Phe Val Phe Gly Leu Lys Ala Ala Phe Cys Ile Gly
1               5                  10                  15
Ile Phe Phe Tyr Gly Ala Tyr Tyr Phe Leu Asp Glu Phe Leu Ile Lys
            20                  25                  30
Leu
```

(2) INFORMATION FOR SEQ ID NO:507:

(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:507

```
Met Lys Glu Gln Glu Trp Asp Leu Ser Ala Leu Phe Glu Asn Lys Glu
1               5                  10                  15
Ser Ala Glu Glu Phe Leu Lys Thr Leu Gln Thr Glu Val Gln Glu Phe
            20                  25                  30
Glu Asn Ala Tyr Gln Asn Asn Leu Lys Asn Leu Asp Ala Ala Lys Phe
        35                  40                  45
Ala Asn Thr Leu Lys His Tyr Glu Asn Leu Ser Glu Lys Ile Ser Arg
    50                  55                  60
Ala Met Ala Tyr Ala Asn Tyr Phe Leu Pro Arg Thr Leu Lys Lys Arg
65                  70                  75                  80
Ser Phe Ile Arg Asn Ala Asn Gly Leu Cys Lys Tyr Pro Thr Thr Pro
                85                  90                  95
Phe Ile Leu
```

(2) INFORMATION FOR SEQ ID NO:507:

(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:507

```
Met Lys Glu Gln Glu Trp Asp Leu Ser Ala Leu Phe Glu Asn Lys Glu
1               5                  10                  15
Ser Ala Glu Glu Phe Leu Lys Thr Leu Gln Thr Glu Val Gln Glu Phe
            20                  25                  30
Glu Asn Ala Tyr Gln Asn Asn Leu Lys Asn Leu Asp Ala Ala Lys Phe
        35                  40                  45
Ala Asn Thr Leu Lys His Tyr Glu Asn Leu Ser Glu Lys Ile Ser Arg
    50                  55                  60
Ala Met Ala Tyr Ala Asn Tyr Phe Leu Pro Arg Thr Leu Lys Lys Arg
65                  70                  75                  80
Ser Phe Ile Arg Asn Ala Asn Gly Leu Cys Lys Tyr Pro Thr Thr Pro
                85                  90                  95
Phe Ile Leu
```

(2) INFORMATION FOR SEQ ID NO:508:

This Sheet Has Been Replaced



SUBSTITUTE SHEET (RULE 26)

(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:508

```
Leu Arg Val Gly Met Tyr Glu Val Cys Asn His Lys Asp Gly Thr Ala
1               5                  10                  15
Tyr His Ser Thr Arg Gly Ser Lys Val Thr Leu Ala Cys Lys Thr Gly
            20                  25                  30
Thr Ala Gln Val Val Glu Ile Ala Gln Asn Ile Val Asn Arg Met Lys
        35                  40                  45
Glu Lys Asp Met Glu Tyr Phe His Unk Ser His Unk Trp Ile Thr Unk
    50                  55                  60
Tyr Leu Unk Pro Met Lys Asn Pro Asn Thr Leu Ser Leu Phe
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:508:

This Sheet Has Been Replaced



(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:508

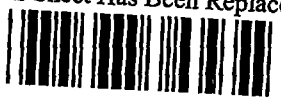
```
Leu Arg Val Gly Met Tyr Glu Val Cys Asn His Lys Asp Gly Thr Ala
1               5                  10                  15
Tyr His Ser Thr Arg Gly Ser Lys Val Thr Leu Ala Cys Lys Thr Gly
            20                  25                  30
Thr Ala Gln Val Val Glu Ile Ala Gln Asn Ile Val Asn Arg Met Lys
        35                  40                  45
Glu Lys Asp Met Glu Tyr Phe His Unk Ser His Unk Trp Ile Thr Unk
    50                  55                  60
Tyr Leu Unk Pro Met Lys Asn Pro Asn Thr Leu Ser Leu Phe
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:509

```
Val Arg Ser Gly Lys Arg Leu Gly Tyr Thr Asn Gln Val Ile Thr Asp
1               5                  10                  15
Ile Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Ala Leu Met Val
            20                  25                  30
Cys Thr Ala Leu Lys Arg Tyr Gly His Pro Arg Leu Lys Met His Phe
        35                  40                  45
Val Ser Asn Val Glu Trp His Ala Asp Phe Arg Arg Phe Gly Lys Asn
    50                  55                  60
Gln Pro Gly Gln Arg Ala
65                  70
```

(2) INFORMATION FOR SEQ ID NO:510:

(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

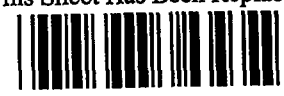
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510

```
Met Asn Leu Val Phe Leu Trp Ala Ala Leu Gly Gly Ala Ile Gly Ser
1               5                  10                  15
Ser Leu Arg Tyr Phe Val Gly Lys Met Met Pro Ser Lys Phe Leu Met
            20                  25                  30
Phe Glu Ser Phe Pro Leu Gly Thr Phe Ser Val Asn Leu Ile Gly Cys
        35                  40                  45
Phe Ile Ile Gly Phe Met Gly His Leu Ala Ala Lys Lys Val Phe Gly
    50                  55                  60
Asp Asp Phe Gly Ile Phe Phe Val Thr Gly Val Leu Gly Gly Phe Thr
65                  70                  75                  80
Thr Phe Ser Ser Tyr Gly Leu Asp Thr Leu Lys Leu Leu Gln Lys Ser
                85                  90                  95
Gln Tyr Leu Glu Ala Ile Ser Tyr Val Leu Gly Thr Asn Leu Leu Gly
            100                 105                 110
Leu Ile Gly Val Ala Ile Gly Trp Phe Leu Ala Lys Asn Phe Val Gly
        115                 120                 125
```

Val Asn
130

(2) INFORMATION FOR SEQ ID NO:511:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511

```
Leu Gly Leu Val Unk Gly Ile Ser Leu Leu His Leu Ser Leu Glu Gln
1               5                  10                  15
Lys Ile Ser Val Phe Leu Gly Unk Asn Leu Met Leu Tyr Pro Val Unk
            20                  25                  30
Glu Val Leu Phe Ser Ile Leu Arg Arg Lys Ile Lys Arg Gln Lys Ala
        35                  40                  45
Thr His Ala Gly
    50
```

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511

```
Leu Gly Leu Val Unk Gly Ile Ser Leu Leu His Leu Ser Leu Glu Gln
1               5                  10                  15
Lys Ile Ser Val Phe Leu Gly Unk Asn Leu Met Leu Tyr Pro Val Unk
            20                  25                  30
Glu Val Leu Phe Ser Ile Leu Arg Arg Lys Ile Lys Arg Gln Lys Ala
        35                  40                  45
Thr His Ala Gly
    50
```

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512

```
Met Leu Glu Lys Leu Ile Glu Arg Val Leu Phe Ala Thr Arg Trp Leu
1               5                  10                  15
Leu Ala Pro Leu Cys Ile Ala Met Ser Leu Val Leu Val Val Leu Gly
            20                  25                  30
Tyr Val Phe Met Lys Glu Leu Trp His Met Leu Ser His Leu Asn Thr
        35                  40                  45
Ile Ser Glu Thr Asp Leu Val Leu Ser Ala Leu Gly Leu Val Asp Leu
    50                  55                  60
Leu Val His Gly Arg Ala Cys Phe Asp Gly Ala Ala Arg Gln Leu
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513

```
Met His Tyr Gln Leu Thr Ser Phe Asn Ile Ile Gln Asp Leu Phe Ile
1               5                  10                  15
Thr Cys His Val Leu Arg Ile Lys Met Arg Val Phe Val Cys Phe Leu
            20                  25                  30
Gly Val Phe Val Ser Asn Gly Leu Ala Arg Phe Gly Tyr Val Val Leu
        35                  40                  45
Ile Pro Leu Leu Ile Leu Ser Gly Ser Leu Thr Pro His Gln Ser Phe
    50                  55                  60
Gln Leu Gly Ile Ala Val Leu Met Gly Tyr Val Phe Gly Ser Phe Leu
65                  70                  75                  80
Ile Gln Phe Leu Ser Pro Leu Met Ser Leu Lys Ser Ile Ala Lys Ile
                85                  90                  95
Ser Phe Lys Leu Thr Leu
            100
```

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...15

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514

```
Val Asp Met Lys Asp Ala Val Gly Thr Tyr Lys Leu Unk Arg Ala
1               5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...377

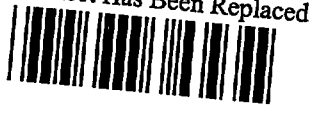
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515

```
Leu Ala Gln Pro Val Gln Val Arg Thr Val Phe Met Ser Met Thr Leu
1               5                   10                  15
Asn Ala Met Gly Gln Phe Ala Tyr Asn Phe Pro Ala Asn Ile Ser Lys
            20                  25                  30
Asp Lys Gln Lys Leu Thr Met Val Tyr Met Asp Lys Asp Tyr Gly Ala
        35                  40                  45
Tyr Gly Asn Ile Val Ala Met Gly Gly Glu Tyr Val Lys Ile Glu Leu
    50                  55                  60
Gly Thr Asp Thr Gly Leu Asn Pro Phe Ala Trp Ala Ala Cys Val Gln
65                  70                  75                  80
Lys Thr Asn Ala Thr Met Glu Gln Lys Gln Thr Ala Ile Ser Val Val
                85                  90                  95
Lys Glu Leu Val Lys Asn Leu Ala Thr Lys Ser Asp Glu Lys Asp Glu
            100                 105                 110
Asn Gly Asn Ser Ile Ser Phe Ser Leu Ala Asp Ser Asn Thr Leu Ala
        115                 120                 125
Ala Ala Val Thr Asn Leu Ile Thr Gly Asp Met Asn Leu Asp Tyr Pro
    130                 135                 140
Ile Thr Gln Leu Ile Asn Ala Phe Gly Lys Asp His Asn Asp Pro Asn
```

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

(2) INFORMATION FOR SEQ ID NO:515:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515

```
Leu Ala Gln Pro Val Gln Val Arg Thr Val Phe Met Ser Met Thr Leu
1               5                   10                  15
Asn Ala Met Gly Gln Phe Ala Tyr Asn Phe Pro Ala Asn Ile Ser Lys
            20                  25                  30
Asp Lys Gln Lys Leu Thr Met Val Tyr Met Asp Lys Asp Tyr Gly Ala
        35                  40                  45
Tyr Gly Asn Ile Val Ala Met Gly Gly Glu Tyr Val Lys Ile Glu Leu
    50                  55                  60
Gly Thr Asp Thr Gly Leu Asn Pro Phe Ala Trp Ala Ala Cys Val Gln
65                  70                  75                  80
Lys Thr Asn Ala Thr Met Glu Gln Lys Gln Thr Ala Ile Ser Val Val
                85                  90                  95
Lys Glu Leu Val Lys Asn Leu Ala Thr Lys Ser Asp Glu Lys Asp Glu
            100                 105                 110
```

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

(2) INFORMATION FOR SEQ ID NO:516:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1027 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516

```
Val Cys Leu Asp His Gln Val Gly Ala Gly Lys Thr Leu Cys Ala Ile
1               5                   10                  15
Ala Ser Cys Met Glu Gln Lys Arg Met Gly Leu Val Asn Lys Thr Leu
            20                  25                  30
Ile Ala Val Pro Asn His Leu Thr Lys Gln Trp Gly Asp Glu Phe Tyr
        35                  40                  45
Lys Ala Tyr Pro Asn Ala Asn Val Leu Val Val Asp Ser Lys Asp Thr
    50                  55                  60
Thr Glu Lys Glu Arg Glu Leu Leu Phe Asn Gln Ile Ala Asn Asn Asn
```

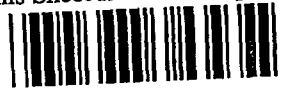
65 70 75 80
Tyr Asp Ala Val Val Ile Ala His Thr His Leu Glu Leu Leu Ser Asn
85 90 95
Pro Arg Gly Ile Ile Glu Glu Leu Lys Glu Glu Glu Leu Val Asn Ala
100 105 110
Glu Lys Asn Phe Glu Arg Gln Glu Leu Ala Tyr Lys Asn Asn Pro Arg
115 120 125
Glu Thr Lys Lys Pro Asn Glu Arg Ala Phe Lys Asn Lys Leu Asp Lys
130 135 140
Ile Arg Ala Lys Tyr Asp Ala Ile Leu Glu Lys Gln Gly Ser His Ile
145 150 155 160
Asp Ile Ser Gln Met Gly Ile Asp Asn Leu Ile Val Asp Glu Ala His
165 170 175
Leu Phe Lys Asn Leu Ala Phe Glu Thr Ser Met Glu Lys Ile Ala Gly
180 185 190
Leu Gly Asn Gln Gln Gly Ser Asn Arg Ala Arg Asp Leu Phe Ile Lys
195 200 205
Thr Arg Tyr Leu His Gln Asn Asp Lys Lys Ile Met Phe Leu Thr Gly
210 215 220
Thr Pro Ile Ala Asn Ser Leu Ser Glu Met Tyr His Leu Gln Arg Tyr
225 230 235 240
Leu Thr Pro Asp Val Leu Lys Glu Arg Gly Leu Glu Phe Phe Asp Asp
245 250 255
Trp Ala Lys Thr Tyr Gly Glu Val Val Asn Asp Phe Glu Leu Asp Thr
260 265 270
Ser Ala Gln Ser Tyr Lys Met Val Asn Arg Phe Ser Lys Phe Ser Asp
275 280 285
Val Gln Gly Leu Ser Thr Met Tyr Arg Ala Phe Ala Asp Ile Val Ser
290 295 300
Asn Asp Asp Ile Leu Lys His Asn Pro His Phe Val Pro Lys Val Tyr
305 310 315 320
Gly Asp Lys Pro Ile Asn Val Val Val Lys Arg Ser Glu Glu Val Ala
325 330 335
Gln Phe Ile Gly Val Ala Leu Glu Asn Gly Lys Tyr Asn Glu Gly Ser
340 345 350
Ile Ile Asp Arg Met Gln Lys Cys Glu Gly Lys Lys Ser Gln Lys Gly
355 360 365
Gln Asp Asn Ile Leu Ser Cys Thr Thr Asp Ala Arg Lys Val Ala Leu
370 375 380
Asp Tyr Arg Leu Ile Asp Pro Asn Ala Lys Val Glu Lys Glu Phe Ser
385 390 395 400
Lys Ser Tyr Ala Met Ala Lys Asn Ile Tyr Glu Asn Tyr Leu Glu Thr
405 410 415
His Ala Thr Lys Gly Thr Gln Leu Gly Phe Ile Gly Leu Ser Thr Pro
420 425 430
Lys Thr His Ser Gln Lys Val Ser Leu Glu Ala Leu Asp Asn Ala His
435 440 445
Glu Thr Glu Asn Lys Asn Pro Leu Asp Lys Ala Gln Glu Leu Leu Glu
450 455 460
Ser Leu Ser Ser Tyr Asp Glu Lys Gly Asn Leu Ile Ala Pro Ser Lys
465 470 475 480
Lys Glu Leu Glu Asn Glu Leu Lys Glu Lys Glu Ala Lys Ser Val Asn
485 490 495
Leu Asp Glu Glu Ile Ala Lys Gly Cys Ser Phe Asp Val Tyr Ser Asp
500 505 510
Val Leu Arg His Leu Val Gln Met Gly Ile Pro Gln Asn Glu Ile Ala
515 520 525
Phe Ile His Asp Ala Lys Thr Glu Glu Gln Lys Gln Asp Leu Phe Lys
530 535 540
Lys Leu Asn Arg Gly Gly Val Arg Val Leu Leu Gly Ser Pro Ala Lys
545 550 555 560
Met Gly Val Gly Thr Asn Val Gln Glu Arg Leu Val Ala Met His Glu
565 570 575
Leu Asp Cys Pro Trp Arg Pro Asp Glu Leu Leu Gln Met Glu Gly Arg
580 585 590

This Sheet Has Been Replaced



```
Gly Ile Arg Gln Gly Asn Ile Leu His Gln Asn Asp Pro Glu Asn Phe
        595                 600                 605
Arg Met Lys Ile Tyr Arg Tyr Ala Thr Glu Lys Thr Tyr Asp Ser Arg
    610                 615                 620
Met Trp Gln Ile Ile Glu Thr Lys Ser Lys Gly Ile Glu Gln Phe Arg
625                 630                 635                 640
Asn Ala His Lys Leu Gly Leu Asn Glu Leu Glu Asp Phe Asn Met Gly
                645                 650                 655
Ser Ser Asn Ala Ser Glu Met Lys Ala Glu Ala Thr Gly Asn Pro Leu
            660                 665                 670
Ile Ile Glu Glu Val Lys Leu Arg Ala Glu Ile Lys Ser Glu Glu Ser
        675                 680                 685
Lys Tyr Lys Ala Phe Asn Lys Glu His Tyr Phe Asn Glu Glu Ser Leu
    690                 695                 700
Lys Asn Asn Ala Ser Lys Leu Asp Tyr Leu Lys Gln Glu Leu Lys Asp
705                 710                 715                 720
Leu Glu Thr Leu Gln Arg Ser Val Ile Ile Pro Thr His Thr Glu Ile
                725                 730                 735
Lys Leu Tyr Asp Leu Lys Asn Glu Glu Ser Lys Asp Tyr Glu Leu Ile
            740                 745                 750
Lys Val Lys Glu Val Glu Pro Leu Lys Glu Asn Ala Ser Met Ser Glu
        755                 760                 765
Glu Leu Thr His Lys Lys Leu Lys Glu Gln Asn Lys Gln Ile Ala Glu
    770                 775                 780
Gln Asn Lys Glu Lys Leu Asp Ala Ile Lys Lys Gln Phe Ala Ser Asn
785                 790                 795                 800
Leu Asn Thr Leu Phe Val Asn Glu Glu Glu Asp Tyr Lys Leu Leu Glu
                805                 810                 815
Tyr Lys Gly Phe Val Val Asn Ala Tyr Lys Thr Lys Tyr Gln Val Glu
            820                 825                 830
Phe Ser Leu Ser Pro Lys Asp Asn Pro Asn Ile Ala Tyr Ser Pro Ser
        835                 840                 845
Asn Met Val Tyr Lys Asn Asp Thr Ile Asn Met Phe Ser Ser Tyr Asn
    850                 855                 860
Phe Cys Ala Glu Ile Lys Phe Asp Gly Phe Leu Lys Arg Leu Asp Asn
865                 870                 875                 880
Ala Ile Thr Lys Leu Pro Glu Lys Ile Lys Glu Leu Glu Asn Ser Ile
                885                 890                 895
Glu Ile Thr Lys Lys Asn Ile Ala Lys Tyr Thr Arg Leu Val Glu Gln
            900                 905                 910
Lys Pro Ser Tyr Pro Arg Leu Glu Tyr Leu Gln Ala Leu Lys Trp Asp
        915                 920                 925
His Lys Thr Leu Ile Asp Asp Leu Ala Lys Met Ser Lys Asp Arg Asn
    930                 935                 940
Tyr Lys Pro Ala Phe Asn Pro Lys Ser Lys Glu Val Leu Lys Asn Leu
945                 950                 955                 960
Asn Ala Glu Lys Arg Ala Ser Leu Glu Asn Glu Arg Glu Glu Gln Gly
                965                 970                 975
Val Lys Gly Asn Thr Lys Ser His Asp Glu Ile Glu Pro Ala Thr Glu
            980                 985                 990
Gln Val Ile Glu Lys Glu Ile Glu Lys Gly Asp Glu Ile Ala Asn Asn
        995                 1000                1005
Val Asp Tyr Tyr Glu Asn Glu Gln Glu Val Glu Ile Thr Lys Ser Met
    1010                1015                1020
Gly Arg Arg
1025
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:517:

(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:517

```
Met Lys Leu Val Ser Leu Ile Val Ala Leu Val Phe Cys Cys Phe Leu
1               5                  10                  15
Gly Ala Val Glu Leu Pro Gly Val Tyr Gln Thr Gln Glu Phe Leu Tyr
            20                  25                  30
Met Lys Ser Ser Phe Val Glu Phe Phe Glu His Asn Gly Lys Phe Tyr
        35                  40                  45
Ala Tyr Gly Ile Ser Asp Val Unk Unk Ser Lys Ala Lys Lys Asp Lys
    50                  55                  60
Leu Asn Pro Asn Pro Lys Leu Arg Asn Arg Ser Asp Lys Gly Val Val
65                  70                  75                  80
Phe Leu Ser Asp Leu Ile Lys Val Gly Glu Gln Ser Tyr Lys Gly Gly
                85                  90                  95
Lys Ala Unk Asn Phe Unk Asp Gly Lys Thr Unk His Val Arg Val Thr
            100                 105                 110
Gln Unk Ser Asn Gly Asp Leu Unk Phe Thr Ser Ser Tyr Unk Lys Trp
        115                 120                 125
Gly Tyr Val Gly Lys Thr Phe Thr Trp Lys Arg Leu Ser Asp Glu Glu
    130                 135                 140
Ile Lys Asn Leu Lys Leu Lys Arg Phe Asn
145                 150
```

(2) INFORMATION FOR SEQ ID NO:517:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517

```
Met Lys Leu Val Ser Leu Ile Val Ala Leu Val Phe Cys Cys Phe Leu
1               5                  10                  15
Gly Ala Val Glu Leu Pro Gly Val Tyr Gln Thr Gln Glu Phe Leu Tyr
            20                  25                  30
Met Lys Ser Ser Phe Val Glu Phe Phe Glu His Asn Gly Lys Phe Tyr
        35                  40                  45
Ala Tyr Gly Ile Ser Asp Val Unk Unk Ser Lys Ala Lys Lys Asp Lys
    50                  55                  60
Leu Asn Pro Asn Pro Lys Leu Arg Asn Arg Ser Asp Lys Gly Val Val
65                  70                  75                  80
```

```
Phe Leu Ser Asp Leu Ile Lys Val Gly Glu Gln Ser Tyr Lys Gly Gly
                85                  90                  95
Lys Ala Unk Asn Phe Unk Asp Gly Lys Thr Unk His Val Arg Val Thr
            100                 105                 110
Gln Unk Ser Asn Gly Asp Leu Unk Phe Thr Ser Ser Tyr Unk Lys Trp
        115                 120                 125
Gly Tyr Val Gly Lys Thr Phe Thr Trp Lys Arg Leu Ser Asp Glu Glu
    130                 135                 140
Ile Lys Asn Leu Lys Leu Lys Arg Phe Asn
145                 150
```

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518

```
Met Ala Glu Glu Glu Lys Thr Glu Leu Pro Ser Ala Lys Lys Ile Gln
1               5                   10                  15
Lys Ala Arg Glu Glu Gly Asn Val Pro Lys Ser Met Glu Val Val Gly
            20                  25                  30
Val Phe Arg Val Ile Gly Trp Ala Asn Glu Tyr Phe Cys Phe Phe Tyr
        35                  40                  45
Met Val Gly Gly Met Ala Leu Ala Arg Cys Ile Ala Met Cys
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

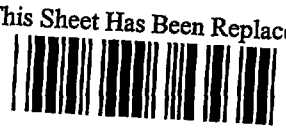
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519

```
Met Lys Thr Leu Val Lys Asn Thr Ile Tyr Ser Phe Leu Leu Leu Ser
1               5                   10                  15
Val Leu Met Ala Glu Asp Ile Thr Ser Gly Leu Lys Gln Leu Asp Asn
```

This Sheet Has Been Replaced



```
            20                  25                  30
Thr Tyr Gln Glu Thr Asn Gln Gln Val Leu Lys Asn Leu Asp Glu Ile
        35                  40                  45
Phe Ser Thr Thr Ser Pro Ser Ala Asn Asn Lys Ile Gly Gln Glu Asp
    50                  55                  60
Ala Leu Asn Ile Lys Lys Ala Ala Ile Ala Leu Arg Gly Asp Leu Ala
65                  70                  75                  80
Leu Leu Lys Ala Asn Phe Glu Ala Asn Glu Leu Phe Phe Ile Ser Glu
                85                  90                  95
Asp Val Ile Phe Lys Thr Tyr Met Ser Ser Pro Glu Leu Leu Leu Thr
            100                 105                 110
Tyr Met Lys Ile Asn Pro Leu Asp Gln Lys Thr Ala Glu Gln Gln Cys
        115                 120                 125
Gly Ile Ser Asp Lys Val Leu Val Leu Tyr Cys Glu Gly Lys Leu Lys
    130                 135                 140
Ile Glu Gln Glu Lys Gln Asn Ile Arg Glu Arg Leu Glu Thr Ser Leu
145                 150                 155                 160
Lys Ala Tyr Gln Ser Asn Ile Gly Gly Thr Ala Ser Leu Ile Thr Ala
                165                 170                 175
Ser Gln Thr Leu Val Glu Ser Leu Lys Asn Lys Asn Phe Ile Lys Gly
            180                 185                 190
Ile Lys Lys Leu Met Leu Ala His Asn Lys Val Phe Leu Asn Tyr Leu
        195                 200                 205
Glu Glu Leu Asp Ala Leu Glu Arg Ser Leu Glu Gln Ser Lys Arg Gln
    210                 215                 220
Tyr Leu Gln Glu Arg Gln Ser Ser Lys Ile Ile Val Lys
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:520:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520

```
Val Ser Glu Lys Asp Arg Ala Phe Leu Leu Ala Ser Leu Ser Cys Val
1               5                   10                  15
Asp Tyr Val Val Val Phe Gly Glu Asp Thr Pro Ile Lys Leu Ile Gln
            20                  25                  30
Ala Leu Lys Pro Asp Ile Leu Val Lys Gly Ala Asp Tyr Leu Asn Lys
        35                  40                  45
Glu Val Ile Gly Ser Glu Leu Ala Lys Glu Thr Arg Leu Ile Glu Phe
    50                  55                  60
Glu Glu Gly Tyr Ser Thr Ser Ala Ile Ile Glu Lys Ile Lys Arg Thr
65                  70                  75                  80
His Asn Asp
```

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521

Leu Glu Thr Leu Phe Leu Val
1 5

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521

Leu Glu Thr Leu Phe Leu Val
1 5

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:522:

(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:522

```
Val Tyr Asp Lys Ser Leu Cys Lys Thr Met Ala Leu Ala Leu Lys Ala
1               5                  10                  15
Leu Gly Val Lys Arg Ala Met Val Val Asn Gly Gly Gly Thr Gly Glu
            20                  25                  30
Ile Val Leu His Asp Ile Thr His Ala Cys Glu Leu Lys Asn Asn Glu
        35                  40                  45
Ile Leu Glu Tyr Asp Leu Ser Ala Lys Asp Phe Asp Leu Pro Pro Ser
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:523:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523

```
Met Leu Val Glu Ile Glu Asn Leu Thr Lys Thr Tyr Gly Ser Leu Lys
1               5                  10                  15
Ala Leu Asp Asn Ile Ser Leu Lys Leu Pro Lys Gln Gln Phe Ile Gly
            20                  25                  30
Leu Leu Gly Pro Asn Gly Ala Gly Lys Thr Thr Leu Leu Lys Ile Leu
        35                  40                  45
Ala Gly Leu Asn Leu Asn Tyr Gln Gly Glu Val Lys Ile Leu Asn Gln
    50                  55                  60
Lys Ile Gly Ile Glu Thr Lys Lys Ser Val Ala Phe Leu Ser Asp Gly
65                  70                  75                  80
Asp Phe Leu Asp Pro Lys Leu Thr Pro Leu Lys Ala Ile Ala Phe Tyr
                85                  90                  95
Lys Asp Phe Phe Ser Asp Phe Asp Glu Ser Lys Ala Leu Asn Leu Leu
            100                 105                 110
Lys Arg Phe Ser Val Pro Leu Lys Arg Glu Phe Lys Ala Leu Ser Lys
        115                 120                 125
Gly Met Arg Glu Lys Leu Gln Leu Ile Leu Thr Leu Ser Arg Asn Ala
    130                 135                 140
Ser Leu Tyr Leu Phe Asp Glu Pro Val Ala Gly Ile Asp Pro Ile Ala
145                 150                 155                 160
Arg Glu Glu Ile Phe Glu Leu Ile Ala Lys Glu Phe Ser Gln Asn Ala
                165                 170                 175
Ser Leu Leu Val Ser Thr His Leu Val Val Asp Val Glu Lys Tyr Leu
            180                 185                 190
Asp Ser Ala Ile Phe Leu Lys Glu Ala Lys Val Val Ala Phe Gly Asp
        195                 200                 205
Val Gly Glu Leu Lys Lys Gly Tyr Ser Ser Leu Glu Ala Ala Tyr Lys
    210                 215                 220
Glu Arg Leu Lys
225
```

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524

```
Met Asn Lys Leu Phe Leu Ala Phe Ile Val Gly Gly Met Leu Leu Ser
1               5                  10                  15
Ala Asp Ala Leu Asn Asp Lys Ile Glu Asn Leu Met Gly Glu Arg Ser
            20                  25                  30
Tyr His Met Asn Lys Leu Phe Leu Glu Arg Leu Phe Lys Asn Arg Lys
        35                  40                  45
Asp Phe Tyr Glu Met Gly Arg Leu Asp Ser Leu Lys Leu Leu Asn Thr
    50                  55                  60
Leu Lys Glu Asn Gly Leu Leu Ser Phe Asn Phe Asp Lys Pro Ser Val
65                  70                  75                  80
Leu Lys Ile Thr Phe Lys Ala Ser Ser Asn Pro Leu Ala Phe Ala Lys
                85                  90                  95
Ser Ile Asn Asn Ser Leu Asn Met Met Gly Tyr Ser Tyr Val Leu Pro
            100                 105                 110
Ile Arg Met Gln Ser Ser Ser Gly Glu Asn Val Phe Ser Tyr Glu Leu
        115                 120                 125
Lys Thr Glu Tyr Val Leu Asp Pro Asn Ile Leu Ile Glu Thr Met Lys
    130                 135                 140
Arg His Gly Phe Asp Phe Met Asp Ile Arg Arg Val Ser Leu Lys Glu
145                 150                 155                 160
Trp Glu Tyr Asp Phe Ala Leu Gln Lys Ile Lys Leu Pro Asn Ala Arg
                165                 170                 175
Ala Leu Val Leu Ser Ser Asp Pro Val Glu Phe Lys Glu Ala Ser Gly
            180                 185                 190
Lys Tyr Trp Leu Ser Val Asn Gln Asn Ala Tyr Leu Lys Ile Ser Ser
        195                 200                 205
Asn Asn Pro Leu Trp Gln Pro Lys Ile Ile Phe Tyr Asp Glu Asn Leu
    210                 215                 220
Lys Ile Ile Gln Ile Ile Ala Lys Glu Asn Arg Gln Gln Glu Ile Ala
225                 230                 235                 240
Leu Asn Leu Leu Asp Gly Val Arg Phe Ile His Ile Thr Asp Ala Lys
                245                 250                 255
Asn Pro Ile Ile Leu Lys Asn Gly Ile Ser Val Val Phe Asp Ala Met
            260                 265                 270
Pro
```

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525

```
Val Ser Arg Pro Phe Lys Thr Ile Lys Lys Pro Pro Gln Pro Pro
1               5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO:526:

(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:526

```
Met Unk Thr His Asp Arg Arg Lys Leu Arg Ile Unk Leu Thr Gln Thr
1               5                   10                  15
Thr Thr Leu Val Ala Thr Ile Gly Ser Asn Ala Pro Tyr Ile Gly Leu
            20                  25                  30
Leu Gly Thr Val Met Gly Ile Met Leu Thr Phe Met Asp Leu Gly Ser
        35                  40                  45
Ala Ser Gly Ile Asp Thr Lys Ala Ile Met Thr Asn Leu Ala Leu Ala
    50                  55                  60
Leu Lys Ala Thr Gly Met Gly Leu Leu Val Ala Ile Pro Ala Ile Val
65                  70                  75                  80
Ile Tyr Asn Leu Leu Val Arg Lys Ser Glu Ile Leu Val Thr Lys Trp
                85                  90                  95
Asp Ile Phe His His Pro Val Asp Thr Gln Ser His Glu Val Tyr Ser
            100                 105                 110
Lys Ala
```

(2) INFORMATION FOR SEQ ID NO:526:

(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:526

```
Met Unk Thr His Asp Arg Arg Lys Leu Arg Ile Unk Leu Thr Gln Thr
1               5                  10                  15
Thr Thr Leu Val Ala Thr Ile Gly Ser Asn Ala Pro Tyr Ile Gly Leu
            20                  25                  30
Leu Gly Thr Val Met Gly Ile Met Leu Thr Phe Met Asp Leu Gly Ser
        35                  40                  45
Ala Ser Gly Ile Asp Thr Lys Ala Ile Met Thr Asn Leu Ala Leu Ala
    50                  55                  60
Leu Lys Ala Thr Gly Met Gly Leu Leu Val Ala Ile Pro Ala Ile Val
65                  70                  75                  80
Ile Tyr Asn Leu Leu Val Arg Lys Ser Glu Ile Leu Val Thr Lys Trp
                85                  90                  95
Asp Ile Phe His His Pro Val Asp Thr Gln Ser His Glu Val Tyr Ser
            100                 105                 110
Lys Ala
```

(2) INFORMATION FOR SEQ ID NO:527:

This Sheet Has Been Replaced



(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:527

```
Met Ile Ala Val Leu Pro Pro Leu Phe Ser Met Gly Ser Phe Asp Glu
1               5                  10                  15
Trp Ile Tyr Arg Gly Leu Val Ala Leu Met Val Ser Cys Pro Cys Ala
            20                  25                  30
Leu Val Ile Ser Val Pro Leu Gly Tyr Phe Gly Gly Val Gly Ala Ala
        35                  40                  45
Ser Arg Lys Gly Ile Leu Met Lys Gly Val His Val Leu Glu Gly Ala
    50                  55                  60
Tyr Pro Asn
65
```

(2) INFORMATION FOR SEQ ID NO:528:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528

```
Val Gln His Phe Asn Phe Leu Tyr Lys Asp Ser Leu Phe Ser Ile Ala
1               5                  10                  15
Leu Phe Thr Phe Ile Ile Ala Leu Val Ile Leu Leu Glu Gln Ala Arg
            20                  25                  30
Ala Tyr Phe Thr Arg Lys Arg Asn Lys Lys Phe Leu Gln Lys Phe Ala
        35                  40                  45
Gln Asn Gln Asn Ala Tyr Ala Ser Ser Glu Asn Leu Asp Glu Leu Leu
    50                  55                  60
Lys His Ala Lys Ile Ser Ser Leu Met Phe Leu Ala Arg Ala Tyr Ser
65                  70                  75                  80
Lys Ala Asp Val Glu Met Ser Ile Glu Ile Leu Lys Gly Leu Leu Asn
                85                  90                  95
Arg Pro Leu Lys Asp Glu Glu Lys Ile Ala Val Leu Asp Leu Leu Ala
            100                 105                 110
Lys Asn Tyr Phe Ser Val Gly Tyr Leu Gln Lys Thr Lys Asp Thr Val
        115                 120                 125
Lys Glu Ile Leu Arg Phe Ser Pro Arg Asn Val Glu Ala Leu Leu Lys
    130                 135                 140
Leu Leu His Ala Tyr Glu Leu Glu Lys Asp Tyr Ser Lys Ala Leu Glu
145                 150                 155                 160
Thr Leu Glu Cys Leu Glu Glu Leu Glu Val Pro Lys Ile Glu Thr Ile
                165                 170                 175
Lys Asn Tyr Leu Tyr Leu Met His Leu Ile Glu Asn Lys Glu Asp Ala
            180                 185                 190
Ala Lys Ile Leu His Val Ser Lys Ala Ser Leu Asp Leu Lys Lys Ile
        195                 200                 205
Ala Leu Asn His Leu Lys Ser His Asp Glu Asn Leu Phe Trp Gln Glu
    210                 215                 220
Ile Asp Thr Thr Glu Arg Leu Glu Asn Val Ile Asp Leu Leu Trp Asp
225                 230                 235                 240
Met Asn Ile Pro Ala Phe Ile Leu Glu Lys His Ala Leu Leu Gln Asp
                245                 250                 255
Ile Ala Arg Ser Gln Gly Leu Leu Leu Asp His Lys Pro Cys Gln Ile
            260                 265                 270
Phe Glu Leu Glu Val Leu Arg Ala Leu Leu His Ser Pro Ile Lys Ala
        275                 280                 285
Ser Leu Thr Phe Glu Tyr Arg Cys Lys His Cys Lys Gln Ile Phe Pro
    290                 295                 300
Phe Glu Ser His Arg Cys Pro Val Cys Tyr Gln Leu Ala Phe Met Asp
305                 310                 315                 320
Met Val Ala
```

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...10

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529

Met Glu His Leu Thr Arg Gly Ile Lys His
1 5 10

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530

Val Val Ile Leu Gly Ser His Gly Lys Glu Glu Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:531:

(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:531

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

```
        35                  40                  45
Asn Met Met Ser Glu Lys Glu Ile Glu Glu Asp Leu Met Ala Phe Lys
    50                  55                  60
Ser Gly Ala Asn Lys Asn Pro Val Met Thr Arg Lys Leu Lys Asn
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:532:

(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:532

```
Met Gly Ile Ala Thr Ser Leu Ile Ser Glu Val Ser Lys Phe Tyr Tyr
1               5                  10                  15
Ala Leu Lys Tyr His Ala Lys Phe Met Ser Leu Gly Glu Leu Gly Cys
            20                  25                  30
Tyr Ala Ser His Tyr Ser Leu Trp Gln Lys Cys Ile Glu Leu Asn Glu
        35                  40                  45
Ala Ile Cys Ile Leu Glu Asp Asp Ile Thr Leu Lys Glu Asp Phe Lys
    50                  55                  60
Glu Gly Leu Asp Phe Leu Glu Lys His Ile Gln Glu Leu Gly Tyr Ala
65                  70                  75                  80
Arg Leu Met His Leu Leu Tyr Asp Ala Ser Val Lys Ser Glu Pro
                85                  90                  95
```

(2) INFORMATION FOR SEQ ID NO:533:

(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:533

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

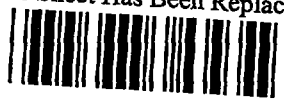
This Sheet Has Been Replaced



```
Lys Pro Pro Gln Val Phe Phe Met Gly Asp Ile Phe His Val Leu Val
        35                  40                  45
Gly Tyr Leu Pro Leu Asp Lys Glu Gln Gln Lys Ile Ile Asp Leu Ile
    50                  55                  60
His Ala Leu Ser Glu Ile Ser Gln Val Phe Tyr Phe Glu Gly Asn His
65                  70                  75                  80
Asp Phe Ser Met Arg Phe Val Phe Asn Ser Lys Val Met Val Phe Glu
                85                  90                  95
Arg Gln Asn Gln Pro Ala Leu Phe Gln Tyr Asp Asn Lys Arg Phe Leu
            100                 105                 110
Leu Ala His Gly Asp Leu Phe Ile Thr Lys Ala Tyr Glu Phe Tyr Ile
        115                 120                 125
Thr Gln Leu Thr Ser Thr Trp Ala Arg Phe Phe Leu Thr Phe Leu Asn
    130                 135                 140
Leu Leu Ser Phe Lys Thr Leu Tyr Pro Phe
145                 150
```

(2) INFORMATION FOR SEQ ID NO:534:

This Sheet Has Been Replaced



(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:534

```
Met Gln Asp Leu Asp Asn Asn Met Ser Leu Asp Thr Ala His Asn Thr
1               5                   10                  15
Leu Ser Ser Asn Gly Lys Asn Ile Thr Ile Ala Gly Val Val Lys Ala
            20                  25                  30
Leu Gln Lys Ile Gly Val Ser Ala Lys Gly Met Val Ser Ile Leu Gln
        35                  40                  45
Ala Leu Lys Lys Ser Gly Ala Ile Ser Ala Lys Trp Arg Tyr Tyr Asp
    50                  55                  60
Lys Gln Gln
65
```

(2) INFORMATION FOR SEQ ID NO:534:

(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:534

```
Met Gln Asp Leu Asp Asn Asn Met Ser Leu Asp Thr Ala His Asn Thr
1               5                  10                  15
Leu Ser Ser Asn Gly Lys Asn Ile Thr Ile Ala Gly Val Val Lys Ala
            20                  25                  30
Leu Gln Lys Ile Gly Val Ser Ala Lys Gly Met Val Ser Ile Leu Gln
        35                  40                  45
Ala Leu Lys Lys Ser Gly Ala Ile Ser Ala Lys Trp Arg Tyr Tyr Asp
    50                  55                  60
Lys Gln Gln
65
```

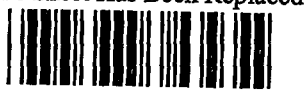
(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535

```
Val Gln Pro Met Lys Ser Lys Lys Leu Tyr Leu Ala Leu Ile Ile Gly
1               5                  10                  15
Val Leu Leu Ala Phe Leu Thr Leu Ser Ser Trp Leu Gly Asn Ser Gly
            20                  25                  30
Leu Val Gly Arg Phe Gly Val Trp Phe Ala Ala Ile Asn Lys Lys Tyr
        35                  40                  45
Phe Gly Tyr Leu Ser Leu Ile Asn Leu Pro Tyr Leu Ala Trp Val Leu
    50                  55                  60
Phe Leu Leu Tyr Arg Ala Lys Asn Pro Phe Thr Glu Ile Val Leu Glu
65                  70                  75                  80
Lys Thr Leu Gly His Leu Leu Gly Ile Leu Ser Leu Leu Phe Leu Gln
                85                  90                  95
Ser Ser Leu Leu Asn Gln Gly Glu Ile Gly Asn Ser Ala Arg Leu Phe
            100                 105                 110
Leu His Pro Phe Ile Gly Asp Phe Gly Leu Tyr Val Leu Ile Met Leu
        115                 120                 125
Met Val Val Ile Ser Tyr Leu Ile Leu Phe Lys Leu Pro Pro Lys Ser
    130                 135                 140
Val Phe Tyr Pro Tyr Met Asn Lys Thr Gln Ser Leu Leu Lys Glu Ile
145                 150                 155                 160
Tyr Lys Gln Cys Leu Gln Ala Phe Ser Pro Asn Phe Ser Leu Lys Lys
                165                 170                 175
Glu Gly Phe Glu Asn Thr Pro Ser Asp Ser Gln Lys Lys Glu Thr Asn
            180                 185                 190
Asn Asp Lys Glu Lys Glu Asn Leu Lys Glu Asn Pro Ile Asp Glu Asn
        195                 200                 205
His Asn Thr Pro Asn Glu Glu Ser Phe Leu Ala Ile Pro Thr Pro Tyr
    210                 215                 220
```

SUBSTITUTE SHEET (RULE 26)

```
Asn Thr Thr Leu Asn Asn Ser Glu Pro Gln Glu Gly Leu Val Gln Ile
225                 230                 235                 240
Ser Pro His Pro Pro Thr His Tyr Thr Ile Tyr Pro Lys Arg Asn Arg
                245                 250                 255
Phe Asp Asp Leu Thr Asn Pro Thr Leu Lys Glu Pro Lys Gln Glu Thr
            260                 265                 270
Lys Glu Arg Glu Pro Thr Leu Lys Lys Glu Thr Pro Thr Thr Leu Lys
        275                 280                 285
Pro Ile Met Pro Ile Ser Ala Ser Thr Gln Lys Ile Met Thr Lys Gln
    290                 295                 300
Lys Thr Thr Lys Pro Leu Thr Thr Pro
305                 310
```

(2) INFORMATION FOR SEQ ID NO:536:

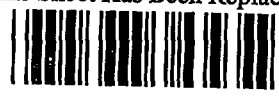
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536

```
Val Met Leu Ser Arg Asp Ile Val Gln Tyr Ser Lys Ile Arg Thr Glu
1               5                  10                  15
Leu Tyr Ala Tyr Leu Thr Tyr Leu Phe Ser His Asn Ile Arg Asn His
            20                  25                  30
Leu Pro Glu Ile Thr Leu Asp Tyr Leu Asn Arg Gln Ile Ser Lys Met
        35                  40                  45
Gln Ala Glu Ile Lys Met Ala Lys Ser Phe Phe Val Leu Asp Ala Lys
    50                  55                  60
Gly Met Leu Met Leu Lys Pro Ser Gln Phe Lys Glu Gln Gly His Lys
65                  70                  75                  80
Glu Gly Leu Leu Glu His Asp Leu Thr Glu Gly Ile Glu Leu Glu Ser
                85                  90                  95
His Val Ser Phe Ser Asp Lys Tyr Tyr Phe Tyr Gln Ala Val Asn Glu
            100                 105                 110
Lys Arg Cys Ile Leu Thr Asp Pro Tyr Pro Ser Lys Lys Gly Asn His
        115                 120                 125
Leu Val Val Ser Ala Ser Tyr Pro Val Tyr Asp Gln Asn Asn Asp Leu
    130                 135                 140
Ala Phe Val Val Cys Leu Gln Ile Pro Leu Arg Val Ala Ile Glu Ile
145                 150                 155                 160
Ser Ser Pro Ser Lys Tyr Phe Lys Thr Phe Ser Glu Gly Ser Met Val
                165                 170                 175
Met Tyr Phe Met Ile Ser Ile Met Leu Thr Leu Val Ser Leu Leu Leu
            180                 185                 190
Phe Val Lys Cys Ile Ser Ser Phe Trp Thr Ala Ile Val His Phe Ser
        195                 200                 205
Ser Phe Asp Ile Lys Glu Val Phe His Pro Ile Val Leu Leu Thr Leu
    210                 215                 220
Ala Leu Ala Thr Phe Asp Leu Val Lys Ala Ile Phe Glu Glu Glu Val
225                 230                 235                 240
Leu Gly Lys Asn Ser Gly Asp Asn His His Ala Ile His Arg Thr Met
```

```
                245                 250                 255
Ile Arg Phe Leu Gly Ser Ile Ile Ile Ala Leu Ala Ile Glu Ala Leu
            260                 265                 270
Met Leu Val Phe Lys Phe Ser Val Ser Glu Pro Asp Lys Ile Thr Tyr
        275                 280                 285
Ala Val Tyr Leu Ala Ile Gly Val Ala Val Leu Leu Ile Ser Leu Ala
    290                 295                 300
Ile Tyr Val Lys Phe Ala Tyr Ser Val Leu Pro Lys Arg Glu Arg
305                 310                 315
```

(2) INFORMATION FOR SEQ ID NO:537:

(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:537

```
Met Val Ile His Glu Lys Ile Lys Ser Arg Phe Ser Arg Asn Trp Ser
1               5                   10                  15
Leu Arg Asn Arg Gly Arg His Phe Ala Ser Ser Ser Val Tyr Phe Phe
            20                  25                  30
Ser Leu Leu Val Ile Thr Ala Val Asn Arg Ser Ser Ala Val Ala Trp
        35                  40                  45
Leu Leu Met Pro Glu His Leu Ile Gly Trp Phe Leu Ile Ser Phe Ser
    50                  55                  60
Gly Glu Phe Val Ala Asp Met Ala Phe Gly Lys Lys Ser Lys Ile Phe
65                  70                  75                  80
Lys Thr Arg Phe Gly Ile Ser Ile Val Ser Gly Val Ser Leu Leu Leu
                85                  90                  95
Gly Ala Tyr Gln Arg Phe Tyr Phe Leu Tyr Gly Leu Ala Leu Leu Ile
            100                 105                 110
Gly Gly Leu Ser Phe Leu
        115
```

(2) INFORMATION FOR SEQ ID NO:538:

This Sheet Has Been Replaced

(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:538

```
Leu His Pro Leu Ala Asp Val Phe Val Val Asn Asp Lys Arg Unk Val
1               5                  10                  15
Leu Ala Met Val Unk Met Leu Ile Unk Ser Leu Ala Asn Ile Phe Phe
            20                  25                  30
Asn Tyr Leu Phe Ile Phe Unk Leu Glu Val Gly Val Gln Gly Unk Ala
        35                  40                  45
Ile Val Thr Val Ile Gly His Ala Ile Gly Gly Leu Val Leu Met Gln
    50                  55                  60
His Phe Trp Arg Lys Lys Gly Glu Leu Tyr Phe Ile Lys Leu Ile Phe
65                  70                  75                  80
Phe Ile Phe Ser His Phe Phe Ser
                85
```

(2) INFORMATION FOR SEQ ID NO:538:

(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:538

```
Leu His Pro Leu Ala Asp Val Phe Val Val Asn Asp Lys Arg Unk Val
1               5                  10                  15
Leu Ala Met Val Unk Met Leu Ile Unk Ser Leu Ala Asn Ile Phe Phe
            20                  25                  30
Asn Tyr Leu Phe Ile Phe Unk Leu Glu Val Gly Val Gln Gly Unk Ala
        35                  40                  45
Ile Val Thr Val Ile Gly His Ala Ile Gly Gly Leu Val Leu Met Gln
    50                  55                  60
His Phe Trp Arg Lys Lys Gly Glu Leu Tyr Phe Ile Lys Leu Ile Phe
65                  70                  75                  80
Phe Ile Phe Ser His Phe Phe Ser
                85
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:539:

(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:539

```
Met Phe Lys Ser Arg Leu Asn Ser Trp Ile Leu Leu Gly Ile Leu Gly
1               5                  10                  15
Val Leu Val Val Val Phe Trp Asp Val Ile Lys Tyr Lys Ile Glu Asp
            20                  25                  30
Leu Gln His Asp His Tyr Leu Ser Gln Val Lys Glu Arg Glu Glu Tyr
        35                  40                  45
Tyr Lys Asn His Ile Glu Glu Ala Leu Lys Lys Asp Ser Glu Cys Phe
    50                  55                  60
Glu Lys Gly Gly Asp Lys Val Asp Cys Ser Ala Ala Met Arg Ile Ala
65                  70                  75                  80
Ala Gly Glu Arg Asn Arg Arg Met Leu Glu Ile Lys
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:540:

(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:540

```
Met Val Phe Trp Gly Ala Val Phe Phe Leu Trp Asp Arg Thr Ala Trp
1               5                  10                  15
Lys Arg Leu Met Val Phe Leu Asn Ser Leu Unk Unk Met Leu Ala Ala
            20                  25                  30
Leu Ser Leu Gly Ser Phe Leu Gly Ala Trp Ile Lys Asn Glu Ala His
        35                  40                  45
Thr Thr Gln Ile Val Leu Ile Ser Ser Leu Pro Leu Ile Phe Met Met
    50                  55                  60
Gly Phe Val Trp Pro Phe Glu Ser Leu Pro Ser Tyr Leu Gln Val Phe
65                  70                  75                  80
Val Gln Ile Val Pro Ala Tyr His Gly Ile Ser Leu Leu Gly Arg Leu
                85                  90                  95
Asn Gln Met His Ala Glu Phe Ile Asp Val Ser Ile His Phe Tyr Ala
            100                 105                 110
Leu Ile Ala Ile Phe Ile Val Ser Phe Ile Gly Cys Val Phe Lys Leu
        115                 120                 125
Ser Ser Leu Lys Lys Ala Cys Glu Asn Ala
    130                 135
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 amino acids

This Sheet Has Been Replaced



(B) TYPE: amino acid
(D) TOPOLOGY: linear

(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:541

```
Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe Leu Leu
1               5                  10                  15
Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu Leu Leu
            20                  25                  30
Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr Phe Phe
        35                  40                  45
Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu Ala Asp
    50                  55                  60
Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Val Phe Leu Ile
65                  70                  75                  80
Ala Ser Phe Ser Leu Val Leu Phe Phe Asp Ser Phe Ile Leu Met Leu
                85                  90                  95
Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser Gly Thr
            100                 105                 110
Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys Asp Leu
        115                 120                 125
Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly Met Ile
    130                 135                 140
Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His Ala Met
145                 150                 155                 160
Leu Tyr Val Val Gly Ile Phe Leu Ile Met Leu Cys Ala Leu Thr Ile
                165                 170                 175
Ile Ile Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln Lys Asn
            180                 185                 190
Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu Leu Lys
        195                 200                 205
Asp Asn Pro Lys Leu Lys Ile Leu Leu Val Gly His Leu Ile Thr Pro
    210                 215                 220
Val Phe Phe Met Ser His Phe Gln Met Trp Gln Ala Tyr Phe Leu Lys
225                 230                 235                 240
Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala Phe Gln
                245                 250                 255
Val Ile Ser Ile Pro His Ser Phe Phe Lys Ser Gln Lys Leu Unk Ala
            260                 265                 270
Lys Lys Ser Pro
        275
```

(2) INFORMATION FOR SEQ ID NO:541:

(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:541

```
Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe Leu Leu
1               5                  10                  15
Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu Leu Leu
            20                  25                  30
Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr Phe Phe
        35                  40                  45
Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu Ala Asp
    50                  55                  60
Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Val Phe Leu Ile
65                  70                  75                  80
Ala Ser Phe Ser Leu Val Leu Phe Phe Asp Ser Phe Ile Leu Met Leu
                85                  90                  95
Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser Gly Thr
            100                 105                 110
Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys Asp Leu
        115                 120                 125
Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly Met Ile
    130                 135                 140
Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His Ala Met
145                 150                 155                 160
Leu Tyr Val Val Gly Ile Phe Leu Ile Met Leu Cys Ala Leu Thr Ile
                165                 170                 175
Ile Ile Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln Lys Asn
            180                 185                 190
Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu Leu Lys
        195                 200                 205
Asp Asn Pro Lys Leu Lys Ile Leu Leu Val Gly His Leu Ile Thr Pro
    210                 215                 220
Val Phe Phe Met Ser His Phe Gln Met Trp Gln Ala Tyr Phe Leu Lys
225                 230                 235                 240
Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala Phe Gln
                245                 250                 255
Val Ile Ser Ile Pro His Ser Phe Phe Lys Ser Gln Lys Leu Unk Ala
            260                 265                 270
Lys Lys Ser Pro
        275
```

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...254

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542

```
Met His Glu Gln Gly Ser Ile Ser Phe Ile Gly Glu Gln Gly Ala Lys
1               5                  10                  15
Arg Leu Leu Tyr Ile Leu Tyr Lys Leu Ala Phe Asn Ala Lys Ser Asn
            20                  25                  30
Lys Ile Ala Leu Asp Arg His Tyr Ala Lys Met Phe Leu Gln Val Val
        35                  40                  45
Ala Arg Thr Leu Ile Lys Asn Val Asn Ile Leu Glu Glu Gln Gly Phe
    50                  55                  60
Ile Glu Val Ile Lys Gly Lys Gln Arg Tyr Leu Tyr Val Tyr Leu Lys
65                  70                  75                  80
Asp Tyr Arg Glu Leu Glu Cys Leu Val Lys Ser Lys Met Ala Lys Tyr
                85                  90                  95
Val Met Tyr Leu Arg Gln Phe Phe Asp Tyr Leu Asp Arg Lys Arg Arg
            100                 105                 110
Tyr Gly Phe Asp Phe Thr Leu Lys Asn Leu Ala Phe Ala Lys Thr Lys
        115                 120                 125
Glu Ser Leu Pro Arg His Leu Asn Asp Lys Asp Leu Lys Ser Phe Leu
    130                 135                 140
Lys Thr Leu Leu Asp Tyr Lys Pro Ala Thr Ser Phe Glu Lys Arg Asn
145                 150                 155                 160
Lys Cys Ile Leu Leu Ile Val Ile Leu Gly Gly Leu Arg Lys Cys Glu
                165                 170                 175
Val Leu Asn Ile Glu Leu Lys His Ile Gln Val Glu Glu Gln Asn Tyr
            180                 185                 190
Ser Ile Leu Ile Gln Gly Lys Gly Arg Lys Glu Arg Lys Ala Tyr Ile
        195                 200                 205
Lys Lys Ser Leu Leu Glu Pro Ser Leu Asn Ala Trp Ile Ser Asp Asp
    210                 215                 220
Tyr Arg Leu Lys Tyr Phe Asn Gly Ala Tyr Leu Phe Lys Lys Asp Lys
225                 230                 235                 240
Gln Lys Ser Gln Asn Ser Leu Thr Leu Tyr Asn Leu Ser Pro
                245                 250
```

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 185 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543

```
Val Val Phe Lys Ile Leu Ser Leu Trp Leu Gly Val Phe Cys Phe Leu
1               5                  10                  15
Arg Ala Thr His Leu Tyr Leu Gly Glu Glu Pro Lys Tyr Lys Asp Asn
            20                  25                  30
Phe Thr His Phe Glu Tyr Ala Asn Pro Asn Ala Arg Lys Gly Gly Val
        35                  40                  45
Leu Arg Asn Asp Ala Ile Gly Thr Phe Asp Ser Leu Asn Pro Phe Ala
    50                  55                  60
Leu Lys Gly Thr Lys Ala Glu Gly Leu Asp Leu Ile Tyr Asp Thr Leu
```

```
65                  70                  75                  80
Met Val Gln Ser Leu Asp Glu Pro Phe Ala Glu Tyr Pro Leu Ile Ala
                85                  90                  95
Lys Asp Ala Glu Val Ala Lys Asp Asn Ser Tyr Val Ile Phe Thr Leu
            100                 105                 110
Asp Lys Arg Ala Arg Phe Ser Asn Asn Ala Pro Ile Leu Ala Ser Asp
        115                 120                 125
Val Lys Phe Ser Phe Asp Thr Ile Met Lys Leu Gly Ser Pro Leu Tyr
    130                 135                 140
Arg Gln Tyr Tyr Gln Asp Val Lys Lys Ala Val Ile Leu Asp Lys His
145                 150                 155                 160
His Val Lys Phe Ile Tyr Lys Thr Thr Glu Asn Lys Glu Leu Pro Leu
                165                 170                 175
Ile Leu Gly Gln Leu Gln Ile Phe Ser
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544

```
Val Ala Met Ile Asp Cys Ala Ile Ile Gly Gly Gly Pro Ala Gly Leu
1               5                  10                  15
Ser Ala Gly Leu Tyr Ala Thr Arg Gly Gly Val Lys Asn Ala Val Leu
            20                  25                  30
Phe Glu Lys Gly Met
        35
```

(2) INFORMATION FOR SEQ ID NO:545:

(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:545

This Sheet Has Been Replaced



```
Leu Tyr Pro Pro Gly Ser Val Val Lys Met Gly Val Gly Leu Ser Phe
1               5                  10                  15
Leu Glu Asn Leu His Ile Thr Glu Asn Thr Thr Ile Pro Thr Pro Pro
            20                  25                  30
Phe Ile Glu Val Gly Lys Arg Lys Phe Arg Asp Trp Lys Lys Thr Gly
        35                  40                  45
His Gly Asn Ser Asn Leu Tyr Lys Ala Ile Arg Glu Ser Val Asp Val
    50                  55                  60
Tyr Phe Tyr Lys Phe Gly Leu Glu Ile Ser Ile Glu Unk Leu Ser Lys
65                  70                  75                  80
Unk Phe Lys Unk Ser Gly Leu Trp Gly Lys Asn Gly Arg
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:545:

(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:545

```
Leu Tyr Pro Pro Gly Ser Val Val Lys Met Gly Val Gly Leu Ser Phe
1               5                  10                  15
Leu Glu Asn Leu His Ile Thr Glu Asn Thr Thr Ile Pro Thr Pro Pro
            20                  25                  30
Phe Ile Glu Val Gly Lys Arg Lys Phe Arg Asp Trp Lys Lys Thr Gly
        35                  40                  45
His Gly Asn Ser Asn Leu Tyr Lys Ala Ile Arg Glu Ser Val Asp Val
    50                  55                  60
Tyr Phe Tyr Lys Phe Gly Leu Glu Ile Ser Ile Glu Unk Leu Ser Lys
65                  70                  75                  80
Unk Phe Lys Unk Ser Gly Leu Trp Gly Lys Asn Gly Arg
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:546:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546

```
Val Gly Lys Ser Leu Arg Tyr Ser Leu Asn Leu Asp Leu Asn Gln Lys
1               5                  10                  15
Ala Asp Leu Phe Phe Thr Glu Leu Glu Pro Thr Gly Leu Thr Leu Ser
            20                  25                  30
Pro Ile Met Lys Arg Phe Thr Ile Lys Gly Asp Phe Asp Ser Gly Leu
        35                  40                  45
Lys Ser Tyr Asp Met Ser Tyr Met Tyr Ala Ser Leu Gln Ala Ile Ser
    50                  55                  60
Ala Ile Arg Arg Leu Pro Leu Gly Leu Tyr Asp Gly Val His Val Tyr
65                  70                  75                  80
Ser Lys Thr Pro Met Lys Asp Ile Glu Lys Leu Arg Asn Ala Leu Lys
                85                  90                  95
Thr Ile Asn His His Gly Ile Gly Ile Glu Gly Trp Trp Gln Gln Asn
            100                 105                 110
Gly Asn Phe Phe Ser Ala Met Glu Leu Glu Lys Arg Ala Leu Phe Ile
        115                 120                 125
Val Leu Met Leu Ile Ile Leu Met Ala Ser Leu Asn Ile Ile Ser Ser
    130                 135                 140
Leu Leu Met Val Val Met Asn Arg Arg Lys Glu Ile Ala Leu Leu Phe
145                 150                 155                 160
Ser Met Gly Ser Ser Gln Lys Glu Ile Gln Lys Thr Phe Phe Tyr Leu
                165                 170                 175
Gly Asn Ile Ile Ser Leu
            180
```

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 247 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

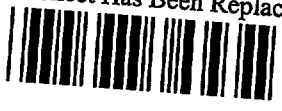
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...247

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547

```
Met Lys Lys Thr Phe Leu Ile Ala Leu Ala Leu Thr Ala Ser Leu Ile
1               5                  10                  15
Gly Ala Glu Asn Thr Lys Trp Asp Tyr Lys Asn Lys Glu Asn Gly Pro
            20                  25                  30
His Arg Trp Asp Lys Leu His Lys Asp Phe Glu Val Cys Lys Ser Gly
        35                  40                  45
Lys Ser Gln Ser Pro Ile Asn Ile Glu His Tyr Tyr His Thr Gln Asp
    50                  55                  60
Lys Ala Asp Leu Gln Phe Lys Tyr Ala Ala Ser Lys Pro Lys Ala Val
65                  70                  75                  80
Phe Phe Thr His His Thr Leu Lys Ala Ser Phe Glu Pro Thr Asn His
                85                  90                  95
Ile Asn Tyr Arg Gly His Asp Tyr Val Leu Asp Asn Val His Phe His
            100                 105                 110
Ala Pro Met Glu Phe Leu Ile Asn Asn Lys Thr Arg Pro Leu Ser Ala
        115                 120                 125
```

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

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 422 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548

```
Met Lys Ile Ser Leu Leu Gly His Gly Lys Thr Thr Leu Ala Leu Gly
1               5                   10                  15
Arg Phe Phe Lys Lys Asn His Asn Glu Val Lys Phe Phe Asp Asp Lys
            20                  25                  30
Phe Pro Ala Phe Phe Lys Asp Ser Glu Gly Phe Leu Cys Tyr Pro Ser
        35                  40                  45
Lys Asp Phe Asn Pro Asn Asp Ser Gln Leu Glu Ile Val Ser Pro Gly
    50                  55                  60
Ile Ser Phe Thr His Pro Leu Val Met Lys Ala Lys His Leu Met Ser
65                  70                  75                  80
Glu Tyr Asp Tyr Ile Asp Ser Leu Phe Asp His Ser Phe Thr Pro Thr
                85                  90                  95
Met Ile Ser Ile Ser Gly Thr Asn Gly Lys Thr Thr Thr Thr Glu Met
            100                 105                 110
Leu Thr Thr Leu Leu Glu Asp Phe Lys Ala Val Ser Gly Gly Asn Ile
        115                 120                 125
Gly Thr Pro Leu Ile Glu Leu Phe Glu Lys Arg Ser Pro Leu Trp Val
    130                 135                 140
Leu Glu Thr Ser Ser Phe Ser Leu His Tyr Thr Asn Lys Ala Tyr Pro
145                 150                 155                 160
Leu Ile Tyr Leu Leu Ile Asn Val Glu Ala Asp His Leu Thr Trp His
                165                 170                 175
Cys Asn Phe Glu Asn Tyr Leu Asn Ala Lys Leu Lys Val Leu Thr Leu
            180                 185                 190
Met Pro Lys Thr Ser Leu Ala Ile Leu Pro Leu Lys Phe Lys Glu His
        195                 200                 205
Pro Ile Val Gln Asn Ser Gln Ala Gln Lys Ile Phe Phe Asp Lys Ser
```

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

(2) INFORMATION FOR SEQ ID NO:549:

(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:549

```
Met Ala His His Unk Glu Gln His Gly Gly His His His His His His
1               5                   10                  15
His Thr His His His His Tyr His Gly Gly Glu His His His His His
            20                  25                  30
His Ser Ser His His Glu Glu Gly Cys Cys Ser Thr Ser Asp Ser His
        35                  40                  45
His Gln Glu Glu Gly Cys Cys His Gly Unk His Glu
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:549

```
Met Ala His His Unk Glu Gln His Gly Gly His His His His His His
1               5                  10                  15
His Thr His His His His Tyr His Gly Gly Glu His His His His His
            20                  25                  30
His Ser Ser His His Glu Glu Gly Cys Cys Ser Thr Ser Asp Ser His
        35                  40                  45
His Gln Glu Glu Gly Cys Cys His Gly Unk His Glu
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:550:

(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:550

```
Met Lys Glu Ile Ile Val Ala Leu Val Gly Gln Pro Asn Val Gly Lys
1               5                  10                  15
Ser Ser Leu Ile Asn Ala Leu Ser Asn Thr His Leu Lys Val Gly Asn
            20                  25                  30
Phe Thr Glu Val Thr Val Asp Lys Met Glu Val Ser Leu Ile Gln Lys
        35                  40                  45
Asp His Gln Ile Asn Ser
    50
```

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551

```
Leu Val Lys Ile Arg Leu Phe Asp Phe Thr Ile Arg Leu Phe Lys Pro
1               5                  10                  15
Glu Phe His Ile Phe Asp Phe Leu Lys Gly Ile Arg Val Leu Met Ile
            20                  25                  30
Glu Trp Met Gln Asn His Arg Lys Tyr Leu Val Val Thr Ile Trp Ile
        35                  40                  45
Ser Thr Ile Ala Phe Ile Ala Ala Gly Met Ile Gly Trp Gly Gln Tyr
    50                  55                  60
Ser Phe Ser Leu Asp Ser Asp Ser Ala Ala Lys Val Gly Gln Ile Lys
65                  70                  75                  80
Ile Ser Gln Glu Glu Leu Ala Gln Glu Tyr Arg Arg Leu Lys Asp Ala
                85                  90                  95
Tyr Ala Glu Ser Ile Pro Asp Phe Lys Glu Leu Thr Glu Asp Gln Ile
            100                 105                 110
Lys Ala Met His Leu Glu Lys Ser Ala Leu Asp Ser Leu Ile Asn Gln
        115                 120                 125
Ala Leu Leu Arg Asn Phe Ala Leu Asp Leu Gly Leu Gly Ala Thr Lys
    130                 135                 140
Gln Glu Val Ala Lys Glu Ile Arg Lys Thr Asn Val Phe Gln Lys Asp
145                 150                 155                 160
Gly Val Phe Asp Glu Glu Leu Tyr Lys Asn Ile Leu Lys Gln Ser His
                165                 170                 175
Tyr Arg Pro Lys His Phe Glu Glu Ser Val Glu Arg Leu Leu Ile Leu
            180                 185                 190
Gln Lys Ile Ser Ala Leu Phe Pro Lys Thr Thr Thr Pro Leu Glu Gln
        195                 200                 205
Ser Ser Leu Ser Leu Trp Ala Lys Leu Gln Asp Lys Leu Asp Ile Leu
    210                 215                 220
Ile Leu Asn Pro Asn Asp Val Lys Ile Ser Leu Asn Glu Glu Glu Met
225                 230                 235                 240
Lys Lys Tyr Tyr Glu Asn His Arg Lys Asp Phe Lys Lys Pro Thr Ser
                245                 250                 255
Phe Lys Thr Arg Ser Leu Tyr Phe Asp Ala Ser Leu Glu Lys Thr Asp
            260                 265                 270
Leu Lys Glu Leu Glu Glu Tyr Tyr His Lys Asn Lys Val Ser Tyr Leu
        275                 280                 285
Asp Unk Unk Gly Glu Ile Thr Gly Phe
    290                 295
```

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature

This Sheet Has Been Replaced



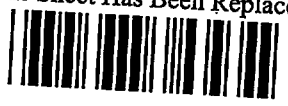
(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551

```
Leu Val Lys Ile Arg Leu Phe Asp Phe Thr Ile Arg Leu Phe Lys Pro
1               5                  10                  15
Glu Phe His Ile Phe Asp Phe Leu Lys Gly Ile Arg Val Leu Met Ile
            20                  25                  30
Glu Trp Met Gln Asn His Arg Lys Tyr Leu Val Val Thr Ile Trp Ile
        35                  40                  45
Ser Thr Ile Ala Phe Ile Ala Ala Gly Met Ile Gly Trp Gly Gln Tyr
    50                  55                  60
Ser Phe Ser Leu Asp Ser Asp Ser Ala Ala Lys Val Gly Gln Ile Lys
65                  70                  75                  80
Ile Ser Gln Glu Glu Leu Ala Gln Glu Tyr Arg Arg Leu Lys Asp Ala
                85                  90                  95
Tyr Ala Glu Ser Ile Pro Asp Phe Lys Glu Leu Thr Glu Asp Gln Ile
            100                 105                 110
Lys Ala Met His Leu Glu Lys Ser Ala Leu Asp Ser Leu Ile Asn Gln
        115                 120                 125
Ala Leu Leu Arg Asn Phe Ala Leu Asp Leu Gly Leu Gly Ala Thr Lys
    130                 135                 140
Gln Glu Val Ala Lys Glu Ile Arg Lys Thr Asn Val Phe Gln Lys Asp
145                 150                 155                 160
Gly Val Phe Asp Glu Glu Leu Tyr Lys Asn Ile Leu Lys Gln Ser His
                165                 170                 175
Tyr Arg Pro Lys His Phe Glu Glu Ser Val Glu Arg Leu Leu Ile Leu
            180                 185                 190
Gln Lys Ile Ser Ala Leu Phe Pro Lys Thr Thr Thr Pro Leu Glu Gln
        195                 200                 205
Ser Ser Leu Ser Leu Trp Ala Lys Leu Gln Asp Lys Leu Asp Ile Leu
    210                 215                 220
Ile Leu Asn Pro Asn Asp Val Lys Ile Ser Leu Asn Glu Glu Glu Met
225                 230                 235                 240
Lys Lys Tyr Tyr Glu Asn His Arg Lys Asp Phe Lys Lys Pro Thr Ser
                245                 250                 255
Phe Lys Thr Arg Ser Leu Tyr Phe Asp Ala Ser Leu Glu Lys Thr Asp
            260                 265                 270
Leu Lys Glu Leu Glu Glu Tyr Tyr His Lys Asn Lys Val Ser Tyr Leu
        275                 280                 285
Asp Unk Unk Gly Glu Ile Thr Gly Phe
    290                 295
```

(2) INFORMATION FOR SEQ ID NO:552:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(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:552

```
Met Val Lys His Tyr Leu Phe Met Ala Val Ser Gln Val Phe Phe Ser
```

```
1               5                   10                  15
Phe Phe Leu Val Leu Phe Phe Ile Ser Ser Ile Val Leu Leu Ile Ser
            20                  25                  30
Ile Ala Ser Val Thr Leu Val Ile Lys Val Ser Phe Leu Asp Leu Val
        35                  40                  45
Gln Leu Phe Leu Tyr Ser Leu Pro Gly Thr Ile Phe Phe Ile Leu Pro
    50                  55                  60
Ile Thr Phe Phe Ala Ala Unk Arg Leu Gly Unk Ser Arg Leu Ser Tyr
65                  70                  75                  80
Asp His Glu Leu Leu Val Phe Phe Leu Unk
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:
(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552

```
Met Val Lys His Tyr Leu Phe Met Ala Val Ser Gln Val Phe Phe Ser
1               5                   10                  15
Phe Phe Leu Val Leu Phe Phe Ile Ser Ser Ile Val Leu Leu Ile Ser
            20                  25                  30
Ile Ala Ser Val Thr Leu Val Ile Lys Val Ser Phe Leu Asp Leu Val
        35                  40                  45
Gln Leu Phe Leu Tyr Ser Leu Pro Gly Thr Ile Phe Phe Ile Leu Pro
    50                  55                  60
Ile Thr Phe Phe Ala Ala Unk Arg Leu Gly Unk Ser Arg Leu Ser Tyr
65                  70                  75                  80
Asp His Glu Leu Leu Val Phe Phe Leu Unk
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:553:

(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:553

```
Val His Arg Phe Ser Arg Asn Pro Cys Ala Ser Cys Asn Arg Ala Arg
1               5                  10                  15
Ser Cys Ser Arg Leu Ser Arg Ser Leu Val Ser Ala Val Thr Trp Trp
            20                  25                  30
Leu Ser Leu Ser Phe Ser Val Val Ser Ala Leu Phe Ser Leu Val Ser
        35                  40                  45
Ser Val Ile Leu Trp Val Ser Ser Val Phe Ser Leu Phe Ser Leu Ser
    50                  55                  60
Phe Ser Val Val Asn Ser Leu Phe Ser Ser Val Ser Arg Ser Leu Ala
65                  70                  75                  80
Ala Asn Lys Arg Val Phe Ser Leu Ala Lys Met Ser Phe Ser Val Phe
                85                  90                  95
Ser Ser Ala Phe Ser Leu Val Ser Leu Leu Leu Phe Cys His Asn
            100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:554:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554

```
Met Gln Lys Met Gly Val Val Ser Tyr Ser Val Phe Gln Ala Phe Glu
1               5                  10                  15
Lys Ala Leu Ser Arg Phe Lys Glu Gly Val Val Leu Ile Val Asp Ser
            20                  25                  30
Leu Arg Arg Leu Ile Met Gly Ser Ala Ser Val Lys Glu Leu Ser Gly
        35                  40                  45
Val Ile Gly Ile Val Gly Ala Leu Ser His Ala Asn Ser Val Ser Met
    50                  55                  60
Leu Leu Leu Phe Gly Ala Phe Leu Ser Ile Asn Leu Gly Ile Leu Asn
65                  70                  75                  80
Leu Leu Pro Ile Pro Ala Leu Asp Gly Ala Gln Met Leu Gly Val Val
                85                  90                  95
Phe Lys Asn Ile Phe His Ile Ala Leu Pro Thr Pro Ile Gln Asn Ala
            100                 105                 110
Leu Trp Leu Val Gly Val Gly Phe Leu Val Phe Val Met Phe Leu Gly
        115                 120                 125
Leu Phe Asn Asp Ile Thr Arg Leu Leu
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:555:

(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:555

```
Val Met Ala Leu Leu Lys Ile Ser Val Val Val Pro Glu Gly Glu Val
1               5                  10                  15
Tyr Thr Gly Glu Val Lys Ser Val Val Leu Pro Gly Val Glu Gly Glu
            20                  25                  30
Phe Gly Val Leu Tyr Gly His Ser Asn Met Ile Thr Leu Leu Gln Ala
        35                  40                  45
Gly Val Val Glu Ile Glu Thr Glu Asn Gln Lys Glu His Ile Ala Ile
    50                  55                  60
Asn Trp Gly Tyr Ala Glu Val Thr Asn Glu Arg Val Asp Ile Leu Ala
65                  70                  75                  80
Asp Gly Ala Val Phe Ile Lys Lys Gly Ser Asp Asp Arg Asp Asp Ala
                85                  90                  95
Ile Ser Arg Ala Lys Lys Leu Leu Glu Asp Ala Ser Ser Asp Arg Leu
            100                 105                 110
Ala Val Ser Ser Val Leu Ala Lys Ile Glu Ser Leu
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:556

```
Met Tyr Ser Leu Leu Leu Asp Leu Asn Lys Lys Thr Ala Leu Leu Gly
1               5                  10                  15
Thr Arg Gly Phe Phe Ile Asp Asp Lys His Ile Lys Glu Lys Gly Leu
            20                  25                  30
Thr Thr Pro Thr Leu Leu Glu Leu Tyr Ser Asp Leu Glu Glu Ala Ile
        35                  40                  45
Arg Leu Lys Cys Glu Tyr Phe Ile Met Glu Val Ser Ser His Ala Ile
    50                  55                  60
Val Gln Asn Ala Ser Leu Gly Leu Ile Ser Leu Leu Lys Phe Ser Pro
65                  70                  75                  80
Ile Ser Gln Ala Ile Ile
                85
```

(2) INFORMATION FOR SEQ ID NO:557:

(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:557

```
Met Ser Lys Arg Ala Ile Arg Phe Pro Asn Lys Leu Phe Ser Tyr Pro
1               5                  10                  15
Lys Pro Lys Ile Lys Ala Thr Asn Thr Ser His Thr Val Leu Phe Ala
            20                  25                  30
Tyr Pro Leu Lys Pro His Glu Met Ala Leu Leu Ala Leu Ala Thr Ser
        35                  40                  45
Leu Leu Ala Pro Ile Phe Asn Ala Ile His Ser Thr Asn Ala Leu Asn
    50                  55                  60
Ala Ile Lys Pro Asp Gly Thr Gly Ser Lys Ile Asn Pro Ile Ile Met
65                  70                  75                  80
Pro Met Lys Ile Gln Lys
                85
```

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

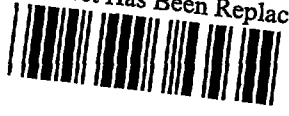
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557

Met Ser Lys Arg Ala Ile Arg Phe Pro Asn Lys Leu Phe Ser Tyr Pro
1 5 10 15
Lys Pro Lys Ile Lys Ala Thr Asn Thr Ser His Thr Val Leu Phe Ala
20 25 30
Tyr Pro Leu Lys Pro His Glu Met Ala Leu Leu Ala Leu Ala Thr Ser
35 40 45
Leu Leu Ala Pro Ile Phe Asn Ala Ile His Ser Thr Asn Ala Leu Asn
50 55 60
Ala Ile Lys Pro Asp Gly Thr Gly Ser Lys Ile Asn Pro Ile Ile Met
65 70 75 80
Pro Met Lys Ile Gln Lys

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:558:

(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:558

```
Met Lys Thr Asn Phe Tyr Lys Ile Lys Leu Leu Phe Ala Trp Cys Leu
1               5                  10                  15
Ile Ile Gly Met Phe Asn Ala Pro Leu Asn Ala Asp Gln Asn Thr Asp
            20                  25                  30
Ile Lys Asp Ile Ser Pro Glu Asp Met Ala Leu Asn Ser Val Gly Leu
        35                  40                  45
Val Ser Arg Asp Gln Leu Lys Ile Glu Ile Pro Lys Glu Thr Leu Glu
    50                  55                  60
Gln Lys Val Thr Ile Leu Asn Asp Tyr Asn Asp Lys Asn Val Asn Ile
65                  70                  75                  80
Lys Phe Asp Asp Ile Ser Leu Gly Ser Phe Gln Pro Asn Asp Asn Leu
                85                  90                  95
Gly Ile Asn Ala Met Trp Gly Ile Gln Asn Leu Leu
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:559:

This Sheet Has Been Replaced



(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:559

```
Val Tyr Ser Arg Phe Phe Ala Asn Gln His Glu Phe Asp Phe Glu Ala
1               5                  10                  15
Gln Gly Ala Leu Gly Ser Asp Gln Ser Ser Leu Asn Phe Lys Ser Thr
            20                  25                  30
Leu Leu Gln Asp Leu Asn Gln Ser Tyr Asn Tyr Leu Ala Tyr Ser Ala
        35                  40                  45
```

```
Thr Ala Arg Ala Ser Tyr Gly Tyr Asp Phe Ala Phe Phe Arg Asn Ala
    50                  55                  60
Leu Val Leu Lys Pro Ser Val Gly Val Ser Tyr Asn His Leu Gly Ser
65                  70                  75                  80
Thr Asn Phe Lys Ser Asn Ser Gln Ser Gln Val Ala Leu Lys Asn Gly
                85                  90                  95
Ala Ser Ser Gln His Leu Phe Asn Ala Asn Ala Thr Trp Lys Arg Val
            100                 105                 110
Ile Ile Met Gly Thr Leu His Thr Phe Ile Cys Met Trp Glu Phe Tyr
        115                 120                 125
Lys Ser Ser Leu Thr Leu Asp Arg Met Met Trp Arg Leu
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559

```
Val Tyr Ser Arg Phe Phe Ala Asn Gln His Glu Phe Asp Phe Glu Ala
1               5                   10                  15
Gln Gly Ala Leu Gly Ser Asp Gln Ser Ser Leu Asn Phe Lys Ser Thr
            20                  25                  30
Leu Leu Gln Asp Leu Asn Gln Ser Tyr Asn Tyr Leu Ala Tyr Ser Ala
        35                  40                  45
Thr Ala Arg Ala Ser Tyr Gly Tyr Asp Phe Ala Phe Phe Arg Asn Ala
    50                  55                  60
Leu Val Leu Lys Pro Ser Val Gly Val Ser Tyr Asn His Leu Gly Ser
65                  70                  75                  80
Thr Asn Phe Lys Ser Asn Ser Gln Ser Gln Val Ala Leu Lys Asn Gly
                85                  90                  95
Ala Ser Ser Gln His Leu Phe Asn Ala Asn Ala Thr Trp Lys Arg Val
            100                 105                 110
Ile Ile Met Gly Thr Leu His Thr Phe Ile Cys Met Trp Glu Phe Tyr
        115                 120                 125
Lys Ser Ser Leu Thr Leu Asp Arg Met Met Trp Arg Leu
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:560:

(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

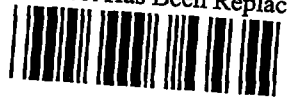
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560

```
Met Ile Asp Asn Leu Asp Gly Ala Lys Asp Ala Gln Leu Ile Lys Lys
1               5                  10                  15
Ala Tyr Ala Phe Leu Cys Leu Gly Gly Asp Gly Thr Ile Leu Gly Ala
            20                  25                  30
Leu Arg Met Thr His Ala His Asn Lys Pro Cys Phe Gly Val Arg Ile
        35                  40                  45
Gly Asn Leu Gly Phe Leu Ser Ala Val Glu Leu Asn Gly Leu Lys Asp
    50                  55                  60
Phe Leu Gln Asp Leu Lys Gln Asn Arg Ile Lys Leu Glu Glu His Leu
65                  70                  75                  80
Ala Leu Glu Gly Arg Ile Gly Asn Thr Ser Phe Tyr Ala Ile Asn Glu
                85                  90                  95
Ile Val Ile Ala Lys Lys Lys Ala Leu Gly Val Leu Asp Ile Lys Ala
            100                 105                 110
Cys Ala Gly His Thr Pro Phe Asn Thr Tyr Lys Gly Asp Gly Leu Ile
        115                 120                 125
Ile Ala Thr Pro Leu Gly Ser Thr Ala Tyr Asn Leu Ser Ala His Gly
    130                 135                 140
Pro Ile Val His Ala Leu Ser Gln Ser Tyr Ile Leu Thr Pro Leu Cys
145                 150                 155                 160
Asp Phe Ser Leu Thr Gln Arg Pro Leu Val Leu Gly Ala Glu Phe Cys
                165                 170                 175
Leu Ser Phe Cys Ala His Glu Asp Ala Leu Val Val Ile Asp Gly Gln
            180                 185                 190
Ala Thr Tyr Asp Leu Lys Ala Asn Gln Pro Leu Tyr Ile Gln Lys Ser
        195                 200                 205
Pro Thr Thr Thr Lys Leu Leu Gln Lys Asn Ser Arg Asp Tyr Phe Lys
    210                 215                 220
Val Leu Lys Glu Lys Leu Leu
225                 230
```

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 185 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:561

```
Met Unk Glu Asn Gly Arg Gly Val Pro Lys Asp Tyr Lys Lys Ala Val
1               5                  10                  15
Glu Tyr Phe Gln Lys Ala Val Asp Asn Asp Ile Pro Arg Gly Tyr Asn
            20                  25                  30
```

```
Asn Leu Gly Val Met Tyr Lys Glu Gly Lys Gly Val Pro Lys Asp Glu
        35                  40                  45
Lys Lys Ala Val Glu Tyr Phe Arg Ile Ala Thr Glu Lys Gly Tyr Thr
    50                  55                  60
Asn Ala Tyr Ile Asn Leu Gly Ile Met Tyr Met Glu Gly Arg Gly Val
65                  70                  75                  80
Pro Ser Asn Tyr Ala Lys Ala Thr Glu Cys Phe Arg Lys Ala Met His
                85                  90                  95
Lys Gly Asn Val Unk Ala Tyr Ile Leu Leu Gly Asp Ile Tyr Tyr Ser
            100                 105                 110
Gly Met Ile Asn Trp Val Leu Ser Arg Thr Lys Ile Arg Leu Val His
        115                 120                 125
Tyr Lys Met Ala Ala Asp Val Ser Ser Ser Arg Ala Tyr Unk Gly Leu
    130                 135                 140
Ser Glu Ser Tyr Unk Tyr Gly Leu Gly Val Glu Lys Unk Unk Lys Lys
145                 150                 155                 160
Ala Glu Glu Tyr Met Gln Lys Ala Cys Asp Phe Asp Ile Asp Lys Asn
                165                 170                 175
Cys Lys Lys Lys Asn Thr Ser Ser Arg
            180                 185
```

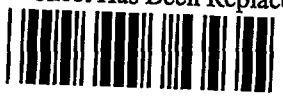
(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 185 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561

```
Met Unk Glu Asn Gly Arg Gly Val Pro Lys Asp Tyr Lys Lys Ala Val
1               5                  10                  15
Glu Tyr Phe Gln Lys Ala Val Asp Asn Asp Ile Pro Arg Gly Tyr Asn
            20                  25                  30
Asn Leu Gly Val Met Tyr Lys Glu Gly Lys Gly Val Pro Lys Asp Glu
        35                  40                  45
Lys Lys Ala Val Glu Tyr Phe Arg Ile Ala Thr Glu Lys Gly Tyr Thr
    50                  55                  60
Asn Ala Tyr Ile Asn Leu Gly Ile Met Tyr Met Glu Gly Arg Gly Val
65                  70                  75                  80
Pro Ser Asn Tyr Ala Lys Ala Thr Glu Cys Phe Arg Lys Ala Met His
                85                  90                  95
Lys Gly Asn Val Unk Ala Tyr Ile Leu Leu Gly Asp Ile Tyr Tyr Ser
            100                 105                 110
Gly Met Ile Asn Trp Val Leu Ser Arg Thr Lys Ile Arg Leu Val His
        115                 120                 125
Tyr Lys Met Ala Ala Asp Val Ser Ser Ser Arg Ala Tyr Unk Gly Leu
    130                 135                 140
Ser Glu Ser Tyr Unk Tyr Gly Leu Gly Val Glu Lys Unk Unk Lys Lys
145                 150                 155                 160
Ala Glu Glu Tyr Met Gln Lys Ala Cys Asp Phe Asp Ile Asp Lys Asn
                165                 170                 175
Cys Lys Lys Lys Asn Thr Ser Ser Arg
```

180 185

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562

```
Met Ile Val Gly Leu Ile Gly Val Val Glu Lys Ile Ser Ala Leu Glu
1               5                  10                  15
Ala His Ile Glu Val Gln Gly Val Val Tyr Gly Val Gln Val Ser Met
            20                  25                  30
Arg Thr Ala Ala Leu Leu Gln Thr Gly Gln Lys Ala Arg Leu Lys Ile
        35                  40                  45
Leu Gln Val Ile Lys Glu Asp Ala His Leu Leu Tyr Gly Phe Leu Glu
    50                  55                  60
Glu Ser Glu Lys Ile Leu Phe Glu Arg Leu Leu Lys Ile Asn Gly Val
65                  70                  75                  80
Gly Gly Arg Ile Ala Leu Ala Ile Leu Ser Ser Phe Ser Pro Asn Glu
                85                  90                  95
Phe Glu Asn Ile Ile Ala Thr Lys Glu Val Lys Arg Leu Gln Gln Val
            100                 105                 110
Pro Gly Ile Gly Lys Lys Leu Ala Asp Lys Ile Met Val Asp Leu Ile
        115                 120                 125
Gly Phe Phe Ile Gln Asp Glu Asn Arg Pro Ala Arg Asn Glu Val Phe
    130                 135                 140
Leu Ala Leu Glu Ser Leu Gly Phe Lys Ser Ala Glu Ile Asn Pro Val
145                 150                 155                 160
Leu Lys Thr Leu Lys Pro His Leu Ser Ile Glu Ala Ala Ile Lys Glu
                165                 170                 175
Ala Leu Gln Gln Leu Arg Ser
            180
```

(2) INFORMATION FOR SEQ ID NO:563:

(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:563

```
Val Gly Val Leu Leu Ala Leu Phe Phe Phe Tyr Ala Lys Asn Asn Leu
1               5                  10                  15
Leu Glu Asn Thr Gln Ile Arg Met Gln Tyr Thr Ala Asp Ala Ile Ala
            20                  25                  30
Lys Ser Leu Leu Glu Leu Asn Asn Ala Ser Ser Leu Glu Pro Leu Lys
        35                  40                  45
Ile Leu Glu Glu Arg Phe Lys Asn Thr Pro Phe Val Leu Leu Asp Ala
    50                  55                  60
Asp Asn Arg Val Lys Phe Ser Asn Ile Gly Val Phe Val Ala Ser Phe
65                  70                  75                  80
Lys Asn Asp Ala Leu Ile Lys Thr Pro Tyr Phe Ala Leu Lys Lys Gln
                85                  90                  95
Gly Phe Tyr Leu Thr Asp Ser Ala Pro Thr Asn Arg Leu Gly Val Ser
            100                 105                 110
Lys Ile Ile Ile Ala Glu Glu Glu Ile Gln Lys Ile Phe Ile Pro Leu
        115                 120                 125
Tyr Lys Met Ile Gly Tyr Val Phe Leu Gly Ala Ser Leu Phe Val Ala
    130                 135                 140
Leu Ile Ala Met Trp Leu Tyr Lys Ile Pro
145                 150
```

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 288 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:564

```
Val Val Ile Met Ile Leu Val Cys Phe Leu Ala Cys Ser Gln Glu Ser
1               5                  10                  15
Phe Ile Lys Met Gln Lys Lys Ala Gln Glu Gln Glu Asn Asp Gly Ser
            20                  25                  30
Lys Arg Pro Ser Tyr Val Asp Ser Asp Tyr Glu Val Phe Ser Glu Thr
        35                  40                  45
Ile Phe Leu Gln Asn Met Val Tyr Gln Pro Ile Glu Glu Arg Asn Ala
    50                  55                  60
Phe Phe Gln Leu Thr Lys Asp Glu Asp Asn Ser Phe Asn Pro Glu Asn
65                  70                  75                  80
Ser Val Ile Leu Leu Asn Glu Pro Ser Asp Asn Ser Glu Lys Asn Leu
                85                  90                  95
Leu Ser Tyr Pro Asn Asp Pro Asn Asn Asn Glu Asp Asn Ala Asn Asn
            100                 105                 110
Ser Gln Lys Asn Pro Phe Leu Tyr Lys Pro Lys Arg Lys Thr Lys Asn
        115                 120                 125
Pro Lys Leu Ile Glu Tyr Ser Gln Gln Asp Phe Tyr Pro Leu Lys Asn
    130                 135                 140
Gly Asp Ile Ile Met Ser Lys Glu Gly Asp Gln Trp Leu Ile Glu Ile
```

```
145                 150                 155                 160
Gln Ser Lys Ala Leu Lys Arg Phe Leu Lys Asp Gln Asn Asp Lys Asp
                165                 170                 175
Arg Gln Ile Gln Thr Phe Thr Phe Asn Asp Thr Lys Thr Gln Ile Ala
            180                 185                 190
Gln Ile Lys Gly Lys Ile Ser Ser Tyr Val Tyr Thr Thr Asn Asn Gly
        195                 200                 205
Ser Leu Ser Leu Arg Pro Phe Tyr Glu Ser Phe Leu Leu Glu Lys Lys
    210                 215                 220
Ser Asp Asn Val Tyr Thr Ile Glu Asn Lys Ala Leu Asp Thr Met Glu
225                 230                 235                 240
Ile Ser Lys Cys Gln Met Val Leu Lys Lys His Ser Thr Asp Lys Leu
                245                 250                 255
Asp Ser Gln His Lys Ala Ile Ser Ile Asp Leu Asp Phe Lys Lys Glu
            260                 265                 270
Arg Phe Lys Ser Asp Thr Glu Leu Phe Leu Glu Cys Leu Lys Glu Ser
        275                 280                 285
```

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:565

```
Met Ala Ala Pro Leu Leu Ala Leu Pro Phe Leu Ser Asn Pro Leu Val
1               5                  10                  15
Leu Gly Ala Leu Ala Val Ile Gly Val Gly Ala Tyr Leu Tyr Pro Asn
            20                  25                  30
Lys Gln Asp Ser Leu Val Val Gln Ala Asp Gly Leu Tyr Ser Glu Ile
        35                  40                  45
Leu Gly Phe Phe Ile Ser Phe Ser Ser Lys Ile Leu Lys Gly Ile Gly
    50                  55                  60
Glu Pro Leu Ala Asn Val Ile Gln Pro Phe Gly Met Val Leu Gly Met
65                  70                  75                  80
Leu Leu Ile Leu Leu Tyr Ser Phe Lys Arg Tyr Gln Asn Asn Asp Leu
                85                  90                  95
Phe Glu Ile Lys Thr Phe Leu Met Leu Phe Val Phe Val Gly Tyr Leu
            100                 105                 110
Ser Leu Tyr His Tyr Ala Phe Lys Ser Asp Gly Ser Ser Ser Gly Asn
        115                 120                 125
Gly Arg Ser Ser Phe Ala Phe Gln Asn His Val Thr Glu Ile Phe Asp
    130                 135                 140
Thr Pro Ala Asn Leu Leu Asn Ala Gly Ile Ser Asn Val Val Lys Glu
145                 150                 155                 160
Tyr Gln Thr Asn Ser Ala Arg Glu His Lys Asn Ile Asp Thr His His
                165                 170                 175
Ser Ile Thr Asn Ala Asn Ile Ser Phe His Val Arg Gln Ile Leu Thr
            180                 185                 190
Ser Leu Asn Lys Leu Tyr Glu Asp Phe Lys Ile Asn Asn Gly Leu Ser
        195                 200                 205
```

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

(2) INFORMATION FOR SEQ ID NO:566:

This Sheet Has Been Replaced



(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:566

```
Val Leu Lys Phe Gln Lys Leu Pro Leu Leu Phe Val Ser Ile Leu Tyr
1               5                   10                  15
Asn Gln Ser Pro Leu Leu Ala Phe Asp Tyr Lys Phe Ser Gly Val Ala
            20                  25                  30
Glu Ser Val Ser Lys Val Gly Phe Asn His Ser Lys Leu Asn Ser Lys
        35                  40                  45
Glu Gly Ile Phe Pro Thr Ala Thr Phe Val Thr Ala Thr Ile Lys Leu
    50                  55                  60
Gln Val Asn Tyr Lys Ser Ala Pro
65                  70
```

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567

```
Met Gly Asn His Phe Ser Lys Leu Gly Phe Val Leu Ala Ala Leu Gly
1               5                  10                  15
Ser Ala Ile Gly Leu Gly His Ile Trp Arg Phe Pro Tyr Met Thr Gly
            20                  25                  30
Val Ser Gly Gly Gly Ala Phe Val Leu Leu Phe Leu Phe Leu Ser Leu
        35                  40                  45
Ser Val Gly Ala Ala Met Phe Ile Ala Glu Met Leu Leu Gly Gln Ser
    50                  55                  60
Thr Gln Lys Asn Val Thr Glu Ala Phe Lys Glu Leu Asp Ile Asn Pro
65                  70                  75                  80
Lys Lys Arg Trp Lys Tyr Ala Gly Ile Met Leu Ile Ser Gly Pro Leu
                85                  90                  95
Ile Leu Thr Phe Tyr Gly Thr Ile Leu Gly Trp Val Leu Tyr Tyr Leu
            100                 105                 110
Val Ser Ile Ser Phe Asn Leu Pro Ser Ser Ile Gln Glu Ser Glu Gln
        115                 120                 125
Ile Phe Thr Gln Thr Leu Gln Ser Ile Gly Leu Gln Ser Ile Gly Leu
    130                 135                 140
Phe Ser Val Leu Phe Ile Thr Gly Trp Ile Val Ser Arg Gly Ile Lys
145                 150                 155                 160
Glu Gly Ile Glu Lys Leu Asn Leu Val Leu Met Pro Leu Leu Phe Ala
                165                 170                 175
Thr Phe Phe Gly Leu Leu Phe Tyr Ala Met Ser Met Asp Ser Phe Ser
            180                 185                 190
Lys Ala Phe His Phe Met Leu Ile Ser Ser Gln Lys Ile
        195                 200                 205
```

(2) INFORMATION FOR SEQ ID NO:568:

(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:568

This Sheet Has Been Replaced



```
Met Glu Lys Val Cys Val Ser Ala Trp Gly Leu Pro Lys Ile Leu Glu
1               5                  10                  15
Glu Arg Leu Lys Glu Lys Tyr Gly Asp Asp Trp Glu Lys His Val Lys
            20                  25                  30
Ala Lys Ala Ile Asn Glu Glu Glu Leu Glu Glu Gln Val Lys Ala Lys
        35                  40                  45
Ala Lys Glu Gln Gln Lys Thr Gln Arg Glu Lys Thr Leu Asn Gly Phe
    50                  55                  60
Leu Lys Lys Val Gly Leu Lys Lys Arg Asp Met Leu Gln Ser Thr Met
65                  70                  75                  80
Leu Phe Asp Glu Val Lys Glu Ala Asp Val Leu Phe Gln Ala Glu Arg
                85                  90                  95
Lys Ile Gly Asp Trp Ile Phe Ser Ser Ala Val Phe Phe Phe Ala Leu
            100                 105                 110
Ala Leu Ile Glu Ala Ile Ile Ile Val Cys Leu Leu Pro Leu Lys Glu
        115                 120                 125
Lys Val Pro Tyr Leu Val Thr Phe Ser Asn Ala Thr Gln Asn Phe Ala
    130                 135                 140
Ile Val Gln Arg Ala Asp Lys Ser Ile Arg Ala Asn Gln Ala Leu Val
145                 150                 155                 160
Arg Gln Leu Val Ala Ser Tyr Val Asn Asn Arg Glu Asn Ile Ser Ser
                165                 170                 175
Ile Lys Glu Gln Asn Glu Ile Ala His Glu Thr Ile Arg Leu Gln Ser
            180                 185                 190
Ala Phe Glu Val Trp Asp Phe Phe Glu Lys Leu Val Ser Tyr Glu His
        195                 200                 205
Ser Ile Tyr Thr Asn Ile Asn Leu Thr Arg Lys Ile Ser Ile Ile Asn
    210                 215                 220
Ile Ala Leu Ile Ser Lys Thr Gln Ala Asn Ile Glu Ile Ser Ala Gln
225                 230                 235                 240
Leu Phe His Lys Glu Lys Leu Glu Ser Glu Lys Arg Tyr Arg Ile Ile
                245                 250                 255
Met Thr Phe Glu Phe Glu Pro Ile Glu Ile Asp Thr Lys Ser Val Pro
            260                 265                 270
Leu Asn Pro Thr Gly Phe Ile Val Thr Gly Tyr Asp Val Thr Glu Ile
        275                 280                 285
Ala Ile Leu Lys Asp Leu Asp Glu Lys Asn Lys Val Lys Asp Asp Gly
    290                 295                 300
Val Lys Ser Arg Ile Ile His Val Glu Lys Lys Asp Pro His Met Ser
305                 310                 315                 320
Gln Tyr Lys Asp Val Lys Glu Gln
                325
```

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569

```
Leu Leu Asn Met Trp Asp Glu Ala Lys Lys Glu Gly Ile Asn Ile Asn
```

This Sheet Has Been Replaced



```
1               5                   10                  15
Thr Glu Lys Leu Ser Gln Glu Leu Gly Val Val Cys Val Pro Thr Ser
            20                  25                  30
Ala Arg Unk Lys Glu Asp Arg Leu Asn Thr Glu Leu Leu Leu Asp Glu
        35                  40                  45
Ile Val Arg Leu Tyr Ser Gln Asn Thr Thr Asn Asn Glu Asn Ile Lys
    50                  55                  60
Val Pro Ser Gln Ser Phe Lys Glu Ser Leu Lys Tyr Ser Gln Ser Ala
65                  70                  75                  80
Gln Arg Ile Ala Lys Ser Val Ile Ser Glu Asn Lys Gln Asn Ala Ser
                85                  90                  95
Phe Glu His Thr Tyr Lys Ile Asp Lys Ile Phe Asn Ala Pro Ala Leu
            100                 105                 110
Trp Asp Phe His Phe Phe Unk Val Tyr Val Tyr His Leu Phe Phe Glu
        115                 120                 125
Leu Phe Asn Arg Arg Gly Ser Ala Lys Ser Pro
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:569:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...139

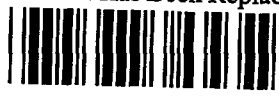
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569

```
Leu Leu Asn Met Trp Asp Glu Ala Lys Lys Glu Gly Ile Asn Ile Asn
1               5                   10                  15
Thr Glu Lys Leu Ser Gln Glu Leu Gly Val Val Cys Val Pro Thr Ser
            20                  25                  30
Ala Arg Unk Lys Glu Asp Arg Leu Asn Thr Glu Leu Leu Leu Asp Glu
        35                  40                  45
Ile Val Arg Leu Tyr Ser Gln Asn Thr Thr Asn Asn Glu Asn Ile Lys
    50                  55                  60
Val Pro Ser Gln Ser Phe Lys Glu Ser Leu Lys Tyr Ser Gln Ser Ala
65                  70                  75                  80
Gln Arg Ile Ala Lys Ser Val Ile Ser Glu Asn Lys Gln Asn Ala Ser
                85                  90                  95
Phe Glu His Thr Tyr Lys Ile Asp Lys Ile Phe Asn Ala Pro Ala Leu
            100                 105                 110
Trp Asp Phe His Phe Phe Unk Val Tyr Val Tyr His Leu Phe Phe Glu
        115                 120                 125
Leu Phe Asn Arg Arg Gly Ser Ala Lys Ser Pro
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:570

```
Met Leu His Lys Ala Lys Val Gly Ile Val Phe Gln Ala Leu Leu Gly
1               5                  10                  15
Ile Phe Cys Val Phe Leu Leu Leu Phe Tyr Leu Ser Ala Phe Leu Met
            20                  25                  30
Val Ala Phe Lys Asp Thr Lys Arg Met Phe Ile Ser Val Leu Ile Gly
        35                  40                  45
Ser Val Val Phe Leu Trp Ser Asp Leu Leu Val Phe Val Gly Phe Lys
    50                  55                  60
Asn Ile Ser Phe Val Leu Asp Ile Gly Tyr Glu Ile
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:571:

(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

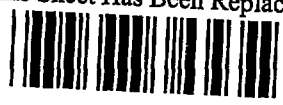
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571

```
Met Gln Glu Ala Leu Leu Arg Phe Gln Glu Gly Phe Lys Glu Trp Gly
1               5                  10                  15
Tyr Leu Ile Leu Phe Leu Tyr Ser Leu Gly Gly Gly Tyr Val Gly Ile
            20                  25                  30
Val Ile Ala Ser Ile Leu Ser Ala Thr Thr His Ala Leu Asp Ile Lys
        35                  40                  45
Ile Thr Ile Leu Val Ala Phe Leu Gly Asn Leu Ile Gly Ser Gly Ala
    50                  55                  60
Leu Val Ile Phe Ala Arg Tyr Gln Lys Arg Glu Phe Leu Lys Tyr Phe
65                  70                  75                  80
Gln Lys His Arg Arg Lys Leu Ala Leu Ala Ser Leu Trp Val Lys Arg
                85                  90                  95
Tyr Ala Leu Leu Met Ile Phe Val Asn Lys Tyr Leu Tyr Gly Ile Lys
            100                 105                 110
Ser Val Val Pro Leu Ala Ile Gly Phe Ser Lys Tyr Pro Leu Lys Lys
        115                 120                 125
Phe Leu Trp Leu Asn Val Phe Ser Ser Phe Leu Trp Ala Leu Ile Val
    130                 135                 140
Gly Ser Val Ser Phe Gln Ala Ser Asp Trp Val Lys Thr Leu Tyr Glu
```

```
145                 150                 155                 160
Arg Leu Ser His Tyr Thr Ser Phe Phe Val Ile Ser Phe Val Leu Ile
                165                 170                 175
Ala Leu Leu Ile Trp Phe Leu Leu Lys Arg Tyr Ser Arg Lys Met Gly
            180                 185                 190
Phe
```

(2) INFORMATION FOR SEQ ID NO:571:

This Sheet Has Been Replaced



(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:571

```
Met Gln Glu Ala Leu Leu Arg Phe Gln Glu Gly Phe Lys Glu Trp Gly
1               5                   10                  15
Tyr Leu Ile Leu Phe Leu Tyr Ser Leu Gly Gly Gly Tyr Val Gly Ile
            20                  25                  30
Val Ile Ala Ser Ile Leu Ser Ala Thr Thr His Ala Leu Asp Ile Lys
        35                  40                  45
Ile Thr Ile Leu Val Ala Phe Leu Gly Asn Leu Ile Gly Ser Gly Ala
    50                  55                  60
Leu Val Ile Phe Ala Arg Tyr Gln Lys Arg Glu Phe Leu Lys Tyr Phe
65                  70                  75                  80
Gln Lys His Arg Arg Lys Leu Ala Leu Ala Ser Leu Trp Val Lys Arg
                85                  90                  95
Tyr Ala Leu Leu Met Ile Phe Val Asn Lys Tyr Leu Tyr Gly Ile Lys
            100                 105                 110
Ser Val Val Pro Leu Ala Ile Gly Phe Ser Lys Tyr Pro Leu Lys Lys
        115                 120                 125
Phe Leu Trp Leu Asn Val Phe Ser Ser Phe Leu Trp Ala Leu Ile Val
    130                 135                 140
Gly Ser Val Ser Phe Gln Ala Ser Asp Trp Val Lys Thr Leu Tyr Glu
145                 150                 155                 160
Arg Leu Ser His Tyr Thr Ser Phe Phe Val Ile Ser Phe Val Leu Ile
                165                 170                 175
Ala Leu Leu Ile Trp Phe Leu Leu Lys Arg Tyr Ser Arg Lys Met Gly
            180                 185                 190
Phe
```

(2) INFORMATION FOR SEQ ID NO:572:

(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

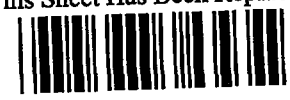
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572

```
Met Pro Phe Leu Lys Asn Trp Ile Trp Ser Leu Lys Met Ala Leu Ser
1               5                  10                  15
Ala Ile Ser Gly Ala Ser Gly Val Gly Lys Ser Val Leu Ile Ala Ser
            20                  25                  30
Leu Leu Gly Ala Phe Gly Leu Lys Glu Ser Asn Ala Ser Asn Ile Glu
        35                  40                  45
Val Glu Leu Ile Ala Pro Phe Leu Asp Thr Glu Glu Tyr Gly Ile Phe
    50                  55                  60
Arg Glu Asp Glu His Glu Pro Leu Val Ile Ser Val Ile Lys Lys Glu
65                  70                  75                  80
Lys Thr Arg Tyr Phe Leu Asn Gln Thr Ser Leu Ser Lys Asn Thr Leu
                85                  90                  95
Lys Ala Leu Leu Lys Gly Leu Ile Lys Arg Leu Ser Asn Asp Arg Phe
            100                 105                 110
Ser Gln Asn Glu Leu Asn Asp Ile Leu Met Leu Ser Leu Leu Asp Gly
        115                 120                 125
Tyr Ile Gln Asn Lys Asn Lys Arg Leu Ala Pro Phe
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:573:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573

```
Met Pro Gln Asn Gln Leu Val Ile Thr Ile Ile Asp Glu Ser Gly Ser
1               5                  10                  15
Lys Gln Leu Lys Phe Ser Lys Asn Leu Lys Arg Asn Leu Ile Ile Ser
            20                  25                  30
Val Val Ile Leu Leu Leu Leu Ile Val Gly Leu Gly Val Gly Phe Leu Lys
        35                  40                  45
Phe Leu Ile Ala Lys Met Asp Thr Met Thr Ser Glu Arg Asn Ala Val
    50                  55                  60
Leu Arg Asp Phe Arg Gly Leu Tyr Gln Lys Asn Tyr Ala Leu Ala Lys
65                  70                  75                  80
Glu Ile Lys Asn Lys Arg Glu Glu Leu Phe Ile Val Gly Gln Lys Ile
                85                  90                  95
Arg Gly Leu Glu Ser Leu Ile Glu Ile Lys Lys Gly Ala Asn Gly Gly
```

```
            100                 105                 110
Gly His Leu Tyr Asp Glu Val Asp Leu Glu Asn Leu Ser Leu Asn Gln
        115                 120                 125
Lys His Leu Ala Leu Met Leu Ile Pro Asn Gly Met Pro Leu Lys Thr
    130                 135                 140
Tyr Ser Ala Ile Lys Pro Thr Lys Glu Arg Asn His Pro Ile Lys Lys
145                 150                 155                 160
Ile Lys Gly Val Glu Ser Gly Ile Asp Phe Ile Ala Pro Leu Asn Thr
                165                 170                 175
Pro Val Tyr Ala Ser Ala Asp Gly Ile Val Asp Phe Val Lys Thr Arg
            180                 185                 190
Ser Asn Ala Gly Tyr Gly Asn Leu Val Arg Ile Glu His Ala Phe Gly
        195                 200                 205
Phe Ser Ser Ile Tyr Thr His Leu Asp His Val Asn Val Gln Pro Lys
    210                 215                 220
Ser Phe Ile Gln Lys Gly Gln Leu Ile Gly Tyr Ser Gly Lys Ser Gly
225                 230                 235                 240
Asn Ser Gly Gly Glu Lys Leu His Tyr Glu Val Arg Phe Leu Gly Lys
                245                 250                 255
Ile Leu Asp Ala Glu Lys Phe Leu Ala Trp Asp Leu Asp His Phe Gln
            260                 265                 270
Ser Ala Leu Glu Glu Asn Lys Phe Ile Glu Trp Lys Asn Leu Phe Trp
        275                 280                 285
Val Leu Glu Asp Ile Val Gln Leu Gln Glu His Val Asp Lys Asp Thr
    290                 295                 300
Leu Lys Gly Gln
305
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:574:

(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:574

```
Met Ile Thr Gly Ser His Asn Pro Lys Glu Tyr Asn Gly Phe Lys Ile
1               5                   10                  15
Thr Leu Asn Gln Asn Pro Phe Tyr Gly Lys Asp Ile Gln Ala Leu Lys
            20                  25                  30
Asn Thr Leu Leu Asn Ala Lys His Glu Ile Lys Pro Leu Lys Glu Thr
        35                  40                  45
Pro Glu Lys Val Asn Ala Leu Glu Ala Tyr His Arg Tyr Leu Ile Lys
    50                  55                  60
Asp Phe Lys His Leu Lys Asn Leu Lys Tyr Lys Ile Ala Leu Asp Phe
65                  70                  75                  80
Gly Asn Gly Val Gly Ala Leu Gly Leu Glu Pro Ile Leu Lys Ala Leu
                85                  90                  95
Asn Ile Asp Phe Ser Ser Leu Tyr Ser Asp Pro Asp Gly Asp Phe Pro
            100                 105                 110
Asn His His Pro Asp Pro Ser Glu Ala Lys Asn Leu Lys Asp Leu Glu
        115                 120                 125
```

```
Lys His Met Arg Glu Asn Ala Ile Leu Ile Gly Phe Ala Phe Asp Gly
    130                 135                 140
Asp Ala Asp Arg Ile Ala Met Leu Ser Ser His His Ile Tyr Ala Gly
145                 150                 155                 160
Asp Glu Leu Ala Ile Leu Phe Ala Lys Arg Leu His Ala Gln Gly Ile
                165                 170                 175
Thr Pro Phe Val Ile Gly Glu Val Lys Cys Ser Gln Val Met Tyr Asn
            180                 185                 190
Ala Ile Asn Thr Phe Gly Lys Thr Leu Met Tyr Lys Thr Gly His Ser
        195                 200                 205
Asn Leu Lys Ile Lys Leu Lys Glu Thr Asn Ala His Phe Ala Ala Glu
    210                 215                 220
Met Ser Gly His Ile Phe Phe Lys Glu Arg Tyr Phe Gly Tyr Asp Asp
225                 230                 235                 240
Ala Leu Tyr Ala Cys Leu Arg Ala Leu Glu Leu Leu Leu Glu Gln Ser
                245                 250                 255
Pro Ser Asp Leu Glu Asn Thr Ile Lys Asn Leu Pro Tyr Ser Tyr Thr
            260                 265                 270
Thr Pro Glu Glu Lys Ile Ala Val Ser Glu Glu Glu Lys Phe Glu Ile
        275                 280                 285
Ile Arg Asn Leu Gln Glu Ala Leu Lys Asn Pro Pro Ser His Phe Pro
    290                 295                 300
Thr Ile Lys Glu Ile Ile Ser Ile Asp Gly Val Arg Val Val Phe Glu
305                 310                 315                 320
His Gly Phe Gly Leu Ile Arg Ala Ser Asn Thr His Pro Leu Phe Ser
                325                 330                 335
Gln Pro Leu
```

(2) INFORMATION FOR SEQ ID NO:575:

This Sheet Has Been Replaced



(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:575

```
Met Ser Lys Asn Leu Gln Lys Lys Asn Pro Lys Lys Ser Unk Pro Gln
1               5                  10                  15
Ala Gln Lys Ala Ile Arg Glu Met Lys Met Phe Glu Thr Ile Ala Phe
            20                  25                  30
Tyr Phe Phe Ala Ile Leu Thr Leu Ser Met Ala Leu Val Val Ile Thr
        35                  40                  45
Thr Thr Asn Ile Leu Tyr Ala Ile Thr Ala Leu Ala Ser Ser Met Val
    50                  55                  60
Phe Ile Ser Ala Phe Phe Phe Leu Leu Asp Ala Glu Phe Leu Gly Val
65                  70                  75                  80
Val Gln Ile Thr Val Tyr Val Gly Ala Val Ile Val Met Tyr Ala Phe
                85                  90                  95
Gly Met Met Phe Phe Asn Ser Ala Ala Glu Val Val Glu Arg Lys Gln
            100                 105                 110
Ser Pro Lys Ile Leu Cys Val Leu Ser Phe Gly Val Ala Leu Leu Leu
```

```
        115                 120                 125
Thr Leu Ile Leu Ser Ala Pro Ser Ile Unk Glu Asn Leu Ser Lys Gln
    130                 135                 140
Val Asn Ser Asn Ala Ile Asp Ala Gln Unk Pro Asn Ile Lys Ala Ile
145                 150                 155                 160
Gly Tyr Val Leu Phe Thr Asn Tyr Leu Ile Pro Phe Glu Ala Ala Ala
                165                 170                 175
Leu Met Leu Leu Val Ala Met Val Gly Gly Ile Ala Thr Gly Ile Gln
            180                 185                 190
Lys Ile His Gly Lys Asn His Thr Gln Phe Ile Lys Glu Ser Leu
        195                 200                 205
```

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

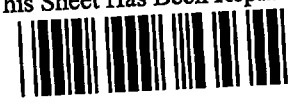
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576

```
Met Gly Ala Ile Leu Ser Ile Leu Lys Leu Glu Ile Lys Ser Tyr Leu
1               5                   10                  15
Thr Asn Thr Ser Ala Leu Phe Trp Thr Phe Ile Tyr Pro Ile Leu Met
            20                  25                  30
Leu Leu Leu Leu Ile Phe Val Phe Ser Lys Asn Thr Thr Glu Ile Phe
        35                  40                  45
Tyr Phe Asn Asn Ile Ile Gly Leu Met Gly Leu Leu Ile Ile Ser Ser
    50                  55                  60
Ala Ile Phe Gly Leu Thr Gln Ala Ile Thr Ser Ser Arg Ser His Asn
65                  70                  75                  80
Ile Phe Leu Phe Tyr Met Leu Ser Pro Ala Thr Phe Lys Gln Ile Thr
                85                  90                  95
Leu Ala Leu Ile Ala Ser Arg Leu Ile Val Val Ile Leu Tyr Ala Phe
            100                 105                 110
Ile Phe Ile Val Leu Ser Phe Tyr Ala Leu Asn Ile Ile Thr Ile Leu
        115                 120                 125
Asn Phe Lys Ala Leu Ile Leu Gly Phe Ile Ser Ile Phe Ser Ser Ala
    130                 135                 140
Leu Phe Cys Phe Cys Leu Ala Ile Phe Val Ala Arg Ile Phe Gln Asn
145                 150                 155                 160
Glu Gln Ser Ile Leu Gly Phe Cys Asn Ile Ile Asn Leu Tyr Ala Leu
                165                 170                 175
Met Ser Cys Asn Val Phe Val Pro Leu Glu Tyr Leu Pro Asn Ile Gly
            180                 185                 190
Gln Leu Phe Ile Lys Thr Ser Ile Phe Tyr Tyr Leu Asn Gln Leu Leu
        195                 200                 205
Ile Lys Ala Phe Gln Gly Ile Asp Thr Ile Leu Val Leu Ala Thr Ser
    210                 215                 220
Thr Phe Phe Ile Ile Gly Gly Ile Ile Leu Phe Leu Leu Ser Ala Asn
225                 230                 235                 240
Arg Met Leu Leu Thr Pro Lys Glu Arg Met Arg
                245                 250
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:577:

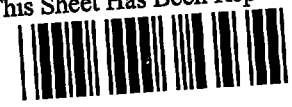
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577

```
Met Ala Gly Thr Gln Ala Ile Tyr Glu Ser Ser Ser Ala Gly Phe Leu
1               5                  10                  15
Ser Gln Val Ser Ser Ile Ile Ser Ser Thr Ser Gly Val Ala Gly Pro
            20                  25                  30
Phe Ala Gly Ile Val Ala Gly Ala Met Thr Ala Ala Ile Ile Pro Ile
        35                  40                  45
Val Val Gly Phe Thr Asn Pro Gln Met Thr Asp Ile Ile Asn Pro Ile
    50                  55                  60
Lys Ser Lys His Arg
65
```

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578

```
Val Ser Arg Ile Leu Gly Leu Ser Asp Asp Leu Ala Met Thr Leu Cys
1               5                  10                  15
Ala Glu Ser Ile Arg Ile Gln Ala Pro Ile Lys Gly Lys Asp Val Val
            20                  25                  30
Gly Ile Glu Ile Pro Asn Ser Gln Ser Gln Ile Ile Tyr Leu Arg Glu
        35                  40                  45
Ile Leu Glu Ser Glu Leu Phe Gln Lys Ser Ser Ser Pro Leu Thr Leu
    50                  55                  60
Ala Leu Gly Lys Asp Ile Val Gly Asn Pro Phe Ile Thr Asp Leu Lys
65                  70                  75                  80
Lys Leu Pro His Leu Leu Ile Ala Gly Thr Thr Gly Ser Gly Lys Ser
```

```
                85                  90                  95
Val Gly Val Asn Ala Met Ile Leu Ser Leu Leu Tyr Lys Lys Pro Pro
            100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:579:

This Sheet Has Been Replaced



(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:579

```
Met Asp Glu Unk Leu Val Tyr Gly Val Ile Cys Met Pro Ser Gln Val
1               5                  10                  15
Phe Ala Asn Thr Gly Thr Asn Val Ser Ile Ile Phe Phe Gln Lys Thr
            20                  25                  30
Pro Ser Ala Lys Glu Val Ile Leu Ile Asp Ala Ser Lys Leu Gly Glu
        35                  40                  45
Glu Tyr Thr Glu Asn Lys Asn Lys Lys Thr Arg Leu Arg Pro Ser Asp
    50                  55                  60
Met Asp Leu Ile Leu Glu Thr Phe Gln Asn Lys Ala Pro Lys Ser Asp
65                  70                  75                  80
Phe Cys Ala Leu Val Ser Phe Asp Glu Ile Thr Glu Lys Asn Tyr Ser
                85                  90                  95
Leu Asn Pro Gly Gln Tyr Phe Thr Ile Glu Asp Thr Ser Glu Thr Ile
            100                 105                 110
Ser Gln Ala Glu Phe Glu Asn Leu Met Gln Gln Tyr Ser Ser Glu Leu
        115                 120                 125
Ala Ser Leu Phe Asp Glu Ser Gln Asn Leu Gln Gln Glu Ile Leu Glu
    130                 135                 140
Thr Leu Lys Gly Val Arg Phe Glu
145                 150
```

(2) INFORMATION FOR SEQ ID NO:580:

(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:580

```
Met Arg Lys Gly Arg Val Met Leu Cys Val Phe Asp Ile Glu Thr Ile
1               5                  10                  15
Pro Asn Ile Ser Leu Cys Lys Glu His Phe Gln Leu Lys Glu Asp Asp
            20                  25                  30
Ala Leu Lys Ile Cys Glu Trp Ser Phe Glu Lys Gln Lys Glu Lys Ser
        35                  40                  45
Gly Ser Glu Phe Leu Pro Leu Tyr Leu His Glu Ile Ile Ser Ile Ala
    50                  55                  60
Ala Val Ile Gly Asp Asp Tyr Gly Gln Phe Ile Lys Val Gly Asn Phe
65                  70                  75                  80
Gly Gln Lys His Glu Asn Lys Glu Asp Phe Ala Ser Glu Lys Glu Leu
                85                  90                  95
Leu Glu Asp Phe Phe Lys Tyr Phe Asn Glu Lys Gln Pro Arg Leu Ile
            100                 105                 110
Ser Phe Unk Gly Arg Gly Phe Gly Tyr Ser Pro Thr His Ala Gln Ser
        115                 120                 125
Pro
```

(2) INFORMATION FOR SEQ ID NO:580:

This Sheet Has Been Replaced



(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:580

```
Met Arg Lys Gly Arg Val Met Leu Cys Val Phe Asp Ile Glu Thr Ile
1               5                  10                  15
Pro Asn Ile Ser Leu Cys Lys Glu His Phe Gln Leu Lys Glu Asp Asp
            20                  25                  30
Ala Leu Lys Ile Cys Glu Trp Ser Phe Glu Lys Gln Lys Glu Lys Ser
        35                  40                  45
Gly Ser Glu Phe Leu Pro Leu Tyr Leu His Glu Ile Ile Ser Ile Ala
    50                  55                  60
Ala Val Ile Gly Asp Asp Tyr Gly Gln Phe Ile Lys Val Gly Asn Phe
65                  70                  75                  80
Gly Gln Lys His Glu Asn Lys Glu Asp Phe Ala Ser Glu Lys Glu Leu
                85                  90                  95
Leu Glu Asp Phe Phe Lys Tyr Phe Asn Glu Lys Gln Pro Arg Leu Ile
            100                 105                 110
Ser Phe Unk Gly Arg Gly Phe Gly Tyr Ser Pro Thr His Ala Gln Ser
        115                 120                 125
Pro
```

(2) INFORMATION FOR SEQ ID NO:581:

(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

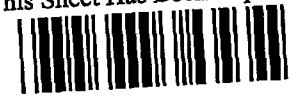
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581

```
Met Arg Arg Ile Ile Lys Asn Thr Leu Ser Arg Leu Gly Tyr Glu Asp
1               5                  10                  15
Val Leu Glu Ala Glu His Gly Val Glu Ala Trp Glu Lys Leu Asp Ala
            20                  25                  30
Asn Ala Asp Thr Lys Val Leu Ile Thr Asp Trp Asn Met Pro Glu Met
        35                  40                  45
Asn Gly Leu Asp Leu Val Lys Lys Val Arg Ala Asp Asn Arg Phe Lys
    50                  55                  60
Glu Ile Pro Ile Ile Met Ile Thr Thr Glu Gly Gly Lys Ala Glu Val
65                  70                  75                  80
Ile Thr Thr Leu Lys Ala Gly Val Asn Asn Tyr Ile Val Lys Pro Phe
                85                  90                  95
Thr Pro Gln Val Leu Lys Glu Lys Leu Glu Val Val Leu Gly Thr Asn
            100                 105                 110
Asp
```

(2) INFORMATION FOR SEQ ID NO:582:

This Sheet Has Been Replaced



(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

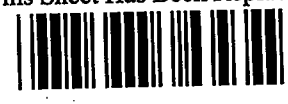
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582

```
Met Ala Glu Glu Gln Glu Asn Thr Ala Gln Gln Pro Gln Lys Lys Ser
1               5                  10                  15
Lys Ala Leu Leu Phe Val Ile Ile Gly Ser Val Leu Val Met Leu Leu
            20                  25                  30
Leu Val Gly Val Ile Ile Met Leu Leu Met Gly Asn Lys Glu Glu Ser
        35                  40                  45
Lys Glu Asn Ala Ser Lys Asn Thr Gln Glu Val Gln Ala Asn Pro Met
    50                  55                  60
Ala Asn Lys Asn Gln Glu Ala Lys Glu Gly Ser Asn Ile Gln Gln Tyr
65                  70                  75                  80
```

```
Leu Val Leu Gly Pro Leu Tyr Ala Ile Asp Ala Pro Phe Ala Val Asn
                85                  90                  95
Leu Val Ser Gln Asn Gly Arg Arg Tyr Leu Lys Ala Ser Ile Ser Leu
            100                 105                 110
Glu Leu Ser Asn Glu Lys Leu Leu Asn Glu Val Lys Val Lys Asp Thr
        115                 120                 125
Ala Ile Lys Asp Thr Ile Ile Glu Ile Leu Ser Ser Lys Ser Val Glu
    130                 135                 140
Glu Val Val Thr Asn Lys Gly Lys Asn Lys Leu Lys Asp Glu Ile Lys
145                 150                 155                 160
Ser His Leu Asn Ser Phe Leu Ile Asp Gly Phe Ile Lys Asn
                165                 170
```

(2) INFORMATION FOR SEQ ID NO:583:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583

```
Met Gly Cys Phe Ser Thr Ile Cys Cys Lys Gly Leu Thr Leu Ser Val
1               5                   10                  15
Gly Gly Phe Leu Val Met Met Arg Phe Leu Ile Phe Lys Asp Phe Cys
            20                  25                  30
Lys Asp Phe
        35
```

(2) INFORMATION FOR SEQ ID NO:584:

(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:584

```
Met Ala Lys Lys Lys Ile Ala Ile Ser Cys Gly Asp Ile Gln Gly Val
1               5                   10                  15
Gly Leu Glu Leu Ile Leu Lys Ser His Lys Glu Val Ser Ala Leu Cys
```

```
            20                  25                  30
Glu Pro Leu Tyr Leu Val His Ser Glu Leu Leu Glu Arg Ala Asn Gln
        35                  40                  45
Leu Leu Asp Asn Ala Tyr Glu Thr Lys Thr Leu Asn Ala Ile Ala Ile
    50                  55                  60
Asp Ala Pro Leu Pro Leu Leu Asn Ser Ser Thr Ile Gly Lys Val Ser
65                  70                  75                  80
Thr Gln Ser Gly Ala Tyr Ser Phe Glu Ser Phe Lys Lys Ala Cys Glu
                85                  90                  95
Leu Ala Asp Ser Lys Glu Val Asp Gly Ile Cys Thr Leu Pro Ile Asn
            100                 105                 110
Lys Leu Ala Trp Gln Gln Ala Gln Ile Pro Phe Val Gly His Thr Asp
        115                 120                 125
Phe Leu Lys Gln Arg Tyr Lys Asp His Gln Ile Ile Met Met Leu Gly
    130                 135                 140
Cys Ser Lys Leu Phe Val Gly Leu Phe Ser Asp His Val Pro Leu Ser
145                 150                 155                 160
Ala Val Ser Gln Leu Ile Gln Val Lys Ala Leu Val Lys Phe Leu Leu
                165                 170                 175
Ala Phe Gln Lys Ser Thr Gln Ala Lys Ile Val Gln Val Cys Gly Phe
            180                 185                 190
Asn Pro His Ala Gly Glu Glu Gly Leu Phe Gly Glu Glu Asp Glu Lys
        195                 200                 205
Ile Leu Lys Ala Ile Gln Glu Ser Asn Gln Thr Leu Gly Phe Glu Cys
    210                 215                 220
Phe Leu Gly Pro Leu Pro Ala Asp Ser Ala Phe Ala Pro Asn Lys Arg
225                 230                 235                 240
Lys Ile Thr Pro Phe Tyr Val Ser Met Ser His Asp Val Gly Leu Ala
                245                 250                 255
Pro Leu Lys Ala Leu Tyr Phe Asp Glu Ser Ile Asn Val Ser Leu Asn
            260                 265                 270
Ala Pro Ile Leu Arg Ala Ser Thr Asp His Gly Thr Ala Phe Asp Ile
        275                 280                 285
Ala Tyr Gln Asn Lys Ala Asn His Lys Ser Tyr Leu Asn Ala Ile Lys
    290                 295                 300
Tyr Leu Ala
305
```

(2) INFORMATION FOR SEQ ID NO:584:

This Sheet Has Been Replaced



(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:584

```
Met Ala Lys Lys Lys Ile Ala Ile Ser Cys Gly Asp Ile Gln Gly Val
1               5                   10                  15
Gly Leu Glu Leu Ile Leu Lys Ser His Lys Glu Val Ser Ala Leu Cys
            20                  25                  30
Glu Pro Leu Tyr Leu Val His Ser Glu Leu Leu Glu Arg Ala Asn Gln
        35                  40                  45
```

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

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 702 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585

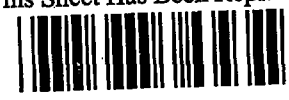
```
Val Ala Arg Leu Val Val Lys Arg Arg Lys Ile Asp Tyr Lys Gln Ser
1               5                   10                  15
Ile Gln Ser Asp Ser Gln Tyr Leu Gln Ala Unk Leu Asn Gln Phe Glu
            20                  25                  30
Asn Lys Glu Val Tyr Glu Asn Gln Tyr Phe Leu Val Leu Glu Ser Thr
        35                  40                  45
His Ser Leu His Gly Val Leu Glu His Lys Lys Lys Ser Phe Met His
    50                  55                  60
Ala Asn Arg Glu Asn Phe Lys Asp Ile Leu Ser Tyr Lys Ala His Phe
```

65 70 75 80
Leu Gln Glu Thr Leu Lys Ser Leu Glu Ile Gln Leu Lys Asn Tyr Ala
85 90 95
Pro Lys Leu Leu Asn Ser Lys Glu Val Leu Asn Phe Tyr Ala Glu Tyr
100 105 110
Ile Asn Gly Phe Glu Leu Pro Leu Lys Pro Leu Val Gly Gly Tyr Leu
115 120 125
Ser Asp Ser Tyr Ile Ala Ser Ser Ile Thr Phe Glu Lys Asp Tyr Phe
130 135 140
Ile Gln Glu Ser Phe Asn Gln Lys Thr Tyr Asn Arg Leu Ile Gly Ile
145 150 155 160
Lys Ala Tyr Glu Ser Glu Arg Ile Thr Ser Ile Ala Val Gly Ala Leu
165 170 175
Leu Tyr Gln Glu Thr Pro Leu Asp Ile Ile Phe Ser Ile Glu Pro Met
180 185 190
Ser Val Asn Lys Thr Leu Ser Phe Leu Lys Glu Arg Ala Lys Phe Ser
195 200 205
Met Ser Asn Leu Val Lys Asn Glu Leu Leu Glu Tyr Gln Glu Leu Val
210 215 220
Lys Thr Lys Arg Leu Ser Met Gln Lys Phe Ala Leu Asn Val Leu Ile
225 230 235 240
Lys Ala Pro Ser Leu Glu Asp Leu Asp Ala Gln Thr Ser Leu Ile Leu
245 250 255
Gly Leu Leu Phe Lys Glu Asn Leu Val Gly Val Ile Glu Thr Phe Gly
260 265 270
Leu Lys Gly Gly Tyr Phe Ser Phe Phe Pro Glu Arg Ile His Leu Asn
275 280 285
His Arg Leu Arg Phe Leu Thr Ser Lys Ala Leu Ala Cys Leu Met Val
290 295 300
Phe Glu Arg Gln Asn Leu Gly Phe Lys Ala Asn Ser Trp Gly Asn Ser
305 310 315 320
Pro Leu Ser Val Phe Lys Asn Leu Asp Tyr Ser Pro Phe Leu Phe Asn
325 330 335
Phe His Asn Gln Glu Val Ser His Asn Asn Ala Lys Glu Ile Ala Arg
340 345 350
Val Asn Gly His Thr Leu Val Ile Gly Ala Thr Gly Ser Gly Lys Ser
355 360 365
Thr Leu Ile Ser Tyr Leu Met Met Ser Ala Leu Lys Tyr Gln Asn Met
370 375 380
Arg Leu Leu Ala Phe Asp Arg Met Gln Gly Leu Tyr Ser Phe Thr Glu
385 390 395 400
Phe Phe Lys Gly His Tyr His Asp Gly Gln Ser Phe Ser Ile Asn Pro
405 410 415
Phe Cys Leu Glu Pro Asn Leu Gln Asn Leu Glu Phe Leu Gln Ser Phe
420 425 430
Phe Leu Ser Met Leu Asp Leu Ala Pro Ser Arg Asp Lys Glu Ala Leu
435 440 445
Glu Asp Met Asn Ala Ile Ser Gly Ala Ile Lys Ser Leu Tyr Glu Thr
450 455 460
Leu Tyr Pro Lys Asp Phe Ser Leu Leu Asp Phe Lys Glu Thr Leu Lys
465 470 475 480
Arg Thr Ser Ser Asn Gln Leu Gly Leu Ser Leu Glu Pro Tyr Leu Asn
485 490 495
Asn Pro Leu Phe Asn Ala Leu Asn Asp Ala Phe Asn Ser Asn Ala Phe
500 505 510
Leu Asn Val Ile Asn Leu Asp Ala Ile Thr Gln Asn Pro Lys Asp Leu
515 520 525
Gly Leu Leu Ala Tyr Tyr Leu Phe Tyr Lys Ile Leu Glu Glu Ser Arg
530 535 540
Lys Asn Asp Ser Gly Phe Leu Val Phe Leu Asp Glu Phe Lys Ser Tyr
545 550 555 560
Val Glu Asn Asp Leu Leu Asn Thr Lys Ile Asn Ala Leu Ile Thr Gln
565 570 575
Ala Arg Lys Ala Asn Gly Val Val Val Leu Ala Leu Gln Asp Ile Tyr
580 585 590

```
Gln Leu Ser Gly Val Lys Asn Ala His Ser Phe Leu Ser Asn Met Gly
        595                 600                 605
Thr Leu Ile Leu Tyr Pro Gln Lys Asn Ala Arg Glu Leu Lys His Asn
    610                 615                 620
Phe Asn Val Pro Leu Ser Glu Thr Glu Ile Ser Phe Leu Glu Asn Thr
625                 630                 635                 640
Pro Leu Tyr Ala Arg Gln Val Leu Val Lys Asn Leu Gly Asn Gly Ser
                645                 650                 655
Ser Asn Met Ile Asp Val Ser Leu Glu Gly Leu Gly Cys Tyr Leu Lys
            660                 665                 670
Ile Phe Asn Ser Asp Ser Ser His Val Asn Lys Val Lys Ala Leu Gln
        675                 680                 685
Lys Asp Tyr Pro Thr Glu Trp Arg Glu Lys Leu Leu Lys Ser
    690                 695                 700
```

(2) INFORMATION FOR SEQ ID NO:586:

This Sheet Has Been Replaced



(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:586

```
Met Gln Glu Asp Trp Gln Ala Val Gln Asp Thr Ile Lys Val Val Ser
1               5                   10                  15
Asp Val Lys Ala Gly Asn Phe Ala Val Arg Ile Thr Ala Glu Pro Ala
            20                  25                  30
Ser Pro Asp Leu Lys Glu Leu Arg Asp Ala Leu Asn Gly Ile Met Unk
        35                  40                  45
Tyr Leu Gln Glu Ser Val Gly Thr His Met Pro Ser Ile Phe Lys Ile
    50                  55                  60
Phe Glu Ser Tyr Ser Gly Leu Asp Phe Arg Gly Arg Ile Gln Asn Ala
65                  70                  75                  80
Ser Gly Arg Val Glu Leu Val Thr Asn Ala Leu Gly Gln Glu Ile Gln
                85                  90                  95
Lys Met Leu Glu Thr Ser Ser Asn Phe Ala Lys Asp Leu Ala Asn Asp
            100                 105                 110
Ser Ala Asn Leu Lys Glu Cys Val Gln Asn Leu Glu Lys Ala Ser Asn
        115                 120                 125
Ser Gln His Lys Ser Leu Met Glu Thr Ser Lys Thr Ile Glu Asn Ile
    130                 135                 140
Thr Thr Ser Ile Gln Gly Val Ser Ser Gln Ser Glu Ala Met Ile Glu
145                 150                 155                 160
Gln Gly Lys Asp Ile Lys Ser Ile Val Glu Ile Ile Arg Asp Ile Ala
                165                 170                 175
Asp Gln Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile Glu Ala Ala Arg
            180                 185                 190
Ala Gly Glu His Gly Arg Gly Phe Ala Val Val Ala Asp Glu Val Arg
        195                 200                 205
Lys Leu Ala Glu Arg Thr Gln Lys Ser Leu Ser Glu Ile Glu Ala Asn
    210                 215                 220
Ile Asn Ile Leu Val Gln Ser Ile Ser Asp Thr Ser Glu Ser Ile Lys
```

```
225                 230                 235                 240
Asn Gln Val Lys Glu Val Glu Glu Ile Asn Ala Ser Ile Glu Ala Leu
                245                 250                 255
Arg Ser Val Thr Glu Gly Asn Leu Lys Ile Ala Ser Asp Ser Leu Glu
            260                 265                 270
Ile Ser Gln Glu Ile Asp Lys Val Ser Asn Asp Ile Leu Glu Asp Val
        275                 280                 285
Asn Lys Lys Gln Phe
    290
```

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587

```
Met Pro Lys Ser Phe Thr Leu Pro Thr Phe Val Trp Cys Leu Phe Val
1               5                  10                  15
Gly Val Ile Leu Arg Asn Ala Leu Ser Phe Phe Lys Ile His Ser Val
            20                  25                  30
Phe Asp Arg Glu Val Ser Val Ile Gly Asn Val Ser Leu Ser Leu Phe
        35                  40                  45
Leu Ala Tyr Ala
    50
```

(2) INFORMATION FOR SEQ ID NO:588:

(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:588

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

```
Ile Gln Ser Ile Leu Ile Glu Ala Leu Arg Phe Ala Tyr Pro Lys Ala
        35                  40                  45
Ser Gln Gln Glu Trp His His Leu Ala Glu Leu Cys Leu Glu Glu Val
    50                  55                  60
Cys Leu Asn Pro Glu Leu Leu Asn Phe Tyr Ala Tyr Glu Leu Ser Gly
65                  70                  75                  80
Gly Glu Arg Gln Arg Val Ala Ile Ala Arg Ala Ile Ala Leu Lys Pro
                85                  90                  95
Arg Ile Ile Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Lys Ser Ile
            100                 105                 110
Gln Lys Ser Val Leu Glu Leu Leu Leu Asn Leu Gln Glu Lys Gln Asp
        115                 120                 125
Leu Ser Tyr Leu Phe Ile Ser His Asp Leu Asp Val Ile Lys Ala Phe
    130                 135                 140
Cys Asp Arg Val Leu Val Val Ser Glu Gly Lys Ile Val Glu Thr Gly
145                 150                 155                 160
Ala Ile Glu Glu Val Phe Asp Asn Pro Lys His Ala Tyr Thr Lys Arg
                165                 170                 175
Leu Leu Glu Ser Arg Leu
            180
```

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

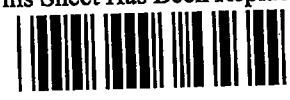
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589

```
Val Ser Leu Ile Lys Val Ser Gly Asp Lys Lys Val Ile Glu Val Ser
1               5                   10                  15
Ile Pro Leu Thr Ser Ile Ser Gly Lys Ala Arg Val Lys Ile Arg His
            20                  25                  30
Ala Phe Ser Asp Tyr Gly Ile Ser Thr Ala Thr Arg Lys Ile Pro Phe
        35                  40                  45
Ser Leu Lys His Tyr Val Glu Trp Gln Ile Gly Tyr Asp Val Pro Ile
    50                  55                  60
Lys Asp Lys Glu Lys Phe Glu Leu Thr Thr Leu Lys Asp Glu Lys Tyr
65                  70                  75                  80
His Phe Leu Gly Ala Asn Asn Lys Val Lys Thr Leu Tyr Glu Leu Ser
                85                  90                  95
Glu Met Ile Tyr Tyr Ala Lys Arg Leu Gly Leu Ile Ser Leu Glu Asn
            100                 105                 110
Leu Glu Asn Thr Leu Lys Phe Leu Glu Lys Gln Lys Gln Phe Ile Glu
        115                 120                 125
Asp Asn Phe Met Ile Thr Arg Glu Arg Phe Arg Ser His Gln Phe Gly
    130                 135                 140
Gly Met Asp Phe Glu Leu Ser Arg Ile Ser Tyr Pro Leu Leu Ile His
145                 150                 155                 160
Ser Phe Asp Asp Asn Glu Leu Ser Glu Ile Val Ile Lys Glu Gln Gln
                165                 170                 175
Tyr Gly Ser Lys Thr Gln Ala Met Leu Tyr Phe Cys Phe Ser Ile Leu
```

This Sheet Has Been Replaced



```
            180                 185                 190
Glu Leu Lys Thr Ala Thr Pro Leu Leu Asn Arg Thr Ala Met Pro Lys
        195                 200                 205
Glu His Ala Leu Leu Ile Ile His Glu Thr Asn Ala Leu Val Phe Leu
    210                 215                 220
Glu Met Leu Lys Ile Phe Gly Leu Leu Ser Gln Val His His Asn Asp
225                 230                 235                 240
Val Leu Lys Ile Leu Glu Lys Ile Leu Gln Asn
                245                 250
```

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590

```
Val Ile Thr Ala Cys Phe Asn Arg Glu Lys Thr Ile Glu Asp Thr Ile
1               5                   10                  15
Leu Ser Val Leu Asn Gln Thr Tyr Lys Asn Ile Glu Tyr Ile Ile Ile
            20                  25                  30
Asp Gly Ala Ser Ala Ile Ala Leu
        35                  40
```

(2) INFORMATION FOR SEQ ID NO:591:

(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:591

```
Val Phe Val Gly Leu Tyr His Gly Ala Ser Ile Phe Asp Leu Lys Phe
1               5                   10                  15
Glu Val Tyr Leu Thr Met Leu Ile Ser Leu Met Pro Phe Val Ala Thr
            20                  25                  30
Ile Tyr Ile Asn Phe Pro Lys Thr Thr Glu Thr Ser His Gly Tyr Ala
        35                  40                  45
```

```
Arg Trp Ala Asn Val Lys Asp Ile Glu Cys Phe Lys Ile Phe Ser Lys
    50                  55                  60
Glu Gly Phe Cys Lys Val Val His Arg Leu Gly Val Gln Phe Asp Asn
65                  70                  75                  80
Gly Phe Ile Leu Gly Lys Phe Gly Phe Pro Lys Leu Arg Asn Val Cys
                85                  90                  95
Tyr Asp Lys Pro Leu Gly Thr Met Ile Val Ala Pro Pro Gly Ala Glu
            100                 105                 110
Lys Leu His Val Trp Leu Cys Gln Ile Tyr
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:592:

(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:592

```
Met Lys Arg Leu Ala Val Ala Leu Ile Leu Val Leu Gly Val Val Trp
1               5                   10                  15
Gly Lys Ser Leu Pro Lys Trp Ala Lys Asp Cys Ser Lys Glu Met Arg
            20                  25                  30
Ile Glu Lys Thr Gln Thr Lys Asp Glu Lys Ile Leu Val Cys Gly Met
        35                  40                  45
Ser Asp Ile Leu Leu Ser Asp Met Asp Tyr Ser Leu Ser Ser Ala Arg
    50                  55                  60
Gln Asn Ala Leu Glu Lys Val Met Glu Ala Phe Lys Gly Asp Arg Ile
65                  70                  75                  80
Glu Ile Lys Ala Gly Glu Leu Lys Ala Thr Phe Ile Asp Thr Asp Lys
                85                  90                  95
Val Tyr Val Leu Leu Arg Ile Thr Lys Lys His Val Ala Leu Met Asn
            100                 105                 110
Glu
```

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 437 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

This Sheet Has Been Replaced



(A) NAME/KEY: misc_feature
(B) LOCATION 1...437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593

```
Met Asn Pro Gln Ile Gln Pro Ala Thr Lys Lys Pro Leu Lys Ser Leu
1               5                  10                  15
Leu Ala Ala Ser Ser Gly Asn Leu Val Glu Trp Tyr Asp Phe Tyr Ala
            20                  25                  30
Tyr Ala Phe Leu Ala Pro Tyr Phe Ala Lys Glu Phe Thr His Thr Asn
        35                  40                  45
Asp Pro Thr Leu Ala Leu Ile Ser Ala Phe Leu Val Phe Met Leu Gly
    50                  55                  60
Phe Phe Met Arg Pro Leu Gly Ser Leu Phe Phe Gly Lys Leu Gly Asp
65                  70                  75                  80
Lys Lys Gly Arg Lys Thr Ser Met Val Tyr Ser Ile Ile Leu Met Ala
                85                  90                  95
Leu Gly Ser Phe Met Leu Ala Leu Leu Pro Thr Lys Glu Ile Val Gly
            100                 105                 110
Glu Trp Ala Phe Leu Phe Leu Leu Leu Ala Arg Leu Leu Gln Gly Phe
        115                 120                 125
Ser Val Gly Gly Glu Tyr Gly Val Val Ala Thr Tyr Leu Ser Glu Leu
    130                 135                 140
Gly Lys Asn Gly Lys Lys Gly Phe Tyr Gly Ser Phe Gln Tyr Val Thr
145                 150                 155                 160
Leu Val Gly Gly Gln Leu Leu Ala Ile Phe Ser Leu Phe Ile Val Glu
                165                 170                 175
Asn Val Tyr Thr His Glu Gln Ile Ser Ala Phe Ala Trp Arg Tyr Leu
            180                 185                 190
Phe Ala Leu Glu Gly Ile Leu Ala Leu Leu Ser Leu Phe Leu Arg Asn
        195                 200                 205
Ile Met Glu Glu Thr Met Asp Asn Glu Ala Thr Pro Gln Lys Lys Thr
    210                 215                 220
Asn Val Asn Asn Thr Lys Glu Thr His Ile Lys Glu Thr Gln Arg Gly
225                 230                 235                 240
Ser Leu Lys Glu Leu Leu Asn His Lys Lys Ala Leu Met Ile Val Phe
                245                 250                 255
Gly Leu Thr Met Gly Gly Ser Leu Cys Phe Tyr Thr Phe Thr Val Tyr
            260                 265                 270
Leu Lys Ile Phe Leu Thr Asn Ser Ser Ser Phe Ser Pro Lys Glu Ser
        275                 280                 285
Ser Phe Ile Met Leu Leu Ala Leu Ser Tyr Phe Ile Phe Leu Gln Pro
    290                 295                 300
Leu Cys Gly Met Leu Ala Asp Lys Ile Lys Arg Thr Gln Met Leu Met
305                 310                 315                 320
Val Phe Ala Ile Thr Gly Leu Ile Val Thr Pro Ile Val Phe Tyr Gly
                325                 330                 335
Ile Lys His Ala Thr Ser Val Tyr Glu Ala Leu Phe Tyr Glu Ile Leu
            340                 345                 350
Ala Leu Ser Ser Met Ser Phe Tyr Thr Cys Ile Ala Gly Val Ile Lys
        355                 360                 365
Ala Glu Leu Phe Pro Glu His Val Arg Ala Leu Gly Val Gly Leu Ala
    370                 375                 380
Tyr Ala Ile Ala Asn Ala Leu Phe Gly Gly Ser Ala Ser Tyr Ile Ala
385                 390                 395                 400
Leu Glu Phe Lys Gln His Gly Phe Glu Glu Gly Phe Val Gly Tyr Val
                405                 410                 415
Met Leu Ser Ile Val Ile Phe Met Val Met Val Ile Ile Phe Pro Lys
            420                 425                 430
Lys Thr Tyr Leu Glu
        435
```

(2) INFORMATION FOR SEQ ID NO:594:

This Sheet Has Been Replaced



SUBSTITUTE SHEET (RULE 26)

(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:594

```
Met Ser Ser Gly Leu Ile Tyr Ile Ser Leu Glu Val Leu Val Unk 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 Unk Glu
        115                 120                 125
Arg Glu Asn Phe Unk Unk Gln Arg Ala Phe Val Unk Unk Unk Unk Ala
    130                 135                 140
Lys Ala
145
```

(2) INFORMATION FOR SEQ ID NO:594:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594

```
Met Ser Ser Gly Leu Ile Tyr Ile Ser Leu Glu Val Leu Val Unk 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 Unk Glu
        115                 120                 125
Arg Glu Asn Phe Unk Unk Gln Arg Ala Phe Val Unk Unk Unk Unk Ala
    130                 135                 140
Lys Ala
145
```

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595

```
Met Asn Ile Lys Ile Leu Lys Ile Leu Val Gly Gly Leu Phe Phe Leu
1               5                   10                  15
Ser Leu Asn Ala His Leu Trp Gly Lys Gln Asp Asn Ser Phe Leu Gly
            20                  25                  30
Ile Gly Glu Arg Ala Tyr Lys Ser Gly Asn Tyr Ser Lys Ala Ala Ser
        35                  40                  45
Tyr Phe Lys Lys Ala Cys Asn Asp Gly Val Ser Glu Gly Cys Thr Gln
    50                  55                  60
Leu Gly Ile Ile Tyr Glu Asn Gly Gln Gly Thr Arg Ile Asp Tyr Lys
65                  70                  75                  80
Lys Ala Leu Glu Tyr Tyr Lys Thr Ala Cys Gln Ala Asp Asp Arg Glu
                85                  90                  95
Gly Cys Phe Gly Leu Gly Gly Leu Tyr Asp Glu Gly Leu Gly Thr Ala
            100                 105                 110
Gln Asn Tyr Gln Glu Ala Unk Asp Ala Tyr Ala Arg His Ala Phe
        115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595

```
Met Asn Ile Lys Ile Leu Lys Ile Leu Val Gly Gly Leu Phe Phe Leu
1               5                  10                  15
Ser Leu Asn Ala His Leu Trp Gly Lys Gln Asp Asn Ser Phe Leu Gly
            20                  25                  30
Ile Gly Glu Arg Ala Tyr Lys Ser Gly Asn Tyr Ser Lys Ala Ala Ser
        35                  40                  45
Tyr Phe Lys Lys Ala Cys Asn Asp Gly Val Ser Glu Gly Cys Thr Gln
    50                  55                  60
Leu Gly Ile Ile Tyr Glu Asn Gly Gln Gly Thr Arg Ile Asp Tyr Lys
65                  70                  75                  80
Lys Ala Leu Glu Tyr Tyr Lys Thr Ala Cys Gln Ala Asp Asp Arg Glu
                85                  90                  95
Gly Cys Phe Gly Leu Gly Gly Leu Tyr Asp Glu Gly Leu Gly Thr Ala
            100                 105                 110
Gln Asn Tyr Gln Glu Ala Unk Asp Ala Tyr Ala Arg His Ala Phe
        115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:596:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596

```
Met Asp Ile Ser Ile Phe Arg Glu Tyr Asp Ile Arg Gly Ile Tyr Pro
1               5                  10                  15
Thr Thr Leu Asp Glu Asn Thr Ala Phe Ser Ile Gly Val Glu Leu Gly
            20                  25                  30
Lys Ile Met Arg Glu Tyr Asp Lys Ser Val Phe Val Gly His Asp Ala
        35                  40                  45
Arg Val His Gly Arg Phe Leu Phe Glu Val Leu Ser Ala Gly Leu Gln
    50                  55                  60
Ser Ser Gly Leu Lys Val Tyr Asp Leu Gly Leu Ile Pro Thr Pro Val
65                  70                  75                  80
Ala Tyr Phe Ala Ala Phe Asn Glu Ile Asp Asn Ile Gln Trp Pro
                85                  90                  95
```

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597

```
Val Cys Asp Ile Phe Ser Asp Gly Val Leu Leu Asp Lys Ala Leu Val
1               5                  10                  15
Ile Tyr Phe Lys Ala Pro Tyr Ser Phe Thr Gly Glu Asp Val Cys Glu
            20                  25                  30
Ile Gln Cys His Gly Ser Pro Leu Leu Ala Gln Asn Ile Leu Gln Ala
        35                  40                  45
Cys Leu Asn Leu Gly Ala Arg Leu Ala Lys Ala Gly Glu Phe Ser Lys
    50                  55                  60
Lys Ala Phe Leu Asn His Lys Met Asp Leu Ser Glu Ile Glu Ala Ser
65                  70                  75                  80
Val Gln Leu Ile Leu Cys Glu Asp Glu Ser Val Leu Asn Ala Leu Ala
                85                  90                  95
Arg Gln Leu Gln Gly Gly
            100
```

(2) INFORMATION FOR SEQ ID NO:598:

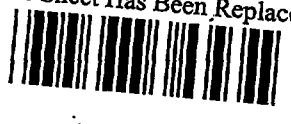
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598

```
Met Phe Lys Lys Met Cys Leu Ser Leu Leu Met Ile Ser Gly Val Cys
1               5                  10                  15
Val Gly Ala Lys Asp Leu Asp Phe Lys Leu Asp Tyr Arg Ala Thr Gly
            20                  25                  30
Gly Lys Phe Met Gly Lys Met Thr Asp Ser Ser Leu Leu Ser Ile Thr
        35                  40                  45
Ser Met Asn Asp Glu Pro Val Val Ile Lys Asn Leu Ile Val Asn Arg
    50                  55                  60
Gly Asn Ser Val Glu Ala Thr Lys Lys Val Glu Pro Lys Phe Gly Asp
65                  70                  75                  80
Lys Phe Lys Lys Glu Lys Leu Phe Asp His Glu Leu Lys Tyr Ser Gln
                85                  90                  95
```

```
Gln Ile Phe Tyr Arg Leu Asp Cys Lys Pro Asn Gln Leu Leu Glu Val
            100                 105                 110
Lys Ile Ile Thr Asp Lys Gly Glu Tyr Tyr His Lys Phe Ser Lys
        115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 502 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

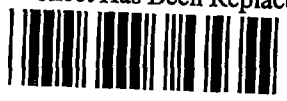
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599

```
Met Thr Leu Lys Pro Tyr Pro Thr Lys Glu Thr Gly Leu Ala Ser Gln
1               5                  10                  15
Leu Ser Gly His Trp Phe Phe Gln Leu Ser Leu Phe Asn Lys Thr Asn
            20                  25                  30
Phe Asn Pro Asn Lys Ile Trp Ile Pro Leu Glu Phe Asn Lys Arg Ser
        35                  40                  45
Lys Ile Lys Phe Asp Lys Asp Leu Glu Ile Tyr Phe Asp Ser His Glu
    50                  55                  60
Ser Phe Asn Ile Ser Lys Lys Tyr Leu Gln Glu Ile Asp Gln Glu Ser
65                  70                  75                  80
Leu Lys Lys Ile Lys Gln Ser Lys Asp Phe Phe Ser Ile Gln Lys Ile
                85                  90                  95
Glu Ser Lys His Asp Asn Asn Asp Ile Leu Gln Leu Glu Phe Phe Glu
            100                 105                 110
Asn Asp Thr Ser Phe Leu Phe Ala Lys Gly Ser Phe Ala Glu Ile Leu
        115                 120                 125
Glu Tyr Asn Met Gln Leu Lys Ile Asp Ser Leu Ile Thr Lys Glu Phe
    130                 135                 140
Asn Lys Leu Leu Ala Ile Val Gln Asp Ser Pro Gln Asp Ser Tyr Gln
145                 150                 155                 160
Leu Lys Ile Arg Val Arg His Asn Asn Lys Leu Pro Arg Glu Lys Tyr
                165                 170                 175
Thr Glu His Glu Ile Lys Leu Glu Val Tyr Asp Cys Arg Lys Ser His
            180                 185                 190
Asp His Asn Glu Pro Ile Ile Leu Ser Gln Gln Ser Thr Gly Phe Gln
        195                 200                 205
Trp Ala Phe Asn Phe Met Phe Gly Phe Leu Tyr Asn Val Gly Ser His
    210                 215                 220
Phe Ser Phe Asn His Asn Ile Ile Tyr Val Met Asp Glu Pro Ala Thr
225                 230                 235                 240
His Leu Ser Val Pro Ala Arg Lys Glu Phe Arg Lys Phe Leu Lys Glu
                245                 250                 255
Tyr Ala His Lys Asn His Val Thr Phe Val Leu Ala Thr His Asp Pro
            260                 265                 270
Phe Leu Val Asp Thr Asp His Leu Asp Glu Ile Arg Ile Val Glu Lys
        275                 280                 285
Glu Thr Glu Gly Ser Val Ile Lys Asn His Phe Asn Tyr Pro Leu Asn
    290                 295                 300
Asn Ala Ser Lys Asp Ser Asp Ala Leu Asp Lys Ile Lys Arg Ser Leu
```

This Sheet Has Been Replaced



```
305                 310                 315                 320
Gly Val Gly Gln His Val Phe His Asn Pro Gln Lys His Arg Ile Ile
                325                 330                 335
Phe Val Glu Gly Ile Thr Asp Tyr Cys Tyr Leu Ser Ala Phe Lys Leu
            340                 345                 350
Tyr Leu Arg Tyr Lys Glu Tyr Lys Asp Asn Pro Ile Pro Phe Thr Phe
        355                 360                 365
Leu Pro Ile Ser Gly Leu Lys Asn Asp Ser Asn Asp Met Lys Glu Thr
    370                 375                 380
Ile Glu Lys Leu Cys Glu Leu Asp Asn His Pro Ile Val Leu Thr Asp
385                 390                 395                 400
Asp Asp Arg Lys Cys Val Phe Asn Gln Gln Ala Thr Ser Glu Arg Phe
                405                 410                 415
Lys Arg Ala Asn Glu Glu Met His Asp Pro Ile Thr Ile Leu Gln Leu
            420                 425                 430
Ser Asp Cys Asp Arg His Phe Lys Gln Ile Glu Asp Cys Phe Ser Ala
        435                 440                 445
Asn Asp Arg Asn Lys Tyr Ala Lys Asn Lys Gln Met Glu Leu Ser Met
    450                 455                 460
Ala Phe Lys Thr Arg Leu Leu Tyr Gly Gly Glu Asp Ala Ile Glu Lys
465                 470                 475                 480
Gln Thr Lys Arg Asn Phe Leu Lys Leu Phe Lys Trp Ile Ala Trp Ala
                485                 490                 495
Thr Asn Leu Ile Lys Asn
            500
```

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600

```
Val Tyr Phe Phe Leu Ala Leu Ser Gly Glu Lys Val Leu Leu Pro Val
1               5                   10                  15
Ile Gly Gly Leu Glu Lys Asn Ala Leu Glu Ala Gly Leu Leu Lys Gly
            20                  25                  30
Asp Arg Ile Leu Leu Ser Thr Ile Lys Lys
        35                  40
```

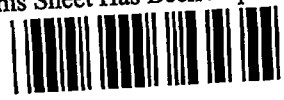
(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 341 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

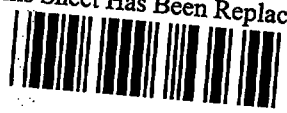
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601

```
Met Glu Asn Phe Lys Leu Ile Asn Phe Phe Thr Gly Gln Asn Asp Ala
1               5                  10                  15
Gly Lys Thr Asn Leu Leu Glu Ala Leu Tyr Thr Asn Thr Gly Leu Cys
            20                  25                  30
Asp Pro Thr Ala Asn Gln Val Ser Leu Pro Pro Glu His Ala Val Asn
        35                  40                  45
Ile Ser Glu Phe Arg Lys Ile Lys Leu Asp Ala Asp Asn Leu Lys Thr
    50                  55                  60
Phe Phe Tyr Gln Gly Asn Thr Ala Asn Pro Ile Ser Ile Arg Thr Glu
65                  70                  75                  80
Phe Glu His Ala Thr Ile Pro Leu Thr Ile Gln Tyr Pro Thr Gln Thr
                85                  90                  95
Ser Tyr Ser Lys Asp Ile Asn Leu Asn Ser Asp Asp Ala His Met Thr
            100                 105                 110
Asn Leu Ile Asn Thr Thr Ile Thr Lys Pro Gln Leu Gln Phe Ser Tyr
        115                 120                 125
Asn Pro Ser Leu Ser Pro Met Thr Met Thr Tyr Glu Phe Glu Arg Gln
    130                 135                 140
Asn Leu Gly Leu Ile His Ser Asn Leu Asp Lys Ile Ala Gln Thr Tyr
145                 150                 155                 160
Lys Glu Asn Ala Met Phe Ile Pro Ile Glu Leu Ser Ile Val Asn Ser
                165                 170                 175
Leu Lys Ala Leu Glu Asn Leu Gln Leu Ala Ser Lys Glu Lys Glu Leu
            180                 185                 190
Ile Glu Ile Leu Gln Cys Phe Asn Pro Asn Ile Leu Asn Ala Asn Thr
        195                 200                 205
Ile Arg Lys Ser Val Tyr Ile Gln Ile Lys Asp Glu Asn Thr Pro Leu
    210                 215                 220
Glu Glu Ser Pro Lys Arg Leu Leu Asn Leu Phe Gly Trp Gly Phe Ile
225                 230                 235                 240
Lys Phe Phe Ile Met Val Ser Ile Leu Ile Asp Asn Arg Val Lys Tyr
                245                 250                 255
Leu Phe Ile Asp Glu Ile Glu Ser Gly Leu His His Thr Lys Met Gln
            260                 265                 270
Glu Phe Leu Lys Ala Leu Phe Lys Leu Ala Gln Lys Leu Gln Ile Gln
        275                 280                 285
Ile Phe Ala Thr Thr His Asn Lys Glu Phe Leu Leu Asn Ala Ile Asn
    290                 295                 300
Thr Ile Ser Asp Asn Glu Thr Gly Val Phe Lys Asp Ile Ala Leu Phe
305                 310                 315                 320
Glu Leu Glu Lys Glu Ser Ala Ser Asp Phe Ile Arg His Ser Tyr Ser
                325                 330                 335
Met Leu Glu Lys Ala
            340
```

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602

```
Met Asp Phe Lys Lys Cys Pro Asn Phe Glu Lys Lys Cys Ala Phe Leu
1               5                  10                  15
Cys Phe Ser Asn Leu Val Leu Leu Ile Glu Ile His Ser Lys Gly Leu
            20                  25                  30
His Met Gln Lys Lys Lys Pro Lys Asn Pro Gln Pro Asn Leu Phe Ser
        35                  40                  45
Ile Leu Asp Lys Gly Asp Val Ala Thr Asn Asn Pro Val Glu Glu Ser
    50                  55                  60
Asp Lys Ala Asn Lys Ile Gln Glu Pro Leu Pro Tyr Val Val Lys Thr
65                  70                  75                  80
Gln Ile Asn Lys Ala Ser Met Ile Ser Arg Asp Pro Ile Glu Trp Ala
                85                  90                  95
Lys Tyr Leu Ser Phe Glu Lys Arg Val Tyr Lys Asp Asn Ser Lys Glu
            100                 105                 110
Asp Val Asn Phe Phe Ala Asn Gly Glu Ile Lys Glu Ser Ser Arg Val
        115                 120                 125
Tyr Glu Ala Asn Lys Glu Gly Phe Glu Arg Arg Ile Thr Lys Arg Tyr
    130                 135                 140
Asp Leu Ile Asp Arg Asn Ile Asp Arg Asn Arg Glu Phe Phe Ile Lys
145                 150                 155                 160
Glu Ile Glu Ile Leu Thr His Thr Asn Ser Leu Lys Glu Leu Lys Glu
                165                 170                 175
Gln Gly Leu Glu Ile Gln Leu Thr His His Asn Glu Thr His Lys Lys
            180                 185                 190
Ala Leu Glu Asn Gly Asn Glu Ile Val Lys Glu Tyr Asp His Leu Lys
        195                 200                 205
Asp Ile Tyr Gln Glu Val Glu Arg Thr Lys Asp Gly Gly Leu Val Arg
    210                 215                 220
Glu Ile Ile Pro Ser Ile Ser Ser Ala Glu Tyr Phe Lys Leu Tyr Asn
225                 230                 235                 240
Lys Leu Pro Phe Glu Ser Ile Asn Asn Glu Asn Thr Lys Leu Asn Thr
                245                 250                 255
Asn Asp Asn Glu Glu Val Lys Lys Leu Glu Phe Glu Leu Ala Lys Glu
            260                 265                 270
Val His Ile Leu Ile Leu Glu Gln Gln Leu Leu Ser Ala Thr Asn Tyr
        275                 280                 285
Tyr Ser Trp Ile Asp Lys Asp Asp Asn Ala Asn Phe Ala Trp Lys Met
    290                 295                 300
His Arg Leu Ile Asn Glu Asn Lys Leu Lys Glu Asn His Leu Ser Ala
305                 310                 315                 320
Asn Asn Ala Asn Lys Ile Lys Gln Phe Phe Phe Asn Asn Gly Ser Ile
                325                 330                 335
Leu Gly Trp Thr Lys Glu Glu Gln Ser Ala Ile Gln Glu Asn Arg Asp
            340                 345                 350
Tyr Ser Leu Arg Ser Ala Leu Leu Ser Leu Glu Glu Ile Ala Gln Ala
        355                 360                 365
Lys Ile Glu Leu Gln Lys Tyr Tyr Glu Ser Val Tyr Val Asn Gly Asp
    370                 375                 380
Gly Asn Lys Arg Glu Ile Lys Pro Phe Lys Glu Ile Leu Arg Asp Thr
385                 390                 395                 400
Asn Asn Phe Glu Lys Ala Tyr Lys Glu Arg Tyr Asp Lys Leu Val Ser
                405                 410                 415
Leu Ser Ala Ala Ile Ile Gln Ala Lys Glu Gly Gly Asn Glu Arg Gln
            420                 425                 430
```

```
Asn Ser Ser Ala Asn Asn Asn Asn Pro Ile Lys Asn Thr Ile Glu Thr
        435                 440                 445
Asn Thr Ser Asn Asn Ile Ile Gln Asn Asn Asp Asn Ile Ile Ile Gln
    450                 455                 460
Ile
465
```

(2) INFORMATION FOR SEQ ID NO:603:

This Sheet Has Been Replaced



(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:603

```
Met Ala Leu Glu Val Val Leu Trp Asp Phe Asp Gly Val Ile Phe Asp
1               5                  10                  15
Ser Met His Leu Lys Tyr Glu Gly Phe Lys Ala Leu Phe Gln Lys His
            20                  25                  30
Gly Asn Asp Ser Lys Glu Gly Leu Lys Gln Phe Glu Val Tyr His Tyr
        35                  40                  45
Gln Ser Gly Gly Ile Ser Arg Asn Glu Lys Ile Gln Tyr Phe Tyr Asn
    50                  55                  60
Glu Ile Leu Lys Thr Pro Ile Ala Gln Glu Glu Ile Asp Ala Leu Ala
65                  70                  75                  80
Leu Glu Phe Gly Ala Ile Ile Glu Gln Lys Leu Phe Asp Arg Gly His
                85                  90                  95
Leu Asn Ser Glu Val Met Ala Phe Ile Asp Lys His Tyr Gln Asn Tyr
            100                 105                 110
Ile Phe His Ile Ala Ser Ala Ala Leu His Ser Glu Leu Gln Val Leu
        115                 120                 125
Cys Glu Phe Leu Gly Ile Thr Lys Tyr Phe Lys Ser Val Glu Gly Ser
    130                 135                 140
Pro Pro Asp Lys Pro Lys Ile Ile Ala Asn Ile Ile Gln Lys Tyr Ala
145                 150                 155                 160
Tyr Asp Pro Ser Arg Met Leu Met Ile Ala Ile Ala Ser Met Ile Met
                165                 170                 175
Lys Ala Leu Arg Leu Ile Lys Trp Arg Phe Trp Ala Ile Thr Ala Arg
            180                 185                 190
Phe
```

(2) INFORMATION FOR SEQ ID NO:604:

(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:604

```
Met Leu Lys Lys Lys Ile Asp Leu His Lys Asp Ser Ile Arg Lys Leu
1               5                  10                  15
Phe Phe Tyr Tyr Phe Ile Pro Leu Val Phe Ser Met Ile Ser Leu Ser
            20                  25                  30
Thr Tyr Ser Met Val Asp Asp Met Phe Val Gly Lys Lys Leu Gly Lys
        35                  40                  45
Glu Ala Ile Ala Ala Val Asn Ile Ala Trp Pro Ile Phe Pro Gly Leu
    50                  55                  60
Ile Ala Tyr Glu Leu Leu Phe Gly Phe Gly Ala Ala Ser Ile Val Gly
65                  70                  75                  80
Tyr Phe Leu Gly Gln Asn Lys Thr His Arg Ala Arg Leu Val Phe Ser
                85                  90                  95
Ser Val Phe Tyr Phe Val Ala Leu Ser Ala Phe Ile Leu Ser Met Ala
            100                 105                 110
Leu Leu Pro Phe Ser Glu Asn Ile Ala Gln Phe Phe Gly Ser Asn Asp
        115                 120                 125
Ala Leu Leu Asn Met Ser Asn Ala Ile Leu Lys Ser Phe
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:605

```
Val Lys Cys Leu Leu Ile Lys Lys Ser Leu Leu Phe Ala Leu Lys Pro
1               5                  10                  15
Leu Pro Asp Leu Lys Thr Thr Thr Pro Ile Leu Ala Pro Met Ser Val
            20                  25                  30
Val Ala Gly Arg Leu Unk Unk His Leu Val Gln His Tyr Leu Leu Ala
        35                  40                  45
Leu Glu His Val Lys Gly Phe Met Gly Lys Gly Val Ile Leu Gly Gly
    50                  55                  60
Leu Ser Gly Ala Gln Arg Ala Lys Ile Val Val Ile Gly Gly Gly Val
65                  70                  75                  80
Val Gly Met Glu Ser Ala Lys Val Leu Unk Gln Met Gly Unk Lys Val
                85                  90                  95
Thr Ile Leu Glu Leu Asp Tyr Ala Lys Leu Gln Asn His Pro Tyr Tyr
            100                 105                 110
```

His Leu Tyr Asp Leu Glu Val Leu Ser Val Asn Glu Ala Asn Ile Ile
115 120 125
Gln Ala Leu Asn Gly Unk Val Gly Leu Val Gly Ala Val Leu Val Thr
130 135 140
Unk Ser Gln Thr Pro Lys Val Unk Leu Arg Arg His Leu Lys Tyr
145 150 155

(2) INFORMATION FOR SEQ ID NO:606:

(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:606

Met Leu Ala Lys Ile Val Phe Ser Ser Leu Val Ala Phe Gly Val Leu
1 5 10 15
Ser Ala Asn Val Glu Gln Phe Gly Ser Phe Phe Asn Glu Ile Lys Lys
20 25 30
Glu Gln Glu Glu Val Ala Ala Lys Glu Asp Ala Leu Lys Ala Arg Lys
35 40 45
Lys Leu Leu Asn Asn Thr His Asp Phe Leu Glu Asp Leu Val Phe Arg
50 55 60
Lys Gln Lys Ile Lys Glu Leu Val Asp Tyr Arg Ala Lys Val Leu Leu
65 70 75 80
Asp Leu Glu Asn Lys Tyr Lys Lys Glu Lys Glu Ala Leu Glu Lys Glu
85 90 95
Thr Arg Gly Lys Ile Leu Thr Ala Lys Ser Lys Ala Tyr Gly Asp Leu
100 105 110
Glu Gln Ala Leu Lys Asp Asn Pro Leu Tyr Lys Lys Leu Leu Pro Asn
115 120 125
Pro Tyr Ala Tyr Val Leu Asn Gln Glu Thr Phe Thr Gln Glu Asp Lys
130 135 140
Glu Arg Leu Ser Tyr Tyr Tyr Pro Gln Val Lys Thr Ser Ser Ile Phe
145 150 155 160
Lys Lys Thr Thr Ala Thr Thr Lys Asp Lys Ala Gln Ala Leu Leu Gln
165 170 175
Met Gly Val Phe Ser Leu Asp Glu Glu Gln Asn Lys Lys Ala Ser Arg
180 185 190
Leu Ala Leu Ser Tyr Lys Gln Ala Ile Glu Glu Tyr Ser Asn Asn Ile
195 200 205
Ser Asn Leu Leu Ser Arg Lys Glu Leu Asp Asn Ile Asp Tyr Tyr Leu
210 215 220
Gln Leu Glu Arg Asn Lys Phe Asp Ser Lys Ala Lys Asp Ile Ala Gln
225 230 235 240
Lys Ala Thr Asn Thr Leu Ile Phe Asn Ser Glu Arg Leu Ala Phe Ser
245 250 255
Met Ala Ile Asp Lys Ile Asn Glu Lys Tyr Leu Arg Gly Tyr Glu Ala
260 265 270
Phe Ser Asn Leu Leu Lys Asn Val Lys Asp Asp Val Glu Leu Asn Thr
275 280 285
Leu Thr Lys Asn Phe Thr Asn Gln Lys Leu Ser Phe Ala Gln Lys Gln

This Sheet Has Been Replaced

```
    290                 295                 300
Lys Leu Cys Leu Leu Val Leu Asp Ser Phe Asn Phe Asp Thr Gln Ser
305                 310                 315                 320
Lys Lys Ser Ile Leu Lys Lys Thr Asn Glu Tyr Asn Ile Phe Val Asp
                325                 330                 335
Ser Asp Pro Met Met Ser Asp Lys Thr Thr Met Gln Lys Glu His Tyr
            340                 345                 350
Lys Ile Phe Asn Phe Phe Lys Thr Val Val Ser Ala Tyr Arg Asn Asn
        355                 360                 365
Val Ala Lys Asn Asn Pro Phe Glu
    370                 375
```

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

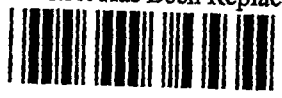
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607

```
Met Asp Phe Val Gly Phe Glu Asp Leu Lys Cys Lys Asp Lys Glu Asn
1               5                  10                  15
Ser Gln Lys Val Phe Val Ile Arg Asn Asp Lys Leu Gly Asp Phe Ile
            20                  25                  30
Leu Glu Ile Pro Ala Leu Ile Ala Leu Lys His Ala Phe Leu Glu Lys
        35                  40                  45
Gly Val Glu Val Tyr Leu Gly Val Val Val Pro Ser Tyr Thr Thr Pro
    50                  55                  60
Ile Ala Leu Glu Phe Pro Phe Ile Asp Glu Val Ile Ile Glu Asp Asn
65                  70                  75                  80
His Leu Ala Thr Thr His Lys Asn Arg Ser Ile Asp Ala Leu Ile Phe
                85                  90                  95
Leu Phe Ser Asn Phe Lys Asn Ala Lys Leu Ala Phe Ser Leu Arg Lys
            100                 105                 110
Ser Ile Pro Tyr Ile Leu Ala Pro Lys Thr Lys Ile Tyr Ser Trp Leu
        115                 120                 125
Tyr Gln Lys Arg Val Arg Gln Asn Arg Ser Leu Cys Leu Lys Thr Glu
    130                 135                 140
Tyr Glu Tyr Asn Leu Asp Leu Ile His Ala Phe Cys Lys Asp Tyr Asp
145                 150                 155                 160
Leu Pro Asn Ala Gln Leu Lys Lys Ile Ala Trp Lys Leu Lys Asp Lys
                165                 170                 175
Ser Lys Glu Arg Ser Ile Ile Ala Ser Lys Leu Asn Ala Asn Val Asp
            180                 185                 190
Leu Leu Trp Ile Gly Val His Met His Ser Gly Gly Ser Ser Pro Val
        195                 200                 205
Leu Pro Ala Ser His Phe Ile Glu Leu Ile Ala Ile Leu His Glu Lys
    210                 215                 220
Leu Ser Cys Glu Ile Ile Leu Ile Cys Gly Pro Gly Glu Arg Lys Ala
225                 230                 235                 240
Thr Glu Glu Leu Leu Lys Glu Val Pro Phe Ala His Leu Tyr Asp Thr
                245                 250                 255
```

This Sheet Has Been Replaced



```
Ser His Ser Leu Val Asp Leu Ala Lys Leu Cys Ala Asn Leu Ser Val
            260                 265                 270
Cys Ile Gly Asn Ala Ser Gly Pro Leu His Val Asn Ala Leu Phe Asp
        275                 280                 285
Asn Gln Ser Ile Gly Phe Tyr Pro Asn Glu Leu Thr Ala Ser Ile Ala
    290                 295                 300
Arg Trp Arg Pro Phe Asn Glu Gln Phe Leu Gly Ile Thr Pro Pro Asn
305                 310                 315                 320
Gly Ser Asn Asp Met Gly Leu Ile Asp Ile Gln Lys Glu Ser Glu Lys
                325                 330                 335
Ile Met Gly Phe Ile Thr Lys Asn Leu Ser His His Met Gln Glu Arg
            340                 345                 350
```

(2) INFORMATION FOR SEQ ID NO:608:

(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:608

```
Val Gly Val Leu Ser Leu Lys Ile Glu Ala Ile Ser Asn Phe Tyr Gly
1               5                   10                  15
Leu Cys Val Leu Gly Val Leu Leu Ala Cys Phe Tyr Leu Leu Asp Ala
            20                  25                  30
Tyr Tyr Leu Met Gln Glu Arg Leu Phe Arg Glu Gln Tyr Gln Trp Leu
        35                  40                  45
Ile Lys Asn Arg Leu Lys Thr Asp Glu Arg Leu Phe Glu Val Phe Pro
    50                  55                  60
Ile His Gln Thr Cys Gln Ser Thr Gln Phe Leu Ser Pro Cys Val Arg
65                  70                  75                  80
Leu Val Phe Ser Pro Ile Gly Arg
                85
```

(2) INFORMATION FOR SEQ ID NO:609:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609

```
Met Ser Leu Gly Ala Val Val Ser Ser Leu Leu Cys His Lys Leu Glu
1               5                  10                  15
Gly Ala Ile Leu Asp Leu Arg Ala Tyr Arg Unk Unk Ala Tyr Tyr His
            20                  25                  30
Glu Asn Lys Asp Thr Leu Leu Ile Lys Gly Lys Lys Arg Leu Leu Tyr
        35                  40                  45
Asn Tyr Ile Lys Ala His Ile Unk Leu Asn Leu Leu Trp Thr Ile Arg
    50                  55                  60
Asn Arg Thr Unk Ser Leu Gly Lys Phe Thr Gln Asn Pro Thr Glu Gln
65                  70                  75                  80
Pro Pro Thr Asn Asn His
                85
```

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:610

```
Met Lys Lys Thr Thr Leu Phe Val Leu Gly Leu Leu Phe Asn Ser Ser
1               5                  10                  15
Leu Ser Ala Val Asp Gly Ile Ser Gln Thr Glu Pro Ser Ser Leu Asn
            20                  25                  30
Leu Ala Glu Asp Ser Leu Pro Leu Asn His Ser Asn Ala Gln Lys Leu
        35                  40                  45
Ser Leu Lys Asn Ala Trp Asn Arg Val Leu Ser Asn His Glu Gly Leu
    50                  55                  60
His Ala Gln Asn Thr Pro Leu Ser Glu Arg Val Lys
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:611:

(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:611

```
Val Lys Lys Val Glu Ser Met Asn Val Val Pro Phe Ile Asp Ile Met
1               5                  10                  15
Leu Val Leu Leu Val Ile Val Leu Thr Thr Ala Ser Phe Val Gln Thr
            20                  25                  30
Ser Lys Leu Pro Ile Ser Ile Pro Gln Val Asp Lys Asp Ser Thr Asp
        35                  40                  45
Ser Lys Asp Val Leu Asp Lys Lys Gln Val Thr Ile Ala Ile Ser Asn
    50                  55                  60
Lys Gly Ser Phe Tyr Phe Asp Asp Lys Glu Ile Ser Phe Glu Asn Leu
65                  70                  75                  80
Lys His Lys Val Ser Thr Leu Ala Lys Asp Thr Pro Ile Val Phe Ala
                85                  90                  95
Arg Arg
```

(2) INFORMATION FOR SEQ ID NO:612:

(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

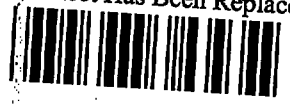
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612

```
Met Gly Ser Tyr Thr Phe Pro Leu Ile Leu Lys Pro Ile Phe Ile Asn
1               5                  10                  15
Lys Val Pro Val Thr Ile Asp Phe Tyr Ala Asn Ala Asn Tyr Phe Leu
            20                  25                  30
Ile Tyr Gly Ala Leu Ala Asn Ala Val Val Gly Ser Ile Asn Ala Leu
        35                  40                  45
Asn Asp Glu Ile Arg Phe Lys Arg Asn Ala Gln Ile Glu Glu Ala Glu
    50                  55                  60
Leu Gly Thr Asp Gly Ile Lys Ile Lys Pro Ile Ala Leu Tyr Asn Pro
65                  70                  75                  80
Ser Glu Gly Tyr Leu Asn Tyr Ala Leu Ser Ser Val Phe Ile Phe Ile
                85                  90                  95
Leu His Gln Val Met Leu Ile Ala Ser Ser Met Phe Thr Ser Ser Arg
            100                 105                 110
Arg Leu Glu Leu Ala Leu Leu Asp Lys Lys Gln Ile Ala Leu Arg Leu
        115                 120                 125
Cys Ala Arg Leu Leu Val Phe Met Gly Ala Phe Ser Val Phe Val Leu
    130                 135                 140
Trp Tyr Phe Gly Ala Leu Phe Ser Phe Tyr Gly Ile Glu Arg His Gly
145                 150                 155                 160
Ser Ala
```

(2) INFORMATION FOR SEQ ID NO:613:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613

```
Val Ile Met Thr Lys Leu Asp Gly Thr Ser Lys Gly Gly Ala Ile Leu
1               5                  10                  15
Unk Val Leu Tyr Glu Leu Lys Leu Pro Ile Leu Tyr Leu Gly Met Gly
            20                  25                  30
Glu Lys Glu Asp Asp Leu Ile Ala Phe Asp Glu Glu Arg Phe Ile Glu
        35                  40                  45
Asp Leu Val Asp Ala Val Phe Val Glu Gln
    50                  55
```

(2) INFORMATION FOR SEQ ID NO:614:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614

```
Val Cys Gly Ala His Gly Lys Ser Ser Ile Thr Unk Met Leu Ser Ala
1               5                  10                  15
Ile Cys Pro Ala Phe Gly Unk Ile Ile Gly Arg His Ser Lys Glu Phe
            20                  25                  30
Asp Ser Asn Val Unk Glu Ser Ala Asp Met Ser Leu Val Phe Glu Unk
        35                  40                  45
Asp Glu Ser Asp Ser Ser Phe Phe Ile Phe Gln Pro Phe Leu Arg Asp
    50                  55                  60
Cys Ala
65
```

(2) INFORMATION FOR SEQ ID NO:615:

(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:615

```
Met Ala Ile Ala Ile Lys Asp Leu Leu Ser Ala Tyr Lys Val Val Leu
1               5                  10                  15
Pro Leu Asp Lys Ile Ser Met Pro Ser Ser Ala Asp Leu Lys Leu Thr
            20                  25                  30
Leu Gln Phe Leu Lys Asn Thr Ala Pro Leu Phe Ser Val Gln Gly Ser
        35                  40                  45
Val Asn Leu Gln Glu Gly Thr Phe Ser Leu Tyr Asn Ile Pro Leu Tyr
    50                  55                  60
Thr Gln Ser Ala Gln Ile Asn Leu Asp Ile Ala Gln Glu Tyr Gln Tyr
65                  70                  75                  80
Ile Tyr Ile Asp Thr Ile His Thr Arg Tyr Ala Asn Met Unk Asp Leu
                85                  90                  95
Asp Ala Lys Ile Ala Leu Asp Leu Gly Gln Lys Asn Leu Ser Unk Unk
            100                 105                 110
Unk Leu Gly Pro
        115
```

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(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:615

```
Met Ala Ile Ala Ile Lys Asp Leu Leu Ser Ala Tyr Lys Val Val Leu
1               5                  10                  15
Pro Leu Asp Lys Ile Ser Met Pro Ser Ser Ala Asp Leu Lys Leu Thr
            20                  25                  30
Leu Gln Phe Leu Lys Asn Thr Ala Pro Leu Phe Ser Val Gln Gly Ser
        35                  40                  45
Val Asn Leu Gln Glu Gly Thr Phe Ser Leu Tyr Asn Ile Pro Leu Tyr
    50                  55                  60
Thr Gln Ser Ala Gln Ile Asn Leu Asp Ile Ala Gln Glu Tyr Gln Tyr
65                  70                  75                  80
Ile Tyr Ile Asp Thr Ile His Thr Arg Tyr Ala Asn Met Unk Asp Leu
```

```
                85                  90                  95
Asp Ala Lys Ile Ala Leu Asp Leu Gly Gln Lys Asn Leu Ser Unk Unk
            100                 105                 110
Unk Leu Gly Pro
        115
```

(2) INFORMATION FOR SEQ ID NO:616:

(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:616

```
Met Pro Asp Asn Leu His Leu His Thr Leu Leu Unk Lys Phe Leu Gln
1               5                  10                  15
Gln Arg Ser Phe Asn Tyr Pro Asn Pro Leu Cys Ala Phe Ile Leu Ile
            20                  25                  30
Leu Cys Asn Leu Pro Phe Ile Leu Ile Ser Val Leu Phe Arg Leu Asp
        35                  40                  45
Ala Tyr Ala Leu Ile Val Ile Ser Leu Val Phe Ile Unk Cys Tyr Leu
    50                  55                  60
Ile Gly Unk Ala Tyr Leu Asn Arg Gln Val Cys Ala Leu Glu Lys Arg
65                  70                  75                  80
Ala Phe
```

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

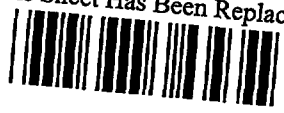
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616

```
Met Pro Asp Asn Leu His Leu His Thr Leu Leu Unk Lys Phe Leu Gln
1               5                  10                  15
Gln Arg Ser Phe Asn Tyr Pro Asn Pro Leu Cys Ala Phe Ile Leu Ile
            20                  25                  30
```

This Sheet Has Been Replaced



```
Leu Cys Asn Leu Pro Phe Ile Leu Ile Ser Val Leu Phe Arg Leu Asp
        35                  40                  45
Ala Tyr Ala Leu Ile Val Ile Ser Leu Val Phe Ile Unk Cys Tyr Leu
    50                  55                  60
Ile Gly Unk Ala Tyr Leu Asn Arg Gln Val Cys Ala Leu Glu Lys Arg
65                  70                  75                  80
Ala Phe
```

This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...77

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617

```
Val Asn Glu Leu Lys Asn Ser Lys Gln Val Leu Gly Asn Gly Lys Ala
1               5                  10                  15
Asp Leu Ser Asn Glu Asn Thr Lys Val Arg Gln Thr Lys Thr Asn Leu
            20                  25                  30
Thr Glu Lys Asn Gln Arg Leu Thr Thr Glu Lys Thr Glu Leu Asn Asn
        35                  40                  45
Lys Ile Thr Gly Leu Ala Thr Glu Lys Glu Arg Leu Ala Ala Asp Lys
    50                  55                  60
Glu Asn Leu Thr Lys Glu Ser Arg Gln Arg Lys Pro Asn
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:618:

(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:618

```
Met Asp Leu Gln Gln Ile Asp Glu Leu Glu Asn Lys Phe Glu Glu Gln
1               5                  10                  15
Glu Glu Gln Ala Gln Asp Thr Pro Leu Lys Gln Glu Pro Ser Thr Lys
```

```
            20                  25                  30
Glu Val Lys Ile Pro Lys Lys Arg Gly Arg Lys Lys Ser Leu Leu Asp
        35                  40                  45
Glu Asp Lys Lys Lys Ser Phe Asn Ile Ala Phe Ser Pro Cys Val Ile
    50                  55                  60
Lys Glu Leu Asn Glu Phe Leu Leu Glu Phe Gly Ser Phe Lys Glu Thr
65                  70                  75                  80
Arg Ser Thr Phe Ile Glu Glu Ala Leu Ile Arg His Leu Lys His Arg
                85                  90                  95
Lys Asn Thr Gln Glu Gln Lys Leu Leu Lys Gln Leu Glu Arg Leu Gln
            100                 105                 110
Asn Lys Glu Lys Gly Ile Met Lys Thr Met Asn Leu Asn Glu Phe Phe
        115                 120                 125
Thr His Lys Ile Ile Tyr Lys Asp Thr Pro Leu Lys Phe Lys Asp Thr
    130                 135                 140
Leu Glu Gln Glu Ile Ser Gln Ala Ser Leu Val Glu Lys Leu Ile Leu
145                 150                 155                 160
Ala Asn Ile Leu Ala Asn Met Val Phe Ala Lys Ile Ser Asn Glu Asn
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:619:

(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

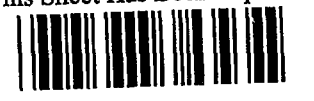
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619

```
Met Gly Cys Tyr Gly Ile Gly Ile Ser Arg Leu Leu Ser Val Ile Leu
1               5                   10                  15
Glu Gln Lys Ser Asp Asp Leu Asp Cys Val Trp Thr Lys Asn Thr Ala
            20                  25                  30
Pro Phe Asp Val Val Ile Val Val Ser Asn Leu Lys Asp Glu Ala Gln
        35                  40                  45
Lys Lys Leu Ala Phe Glu Val Tyr Glu Arg Leu Leu Gln Lys Gly Val
    50                  55                  60
Asp Ala Leu Leu Asp Asp Arg Asp Ala Arg Phe Gly Ala Lys Met Arg
65                  70                  75                  80
Asp Phe Glu Leu Ile Gly Glu Arg Leu Ala Leu Ile Val Gly Lys Gln
                85                  90                  95
Thr Leu Glu Ser Lys Glu Phe Glu Cys Ile Lys Arg Ala Asn Leu Glu
            100                 105                 110
Lys Gln Thr Ile Lys Asp Ile Gly Ile Arg Arg Lys Asn Phe Arg Asn
        115                 120                 125
Val Ser Glu Arg Ile Arg Gly Gly Asn Gly Lys Asn Ser Asp Trp Leu
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 amino acids

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(B) TYPE: amino acid
(D) TOPOLOGY: linear

(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:620

```
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 Leu
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:621:

(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:621

```
Met Ser Glu Lys Glu Arg Leu Asn Glu Val Ile Leu Glu Glu Glu Asn
1               5                  10                  15
Asn Gly Ser Gly Thr Lys Lys Val Phe Leu Ile Val Ala Ile Ala Ile
            20                  25                  30
Ile Ile Leu Ala Val Leu Leu Met Val Phe Trp Lys Ser Thr Arg Val
        35                  40                  45
Ala Pro Lys Glu Thr Phe Leu Gln Thr Asp Ser Gly Met Gln Lys Ile
    50                  55                  60
Gly Asn Thr Lys Asp Glu Lys Lys Asp Asp Glu Phe Glu Ser Leu Asn
65                  70                  75                  80
Met Asp Ser Pro Lys Gln Glu Asp Lys Leu Asp Lys Val Val Asp Asn
                85                  90                  95
Ile Lys Lys Gln Glu Ser Glu Asn Ser Met Pro Ile Gln Thr Asp Gln
            100                 105                 110
Ala Gln Met Glu Met Lys Thr Thr Glu Glu Lys Gln Glu Ser Gln Lys
```

```
        115                 120                 125
Glu Leu Lys Ala Val Glu Pro Ile Pro Met Ser Thr Gln Lys Glu Ser
    130                 135                 140
Gln Ala Val Ala Lys Lys Glu Thr Pro His Lys Lys Pro Lys Val Ala
145                 150                 155                 160
Pro Lys Asp Lys Glu Ala His Lys Asp Lys Ala Lys His Ala Ala Lys
                165                 170                 175
Glu Pro Lys Val Lys Lys Glu Ala Arg Lys Glu Val Ser Lys Lys Ala
            180                 185                 190
Asn Ser Lys Thr Asn Leu Thr Lys Gly His Tyr Leu Gln Val Gly Val
        195                 200                 205
Phe Ala His Thr Pro Asn Lys Ala Phe Leu Gln Glu Phe Asn Gln Phe
    210                 215                 220
Pro His Lys Ile Glu Asp Arg Gly Ala Thr Lys Arg Tyr Leu Ile Gly
225                 230                 235                 240
Pro Tyr Lys Ser Lys Gln Glu Ala Leu Met His Ala Asp Glu Val Ser
                245                 250                 255
Lys Lys Met Thr Lys Pro Val Val Ile Glu Val Arg
            260                 265
```

(2) INFORMATION FOR SEQ ID NO:622:

This Sheet Has Been Replaced



(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:622

```
Val Glu Tyr Tyr Ala Phe Asn Phe Ser Val Leu Asp Phe Val Leu Met
1               5                  10                  15
Gly Lys Ala Thr His Leu Asn Leu Phe Ala Met Pro Lys Ala Lys His
            20                  25                  30
Ile Lys Glu Ala Thr Ser Val Leu Glu Arg Leu Asp Leu Glu Ser Leu
        35                  40                  45
Lys Asp Gln Gly Ile Asn Asp Leu Ser Gly Gly Gln Arg Gln Met Val
    50                  55                  60
Leu Leu Ala Arg Ser Leu Leu Gln Arg Thr Pro Leu Leu Leu Leu Asp
65                  70                  75                  80
Glu Pro Thr Ser Ala Leu Asp Leu Lys Asn Gln Ala Leu Phe Phe Asp
                85                  90                  95
Ala Ile Lys Asp Glu Met Lys Lys Arg Glu Leu Ser Val Leu Val Asn
            100                 105                 110
Ile His Asp Pro Asn Leu Val Ala Arg His Ser Thr His Val Val Met
        115                 120                 125
Leu Lys Asp Lys Lys Leu Phe Leu Gln Ala Ser Thr Pro Ile Ala Met
    130                 135                 140
Thr Ser His Asn Leu Ser Ala Leu Tyr Asp Thr Pro Leu Unk Ala Ile
145                 150                 155                 160
Trp His Asp Asp Lys Leu Val Val Tyr Ala Leu
                165                 170
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623

```
Met Met Ala His Ser Leu Ile Leu Val Ser Lys Thr Ser Leu Ser Asn
1               5                  10                  15
Leu Leu Ile Phe Val Val Gln Pro Asp Gly Lys Leu Ser Met Thr Asp
            20                  25                  30
Ala Ala Ile Asp Pro Asn Met Thr Asn Ser Gly Leu Arg Trp Tyr Arg
        35                  40                  45
Val Asn Glu Ile Ala Glu Lys Phe Lys Leu Ile Lys Asp Lys Ala Leu
    50                  55                  60
Val Thr Val Ile Asn Lys Gly Tyr Gly Lys Asn Pro Leu Thr Lys Asn
65                  70                  75                  80
Tyr Asn Ile Lys Asn Tyr Gly Glu Leu Glu Arg Val Ile Lys Lys Leu
                85                  90                  95
Pro Leu Val Arg Asp Lys
            100
```

(2) INFORMATION FOR SEQ ID NO:624:

(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

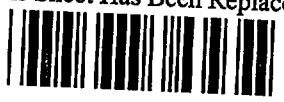
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624

```
Leu Lys Val Thr Asn Pro His Leu Leu Val Val Ile Gln Asp Leu Asn
1               5                  10                  15
Ala Arg Ile Ala Leu Met Lys Leu Leu Phe Gln Asn Val Lys Ser Ala
            20                  25                  30
Asn Lys Glu Leu Val Phe Cys Asn Lys Glu Lys Arg Leu Ile Arg Ser
        35                  40                  45
Phe Asp Ala Gln Lys Glu Tyr Gly Ile Thr Pro Val Glu Asn Ile Leu
    50                  55                  60
Ser Val Leu Asp Thr Ala Met Asn Pro Asn Ser Ala Leu Val Ile Asp
```

65 70 75 80
Asn Leu Asn Glu Ala Lys Glu Leu His Asp Lys Val Gly Ala Glu Lys
85 90 95
Leu Lys Ser Phe Leu Glu Lys Ala Unk Arg Gln Arg Ala Val Leu Arg
100 105 110
His Phe Cys Ala
115

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:624:

(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:624

Leu Lys Val Thr Asn Pro His Leu Leu Val Val Ile Gln Asp Leu Asn
1 5 10 15
Ala Arg Ile Ala Leu Met Lys Leu Leu Phe Gln Asn Val Lys Ser Ala
20 25 30
Asn Lys Glu Leu Val Phe Cys Asn Lys Glu Lys Arg Leu Ile Arg Ser
35 40 45
Phe Asp Ala Gln Lys Glu Tyr Gly Ile Thr Pro Val Glu Asn Ile Leu
50 55 60
Ser Val Leu Asp Thr Ala Met Asn Pro Asn Ser Ala Leu Val Ile Asp
65 70 75 80
Asn Leu Asn Glu Ala Lys Glu Leu His Asp Lys Val Gly Ala Glu Lys
85 90 95
Leu Lys Ser Phe Leu Glu Lys Ala Unk Arg Gln Arg Ala Val Leu Arg
100 105 110
His Phe Cys Ala
115

(2) INFORMATION FOR SEQ ID NO:625:

(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:625

```
Val Leu Asn Glu Glu Gln Asn Ser Leu Glu Glu Lys Gly Gly Glu Asn
1               5                  10                  15
Lys Asn Glu Lys Glu Thr Pro Leu Lys Gly Ile His Ser Lys Ile Pro
            20                  25                  30
Ser Leu Lys Gln Ala Leu Glu Gln Thr Ile Ser Lys Ile Lys Ser Ser
        35                  40                  45
Lys Glu Phe Phe Lys Gln Leu Leu His Asn Lys Lys Lys Leu Tyr Ile
    50                  55                  60
Ala Leu Gly Ile Leu Leu Ser Leu Ile Ala Leu Ile Val Ala Leu Ser
65                  70                  75                  80
Leu Leu Leu Gly His Lys Lys Glu Asn Lys Gln Thr Ser Leu Gln Thr
                85                  90                  95
Asn Thr Ala Thr Thr Asn Asn Glu Thr Pro Asn Asp Thr Asn Asn Ala
            100                 105                 110
Glu Ala Glu Gly Gln Ile Glu Asn Leu Asp Leu Pro Asp Leu Ile Gly
        115                 120                 125
Lys Asp Ser Leu Lys Arg Asn Asp Glu Ser Gln Val Asp Ala Met Met
    130                 135                 140
Gln Lys Ala Ser Leu Leu Tyr Glu Gln Gly Gln Lys Asp Glu Ala Leu
145                 150                 155                 160
His Leu Phe Asp Lys Ile Ala Ser Phe Ser Gln Gly Ile Ala Ser His
                165                 170                 175
Asn Leu Gly Val Ile Lys Phe Lys Glu Lys Asp Phe Asn Gly Ala Leu
            180                 185                 190
Asp Leu Phe Asp Ser Ser Ile Ala Ser Lys Glu Asn Ala Ser Val Ser
        195                 200                 205
Ala Ile Asp Ala Leu Val Thr Ala Tyr His Leu Gln Asp Ala Asp Leu
    210                 215                 220
Tyr Tyr His Tyr Leu Lys Ile Val Lys Arg His Phe Val
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:626:

This Sheet Has Been Replaced



(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:626

```
Met Lys Glu Ser Phe Tyr Ile Glu Gly Met Thr Cys Thr Ala Cys Ser
1               5                  10                  15
Ser Gly Ile Glu Arg Ser Leu Gly Arg Lys Ser Phe Val Lys Lys Ile
            20                  25                  30
Glu Val Ser Leu Leu Asn Lys Ser Ala Asn Ile Glu Phe Asn Glu Asn
        35                  40                  45
Glu Thr Asn Leu Asp Glu Ile Phe Lys Leu Ile Glu Lys Leu Gly Tyr
    50                  55                  60
Ser Pro Lys Lys Thr Leu Ala Glu Glu Lys Lys Glu Phe Phe Ser Pro
65                  70                  75                  80
Asn Val Lys Leu Ala Leu Ala Val Ile Phe Thr Leu Phe Val Val Tyr
```

```
                85                  90                  95
Leu Ser Met Gly Ala Met Leu Ser Pro Ser Leu Leu Pro Glu Ser Leu
            100                 105                 110
Leu Thr Ile Asn His His Ser Asn Phe Leu Asn Ala Cys Leu Gln Leu
        115                 120                 125
Ile Gly Ala Leu Ile Val Met His Leu Gly Arg Asp Phe Tyr Ile Gln
    130                 135                 140
Gly Phe Lys Ala Leu Trp His Arg Gln Pro Asn Met Ser Ser Leu Ile
145                 150                 155                 160
Ala Ile Gly Thr Ser Ala Ala Leu Ile Ser Ala Cys Gly Asn Cys Ile
                165                 170                 175
Trp Phe Ile Pro Ile Ile Ile Pro Ile Ser Gly Leu Met Gly Ile Ile
            180                 185                 190
Ile Leu Lys Ala Cys Ala
        195
```

(2) INFORMATION FOR SEQ ID NO:626:

(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:626

```
Met Lys Glu Ser Phe Tyr Ile Glu Gly Met Thr Cys Thr Ala Cys Ser
1               5                   10                  15
Ser Gly Ile Glu Arg Ser Leu Gly Arg Lys Ser Phe Val Lys Lys Ile
            20                  25                  30
Glu Val Ser Leu Leu Asn Lys Ser Ala Asn Ile Glu Phe Asn Glu Asn
        35                  40                  45
Glu Thr Asn Leu Asp Glu Ile Phe Lys Leu Ile Glu Lys Leu Gly Tyr
    50                  55                  60
Ser Pro Lys Lys Thr Leu Ala Glu Glu Lys Lys Glu Phe Phe Ser Pro
65                  70                  75                  80
Asn Val Lys Leu Ala Leu Ala Val Ile Phe Thr Leu Phe Val Val Tyr
                85                  90                  95
Leu Ser Met Gly Ala Met Leu Ser Pro Ser Leu Leu Pro Glu Ser Leu
            100                 105                 110
Leu Thr Ile Asn His His Ser Asn Phe Leu Asn Ala Cys Leu Gln Leu
        115                 120                 125
Ile Gly Ala Leu Ile Val Met His Leu Gly Arg Asp Phe Tyr Ile Gln
    130                 135                 140
Gly Phe Lys Ala Leu Trp His Arg Gln Pro Asn Met Ser Ser Leu Ile
145                 150                 155                 160
Ala Ile Gly Thr Ser Ala Ala Leu Ile Ser Ala Cys Gly Asn Cys Ile
                165                 170                 175
Trp Phe Ile Pro Ile Ile Ile Pro Ile Ser Gly Leu Met Gly Ile Ile
            180                 185                 190
Ile Leu Lys Ala Cys Ala
        195
```

This Sheet Has Been Replaced



This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:627:

(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:627

```
Met Asn Thr Ser Leu Leu Thr Gln Ala Gln Val Leu Ser Ser Lys Glu
1               5                  10                  15
Asn Gln Ile His Arg Leu Leu Leu Glu Leu Leu Glu Glu Ala Lys Leu
            20                  25                  30
His Phe Glu Pro Lys Leu Tyr Ile Ile Asn Ala Pro Tyr Met Asn Ala
        35                  40                  45
Phe Ala Ser Gly Trp Asp Glu Ser Asn Ser Leu Ile Ala Leu Thr Ser
    50                  55                  60
Ala Leu Ile Glu Arg Leu Asp Arg Asp Glu Leu Lys Ala Val Ile Ala
65                  70                  75                  80
His Glu Leu Ser His Ile Arg His Asn Asp Ile Arg Leu Thr Met Cys
                85                  90                  95
Val Gly Ile Leu Ser Asn Ile Met Leu Leu Val Ala Asn Phe Ser Val
            100                 105                 110
Tyr Phe Phe Met Gly Asn Arg Lys Asn Ser Gly Ala Asn Leu Ala Arg
        115                 120                 125
Met Ile Leu Trp Val Leu Gln Ile Ile Leu Pro Phe Leu Thr Leu Leu
    130                 135                 140
Leu Gln Met Tyr Leu Ser Arg Thr Arg Glu Tyr Met Ala Asp Ser Gly
145                 150                 155                 160
Ala Ala Phe Leu Met His Asp Asn Lys Pro Met Ile Arg Ala Leu Gln
                165                 170                 175
Lys Ile Ser Asn Asp Tyr Thr Asn Asn Asp Tyr Lys Glu Ile Asp Lys
            180                 185                 190
Asn Ser Thr Arg Ser Ala Ala Tyr Leu Phe Asn Ala Glu Met Phe Ser
        195                 200                 205
Thr His Pro Ser Ile Lys Asn Arg Ile Gln Ser Leu Arg Lys Arg Val
    210                 215                 220
Ile
225
```

(2) INFORMATION FOR SEQ ID NO:628:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628

```
Val Gly Ile Val Pro Asp Asn Leu Trp Lys Leu Lys Arg Phe Asn Gln
1               5                  10                  15
Asp Trp Arg Val Gly Asp Thr Leu Ile Thr Ala Ile Gly Gln Gly Ser
            20                  25                  30
Phe Leu Ala Thr Pro Leu Gln Val Leu Ala Tyr Thr Gly Leu Ile Ala
        35                  40                  45
Thr Gly Lys Leu Ala Thr Pro His Phe Ala Ile His Asn Gln Gln Pro
    50                  55                  60
Leu Lys Asp Pro Leu Asn Arg Phe Ser Lys Lys Glu Ala Pro Ser Leu
65                  70                  75                  80
Ala Arg Gly His Val
                85
```

(2) INFORMATION FOR SEQ ID NO:628:

(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:628

```
Val Gly Ile Val Pro Asp Asn Leu Trp Lys Leu Lys Arg Phe Asn Gln
1               5                  10                  15
Asp Trp Arg Val Gly Asp Thr Leu Ile Thr Ala Ile Gly Gln Gly Ser
            20                  25                  30
Phe Leu Ala Thr Pro Leu Gln Val Leu Ala Tyr Thr Gly Leu Ile Ala
        35                  40                  45
Thr Gly Lys Leu Ala Thr Pro His Phe Ala Ile His Asn Gln Gln Pro
    50                  55                  60
Leu Lys Asp Pro Leu Asn Arg Phe Ser Lys Lys Glu Ala Pro Ser Leu
65                  70                  75                  80
Ala Arg Gly His Val
                85
```

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 496 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629

```
Met Phe Asn Ile Lys Arg Thr Phe Leu Ile Thr Ile Ile Ser Phe Phe
1               5                  10                  15
Leu Ile Val Pro Asn Trp Leu Lys Ala Ile Asp Leu Pro Ile Val Ser
            20                  25                  30
Asn Leu Lys Ile Tyr Gln Thr Val Tyr Cys Met Leu Ile Pro Ser Tyr
        35                  40                  45
Val Leu Thr Asn Lys Ser Phe Ala Asp Ile Leu Thr Gly Tyr Thr Ser
    50                  55                  60
Ile Gly Ala Ser Gly Ser Gly Lys Ser Ser Gly Gln Gly Val Ile Glu
65                  70                  75                  80
Ala Leu Ser Thr Pro Leu Ala Thr Ser Leu Ala Ala Ser Asn Leu Val
                85                  90                  95
Lys Tyr Leu Asn Thr Leu Gly Pro Leu Trp Gly Ser Ala Trp Ala Ser
            100                 105                 110
Val Ala Thr Ala Ile Gln Gly Phe Ala Leu Thr Pro Ser Ser Gly Cys
        115                 120                 125
Asn Phe Gly Trp Asn Ala Leu Ile Asn Lys Asn Ile Asp Val Ser Met
    130                 135                 140
Asp Ser Val Leu Asp Asn Leu Ser Asn Lys Ile Gln Asn Phe Thr Lys
145                 150                 155                 160
Gly Gly Val Glu Asp Asn Val Lys Gly Asn Ile Leu Leu Gln Ile Ile
                165                 170                 175
Gly Ser Ile Thr Ala Gln Ala Ser Thr Asn Ile Thr Ala Asp Gly Leu
            180                 185                 190
Ile Trp Leu Ile Gly Lys Glu Phe Thr Ala Asn Lys Leu Gln Asn Asn
        195                 200                 205
Thr Ile Ala Met Leu Ala Phe Ala Ala Leu Glu Ser Val Val Lys Gly
    210                 215                 220
Ala Asp Ala Ala Val Leu Pro Ala Tyr Gly Val Val Asn Leu Pro Asp
225                 230                 235                 240
Ile Ile Ile Gly Gln Gly Ser Tyr Leu Asp Phe Val Ser Tyr Leu Ile
                245                 250                 255
Tyr Ile Val Phe Gly Ile Phe Val Phe Ile Ser Phe Met Lys Leu Arg
            260                 265                 270
Asp Ile Ser Asn Gly Ile Gln Ile Asn Ile Gly Phe Glu Tyr Met Arg
        275                 280                 285
Phe Val Gly Gly Thr Leu Phe Lys Met Ala Met Val Ser Phe Ile Ala
    290                 295                 300
Tyr Ala Gly Phe Gly Tyr Leu Tyr Lys Ile Ser Tyr Ser Ile Tyr Phe
305                 310                 315                 320
Gly Leu Ala Gly Ala Phe Gly Leu Asn Gln Val Leu Phe Trp Ala Leu
                325                 330                 335
Asp Leu Val Leu Asn Tyr Thr Val Asn Ser Ile Leu Pro Ala Val Arg
            340                 345                 350
Ala Val Phe Ser Asn Val Gly Asn Asn Ala Pro Ser Leu Leu Gln Gly
        355                 360                 365
Leu Gln Val Ala Gly Ile Ser Leu Phe Ala Ile Phe Met Gln Val Thr
    370                 375                 380
Ile Ile Met Arg Ile Ser Thr Val Val Val Lys Pro Leu Ile Ala Gly
385                 390                 395                 400
Ala Phe Ser Gly Ile Val Phe Pro Ile Ala Val Cys Leu Ile Val Leu
                405                 410                 415
Asp Trp Phe Lys Asp Ser Met Lys Asn Ile Leu Ile Trp Phe Ile Asn
            420                 425                 430
Asn Leu Phe Ile Leu Val Leu Ala Ile Pro Ile Leu Leu Phe Gly Val
```

```
        435                 440                 445
Leu Ala Leu Leu Ala Phe Asn Leu Thr Ile Thr Pro Ser Val Ala Ile
    450                 455                 460
Gln Asn Ile Asn Gln Gly Gly Leu Gly Ile Asp Ser Thr Ile Ala Ser
465                 470                 475                 480
Leu Ile Thr Leu Phe Ile Leu Lys Gly Phe Ile Glu Thr Ile Ile Glu
                485                 490                 495
```

(2) INFORMATION FOR SEQ ID NO:630:

This Sheet Has Been Replaced



(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:630

```
Met Ala Phe Trp Gln Ala Ile Arg Trp Trp Ile Leu Lys Leu Pro Phe
1               5                  10                  15
Met Met Gly Ala Thr Met Met Trp Ile Leu Ser Glu Met Ala Phe Lys
            20                  25                  30
Ile Ala Gly Unk Met Ala Phe Lys Glu Ala Ser Arg Ala Ala Asn Pro
        35                  40                  45
Val Leu Leu Glu Pro Met Met Lys Val Glu Val Glu Val Pro Glu Glu
    50                  55                  60
Tyr Met Gly Asp Val Ile Gly Asp Leu Asn Arg Arg Arg Gly Gln Ile
65                  70                  75                  80
Asn Ser Met Asp Asp Arg Leu Gly Leu Lys Ile Val Asn Ala Phe Val
                85                  90                  95
Pro Leu Val Glu Met Phe Gly Tyr Ser Thr Asp Leu Arg Ser Ala Thr
            100                 105                 110
Gln Gly Arg Gly Thr Tyr Ser Met Glu Phe Asp His Tyr Gly Glu Val
        115                 120                 125
Pro Ser Asn Ile Ala Lys Glu Ile Val Glu Lys Arg Lys Gly
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:631:

(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:631

```
Met Gln Asn Leu Pro Gly Met Ala Arg Ala Ala Met Leu Thr Thr Ser
1               5                  10                  15
Ser Ala Pro Ala Pro Glu Gly Glu Gly Ala Phe Arg Ala Met Lys Met
            20                  25                  30
Ala Ser Glu Met Ala Lys Val Glu Val Gly Tyr Val Asn Ala His Gly
        35                  40                  45
Thr Ser Thr His Tyr Asn Asp Trp Tyr Glu Ser Ile Ala Leu Lys Asn
    50                  55                  60
Val Leu Ala Leu Lys Lys Lys Ser Leu Leu Leu Ala Pro Leu Lys Gly
65                  70                  75                  80
Arg Leu Gly Leu Leu Gly Cys Cys Gly Val Arg Ser Arg Tyr Ser Ile
                85                  90                  95
Met Ala Met Unk Gln Gly Ile Leu Pro Pro Thr Ile Asn Gln Glu Thr
            100                 105                 110
Pro Asp Pro Glu Cys Unk Leu Asp Tyr Ile Pro Asn Thr Ala Arg Glu
        115                 120                 125
Lys Gln Val Asn Ala Val Met Ser Asn Ser Phe Gly Phe Gly Gly Thr
    130                 135                 140
Asn Gly Val Val Ile Phe Lys Lys Ala
145                 150
```

(2) INFORMATION FOR SEQ ID NO:632:

This Sheet Has Been Replaced



(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:632

```
Met Gln Asn Leu Leu Ile Gln Ala Glu Asn Ala Ile Ala Leu Leu Phe
1               5                  10                  15
Leu Leu Asn Asp Lys Asn Leu Lys Gly Lys Ile Asp Leu Ile Tyr Ile
            20                  25                  30
Asp Pro Pro Phe Ala Thr Asn Asn His Phe Thr Ile Thr Asn Gly Arg
        35                  40                  45
Ala Thr Thr Ile Ser Asn Ser Lys Asn Gly Asp Ile Ala Tyr Ser Asp
    50                  55                  60
Lys Val Val Gly Met Asp Phe Met Glu Phe Leu Lys Gln Arg Leu Val
65                  70                  75                  80
Leu Leu Lys Glu Leu Leu Ser Glu Gln Gly Ser Ile Tyr Val His Thr
                85                  90                  95
Asp Tyr Lys Ile Gly His Tyr Val Lys Val Met Leu Asp Glu Ile Phe
            100                 105                 110
Gly Ile Gln Asn Phe Arg Asn Glu Ile Thr Arg Ile Lys Cys Asn Pro
        115                 120                 125
Lys Asn Phe Lys Arg Ile Gly Tyr Gly Asn Ile Lys Asp Met Ile Leu
    130                 135                 140
Phe Tyr Ser Lys Gly Lys Asn Pro Ile Phe Asn Glu Pro Lys Ile Pro
```

```
145                 150                 155                 160
Tyr Thr Pro Gln Asp Leu Glu Lys Arg Phe Pro Lys Ile Asp Lys Asp
                165                 170                 175
Lys Arg Arg Tyr Thr Thr Val Pro Ile His Ala Pro Gly Glu Val Glu
            180                 185                 190
Ser Gly Glu Cys Ser Lys Ala Phe Lys Gly Met Leu Pro Pro Lys Gly
        195                 200                 205
Arg His Trp Arg Thr Asp Ile Ala Thr Leu Glu Arg Trp Asp Lys Glu
    210                 215                 220
Gly Leu Ile Glu Tyr Ser Asn Asn Asn Asn Pro Arg Lys Lys Ile Tyr
225                 230                 235                 240
Ala Leu Glu Gln Val Gly Lys Arg Val Gln Asp Ile Trp Glu Phe Lys
                245                 250                 255
Asp Pro Gln Tyr Pro Ser Tyr Pro Thr Glu Lys Asn Ala Gln Leu Leu
            260                 265                 270
Asp Leu Ile Ile Lys Thr Ser Ser Asn Lys Asp Ser Ile Val Leu Asp
        275                 280                 285
Cys Phe Cys Gly Ser Gly Thr Thr Leu Lys Ser Ala Phe Leu Leu Gln
    290                 295                 300
Arg Lys Phe Ile Gly Ile Asp Asn Ser Asp Leu Ala Ile Gln Ala Cys
305                 310                 315                 320
Lys Asn Lys Leu Glu Thr Ile Thr Lys Asp Leu Phe Val Ser Gln Asn
                325                 330                 335
Phe Tyr Asp Phe Leu Val Phe
            340
```

(2) INFORMATION FOR SEQ ID NO:632:

This Sheet Has Been Replaced



(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:632

```
Met Gln Asn Leu Leu Ile Gln Ala Glu Asn Ala Ile Ala Leu Leu Phe
1               5                   10                  15
Leu Leu Asn Asp Lys Asn Leu Lys Gly Lys Ile Asp Leu Ile Tyr Ile
            20                  25                  30
Asp Pro Pro Phe Ala Thr Asn Asn His Phe Thr Ile Thr Asn Gly Arg
        35                  40                  45
Ala Thr Thr Ile Ser Asn Ser Lys Asn Gly Asp Ile Ala Tyr Ser Asp
    50                  55                  60
Lys Val Val Gly Met Asp Phe Met Glu Phe Leu Lys Gln Arg Leu Val
65                  70                  75                  80
Leu Leu Lys Glu Leu Leu Ser Glu Gln Gly Ser Ile Tyr Val His Thr
                85                  90                  95
Asp Tyr Lys Ile Gly His Tyr Val Lys Val Met Leu Asp Glu Ile Phe
            100                 105                 110
Gly Ile Gln Asn Phe Arg Asn Glu Ile Thr Arg Ile Lys Cys Asn Pro
        115                 120                 125
Lys Asn Phe Lys Arg Ile Gly Tyr Gly Asn Ile Lys Asp Met Ile Leu
    130                 135                 140
```

```
Phe Tyr Ser Lys Gly Lys Asn Pro Ile Phe Asn Glu Pro Lys Ile Pro
145                 150                 155                 160
Tyr Thr Pro Gln Asp Leu Glu Lys Arg Phe Pro Lys Ile Asp Lys Asp
                165                 170                 175
Lys Arg Arg Tyr Thr Thr Val Pro Ile His Ala Pro Gly Glu Val Glu
            180                 185                 190
Ser Gly Glu Cys Ser Lys Ala Phe Lys Gly Met Leu Pro Pro Lys Gly
        195                 200                 205
Arg His Trp Arg Thr Asp Ile Ala Thr Leu Glu Arg Trp Asp Lys Glu
    210                 215                 220
Gly Leu Ile Glu Tyr Ser Asn Asn Asn Asn Pro Arg Lys Lys Ile Tyr
225                 230                 235                 240
Ala Leu Glu Gln Val Gly Lys Arg Val Gln Asp Ile Trp Glu Phe Lys
                245                 250                 255
Asp Pro Gln Tyr Pro Ser Tyr Pro Thr Glu Lys Asn Ala Gln Leu Leu
            260                 265                 270
Asp Leu Ile Ile Lys Thr Ser Ser Asn Lys Asp Ser Ile Val Leu Asp
        275                 280                 285
Cys Phe Cys Gly Ser Gly Thr Thr Leu Lys Ser Ala Phe Leu Leu Gln
    290                 295                 300
Arg Lys Phe Ile Gly Ile Asp Asn Ser Asp Leu Ala Ile Gln Ala Cys
305                 310                 315                 320
Lys Asn Lys Leu Glu Thr Ile Thr Lys Asp Leu Phe Val Ser Gln Asn
                325                 330                 335
Phe Tyr Asp Phe Leu Val Phe
            340
```

(2) INFORMATION FOR SEQ ID NO:633:

(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:633

```
Met Ile Leu Lys Asn Leu Ile Leu Leu Phe Leu Ala Lys Arg Lys Leu
1               5                   10                  15
Ile Phe Ile Glu Ala Asn Phe Tyr Thr Ile Ser Gly Ser Lys Leu Asn
            20                  25                  30
Glu Val Ala Arg Ser Tyr Gln Asp Leu Ala Leu Lys Phe Glu Ala Phe
        35                  40                  45
Pro Asn Tyr Glu Phe Ile Trp Ile Thr Asp Gly Ile Gly Trp Leu Asp
    50                  55                  60
Ala Lys Ser Lys Leu Gln Glu Ala Tyr Lys Ser Val Glu Ile Tyr Asn
65                  70                  75                  80
Leu Ser Tyr Val Asn Asp Phe Ile Ser Lys Val Gln Lys
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(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:634

```
Met Thr Ser Val Val Ile Lys Pro His Ala Tyr Gly Glu Gln Val Gln
1               5                  10                  15
Glu Ile Glu Glu Glu Ser Asp Ser Asp Tyr Glu Lys Asn Asn Asp Gln
            20                  25                  30
Glu Ala Ile Asn Phe Gly Ile Ala Leu His Lys Gly Leu Glu Tyr Gln
        35                  40                  45
Tyr Ala Tyr Asn Ile Pro Lys Gln Ser Val Leu Glu Tyr Leu Asn Tyr
    50                  55                  60
His Tyr Gly Phe Tyr Gly Leu Asp Tyr Gln Ala Leu Glu Glu Ser Leu
65                  70                  75                  80
Glu Leu Phe Glu Asn Asp Ala Gly Ile Gln Ala Leu Phe Lys Asn His
                85                  90                  95
Ala Leu Lys Gly Glu Ala Ala Phe Leu Phe Gln Gly Val Val Ser Arg
            100                 105                 110
Ile Asp Val Leu Leu Trp Asp Arg Gly Gln Asn Leu Tyr Val Leu Asp
        115                 120                 125
Tyr Lys Ser Ser Gln Asn Tyr Gln Gln Ser His Lys Ala Gln Val Ser
    130                 135                 140
His Tyr Ala Glu Phe Leu Arg Thr Gln Unk Pro His Phe Lys Ile Gln
145                 150                 155                 160
Ala Gly Ile Ile Tyr Ala His Lys Arg Leu Leu Glu Lys Unk Trp Unk
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:634:

(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:634

```
Met Thr Ser Val Val Ile Lys Pro His Ala Tyr Gly Glu Gln Val Gln
1               5                  10                  15
Glu Ile Glu Glu Glu Ser Asp Ser Asp Tyr Glu Lys Asn Asn Asp Gln
            20                  25                  30
```

```
Glu Ala Ile Asn Phe Gly Ile Ala Leu His Lys Gly Leu Glu Tyr Gln
        35                  40                  45
Tyr Ala Tyr Asn Ile Pro Lys Gln Ser Val Leu Glu Tyr Leu Asn Tyr
    50                  55                  60
His Tyr Gly Phe Tyr Gly Leu Asp Tyr Gln Ala Leu Glu Glu Ser Leu
65                  70                  75                  80
Glu Leu Phe Glu Asn Asp Ala Gly Ile Gln Ala Leu Phe Lys Asn His
                85                  90                  95
Ala Leu Lys Gly Glu Ala Ala Phe Leu Phe Gln Gly Val Val Ser Arg
            100                 105                 110
Ile Asp Val Leu Leu Trp Asp Arg Gly Gln Asn Leu Tyr Val Leu Asp
        115                 120                 125
Tyr Lys Ser Ser Gln Asn Tyr Gln Gln Ser His Lys Ala Gln Val Ser
    130                 135                 140
His Tyr Ala Glu Phe Leu Arg Thr Gln Unk Pro His Phe Lys Ile Gln
145                 150                 155                 160
Ala Gly Ile Ile Tyr Ala His Lys Arg Leu Leu Glu Lys Unk Trp Unk
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:635:

(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:635

```
Met Glu Ser Gln Leu Met Lys Leu Ala Ile Glu Thr Tyr Lys Ile Thr
1               5                   10                  15
Leu Met Ile Ser Leu Pro Val Leu Leu Ala Gly Leu Val Val Gly Leu
            20                  25                  30
Leu Val Ser Ile Phe Gln Ala Thr Thr Gln Ile Asn Glu Met Thr Leu
        35                  40                  45
Ser Phe Val Pro Lys Ile Leu Ala Val Ile Gly Val Leu Ile Leu Thr
    50                  55                  60
Met Pro Trp Met Thr Asn Met Leu Leu Asp Tyr Thr Lys Thr Leu Ile
65                  70                  75                  80
Lys Leu Ile Pro Lys Ile Ile Gly
                85
```

(2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

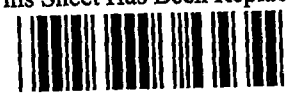
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636

```
Met Lys Phe Phe Thr Arg Ile Thr Asp Ser Tyr Lys Lys Val Val Val
1               5                  10                  15
Thr Leu Gly Leu Val Val Thr Thr Asn Pro Leu Met Ala Val Thr Ser
            20                  25                  30
Pro Ala Thr Gly Val Thr Glu Thr Lys Ser Leu Val Ile Gln Ile Ile
        35                  40                  45
Ser Val Leu Ala Ile Val Gly Gly Cys Ala Leu Gly Val Lys Gly Ile
    50                  55                  60
Ala Asp Ile Trp Lys Ile Ser Asp Asp Ile Lys Arg Gly Gln Ala Thr
65                  70                  75                  80
Val Phe Ala Tyr Ala Gln Pro Ile Ala Met Leu Ala Val Ala Gly Gly
                85                  90                  95
Ile Ile Tyr Leu Ser Thr Lys Phe Gly Phe Asn Ile Gly Glu Ser Gly
            100                 105                 110
Gly Ala Ser
        115
```

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637

```
Met Ser Glu Asp Leu Pro Phe Ala Ser Asp Ser Gln Phe Thr Tyr Asn
1               5                  10                  15
Gly Val Ser Ile Thr Arg Pro Thr Asn Glu Val Asn Asp Val Ile Ser
            20                  25                  30
Gly Val Asn Ile Thr Leu Glu Gln Thr Thr Glu Pro Asn Lys Pro Ala
        35                  40                  45
Ile Ile Ser Val Ser Arg Asp Asn Gln Ala Ile Ile Asp Ser Leu Lys
    50                  55                  60
Glu Phe Val Lys Ala Tyr Asn Glu Leu Ile Pro Lys Leu Asp Glu Asp
65                  70                  75                  80
Thr Arg Tyr Asp Ala Asp Thr Lys Ile Ala Gly Ile Phe Asn Gly Val
                85                  90                  95
Gly Asp Ile Arg Ala Ile Arg Ser Ser Leu Asn Asn Val Phe Ser Tyr
            100                 105                 110
Ser Val His Thr Asp Asn Gly Val Glu Ser Leu Met Lys Tyr Gly Leu
        115                 120                 125
Ser Leu Asp Asp Lys Gly Val Met Ser Leu Asp Glu Ala Lys Leu Ser
    130                 135                 140
```

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

(2) INFORMATION FOR SEQ ID NO:637:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637

```
Met Ser Glu Asp Leu Pro Phe Ala Ser Asp Ser Gln Phe Thr Tyr Asn
1               5                   10                  15
Gly Val Ser Ile Thr Arg Pro Thr Asn Glu Val Asn Asp Val Ile Ser
            20                  25                  30
Gly Val Asn Ile Thr Leu Glu Gln Thr Thr Glu Pro Asn Lys Pro Ala
        35                  40                  45
Ile Ile Ser Val Ser Arg Asp Asn Gln Ala Ile Ile Asp Ser Leu Lys
    50                  55                  60
Glu Phe Val Lys Ala Tyr Asn Glu Leu Ile Pro Lys Leu Asp Glu Asp
65                  70                  75                  80
Thr Arg Tyr Asp Ala Asp Thr Lys Ile Ala Gly Ile Phe Asn Gly Val
                85                  90                  95
Gly Asp Ile Arg Ala Ile Arg Ser Ser Leu Asn Asn Val Phe Ser Tyr
            100                 105                 110
Ser Val His Thr Asp Asn Gly Val Glu Ser Leu Met Lys Tyr Gly Leu
        115                 120                 125
Ser Leu Asp Asp Lys Gly Val Met Ser Leu Asp Glu Ala Lys Leu Ser
    130                 135                 140
Ser Ala Leu Asn Ser Asn Pro Lys Ala Thr Gln Asp Phe Phe Tyr Gly
145                 150                 155                 160
Ser Asp Ser Lys Asp Met Gly Gly Arg Glu Ile His Gln Glu Gly Ile
                165                 170                 175
Phe Ser Lys Phe Asn Gln Val Ile Ala Asn Leu Ile Asp Gly Gly Asn
            180                 185                 190
Ala Lys Leu Lys Ile Tyr Glu Asp Ser Leu Asp Arg Asp Ala Lys Ser
        195                 200                 205
Leu Thr Lys Asp Lys Glu Asn Ala Gln Glu Leu Leu Lys Thr Arg Tyr
```

```
    210                 215                 220
Asn Ile Met Ala Glu Arg Phe Ala Ala Tyr Asp Ser Gln Ile Ser Lys
225                 230                 235                 240
Ala Asn Gln Lys Phe Asn Ser Val Gln Met Met Ile Asp Gln Ala Ala
                245                 250                 255
Ala Lys Lys Asn
            260
```

(2) INFORMATION FOR SEQ ID NO:638:

This Sheet Has Been Replaced



(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:638

```
Met Lys Asn Pro Gln Ala Asn Val Leu Lys Leu Phe Leu Asn Gln Val
1               5                   10                  15
Ala Asp Gln Lys Tyr Ile Asp Met Asn Asp Glu Lys Asn Tyr Asp Pro
            20                  25                  30
Arg Glu Pro Glu Pro Pro Tyr Gly Thr Lys Gly Ala Leu Asp Glu Ile
        35                  40                  45
Ile Arg Thr Asp Ala Arg Ser Trp Ala Asn Thr Pro Asp Asp Glu Phe
    50                  55                  60
Gly Ser Ile Met Ser Ser Phe Lys Arg Phe Met Tyr Val Tyr Lys Asp
65                  70                  75                  80
Pro Lys Val Arg Glu Ala Thr Ser Lys Met Ser Phe Asp Tyr Glu Glu
                85                  90                  95
Leu Arg Thr Gly Asn Ile Ser Ile Tyr Ile Val Ile Ala Gln Ile Asp
            100                 105                 110
Ile Gly Thr Leu Ser Ser Leu Val Arg Ala Phe Leu Glu Ser Ile Ala
        115                 120                 125
Lys Asn Leu Met Val Lys Glu Ser Ser Lys Pro Glu Glu Arg Ile Phe
    130                 135                 140
Ile Ile Ala Asp Glu Phe Val Arg Phe Gly Lys Leu Pro Phe Leu Leu
145                 150                 155                 160
Glu Met Pro Ala Leu Cys Arg Ser Tyr Asn Val Val Pro Leu Phe Ile
                165                 170                 175
Thr Gln Asp Tyr Ala Met Ile Arg Asn Thr Ile Ala Met Met Ile
            180                 185                 190
```

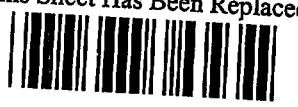
(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639

```
Met Ile Ser Glu Ile Ile Lys Phe Gln Leu Lys Gly Ile Lys Met Ile
1               5                  10                  15
Arg Leu Lys Gly Leu Asn Lys Thr Leu Lys Thr Ser Leu Leu Ala Gly
            20                  25                  30
Val Leu Leu Gly Ala Thr Ala Pro Leu Met Ala Lys Pro Leu Leu Ser
        35                  40                  45
Asp Glu Asp Leu Leu Lys Arg Val Lys Leu His Asn Ile Lys Glu Asp
    50                  55                  60
Thr Leu Thr Ser Cys Asn Ala Lys Val Asp Gly Ser Gln Tyr Leu Asn
65                  70                  75                  80
Ser Gly Trp Asn Leu Ser Lys Glu Phe Pro Gln Glu Tyr Arg Glu Lys
                85                  90                  95
Ile Phe Glu Cys Val Glu Glu Glu Lys His Lys Gln Ala Leu Asn Leu
            100                 105                 110
Ile Asn Lys Glu Asp Thr Glu Asp Lys Glu Glu Leu Ala Lys Lys Ile
        115                 120                 125
Lys Glu Ile Lys Glu Lys Ala Lys Val Leu Arg Gln Lys Phe Met Ala
    130                 135                 140
Phe Glu Met Lys Glu His Ser Lys Glu Phe Pro Asn Lys Lys Gln Leu
145                 150                 155                 160
Gln Thr Met Leu Glu Asn Ala Phe Asp Asn Gly Ala Glu Ser Phe Ile
                165                 170                 175
Asp Asp Trp His Glu Arg Phe Gly Gly Ile Ser Arg Glu Asn Thr Tyr
            180                 185                 190
Lys Ala Leu Gly Ile Lys Glu Tyr Ser Asp Glu Gly Lys Ile Leu Ala
        195                 200                 205
Phe Gly Glu Arg Ser Tyr Ile Arg Gln Tyr Lys Lys Asp Phe Glu Glu
    210                 215                 220
Ser Thr Tyr Asp Thr Arg Gln Thr Leu Ser Ala Met Ala Asn Met Ser
225                 230                 235                 240
Gly Glu Asn Asp Tyr Lys Ile Thr Trp Leu Lys Pro Lys Tyr Gln Leu
                245                 250                 255
His Ser Ser Asn Asn Ile Lys Pro Leu Met Ser Asn Thr Glu Leu Leu
            260                 265                 270
Asn Met Ile Glu Leu Thr Asn Ile Lys Lys Glu Tyr Val Met Gly Cys
        275                 280                 285
Asn Met Glu Ile Asp Gly Ser Lys Tyr Pro Ile His Lys Asp Trp Gly
    290                 295                 300
Phe Phe Gly Lys Ala Lys Val Pro Glu Thr Trp Arg Asn Lys Ile Trp
305                 310                 315                 320
Glu Cys Ile Lys Asn Lys Val Lys Ser Tyr Asp Asn Thr Thr Ala Glu
                325                 330                 335
Ile Gly Ile Val Trp Lys Lys Asn Thr Tyr Ser Ile Ser His His
            340                 345                 350
```

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640

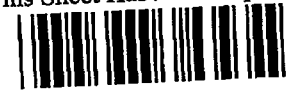
```
Met Ala Asp Ile Leu Ser Gln Glu Glu Ile Asp Ala Leu Leu Glu Val
1               5                  10                  15
Val Asp Glu Asn Val Asp Ile Gln Asn Val Gln Lys Lys Asp Ile Ile
            20                  25                  30
Pro Gln Arg Ser Val Thr Leu Tyr Asp Phe Lys Arg Pro Asn Arg Val
        35                  40                  45
Ser Lys Glu Gln Leu Arg Ser Phe Arg Ser Ile His Asp Lys Met Ala
    50                  55                  60
Arg Asn Leu Ser Ser Gln Val Ser Ser Ile Met Arg Ser Ile Val Glu
65                  70                  75                  80
Ile Gln Leu His Ser Val Asp Gln Met Thr Tyr Gly Glu Phe Leu Met
                85                  90                  95
Ser Leu Pro Ser Pro Thr Ser Phe Asn Val Phe Ser Met Lys Pro Met
            100                 105                 110
Gly Gly Thr Gly Val Leu Glu Ile Asn Pro Ser Ile Ala Phe Pro Met
        115                 120                 125
Ile Asp Arg Leu Leu Gly Gly Lys Gly Ser Ala Tyr Asp Gln Asn Arg
    130                 135                 140
Glu Phe Ser Asp Ile Glu Leu Asn Leu Leu Asp Thr Ile Leu Arg Gln
145                 150                 155                 160
Val Met Gln Ile Leu Lys Glu Val Trp Ser Pro Val Val Glu Met Tyr
                165                 170                 175
Pro Thr Ile Asp Ala Lys Glu Ser Ser Ala Asn Val Val Gln Ile Val
            180                 185                 190
Ala Gln Asn Glu Ile Ser Ile Met Val Val Leu Glu Ile Ile Ile Gly
        195                 200                 205
His Ser Arg Gly Met Met Asn Ile Cys Tyr Pro Val Ile Ser Ile Glu
    210                 215                 220
Ser Ile Leu Ser Lys Met Gly Ser Arg Asp Phe Met Leu Ser Glu Thr
225                 230                 235                 240
Asn Ser Lys Lys Ser Arg Asn Lys Glu Leu Gln Ala Leu Leu Ser Gly
                245                 250                 255
Val Ser Val Asp Met Met Val Phe Leu Gly Ala Val Glu Leu Ser Leu
            260                 265                 270
Lys Glu Met Leu Asp Leu Asp Val Gly Asp Thr Ile Arg Leu Asn Lys
        275                 280                 285
Val Ala Asn Asp Glu Val Ser Val Tyr Val His Lys Lys Lys Arg Tyr
    290                 295                 300
Leu Ala Ser Val Gly Phe Gln Gly Tyr Arg Lys Thr Ile Gln Ile Lys
305                 310                 315                 320
Glu Val Val Tyr Ser Glu Lys Glu Arg Thr Lys Glu Ile Leu Glu Met
                325                 330                 335
Leu Glu Glu Gln Arg Arg Arg Gln Ser Trp Ala Met Leu Trp Ser
            340                 345                 350
```

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641

```
Met Arg Ile Val Phe Met Gly Thr Pro Ser Phe Ala Glu Val Ile Leu
1               5                  10                  15
Arg Ala Leu Val Glu Asn Glu Asp Lys Lys Ile Glu Val Val Gly Leu
            20                  25                  30
Phe Thr Gln Arg Asp Lys Pro Phe Gly Arg Lys Lys Glu Leu Lys Ala
        35                  40                  45
Pro Glu Thr Lys Thr Tyr Ile Leu Glu Asn His Leu Asn Ile Pro Ile
    50                  55                  60
Phe Gln Pro Gln Ser Leu Lys Glu Pro Glu Val Gln Ile Leu Lys Gly
65                  70                  75                  80
Leu Lys Pro Asp Phe Ile Val Val Val Ala Tyr Gly Lys Ile Leu Pro
                85                  90                  95
Lys Glu Val Leu Thr Ile Ala Pro Cys Ile Asn Leu His Ala Ser Leu
            100                 105                 110
Leu Pro Lys Tyr Arg Gly Ala Ser Pro Ile His Glu Met Ile Leu Asn
        115                 120                 125
Asp Asp Arg Ile Tyr Gly Ile Ser Thr Met Leu Met Unk Phe Gly Ile
    130                 135                 140
Gly
145
```

(2) INFORMATION FOR SEQ ID NO:641:

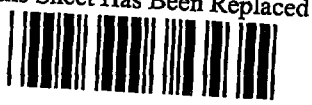
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641

```
Met Arg Ile Val Phe Met Gly Thr Pro Ser Phe Ala Glu Val Ile Leu
1               5                  10                  15
Arg Ala Leu Val Glu Asn Glu Asp Lys Lys Ile Glu Val Val Gly Leu
            20                  25                  30
Phe Thr Gln Arg Asp Lys Pro Phe Gly Arg Lys Lys Glu Leu Lys Ala
        35                  40                  45
Pro Glu Thr Lys Thr Tyr Ile Leu Glu Asn His Leu Asn Ile Pro Ile
    50                  55                  60
Phe Gln Pro Gln Ser Leu Lys Glu Pro Glu Val Gln Ile Leu Lys Gly
65                  70                  75                  80
Leu Lys Pro Asp Phe Ile Val Val Val Ala Tyr Gly Lys Ile Leu Pro
```

```
                85                  90                  95
Lys Glu Val Leu Thr Ile Ala Pro Cys Ile Asn Leu His Ala Ser Leu
            100                 105                 110
Leu Pro Lys Tyr Arg Gly Ala Ser Pro Ile His Glu Met Ile Leu Asn
        115                 120                 125
Asp Asp Arg Ile Tyr Gly Ile Ser Thr Met Leu Met Unk Phe Gly Ile
    130                 135                 140
Gly
145
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 190 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642

```
Met Pro Thr Met Leu Ala Val Gly Phe Trp Val Leu Val Phe Leu Ser
1               5                   10                  15
Thr Ser Asn Ala Val Asn Leu Thr Asp Gly Leu Asp Gly Leu Ala Ser
            20                  25                  30
Val Pro Ser Ile Phe Thr Leu Leu Ser Leu Ser Ile Phe Val Tyr Val
        35                  40                  45
Ala Gly Asn Ala Glu Phe Ser Lys Tyr Leu Leu Tyr Pro Lys Val Ile
    50                  55                  60
Asp Val Gly Glu Leu Phe Val Ile Ser Leu Ala Leu Val Gly Ser Leu
65                  70                  75                  80
Phe Gly Phe Leu Trp Tyr Asn Cys Asn Pro Ala Ser Val Phe Met Gly
                85                  90                  95
Asp Ser Gly Ser Leu Ala Ile Gly Gly Phe Ile Ala Tyr Asn Ala Ile
            100                 105                 110
Val Ser His Asn Glu Ile Leu Leu Val Leu Met Gly Ser Ile Phe Val
        115                 120                 125
Ile Glu Thr Leu Ser Val Ile Leu Gln Val Gly Ser Tyr Lys Thr Arg
    130                 135                 140
Lys Lys Arg Leu Phe Leu Met Ala Pro Ile His His His Phe Glu Gln
145                 150                 155                 160
Lys Gly Trp Ala Glu Asn Lys Val Ile Val Arg Phe Trp Ile Ile Ser
                165                 170                 175
Met Leu Ser Asn Leu Val Ala Leu Leu Ser Leu Lys Val Cys
            180                 185                 190
```

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...489

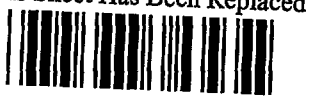
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643

```
Val Arg Phe Glu Asn Phe Ile Asn Arg Leu Ala Phe Tyr Met Ala Thr
1               5                  10                  15
Gly Ser Gly Lys Thr Ile Val Ile Ile Lys Leu Val Glu Leu Leu Ser
            20                  25                  30
Val Ala Met Gly Met Gly Leu Ile Pro Lys Lys Asn Ile Met Phe Phe
        35                  40                  45
Ser Ala Asn Glu His Leu Ile Lys Gln Phe Glu Lys Glu Ile Glu Lys
    50                  55                  60
Tyr Asn Arg Asn Lys Asp Tyr Ser Lys Gln Ile Asp Phe Lys Asn Leu
65                  70                  75                  80
Lys Ser Val Lys Asn Lys Asp Phe Tyr Arg Ala Pro Lys Asp Ser Leu
                85                  90                  95
Met Lys Glu Ile Ala Leu Phe Tyr Tyr Arg Ala Asp Leu Met Ser Asp
            100                 105                 110
Glu Glu Ser Lys Glu Asn Leu Leu Asn Tyr Lys Asp Cys Trp Asp Asn
        115                 120                 125
Gly Glu Asn Tyr Val Ile Leu Asp Glu Ala His Lys Gly Asn Lys Thr
    130                 135                 140
Glu Ser Lys Arg Gln Ala Ile Phe Ser Leu Leu Ser Leu Lys Gly Phe
145                 150                 155                 160
Leu Phe Asn Phe Ser Ala Thr Phe Thr Glu Glu Ser Asp Leu Ile Thr
                165                 170                 175
Ala Val Tyr Asn Leu Ser Val Gly Glu Trp Val Lys Leu Gly Tyr Gly
            180                 185                 190
Lys Glu Ser Val Leu Leu Lys Lys Asn Asn Leu Asn Ala Phe Lys Glu
        195                 200                 205
Leu Lys Asp Leu Asn Asp Arg Glu Lys Glu Ile Ala Leu Leu Lys Ala
    210                 215                 220
Leu Leu Leu Leu Gly Met Gln Lys Arg Tyr Lys Val Glu Gly Tyr Phe
225                 230                 235                 240
His Asp Pro Leu Met Leu Val Phe Thr His Ser Val Asn Met Glu Asn
                245                 250                 255
Ser Asp Ala Unk Ile Phe Phe Lys Thr Leu Ala Arg Val Ile Glu Asn
            260                 265                 270
Asp Asp Glu Ser Asp Phe Ser Lys Ala Lys Asp Asp Leu Leu Glu Glu
        275                 280                 285
Leu Lys Asn Pro Glu Phe Leu Phe Ser Asp Gly Lys Asp Lys Glu Lys
    290                 295                 300
Asp Tyr Lys Ile Glu Val Phe Lys Glu Ser Leu Lys Gly Met Asp Phe
305                 310                 315                 320
Lys Gly Leu Lys Glu Ala Val Phe Tyr Ala Ser Asn Gly His Ile Glu
                325                 330                 335
Val Ile Ile Asn Pro Lys Asn Asn Gln Glu Ile Ala Phe Lys Leu Asn
            340                 345                 350
Thr Ser Asp Lys Val Phe Cys Leu Ile Arg Ile Gly Asp Ile Thr Glu
        355                 360                 365
Trp Ile Arg Glu Lys Leu Lys Ser Val Lys Val Val Ser Lys Asn Leu
    370                 375                 380
Ser Phe Lys Glu Glu Ser Tyr Phe Ser Gln Ile Asp Lys Ser Ser Ile
385                 390                 395                 400
Asn Ile Leu Val Gly Ser Arg Ala Phe Asp Thr Gly Trp Asp Ser Thr
                405                 410                 415
Arg Pro Ser Val Ile Leu Phe Leu Asn Ile Gly Leu Asp Asp Asp Ala
```

```
            420                 425                 430
Lys Lys Leu Val Lys Gln Ser Phe Gly Arg Gly Val Arg Ile Glu Ser
        435                 440                 445
Val Lys Asn Gln Arg Gln Arg Leu Ala Tyr Leu Glu Ile Asp Glu Ala
    450                 455                 460
Ile Lys Glu Gln Ala Glu Thr Lys Arg Cys Asn Ala Gly Asn Ala Phe
465                 470                 475                 480
Cys Asp Thr Tyr Gln Pro Cys Lys Pro
                485
```

(2) INFORMATION FOR SEQ ID NO:644:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644

```
Met Arg Phe Tyr Phe Lys Phe Leu Trp Leu Leu Gly Ile Phe Leu Ile
1               5                  10                  15
Phe Tyr Phe Leu Asp Ile Lys Gly Ser Ser Ser Tyr Ile Ser Asp Arg
            20                  25                  30
Val Lys Ser Ala Leu Met Ser Ala Lys Asn Ser Leu Leu Asp Asn Val
        35                  40                  45
Gln Ala Tyr Phe Phe Gln Ala Gln Asn Ile Lys Glu Phe Gln Lys Glu
    50                  55                  60
Arg Leu Ile Leu Glu Ala Leu Lys Leu Glu Asn Ala Asp Leu Lys Glu
65                  70                  75                  80
Arg Leu Asn Ser Ile Tyr Pro Leu Glu Asn Pro Lys Met Thr Tyr Thr
                85                  90                  95
Pro Thr Phe Met Thr Ser Phe Ile Asn Leu Glu Asp Thr His Ser Val
            100                 105                 110
Ser Leu Asn Pro Ile Val Asn Leu Glu Glu Asn Lys Ile Tyr Gly Leu
        115                 120                 125
Val Ser His Asn Gln Ala Ile Gly Ile Ala Val Leu Glu Lys Gly Arg
    130                 135                 140
Leu Asn Gly Phe Leu Asn Ala His Lys Arg Cys Ala Tyr Ser Val Met
145                 150                 155                 160
Ile Gly Gln Asn Gln Val Leu Gly Phe Ile Gly Thr Asn Phe Lys Gln
                165                 170                 175
Glu Leu Val Val Asp Phe Ile Val Pro Ser Ala Glu Ile Asn Ile Gly
            180                 185                 190
Asp Gln Val Leu Thr Ser Gly Leu Asp Gly Ile Phe Gly Ala Gly Val
        195                 200                 205
Phe Val Gly Glu Val Ser Ser Val Glu Asp His Tyr Thr Tyr Lys Ser
    210                 215                 220
Ala Val Leu Lys Asn Ala Phe Leu Ser Glu Ala Lys Leu Leu Arg His
225                 230                 235                 240
Val Phe Leu Ser Gly Val Lys Asn
                245
```

(2) INFORMATION FOR SEQ ID NO:644:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644

```
Met Arg Phe Tyr Phe Lys Phe Leu Trp Leu Leu Gly Ile Phe Leu Ile
1               5                  10                  15
Phe Tyr Phe Leu Asp Ile Lys Gly Ser Ser Ser Tyr Ile Ser Asp Arg
            20                  25                  30
Val Lys Ser Ala Leu Met Ser Ala Lys Asn Ser Leu Leu Asp Asn Val
        35                  40                  45
Gln Ala Tyr Phe Phe Gln Ala Gln Asn Ile Lys Glu Phe Gln Lys Glu
    50                  55                  60
Arg Leu Ile Leu Glu Ala Leu Lys Leu Glu Asn Ala Asp Leu Lys Glu
65                  70                  75                  80
Arg Leu Asn Ser Ile Tyr Pro Leu Glu Asn Pro Lys Met Thr Tyr Thr
                85                  90                  95
Pro Thr Phe Met Thr Ser Phe Ile Asn Leu Glu Asp Thr His Ser Val
            100                 105                 110
Ser Leu Asn Pro Ile Val Asn Leu Glu Glu Asn Lys Ile Tyr Gly Leu
        115                 120                 125
Val Ser His Asn Gln Ala Ile Gly Ile Ala Val Leu Glu Lys Gly Arg
    130                 135                 140
Leu Asn Gly Phe Leu Asn Ala His Lys Arg Cys Ala Tyr Ser Val Met
145                 150                 155                 160
Ile Gly Gln Asn Gln Val Leu Gly Phe Ile Gly Thr Asn Phe Lys Gln
                165                 170                 175
Glu Leu Val Val Asp Phe Ile Val Pro Ser Ala Glu Ile Asn Ile Gly
            180                 185                 190
Asp Gln Val Leu Thr Ser Gly Leu Asp Gly Ile Phe Gly Ala Gly Val
        195                 200                 205
Phe Val Gly Glu Val Ser Ser Val Glu Asp His Tyr Thr Tyr Lys Ser
    210                 215                 220
Ala Val Leu Lys Asn Ala Phe Leu Ser Glu Ala Lys Leu Leu Arg His
225                 230                 235                 240
Val Phe Leu Ser Gly Val Lys Asn
                245
```

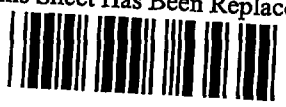
(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645

```
Leu Ala Leu Arg Leu Pro Phe Leu Ile Ala His Val Ile Asn Met Phe
1               5                  10                  15
Leu Phe Tyr Leu Ile Gly Arg Lys Ile Leu Lys Lys Pro Lys Asp Ala
            20                  25                  30
Leu Tyr Val Val Leu Thr Tyr Ala Leu Leu Pro Gly Val Asn Leu Phe
        35                  40                  45
Ala Ile Leu Leu Ala Lys Ser Val Leu Val Leu Ser Leu Gly Leu Leu
    50                  55                  60
Ile Ser Tyr Leu Tyr Ile Lys Thr Gln Lys Ile Pro Tyr Leu Thr Leu
65                  70                  75                  80
Ser Ala Cys Ala Phe Leu Asp Gly Ala Phe Ile Pro Leu Leu Leu Gly
                85                  90                  95
Val Phe Ala Tyr Ala Leu Arg Lys Thr Ala Ile Leu Arg Ala Arg Ser
            100                 105                 110
Leu Leu Trp Trp Phe Unk Leu
        115
```

(2) INFORMATION FOR SEQ ID NO:645:

(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:645

```
Leu Ala Leu Arg Leu Pro Phe Leu Ile Ala His Val Ile Asn Met Phe
1               5                  10                  15
Leu Phe Tyr Leu Ile Gly Arg Lys Ile Leu Lys Lys Pro Lys Asp Ala
            20                  25                  30
Leu Tyr Val Val Leu Thr Tyr Ala Leu Leu Pro Gly Val Asn Leu Phe
        35                  40                  45
Ala Ile Leu Leu Ala Lys Ser Val Leu Val Leu Ser Leu Gly Leu Leu
    50                  55                  60
Ile Ser Tyr Leu Tyr Ile Lys Thr Gln Lys Ile Pro Tyr Leu Thr Leu
65                  70                  75                  80
Ser Ala Cys Ala Phe Leu Asp Gly Ala Phe Ile Pro Leu Leu Leu Gly
                85                  90                  95
Val Phe Ala Tyr Ala Leu Arg Lys Thr Ala Ile Leu Arg Ala Arg Ser
            100                 105                 110
Leu Leu Trp Trp Phe Unk Leu
        115
```

(2) INFORMATION FOR SEQ ID NO:646:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646

```
Val Asn Leu Met Asp Tyr Phe Ser Lys Ser Leu Phe Leu Asn Ser Leu
1               5                  10                  15
Asn Thr Gln Arg Leu Ile Val Ser Asn Lys Leu Ala Ile Asp Val Gln
            20                  25                  30
Tyr Gly Met Leu Gln Ser Val Arg Lys Asn Tyr Pro Asp Val Val Asp
        35                  40                  45
Gly Gly Val Arg Glu Gly Pro Phe Trp Val Leu Ala Gly Ala Leu Met
    50                  55                  60
Pro Ser Ile Leu Ile Glu Ile Gly Tyr Asn Ser His Ala Ile Glu Ser
65                  70                  75                  80
Lys Arg Ile Gln Ser Lys Pro Tyr Gln Lys Ile Leu Ala Lys Gly Ile
                85                  90                  95
Ala Asp Gly Ile Asp Ser Phe Phe Ser Lys Asn Asp
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:646:

(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:646

```
Val Asn Leu Met Asp Tyr Phe Ser Lys Ser Leu Phe Leu Asn Ser Leu
1               5                  10                  15
Asn Thr Gln Arg Leu Ile Val Ser Asn Lys Leu Ala Ile Asp Val Gln
            20                  25                  30
Tyr Gly Met Leu Gln Ser Val Arg Lys Asn Tyr Pro Asp Val Val Asp
        35                  40                  45
Gly Gly Val Arg Glu Gly Pro Phe Trp Val Leu Ala Gly Ala Leu Met
    50                  55                  60
Pro Ser Ile Leu Ile Glu Ile Gly Tyr Asn Ser His Ala Ile Glu Ser
```

65 70 75 80
Lys Arg Ile Gln Ser Lys Pro Tyr Gln Lys Ile Leu Ala Lys Gly Ile
85 90 95
Ala Asp Gly Ile Asp Ser Phe Phe Ser Lys Asn Asp
100 105

(2) INFORMATION FOR SEQ ID NO:647:

This Sheet Has Been Replaced



(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:647

Val Phe Lys Asn Ser Leu Phe Gly Ile Ser Ile Ser Met Leu Ile Thr
1 5 10 15
Trp Val Leu Thr Ala Cys Ile Leu Ile Phe Ile Leu Phe Val Pro Asn
20 25 30
Phe Thr Leu Thr His Pro Asn Phe His Phe Thr Pro Phe Glu Lys Thr
35 40 45
Tyr Phe Gln Ile Leu Gly Leu Val Gly Ile Val Ser Ser Ile Ile Phe
50 55 60
Thr Gly Phe Leu Ala Asp Lys Ile Lys Pro His Lys Val Cys Met Ala
65 70 75 80
Phe Ser Thr Thr Phe Gly Phe Phe Gly Phe Leu Phe Phe Lys Glu Phe
85 90 95
Tyr Ser Asn Ala Pro Ser Leu Val Asn Thr Ile Ile Leu Tyr Phe Leu
100 105 110
Ala Cys Phe Cys Ala Gly Ile Met Asn Phe Cys Pro Ile Phe Met Ser
115 120 125
Asp Val Phe Ser Ala Lys Ile Arg Phe Ser Gly Ile Ser Phe Ala Tyr
130 135 140
Asn Ile Ala Tyr Ala Ile Thr Ala Gly Phe Thr Pro Gln Leu Ser Ser
145 150 155 160
Trp Leu Asn Ala Lys Ala Ile Ala Val Pro Glu Ser Leu Gln Ser Tyr
165 170 175
Gly Leu Ser Phe Tyr Ile Leu Ile Val Ser Leu Ile Ala Phe Ile Thr
180 185 190
Ser Leu Leu Met Ala Pro Ile Tyr His Lys Ser Asn Thr Gln His Glu
195 200 205
Val Ser Pro Thr Ala
210

(2) INFORMATION FOR SEQ ID NO:648:

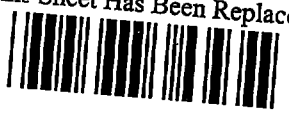
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648

```
Leu Ala Ser Arg Tyr Ser Val Ala Val Gly Asn Leu Phe Ser Glu His
1               5                  10                  15
Leu Tyr Asp Leu Arg Asn Glu Thr Met Thr Asn Leu Ile Gly Phe Leu
            20                  25                  30
Leu Val Leu Ala Ser Ile Trp Val Phe Phe Leu Ala Leu Gly Val Leu
        35                  40                  45
Leu Gly Lys Met Leu Val Phe Ser Gly Leu Gly Ile Ile Asp Lys Ala
    50                  55                  60
Leu Gly Phe Ile Phe Ser Cys Leu Lys Thr Phe Leu Val Leu Ser Phe
65                  70                  75                  80
Ile Leu Tyr Ala Leu Ser Lys Met Asp Leu Met Lys Asp Ala Asn Ala
                85                  90                  95
Tyr Leu Gln Glu Lys Unk Unk Ile Phe Pro Thr Unk Lys Unk Unk Unk
            100                 105                 110
Ser Lys Ile Met Arg Leu Asp Gly Val Lys His Val Glu Lys Asn Leu
        115                 120                 125
Lys Asp Asn Leu Glu Glu Met Ser Asp Glu Val Lys Asn Lys Gly Ser
    130                 135                 140
Ile Asp Asn Ala Lys Glu Ser Phe Asn Lys Gly Tyr Gly
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:648:

(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:648

```
Leu Ala Ser Arg Tyr Ser Val Ala Val Gly Asn Leu Phe Ser Glu His
1               5                  10                  15
Leu Tyr Asp Leu Arg Asn Glu Thr Met Thr Asn Leu Ile Gly Phe Leu
            20                  25                  30
Leu Val Leu Ala Ser Ile Trp Val Phe Phe Leu Ala Leu Gly Val Leu
        35                  40                  45
Leu Gly Lys Met Leu Val Phe Ser Gly Leu Gly Ile Ile Asp Lys Ala
    50                  55                  60
Leu Gly Phe Ile Phe Ser Cys Leu Lys Thr Phe Leu Val Leu Ser Phe
65                  70                  75                  80
Ile Leu Tyr Ala Leu Ser Lys Met Asp Leu Met Lys Asp Ala Asn Ala
```

```
                85                  90                  95
Tyr Leu Gln Glu Lys Unk Unk Ile Phe Pro Thr Unk Lys Unk Unk Unk
            100                 105                 110
Ser Lys Ile Met Arg Leu Asp Gly Val Lys His Val Glu Lys Asn Leu
        115                 120                 125
Lys Asp Asn Leu Glu Glu Met Ser Asp Glu Val Lys Asn Lys Gly Ser
    130                 135                 140
Ile Asp Asn Ala Lys Glu Ser Phe Asn Lys Gly Tyr Gly
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:649

```
Met Lys Ser Asp Lys Pro Phe Leu Glu Arg Tyr Phe Tyr Asp Pro Thr
1               5                  10                  15
Leu Leu Gln Lys Gly Leu Ile Phe Ala Leu Tyr Pro Phe Ser Leu Ile
            20                  25                  30
Tyr Gln Cys Ile Ala Thr Ile Lys Arg Lys Thr Ala Lys Lys His Asp
        35                  40                  45
Phe Lys Ile Pro Ile Ile Ser Ile Gly Asn Leu Ile Ala Gly Gly Ser
    50                  55                  60
Gly Lys Thr Pro Phe Ile Leu Glu Ile Ala Pro Arg Tyr Gln Glu Val
65                  70                  75                  80
Ala Val Val Ser Arg Gly Tyr Gln Arg Asp Ser Lys Gly Leu Val Val
                85                  90                  95
Val Ser Val Lys Gly Asn Ile Leu Val Pro Gln Lys Thr Ala Gly Asp
            100                 105                 110
Glu Ala Tyr Leu Leu Ala Leu Asn Leu Lys Gln Ala Ser Val Ile Val
        115                 120                 125
Ser Glu Lys Arg Glu Leu Gly Val Leu Lys Ala Leu Glu Leu Gly Ser
    130                 135                 140
Lys Ile Val Phe Leu Asp Asp Gly Phe Arg Phe Asn Phe Asn Gln Phe
145                 150                 155                 160
Asn Ala Leu Leu Lys Pro Lys Val Pro Pro Tyr Tyr Pro Phe Cys Leu
                165                 170                 175
Pro Ser Gly Leu Tyr Arg Glu Asn Ile Lys Ser Tyr Lys Glu Ala His
            180                 185                 190
Leu Val Ile Thr Glu Asp Lys Asp Tyr Gln Arg Ile Thr Ser Ile Thr
        195                 200                 205
Asn Pro Thr Lys Arg Met Leu Leu Val Thr Ala Ile Ala Asn Pro Ser
    210                 215                 220
Arg Leu Asp Ala Phe Leu Pro Lys Glu Val Val Lys Lys Leu Tyr Phe
225                 230                 235                 240
Arg Asp His Ala Pro Phe Asp Leu Lys Leu Leu Glu Lys Glu Phe Tyr
                245                 250                 255
Gln Asn Asn Ala Thr Ser Leu Leu Val Thr Ser Lys Asp Leu Val Lys
            260                 265                 270
```

```
Leu Gln Asp Cys Lys Leu Pro Leu Ser Val Leu Asp Leu Lys Leu Glu
        275                 280                 285
Ile Cys Pro Lys Val Leu Glu Glu Ile Asp Arg Tyr Ile Leu Ser Tyr
    290                 295                 300
Pro Cys Asn Ile Lys Glu His Leu
305                 310
```

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...56

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650

```
Met Ser Leu Gly Ala Val Ile Arg Leu Ile Phe Cys Tyr Lys Leu Glu
1               5                   10                  15
Gly Val Ile Leu Asp Leu Lys Arg Ile Asn Phe Lys Ser Tyr Tyr Pro
            20                  25                  30
Asn Asn Lys Asn Ala Leu Phe Ile Asn Asn Lys Lys Asn Pro Leu Ser
        35                  40                  45
Ser Thr Ser Lys Phe Ile Leu Leu
    50                  55
```

(2) INFORMATION FOR SEQ ID NO:651:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651

```
Met Leu Glu Thr Thr Ile Asp Phe Ser Arg Tyr Ser Ser Val Lys Ile
1               5                   10                  15
Gly Ala Pro Leu Lys Val Ser Val Leu Glu Asn Asp Asn Glu Ile Ser
            20                  25                  30
Gln Glu His Gln Ile Ile Gly Leu Ala Asn Asn Leu Leu Ile Ala Pro
        35                  40                  45
Asp Val Lys Asn Leu Ala Leu Leu Gly Lys Asn Tyr Asp Tyr Ile Cys
```

```
    50                  55                  60
Asp Lys Gly Glu Trp Val Glu Val Gly Gly Ala Ala Asn Ala Ser Lys
65                  70                  75                  80
Ile Phe Asn Tyr Phe Arg Ala Asn Asp Leu Glu Gly Leu Glu Phe Leu
                85                  90                  95
Gly Gln Leu Pro Gly Thr Leu Gly Ala Leu Val Lys Met Asn Ala Gly
            100                 105                 110
Met Lys Glu Phe Glu Ile Lys Asn Val Leu Glu Ser Ala Cys Val Asn
        115                 120                 125
Gly Glu Trp Leu Glu Lys Glu Ala Leu Gly Leu Asp Tyr Arg Ser Ser
    130                 135                 140
Gly Phe Asn Gly Val Val Leu Arg Ala Arg Phe Lys Lys Thr His Gly
145                 150                 155                 160
Phe Arg Glu Gly Val Leu Lys Ala Cys Lys Ser Met Arg Lys Ser His
                165                 170                 175
Pro Lys Leu Pro Asn Phe Gly Ser Cys Phe Lys Asn Pro Pro Asn Asp
            180                 185                 190
Tyr Ala Gly Arg Leu Leu Glu
        195
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:652:

(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:652

```
Leu Ser Lys Gln Ser Ala Asp Ile Val Ile Thr Asn Asp Ser Leu Ser
1               5                   10                  15
Ser Leu Val Lys Val Leu Ala Ile Ala Lys Lys Thr Lys Ser Ile Thr
            20                  25                  30
Trp Gln Asn Ile Leu Phe Ala Leu Gly Ile Lys Ala Val Phe Ile Val
        35                  40                  45
Leu Gly Leu Met Gly Val Ala Ser Leu Trp Glu Ala Val Phe Gly Asp
    50                  55                  60
Val Gly Val Thr Leu Leu Ala Leu Ala Asn Ser Unk Arg Thr Met Arg
65                  70                  75                  80
Ala
```

(2) INFORMATION FOR SEQ ID NO:652:

(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:652

```
Leu Ser Lys Gln Ser Ala Asp Ile Val Ile Thr Asn Asp Ser Leu Ser
1               5                  10                  15
Ser Leu Val Lys Val Leu Ala Ile Ala Lys Lys Thr Lys Ser Ile Thr
            20                  25                  30
Trp Gln Asn Ile Leu Phe Ala Leu Gly Ile Lys Ala Val Phe Ile Val
        35                  40                  45
Leu Gly Leu Met Gly Val Ala Ser Leu Trp Glu Ala Val Phe Gly Asp
    50                  55                  60
Val Gly Val Thr Leu Leu Ala Leu Ala Asn Ser Unk Arg Thr Met Arg
65                  70                  75                  80
Ala
```

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653

```
Met Leu Lys Asn Gly Asp Lys Ile Pro Asp Ala Ile Leu Val Asp Ile
1               5                  10                  15
Glu Met Pro Lys Met Asp Gly Tyr Thr Phe Ala Ser Glu Val Arg Lys
            20                  25                  30
Tyr Asn Lys Phe Lys Asn Leu Pro Leu Ile Ala Val Thr Ser Arg Val
        35                  40                  45
Thr Lys Thr Asp Arg Met Arg Gly Val Glu Ser Gly Met Thr Glu Tyr
    50                  55                  60
Ile Thr Lys Pro Tyr Ser Gly Glu Tyr Leu Thr Thr Val Val Lys Arg
65                  70                  75                  80
Ser Ile Lys Leu Glu Gly Asp Gln Ser
                85
```

(2) INFORMATION FOR SEQ ID NO:654:

(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:654

```
Val Phe Glu Pro Val Ile Ala Tyr Lys Leu Phe His Ser Phe Val Ile
1               5                  10                  15
Leu Gly Cys Ala Ile Glu Thr Leu Thr Thr Lys Cys Val Glu Gly Ile
            20                  25                  30
Thr Ala Asn Glu Lys Ile Cys His Asp Tyr Val Phe Asn Ser Ile Gly
        35                  40                  45
Ile Val Thr Ala Leu Asn Pro His Ile Gly Tyr Glu Lys Ser Ala Met
    50                  55                  60
Ile Ala Lys Glu Ala Leu Lys Ser Asp Arg Ser Ile Tyr Asp Ile Ala
65                  70                  75                  80
Leu Glu Lys Lys Ile Leu Thr Lys Glu Gln Leu Asp Asp Ile Phe Lys
                85                  90                  95
Pro Glu Asn Met Leu Arg Thr His Ala Phe Lys Lys His Lys Asp
            100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655

```
Met Leu Arg Leu Leu Ala Gln Lys Ser Ala Ile Lys Leu Ile Leu Ile
1               5                  10                  15
Pro Pro Ser Ala Asn Ala Leu Gly Ile Ala Ser Ile Cys Glu Leu Ser
            20                  25                  30
Glu Glu Val Phe Glu His Glu Lys Ile Val Gly Ile Arg Ala Gln Gly
        35                  40                  45
Asp Phe Thr Ile Asn Ser Asp Asp Arg Gly Phe Trp Glu Arg Arg Cys
    50                  55                  60
Gln
65
```

(2) INFORMATION FOR SEQ ID NO:656:

(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:656

```
Met Lys Lys Leu Leu Leu Leu Leu Glu His Lys Ile Val Lys Ile Gly
1               5                  10                  15
Leu Ile Ile Val Ile Val Leu Val Gly Phe Phe Leu Phe Tyr Glu Gln
            20                  25                  30
Glu Ile Lys Glu Lys Ala Val Asn Val Ser Gln Gly Lys Phe Pro Thr
        35                  40                  45
Ser Ser Tyr Leu Phe Gln Ala Tyr Glu Gly Ile Lys Asn Lys Ile Asp
    50                  55                  60
Thr Ile Asn Gln Val Lys Pro Asn Asp Glu Thr Lys Ser Val Asn Glu
65                  70                  75                  80
Asn Ile Glu Lys Thr Gln Lys Asp Leu Asp Asp Phe Asn Ala Leu Val
                85                  90                  95
Gln Lys Leu Pro Asn Leu Pro Lys Asp Phe Asn Lys Thr Leu Ile Lys
            100                 105                 110
Pro Gln Ser Pro Phe Phe Asn Tyr Asn Thr Ala Asn Glu Asp Glu Lys
        115                 120                 125
Asn Arg Leu Val Ile Leu Ala Ser Arg Ile Ser Ser Gln Lys Glu Thr
    130                 135                 140
Gln Pro Pro Ile Ser Ile Lys Asn Ser Val Ser His Ile Lys Ser Lys
145                 150                 155                 160
Glu Lys Arg Glu Leu Glu Lys Glu Trp Ala Lys Pro Ser Val Ser Phe
                165                 170                 175
Gly Ser Phe Ser Leu Leu Ser Ser Ser Ser Ser Phe Ser Ser Phe Glu
            180                 185                 190
Val Ser Phe Leu Ser Arg Gly Ile Gly Leu Asp Cys Glu Lys Leu Lys
        195                 200                 205
Ser Phe Leu Lys Ala Phe Ser Ser Ser Leu Phe Ser Leu Leu Ser Ser
    210                 215                 220
Leu Phe Cys His Pro Leu Ser Leu Phe Cys Ser Leu Ile Gly Leu Ile
225                 230                 235                 240
Phe Cys Phe Ser Lys Phe Ser Arg Glu Leu Val Asn Ala Ser Asn Asn
                245                 250                 255
Ser Leu Glu Phe Ser Ser Leu Ser Arg Leu Gly Ser
            260                 265
```

(2) INFORMATION FOR SEQ ID NO:657:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657

```
Met Gly Ala Ile Ala Ser Cys Tyr Ala His Gln Ile Ile Leu Thr Ser
1               5                  10                  15
Asp Asn Pro Arg Ser Glu Asn Glu Glu Asp Ile Ile Lys Asp Ile Leu
            20                  25                  30
Lys Gly Ile Asn Asn Ser Ser Lys Val Ile Val Glu Lys Asp Arg Lys
        35                  40                  45
Lys Ala Ile Leu Asn Ala Leu Glu Asn Leu Lys Asp Asp Glu Val Leu
    50                  55                  60
Leu Ile Leu Gly Lys Gly Asp Glu Asn Ile Gln Ile Phe Lys Asp Lys
65                  70                  75                  80
Thr Ile Phe Phe Ser Asp Gln Glu Val Val Lys Asp Tyr Tyr Leu Asn
                85                  90                  95
Leu Lys Gln Gly
            100
```

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:658

```
Val Met Asp Lys Leu Thr Lys Ser Leu Gln Thr Gln Lys Asn Phe Ala
1               5                  10                  15
Tyr Leu Gly Lys Ile Lys Pro Gln Gln Leu Ala Asp Phe Ile Ile Asn
            20                  25                  30
Glu His Pro Gln Thr Ile Ala Leu Ile Leu Ala His Met Glu Unk Pro
        35                  40                  45
Asn Ala Ala Glu Thr Leu Ser Tyr Phe Pro Asp Glu Met Lys Ala Glu
    50                  55                  60
Ile Ser Ile Arg Met Ala Asn Phe Arg Arg Asn Ile Ala Pro Ser Gly
65                  70                  75                  80
```

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659

```
Met Arg Tyr Phe Arg Ser Ala Phe Leu Leu Phe Phe Met Thr Leu Phe
1               5                  10                  15
Phe Val Ser Cys Ser Lys His Pro Phe Ser Lys Gln Thr Pro Lys Thr
            20                  25                  30
Lys Glu Arg Ile Arg Gln Glu Glu Ala Asn Lys Lys Arg Glu Glu Thr
        35                  40                  45
Leu Asn Ala Leu Arg Gln Phe Arg Leu Ile Tyr Ile Asn Thr Pro Val
    50                  55                  60
Phe Arg Phe Tyr Asp Tyr Gly Thr Ile Lys Thr Asp Lys Asp His Asn
65                  70                  75                  80
Thr Glu Val Thr Leu Tyr Lys Leu Ser Gln Lys Val Gly Asp Ile Tyr
                85                  90                  95
Met Thr Lys Arg Ser Ile Cys Phe Ser Gln Lys Cys Ser Ala Lys Trp
            100                 105                 110
Ile Ala Ala Arg Asp Leu Phe Gly Lys Val Ser Tyr Gly Asp Leu Phe
        115                 120                 125
Asp Asp Ile Val Leu Gly Arg Asp Ile Phe Lys Gly Leu Gly Lys Arg
    130                 135                 140
His Leu Thr Pro Glu Tyr Val Ile Gln Arg Phe Gln Lys Ser Gly Glu
145                 150                 155                 160
Ile Ile Leu Tyr Glu Arg Lys Asn Gly Leu Ile Ser Phe Gln Asn Leu
                165                 170                 175
Thr Gln Lys Ile Ala Ile Arg Ile Glu Pro Tyr Glu Pro Ser Leu Gln
            180                 185                 190
Asp Leu Glu Asp Asn Glu Asn Ala Asp Ser Glu Leu Gln
        195                 200                 205
```

(2) INFORMATION FOR SEQ ID NO:660:

This Sheet Has Been Replaced



(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:660

```
Met Arg Ile Glu Glu Asn Gly Val Ile Ser Leu Ala Phe Ser Asn Gly
1               5                  10                  15
Val Val Glu Pro Val Ala Arg Ile Gly Ile Unk Ala Phe Thr Asn Asp
            20                  25                  30
Gln Gly Leu Arg Lys Ile Gly Gly Asn Leu Tyr Glu Met Gln Glu Gly
        35                  40                  45
Thr Ile Asn Gly Glu Asn Arg Pro Leu Unk Gly Asn Pro Ile Leu Gly
```

```
    50                  55                  60
Trp Asp Glu Glu Gly Lys Leu Lys Phe Gly Lys Ile Arg His Lys Tyr
65                  70                  75                  80
Leu Glu Thr Ser Asn Val Asn Ala Gly Asn Ala Leu Thr Asn Leu Ile
                85                  90                  95
Leu Met Gln Arg Gly Tyr Ser Met Asn Ala Arg Ala Phe Gly Ala Gly
            100                 105                 110
Asp Asp Met Ile Lys Glu Ala Ile Ser Leu Lys Lys
        115                 120
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:661:

(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:661

```
Val Glu Ala Arg Tyr Tyr Tyr Gly Asp Thr Ser Tyr Phe Tyr Leu His
1               5                   10                  15
Val Gly Val Leu Gln Glu Phe Ala His Phe Gly Ser Asn Asp Val Ala
            20                  25                  30
Ser Leu Asn Thr Phe Lys Ile Asn Ala Ala Arg Ser Pro Leu Ser Thr
        35                  40                  45
Tyr Ala Arg Ala Met Met Gly Gly Glu Leu Gln Leu Ala Lys Glu Val
    50                  55                  60
Phe Leu Asn Leu Gly Val Val Tyr Leu His Asn Leu Ile Ser Asn Ala
65                  70                  75                  80
Ser His Phe Ala Ser Asn Leu Gly Met Arg Tyr Ser Phe
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:662:

(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:662

```
Met Lys Asn Leu Arg His Phe Arg Lys Leu Ile Ala Phe Leu Gly Phe
1               5                  10                  15
Ser Pro Leu Leu Leu Gln Ala Asp Met Thr Thr Phe Phe Asn Ser Ile
            20                  25                  30
Glu Gln Gln Leu Thr Ser Pro Thr Ala Lys Gly Ile Leu Met Val Ile
        35                  40                  45
Phe Leu Gly Leu Ala Ile Phe Ile Trp Lys Asn Leu Asp Arg Trp Lys
    50                  55                  60
Glu Ile Leu Met Thr Val Leu Ala Leu Lys Unk Val Pro Met Gln Unk
65                  70                  75                  80
```

(2) INFORMATION FOR SEQ ID NO:662:

(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:662

```
Met Lys Asn Leu Arg His Phe Arg Lys Leu Ile Ala Phe Leu Gly Phe
1               5                  10                  15
Ser Pro Leu Leu Leu Gln Ala Asp Met Thr Thr Phe Phe Asn Ser Ile
            20                  25                  30
Glu Gln Gln Leu Thr Ser Pro Thr Ala Lys Gly Ile Leu Met Val Ile
        35                  40                  45
Phe Leu Gly Leu Ala Ile Phe Ile Trp Lys Asn Leu Asp Arg Trp Lys
    50                  55                  60
Glu Ile Leu Met Thr Val Leu Ala Leu Lys Unk Val Pro Met Gln Unk
65                  70                  75                  80
```

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 214 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

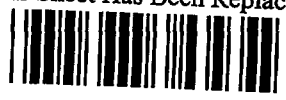
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663

```
Val Glu Glu Leu Ala Lys Leu Ile Asn Asn Asn Asn Asn Asn Lys Lys
```

This Sheet Has Been Replaced



```
1               5                   10                  15
Leu Arg Gly Phe Phe Leu Lys Val Leu Leu Ser Leu Val Val Phe Ser
            20                  25                  30
Ser Tyr Gly Ser Ala Asn Asp Asp Lys Glu Ala Lys Lys Glu Ala Leu
        35                  40                  45
Glu Lys Glu Lys Asn Thr Pro Asn Gly Leu Val Tyr Thr Asn Leu Asp
    50                  55                  60
Phe Asp Ser Phe Lys Ala Thr Ile Lys Asn Leu Lys Asp Lys Lys Val
65                  70                  75                  80
Thr Phe Lys Glu Val Asn Pro Asp Ile Ile Lys Asp Glu Val Phe Asp
                85                  90                  95
Phe Val Ile Val Asn Arg Val Leu Lys Lys Ile Lys Asp Leu Lys His
            100                 105                 110
Tyr Asp Pro Val Ile Glu Lys Ile Phe Asp Glu Lys Gly Lys Glu Met
        115                 120                 125
Gly Leu Asn Val Glu Leu Gln Ile Asn Pro Glu Val Lys Asp Phe Phe
    130                 135                 140
Thr Phe Lys Ser Ile Ser Thr Thr Asn Lys Gln Arg Cys Phe Leu Ser
145                 150                 155                 160
Leu His Gly Glu Thr Arg Glu Ile Leu Cys Asp Asp Lys Leu Tyr Asn
                165                 170                 175
Val Leu Leu Ala Val Phe Asn Ser Tyr Asp Pro Asn Asp Leu Leu Lys
            180                 185                 190
His Ile Ser Thr Ile Glu Ser Leu Lys Lys Ile Phe Tyr Thr Ile Thr
        195                 200                 205
Cys Glu Ala Val Tyr Leu
    210
```

(2) INFORMATION FOR SEQ ID NO:664:

This Sheet Has Been Replaced



(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:664

```
Val Gly Gly Ile Val Ala Asn Met Asn Asp Leu Ser Thr Tyr Met Val
1               5                   10                  15
Glu Asn Leu Leu Met Gly Leu Tyr Leu Phe Ser Ser Ala Leu Asp Leu
            20                  25                  30
Gly Val Lys Lys Ala Ile Asn Leu Ala Ser Ser Cys Ala Tyr Pro Lys
        35                  40                  45
Tyr Ala Pro Asn Pro Leu Lys Glu Ser Asp Leu Leu Asn Gly Ser Leu
    50                  55                  60
Glu Pro Thr Asn Glu Gly Tyr Ala Leu Pro Asn Ser Leu Unk
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:665:

(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:665

```
Met Lys Lys Arg Lys His Val Ser Lys Lys Val Phe Asn Val Ile Ile
1               5                  10                  15
Leu Phe Val Ala Val Phe Thr Leu Leu Val Val Ile His Lys Thr Leu
            20                  25                  30
Ser Asn Gly Ile His Ile Gln Asn Leu Lys Ile Gly Lys Leu Gly Ile
        35                  40                  45
Ser Glu Leu Tyr Leu Lys Leu Asn Asn Lys Leu Ser Leu Glu Val Glu
    50                  55                  60
Arg Val Asp Leu Ser Ser Phe Phe His Gln Lys Pro Thr Lys Lys Arg
65                  70                  75                  80
Leu Glu Val Ser Asp Leu Ile Lys Asn Ile Arg Tyr Gly Ile Trp Ala
                85                  90                  95
Val Ser Tyr Phe Glu Lys Leu Lys Val Lys Glu Ile Ile Leu Asp Asp
            100                 105                 110
Lys Asn Lys Ala Asn Ile Phe Phe Asp Gly Asn Lys Tyr Glu Unk Arg
        115                 120                 125
Ile Ser Arg Asn Gln Arg Gly Ile Phe Pro Arg Arg Arg Leu Lys Ile
    130                 135                 140
Ser Ser Leu Lys Ser Ser Ile Cys Phe Leu Lys Met Leu Lys Ser Lys
145                 150                 155                 160
Trp Met Ala Thr Pro Thr Ile Unk Pro Lys Pro Gly Lys Trp Arg Ser
                165                 170                 175
Ile
```

(2) INFORMATION FOR SEQ ID NO:666:

This Sheet Has Been Replaced



(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:666

```
Val Ser Cys Trp Gly Ala Ser Lys Lys Arg Phe Leu Gly Phe Cys Val
1               5                  10                  15
Trp Gly Arg Cys Val Tyr Ala Gly Gly Leu Met Ala Glu Gln Asp Pro
```

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

(2) INFORMATION FOR SEQ ID NO:667:

This Sheet Has Been Replaced



(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:667

```
Val Ala Leu Thr Leu Gly Ala Arg Gly Gly Val Tyr Leu Cys Gly Gly
1               5                   10                  15
Ile Ile Pro Arg Phe Ile Asp Tyr Phe Lys Thr Ser Pro Phe Arg Ala
            20                  25                  30
Arg Phe Glu Thr Lys Gly Arg Met Gly Ala Phe Leu Ala Ser Ile Pro
        35                  40                  45
Val His Val Val Met Lys Lys Thr Pro Gly Leu Asp Gly Ala Gly Ile
    50                  55                  60
Ala Leu Glu Asn Tyr Leu Leu His Asp Arg Ile
65                  70                  75
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 421 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

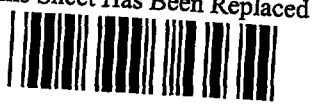
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668

```
Met Lys Gly Leu Thr Met Lys Lys Leu Val Phe Ser Met Leu Leu Cys
1               5                  10                  15
Cys Lys Ser Val Phe Ala Glu Gly Glu Thr Pro Leu Ile Val Asn Asp
            20                  25                  30
Pro Glu Thr His Val Ser Gln Ala Thr Ile Ile Gly Lys Met Val Asp
        35                  40                  45
Ser Ile Lys Arg Tyr Glu Glu Ile Ile Ser Lys Ala Gln Ala Gln Val
    50                  55                  60
Asn Gln Leu Gln Lys Val Asn Asn Met Ile Asn Thr Thr Asn Ser Leu
65                  70                  75                  80
Ile Ser Ser Ser Ala Ile Thr Leu Ala Asn Pro Met Gln Val Leu Gln
                85                  90                  95
Asn Ala Gln Tyr Gln Ile Glu Ser Ile Arg Tyr Asn Tyr Glu Asn Leu
            100                 105                 110
Lys Gln Ser Ile Glu Asn Trp Asn Ala Gln Asn Leu Leu Arg Asn Lys
        115                 120                 125
Tyr Leu Gln Gln Gln Cys Pro Trp Leu Asn Val Asn Ala Leu Thr Asn
    130                 135                 140
Asn Lys Ile Val Asn Leu Lys Asp Leu Asn Asn Leu Ile Thr Lys Asn
145                 150                 155                 160
Gly Glu Gln Thr Gln Thr Ala Arg Asp Val Gln Asn Leu Ile Gln Ser
                165                 170                 175
Ile Ser Gly Ser Gly Tyr Gly Asn Met Gln Ser Leu Ala Gly Glu Leu
            180                 185                 190
Ser Gly Arg Ala Trp Gly Glu Met Leu Cys Lys Met Val Asn Asp Ser
        195                 200                 205
Asn Tyr Glu Ser Glu Gln Ala Leu Leu Ala Thr Gly Asn Asn Pro Glu
    210                 215                 220
Glu Gln Lys Arg Arg Phe Leu Leu Arg Val Lys Lys Lys Val Asn Asp
225                 230                 235                 240
Asn Lys Gln Leu Lys Asp Lys Leu Asp Pro Phe Leu Lys Arg Leu Asp
                245                 250                 255
Val Leu Gln Thr Glu Phe Gly Val Thr Asp Pro Thr Ala Asn His Asn
            260                 265                 270
Lys Gln Gly Ile His Tyr Cys Thr Glu Asn Lys Glu Thr Gly Lys Cys
        275                 280                 285
Asp Pro Ile Lys Asn Val Phe Arg Thr Thr Arg Leu Asp Asn Glu Leu
    290                 295                 300
Glu Gln Glu Ile Gln Thr Leu Thr Leu Asp Leu Ile Lys Ala Ser Asn
305                 310                 315                 320
Lys Asp Ala Gln Ser Gln Ala Tyr Ala Asn Phe Asn Gln Arg Ile Lys
                325                 330                 335
Leu Leu Thr Leu Lys Tyr Leu Lys Glu Ile Thr Asn Gln Met Leu Phe
            340                 345                 350
Leu Asn Gln Thr Met Ala Met Gln Ser Glu Ile Met Thr Asp Asp Tyr
```

```
        355                 360                 365
Phe Arg Gln Asn Asn Asp Gly Phe Gly Glu Lys Glu Asn His Ile Asp
    370                 375                 380
Glu Gln Leu Thr Gln Lys Arg Ile Asn Glu Arg Glu Arg Ala Arg Ile
385                 390                 395                 400
Tyr Phe Gln Asn Pro Asn Val Lys Phe Asp Gln Phe Gly Phe Pro Ile
                405                 410                 415
Phe Ser Ile Trp Asp
            420
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:669:

(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:669

```
Met Ser Val Asn Leu Leu Glu Leu Leu Lys Leu Ala Val Pro Leu Ala
1               5                  10                  15
Val Ile Leu Ser Val Gln Val Ala Val Met Ile Leu Tyr Val Val Leu
            20                  25                  30
Val Thr Phe Arg Val Cys Gly Lys Asp Tyr Asp Ala Ala Val Leu Cys
        35                  40                  45
Ala Gly His Cys Gly Phe Gly Leu Gly Ala Thr Pro Thr Ala Met Val
    50                  55                  60
Asn Met Gln Thr Ile Thr Asn His Tyr Gly Pro Ser His Val Ala Phe
65                  70                  75                  80
Ile
```

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670

```
Met Gln Leu Ser Pro Leu Gln Ser Ala Leu Leu Tyr Phe Arg Tyr Phe
1               5                  10                  15
Ile Tyr Pro Glu Lys Lys Thr Arg Ser Phe Asp Leu Ser Asp Leu Ile
            20                  25                  30
Phe Ile Val Met Val Phe Leu Val Leu Ala Leu Gly Leu Leu Met Ser
        35                  40                  45
Glu Glu Ile Ser Ile Ser Tyr Asn Glu Ala Lys Asp Phe Phe Tyr Ser
    50                  55                  60
Asp Ala Trp Phe Val Lys Ile Ala Gln Lys Ser Val Ala Ile Leu Arg
65                  70                  75                  80
Pro Lys Arg Phe Gly Phe Lys Ile Ala Phe Phe Asp Arg Ser Arg His
                85                  90                  95
Gln His Val Phe Ile Leu Pro His Arg Ala Lys Asp Phe Lys Lys Ala
            100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:671:

This Sheet Has Been Replaced



(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:671

```
Leu Ala Gly Leu Unk Val Gly Cys Unk Arg Met Lys Gln Thr Phe Trp
1               5                  10                  15
Unk Leu Ser Trp Gly Glu Lys Ser Gln Lys Val Cys Val His Arg Pro
            20                  25                  30
Trp Tyr Ala Ile Trp Ser Cys Asp Lys Trp Glu Glu Lys Thr Gln Gln
        35                  40                  45
Phe Thr Gly Asn Gln Leu Ile Thr Lys Thr Trp Ala Gly Gly Asn Ala
    50                  55                  60
Ala Asn Tyr Tyr His Ser Gln Asn Asn Gln Asp Ile Thr Ala Asn Leu
65                  70                  75                  80
Lys Asn Asp Asn Gly Thr Tyr Phe Leu Ser Gly Leu Tyr Asn Tyr Thr
                85                  90                  95
Gly Gly Glu Tyr Asn Gly Gly Asn Leu Asp Ile Glu Leu Gly Ser Asn
            100                 105                 110
Ala Thr Phe Asn Leu Gly Ala Ser Ser Gly Asn Ser Phe Thr Ser Trp
        115                 120                 125
Tyr Pro Asn Gly His Thr Asp Val Thr Phe Ser Ala Gly Thr Ile Asn
    130                 135                 140
Val Asn Asn Ser Val Glu Val Gly Asn Arg Val Gly Ser Gly Ala Gly
145                 150                 155                 160
Thr His Thr Gly Thr Ala Thr Leu Asn Leu Asn Ala Asn Lys Val Thr
                165                 170                 175
Ile Asn Ser Asn Ile Ser Ala Tyr Lys Thr Ser Gln Val Asn Val Gly
            180                 185                 190
Asn Ala Asn Ser Val Ile Thr Ile Asn Ser Val Ser Leu Asn Gly Glu
        195                 200                 205
Thr Cys Unk Ser Leu Ala Arg Val Gly Val Gly Ala Asn Cys Ser Thr
    210                 215                 220
Ser Gly Pro Ser Tyr Ser Phe Lys Gly Thr Thr Asn Ala Thr Asn Thr
```

```
225                 230                 235                 240
Thr Phe Ser Unk Ser Ser Gly Ser Phe Thr Phe Glu Glu Asn Ala Thr
                245                 250                 255
Phe Ser Gly Ala Lys Leu Asn Gly Gly Ala Phe Thr Phe Asn Lys Lys
            260                 265                 270
Phe Asn Ala Thr Asn Asn Thr Ala Phe Asn Ser Gly Ser Phe Thr Phe
        275                 280                 285
Lys Gly Thr Ser Ser Phe Asn Gly Ala Asn Phe Ser Asn Ala Ser Tyr
    290                 295                 300
Thr Phe Asn Asn Gln Ala Thr Phe Gln Asn Ser Ser Phe Asn Gly Gly
305                 310                 315                 320
Thr Phe Thr Phe Asn
                325
```

(2) INFORMATION FOR SEQ ID NO:671:

This Sheet Has Been Replaced



(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:671

```
Leu Ala Gly Leu Unk Val Gly Cys Unk Arg Met Lys Gln Thr Phe Trp
1                   5                  10                  15
Unk Leu Ser Trp Gly Glu Lys Ser Gln Lys Val Cys Val His Arg Pro
            20                  25                  30
Trp Tyr Ala Ile Trp Ser Cys Asp Lys Trp Glu Glu Lys Thr Gln Gln
        35                  40                  45
Phe Thr Gly Asn Gln Leu Ile Thr Lys Thr Trp Ala Gly Gly Asn Ala
    50                  55                  60
Ala Asn Tyr Tyr His Ser Gln Asn Asn Gln Asp Ile Thr Ala Asn Leu
65                  70                  75                  80
Lys Asn Asp Asn Gly Thr Tyr Phe Leu Ser Gly Leu Tyr Asn Tyr Thr
                85                  90                  95
Gly Gly Glu Tyr Asn Gly Gly Asn Leu Asp Ile Glu Leu Gly Ser Asn
            100                 105                 110
Ala Thr Phe Asn Leu Gly Ala Ser Ser Gly Asn Ser Phe Thr Ser Trp
        115                 120                 125
Tyr Pro Asn Gly His Thr Asp Val Thr Phe Ser Ala Gly Thr Ile Asn
    130                 135                 140
Val Asn Asn Ser Val Glu Val Gly Asn Arg Val Gly Ser Gly Ala Gly
145                 150                 155                 160
Thr His Thr Gly Thr Ala Thr Leu Asn Leu Asn Ala Asn Lys Val Thr
                165                 170                 175
Ile Asn Ser Asn Ile Ser Ala Tyr Lys Thr Ser Gln Val Asn Val Gly
            180                 185                 190
Asn Ala Asn Ser Val Ile Thr Ile Asn Ser Val Ser Leu Asn Gly Glu
        195                 200                 205
Thr Cys Unk Ser Leu Ala Arg Val Gly Val Gly Ala Asn Cys Ser Thr
    210                 215                 220
Ser Gly Pro Ser Tyr Ser Phe Lys Gly Thr Thr Asn Ala Thr Asn Thr
225                 230                 235                 240
```

```
Thr Phe Ser Unk Ser Ser Gly Ser Phe Thr Phe Glu Glu Asn Ala Thr
                245                 250                 255
Phe Ser Gly Ala Lys Leu Asn Gly Gly Ala Phe Thr Phe Asn Lys Lys
            260                 265                 270
Phe Asn Ala Thr Asn Asn Thr Ala Phe Asn Ser Gly Ser Phe Thr Phe
        275                 280                 285
Lys Gly Thr Ser Ser Phe Asn Gly Ala Asn Phe Ser Asn Ala Ser Tyr
    290                 295                 300
Thr Phe Asn Asn Gln Ala Thr Phe Gln Asn Ser Ser Phe Asn Gly Gly
305                 310                 315                 320
Thr Phe Thr Phe Asn
                325
```

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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

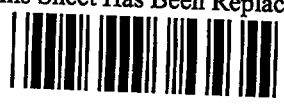
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672

```
Leu Leu Ser Leu Val Lys Gly Lys Thr Met Leu Arg Ser Leu Tyr Ser
1               5                  10                  15
Ala Thr Ser Gly Met Leu Ala Gln Gln Thr His Ile Asp Thr Thr Ser
            20                  25                  30
Asn Asn Ile Ala Asn Val Asn Thr Thr Gly Phe Lys Lys Ser Arg Ala
        35                  40                  45
Asp Phe Asn Asp Leu Phe Tyr Gln Ala Met Gln Tyr Ala Gly Thr Asn
    50                  55                  60
Thr Ser Asn Thr Thr Leu Ser Pro Asp Gly Met Glu Val Gly Leu Gly
65                  70                  75                  80
Val Arg Pro Ser Ala Ile Thr Lys Met Phe Ser Gln Gly Ser Pro Lys
                85                  90                  95
Glu Thr Glu Asn Asn Leu Asp Ile Ala Ile Thr Gly Lys Gly Phe Phe
            100                 105                 110
Gln Val Gln Leu Pro Asp Gly Thr Thr Ala Tyr Thr Arg Ser Gly Asn
        115                 120                 125
Phe Lys Leu Asp Glu Gln Gly Asn Leu Val Thr Ser Glu Gly Tyr Leu
    130                 135                 140
Leu Ile Pro Gln Ile Thr Leu Pro Glu Asp Thr Thr Gln Val Asn Ile
145                 150                 155                 160
Gly Val Asp Gly Thr Val Ser Val Thr Gln Gly Leu Gln Thr Thr Ser
                165                 170                 175
Asn Val Ile Gly Gln Ile Thr Leu Ala Asn Phe Val Asn Pro Ala Gly
            180                 185                 190
Leu His Ser Met Gly Asp Asn Leu Phe Ser Ile Thr Asn Ala Ser Gly
        195                 200                 205
Asp Ala Ile Val Gly Asn Pro Asp Ser Gln Gly Leu Gly Lys Leu Arg
    210                 215                 220
Gln Gly Phe Leu Glu Leu Ser Asn Val Arg Leu Val Glu Glu Met Thr
225                 230                 235                 240
Asp Leu Ile Thr Ala Gln Arg Ala Tyr Glu Ala Asn Ser Lys Ser Ile
```

```
                245                 250                 255
Gln Thr Ala Asp Ala Met Leu Gln Thr Val Asn Ser Leu Lys Arg
            260                 265                 270
```

(2) INFORMATION FOR SEQ ID NO:672:

This Sheet Has Been Replaced



(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:672

```
Leu Leu Ser Leu Val Lys Gly Lys Thr Met Leu Arg Ser Leu Tyr Ser
1               5                  10                  15
Ala Thr Ser Gly Met Leu Ala Gln Gln Thr His Ile Asp Thr Thr Ser
            20                  25                  30
Asn Asn Ile Ala Asn Val Asn Thr Thr Gly Phe Lys Lys Ser Arg Ala
        35                  40                  45
Asp Phe Asn Asp Leu Phe Tyr Gln Ala Met Gln Tyr Ala Gly Thr Asn
    50                  55                  60
Thr Ser Asn Thr Thr Leu Ser Pro Asp Gly Met Glu Val Gly Leu Gly
65                  70                  75                  80
Val Arg Pro Ser Ala Ile Thr Lys Met Phe Ser Gln Gly Ser Pro Lys
                85                  90                  95
Glu Thr Glu Asn Asn Leu Asp Ile Ala Ile Thr Gly Lys Gly Phe Phe
            100                 105                 110
Gln Val Gln Leu Pro Asp Gly Thr Thr Ala Tyr Thr Arg Ser Gly Asn
        115                 120                 125
Phe Lys Leu Asp Glu Gln Gly Asn Leu Val Thr Ser Glu Gly Tyr Leu
    130                 135                 140
Leu Ile Pro Gln Ile Thr Leu Pro Glu Asp Thr Thr Gln Val Asn Ile
145                 150                 155                 160
Gly Val Asp Gly Thr Val Ser Val Thr Gln Gly Leu Gln Thr Thr Ser
                165                 170                 175
Asn Val Ile Gly Gln Ile Thr Leu Ala Asn Phe Val Asn Pro Ala Gly
            180                 185                 190
Leu His Ser Met Gly Asp Asn Leu Phe Ser Ile Thr Asn Ala Ser Gly
        195                 200                 205
Asp Ala Ile Val Gly Asn Pro Asp Ser Gln Gly Leu Gly Lys Leu Arg
    210                 215                 220
Gln Gly Phe Leu Glu Leu Ser Asn Val Arg Leu Val Glu Glu Met Thr
225                 230                 235                 240
Asp Leu Ile Thr Ala Gln Arg Ala Tyr Glu Ala Asn Ser Lys Ser Ile
                245                 250                 255
Gln Thr Ala Asp Ala Met Leu Gln Thr Val Asn Ser Leu Lys Arg
            260                 265                 270
```

(2) INFORMATION FOR SEQ ID NO:673:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673

```
Val Tyr Ala Leu Met Val Ala Phe Phe Ala Tyr Met Ser Tyr Cys Leu
1               5                  10                  15
Gly Tyr Gln Phe Ser Lys Phe Val Ser Lys Asn Asn Ile Ser Ser Leu
            20                  25                  30
Ser Ser Leu Leu Ser Ser Cys Val Arg Val Val Ser Val Leu Ile Leu
        35                  40                  45
Ser Leu Ser Ser Leu Glu Leu Arg Tyr Phe Ser Pro Leu Thr Ile Ile
    50                  55                  60
Thr Met His Phe Ala Leu Thr Leu Ile Ile Leu Phe Phe Phe
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:674:

(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:674

```
Met Arg Ser Trp Met Lys Lys Lys Tyr Phe Thr Leu Leu Leu Gln Ser
1               5                  10                  15
Ser Val Val Leu Ala Val Phe Ile Gly Cys Ser Ser Thr Arg Asn His
            20                  25                  30
Thr Phe Ser Ala Leu Ser Asn Gln Glu Asn Thr Asp Asp Lys Leu Pro
        35                  40                  45
Val Val His Ser Ile Lys Thr Ile Asn Asp Val Ser Ser Val Gly Phe
    50                  55                  60
Glu Trp Ser Lys Val Ala Asp Thr Tyr Asp Ile Asp Gly Phe Val Leu
65                  70                  75                  80
Tyr Arg Leu Lys Lys Asp Ser Lys Leu Lys Arg Ile Ala Thr Ile Lys
                85                  90                  95
Asn Pro Tyr Ala Thr His Tyr Tyr Asp Glu Gly Leu Glu Thr Glu Ser
            100                 105                 110
Ser Tyr Thr Tyr Gln Leu Ala Thr Tyr Lys Gly Asp Lys Ile Ser Lys
        115                 120                 125
Leu Ser Glu Pro Ile Leu Val Lys Thr Ser Phe Ile Asn Pro Val Glu
```

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

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:
(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:675

```
Met Gln Asn Gly Tyr Tyr Ala Ala Thr Gly Ala Met Ala Thr Gln Phe
1               5                  10                  15
Asn Arg Leu Asp Leu Thr Ser Asn Asn Leu Ala Asn Leu Asn Thr Asn
            20                  25                  30
Gly Phe Lys Arg Asp Asp Ala Ile Thr Gly Asp Phe Leu Arg Leu Tyr
        35                  40                  45
Gln Glu Tyr Arg Glu Gln Leu Pro Leu Glu Asp Gln Thr Lys Ala Ser
    50                  55                  60
Ala Lys Tyr Leu Asn Arg Unk Leu Asn Arg Val Pro Ile Leu Ser Unk
65                  70                  75                  80
```

This Sheet Has Been Replaced



Ile Tyr Thr Unk Arg Unk Leu Gly Unk Val
85 90

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:
(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:675

Met Gln Asn Gly Tyr Tyr Ala Ala Thr Gly Ala Met Ala Thr Gln Phe
1 5 10 15
Asn Arg Leu Asp Leu Thr Ser Asn Asn Leu Ala Asn Leu Asn Thr Asn
20 25 30
Gly Phe Lys Arg Asp Asp Ala Ile Thr Gly Asp Phe Leu Arg Leu Tyr
35 40 45
Gln Glu Tyr Arg Glu Gln Leu Pro Leu Glu Asp Gln Thr Lys Ala Ser
50 55 60
Ala Lys Tyr Leu Asn Arg Unk Leu Asn Arg Val Pro Ile Leu Ser Unk
65 70 75 80
Ile Tyr Thr Unk Arg Unk Leu Gly Unk Val
85 90

(2) INFORMATION FOR SEQ ID NO:676:

This Sheet Has Been Replaced

(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:676

Met Leu Pro Thr Lys Thr Arg Ile Arg Asp Pro Asn Lys Gln Glu Leu
1 5 10 15
Thr Gln Pro Lys Ile Lys Gly Leu Ser Met Gly Lys Ile Leu Ala Ser
20 25 30
Leu Leu Gly Gly Gly Thr Asn Leu Phe Thr Gly Leu Ser Ser Asp Leu
35 40 45
Phe Ser Met Ile Leu Asn Phe Leu Phe Phe Leu Met Leu Met Met Gly

```
    50                  55                  60
Leu Asn Glu Ala Leu Gly Lys Lys Phe Asn Leu Pro Met Asp Asn Ile
65                  70                  75                  80
Lys Asn Phe Met Ala Glu Val Leu Lys Asn Gly Phe Asp Ser Ile Lys
                85                  90                  95
Asn Met Gly Ser Ala Leu Val Gly Asn Gly Phe Gly Ser Ser Lys Ser
            100                 105                 110
Asp Lys Thr Thr Asn Lys Met Ser Val Pro Gln Val Arg Leu
        115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 195 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:677

```
Val Gly Ala Met Pro Thr Ile Gln Ile Arg Unk Phe Gly Ala Gly Gly
1               5                   10                  15
Ser Gly His Ser Asp Ala Thr Leu Met Leu Val Asn Gly Ile Pro Val
            20                  25                  30
Tyr Met Ala Pro Tyr Ala His Ile Glu Leu Asp Ile Phe Pro Val Thr
        35                  40                  45
Phe Gln Ala Ile Asp Arg Ile Asp Val Ile Lys Gly Gly Gly Ser Val
    50                  55                  60
Gln Tyr Gly Pro Asn Thr Tyr Gly Gly Ile Val Asn Ile Ile Thr Lys
65                  70                  75                  80
Pro Ile Pro Asn Gln Trp Glu Asn Gln Ala Ala Glu Arg Unk Thr Tyr
                85                  90                  95
Trp Ala Lys Ala Arg Asn Ala Gly Phe Ala Ala Pro Unk Asp Lys Thr
            100                 105                 110
Gly Asp Pro Ser Phe Ile Lys Ser Leu Gly Asn Asn Leu Leu Tyr Asn
        115                 120                 125
Thr Tyr Val Arg Ser Gly Gly Met Ile Asn Lys His Val Gly Ile Gln
    130                 135                 140
Arg Lys Leu Thr Gly Leu Glu Ala Lys Ala Leu Gly Thr Ile Ala Pro
145                 150                 155                 160
Leu Val Phe Gln Thr Ile Gly Trp Met Gly Ser Met Thr Ser Met Lys
                165                 170                 175
Ala Met Gly Leu Lys Pro Ile Thr Asn Thr Thr Ile Leu Ala Ile Unk
            180                 185                 190
Gln Pro Gly
        195
```

(2) INFORMATION FOR SEQ ID NO:677:

(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:677

```
Val Gly Ala Met Pro Thr Ile Gln Ile Arg Unk Phe Gly Ala Gly Gly
1               5                  10                  15
Ser Gly His Ser Asp Ala Thr Leu Met Leu Val Asn Gly Ile Pro Val
            20                  25                  30
Tyr Met Ala Pro Tyr Ala His Ile Glu Leu Asp Ile Phe Pro Val Thr
        35                  40                  45
Phe Gln Ala Ile Asp Arg Ile Asp Val Ile Lys Gly Gly Gly Ser Val
    50                  55                  60
Gln Tyr Gly Pro Asn Thr Tyr Gly Gly Ile Val Asn Ile Ile Thr Lys
65                  70                  75                  80
Pro Ile Pro Asn Gln Trp Glu Asn Gln Ala Ala Glu Arg Unk Thr Tyr
                85                  90                  95
Trp Ala Lys Ala Arg Asn Ala Gly Phe Ala Ala Pro Unk Asp Lys Thr
            100                 105                 110
Gly Asp Pro Ser Phe Ile Lys Ser Leu Gly Asn Asn Leu Leu Tyr Asn
        115                 120                 125
Thr Tyr Val Arg Ser Gly Gly Met Ile Asn Lys His Val Gly Ile Gln
    130                 135                 140
Arg Lys Leu Thr Gly Leu Glu Ala Lys Ala Leu Gly Thr Ile Ala Pro
145                 150                 155                 160
Leu Val Phe Gln Thr Ile Gly Trp Met Gly Ser Met Thr Ser Met Lys
                165                 170                 175
Ala Met Gly Leu Lys Pro Ile Thr Asn Thr Thr Ile Leu Ala Ile Unk
            180                 185                 190
Gln Pro Gly
        195
```

(2) INFORMATION FOR SEQ ID NO:678:

This Sheet Has Been Replaced



(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:678

```
Met Ala Asn Met Met Met Ala Ala Ala Met Leu Gly Ile Asp Ser Cys
1               5                  10                  15
Pro Ile Glu Gly Tyr Asp Gln Glu Lys Val Glu Ala Tyr Leu Glu Glu
```

```
            20                  25                  30
Lys Gly Tyr Leu Asn Thr Ala Glu Phe Gly Val Ser Val Met Ala Ser
        35                  40                  45
Phe Gly Tyr Arg Asn Gln Glu Ile Thr Pro Lys Thr Arg Trp Lys Thr
    50                  55                  60
Glu Val Ile Tyr Glu Val Ile Glu
65                  70
```

(2) INFORMATION FOR SEQ ID NO:679:

(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:679

```
Met Ala Gly Leu Val Leu Met Val Leu Leu Ala Ser Tyr Glu Ser Phe
1               5                   10                  15
Val Ser Lys Leu Asp Lys Val Asp Ala Ser Glu Ile Thr Trp Leu Lys
            20                  25                  30
His Thr Asp Phe Asn Ala Leu Lys Leu Lys Val Ser Leu Ser Ile Val
        35                  40                  45
Ala Ile Ser Ala Ile Phe Leu Leu Lys Arg Tyr Met Ser Leu Glu Asp
    50                  55                  60
Val Leu Ser Ser Ile Pro Lys Asp Thr Pro Leu Ser His Asn Pro Ile
65                  70                  75                  80
Phe Trp Gln Val Val Ile His Leu Val Phe Val Cys Ser Ala Leu Leu
                85                  90                  95
Thr Ala Val Thr Asn Asn Ile Ala Phe Ser Gln Lys Glu Arg His
            100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:680

```
Met Ile Thr Ile Val Ile Ala Lys Ala Gly Asn Ile Val Lys Unk Asp
1               5                  10                  15
Ile Phe Thr His Ile Ser Asp Ile Lys Met Gly Leu Ile Lys Gly Gly
            20                  25                  30
Gln Trp Gly Val Ile Gly Leu Gly Asn Ile Gly Lys Arg Val Ala Lys
        35                  40                  45
Leu Ala Gln Ala Phe Gly Ala Lys Val Val Tyr Phe Ser Pro Lys Asp
    50                  55                  60
Lys Lys Glu Glu Tyr Glu Arg Leu Ser Leu Glu Glu Leu Leu Lys Thr
65                  70                  75                  80
Ser Gly Ile Ile Ser Ile His Ala Pro Leu Asn Glu Ser Thr Arg Asp
                85                  90                  95
Leu Ile Ala Leu Lys Glu Leu Gln Ser Leu Lys Asp Gly Ala Ile Leu
            100                 105                 110
Ile Asn Val Gly Arg Gly Gly Ile Val Asn Glu Lys Unk Leu Ala Unk
        115                 120                 125
Unk Leu Glu Thr Thr Asp Leu Tyr Tyr Ala Ser Asp Val Phe
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:681:

(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:681

```
Val Asn Phe Asn Ala Lys Asn Ile Ser Ile Asp Asn Leu Val Glu Ile
1               5                  10                  15
Asn Asn Arg Val Gly Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val
            20                  25                  30
Leu Thr Leu Gln Ala Ser Glu Gly Ile Thr Unk Ser Lys Asn Ala Glu
        35                  40                  45
Ile Ser Leu Tyr Asp Gly Ala Thr Unk Ile Trp Leu Gln Thr Gly
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:682:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

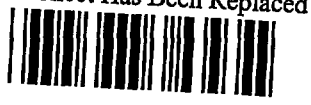
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

This Sheet Has Been Replaced



(A) NAME/KEY: misc_feature
(B) LOCATION 1...310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682

```
Met Arg Thr Leu Ile Leu Ser Leu Leu Lys His Ala Ile Leu Met Gly
1               5                  10                  15
Met Leu Leu Lys Glu Cys Gln Glu Lys Leu Lys Arg Ser Leu Asn Leu
            20                  25                  30
Ser Ala Asn His Cys Val Leu Ser Ala Gly Tyr Gly Ala Ser Ser Ala
        35                  40                  45
Ile Lys Lys Phe Gln Glu Ile Leu Gly Val Cys Ile Pro Ser Lys Thr
    50                  55                  60
Lys Lys Asn Leu Glu Pro Tyr Leu Lys Asp Met Ala Leu Lys Arg Val
65                  70                  75                  80
Ile Val Gly Pro Tyr Glu His His Ser Asn Glu Val Ser Trp Arg Glu
                85                  90                  95
Gly Leu Cys Glu Val Val Arg Ile Pro Leu Asn Glu His Gly Leu Leu
            100                 105                 110
Asp Leu Glu Ile Leu Glu Gln Thr Leu Lys Lys Thr Pro Asn Ser Leu
        115                 120                 125
Val Ser Val Ser Ala Ala Ser Asn Val Thr Gly Ile Leu Thr Pro Leu
    130                 135                 140
Lys Glu Val Ser Ser Leu Cys Lys Glu Tyr Arg Ala Ile Leu Ala Leu
145                 150                 155                 160
Asp Leu Ala Asn Phe Ser Ala His Ala Asn Pro Lys Asp Cys Glu Tyr
                165                 170                 175
Gln Thr Gly Phe Tyr Ala Pro His Lys Leu Leu Gly Gly Val Gly Gly
            180                 185                 190
Cys Gly Leu Leu Gly Ile Ser Lys Asp Leu Ile Asp Thr Gln Ile Pro
        195                 200                 205
Thr Ser Phe Ser Ala Gly Gly Val Ile Lys Tyr Ala Asn Arg Thr Arg
    210                 215                 220
His Glu Phe Ile Asp Glu Leu Pro Leu Arg Glu Glu Phe Gly Thr Pro
225                 230                 235                 240
Gly Leu Leu Gln Phe Tyr Arg Ser Ala Leu Ala Tyr Gln Leu Arg Asp
                245                 250                 255
Glu Cys Gly Leu Asp Phe Ile His Lys Lys Glu Asn Asn Leu Leu Arg
            260                 265                 270
Val Leu Val Tyr Gly Leu Lys Asp Leu Pro Ala Ile Asn Ile Tyr Gly
        275                 280                 285
Asn Leu Thr Ala Ser Arg Val Gly Val Val Thr Phe Asn Ile Gly Gly
    290                 295                 300
Ile Ser Pro Tyr Asp Leu
305                 310
```

(2) INFORMATION FOR SEQ ID NO:683:

(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

This Sheet Has Been Replaced



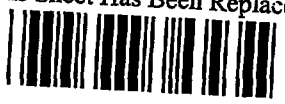
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683

```
Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu Met Gln Lys
1               5                  10                  15
Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser Ile Leu Ala
            20                  25                  30
Ile Lys Arg Gln Val Glu Asp Lys Asn Ala Pro Ile Leu Val Leu Gly
        35                  40                  45
Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala Leu Lys Gln
    50                  55                  60
Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu Phe Val Pro
65                  70                  75                  80
Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu Thr Cys Met
                85                  90                  95
His Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val Ile Ile Leu
            100                 105                 110
Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu Gly Tyr Phe
        115                 120                 125
Met Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile His Ser Gly
    130                 135                 140
Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu Lys Asn Asn
145                 150                 155                 160
Ala Cys Thr Phe Pro Lys Val Glu Phe
                165
```

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:684

```
Met Arg Unk Glu Lys Ile Met Thr Asn Phe Glu Lys Unk Ile Ala Gln
1               5                  10                  15
Asn Arg Leu Lys Thr Asn Ala Val Leu Thr Thr Tyr Cys Ala Ile Phe
            20                  25                  30
Ala Phe Ile Gly Leu Leu Val Asp Ala Ile Arg Ile Asn Ala Asn Asp
        35                  40                  45
Leu Gly Ile Ala Leu Phe Lys Leu Met Thr Phe Gln Ile Phe Pro Thr
    50                  55                  60
Unk Thr Ile Val Met Phe Val Val Ala Phe Val Ile Unk Unk Ser Leu
65                  70                  75                  80
Tyr Pro Lys Phe
```

(2) INFORMATION FOR SEQ ID NO:684:

(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

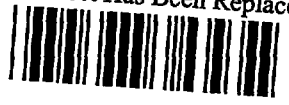
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684

```
Met Arg Unk Glu Lys Ile Met Thr Asn Phe Glu Lys Unk Ile Ala Gln
1               5                  10                  15
Asn Arg Leu Lys Thr Asn Ala Val Leu Thr Thr Tyr Cys Ala Ile Phe
            20                  25                  30
Ala Phe Ile Gly Leu Leu Val Asp Ala Ile Arg Ile Asn Ala Asn Asp
        35                  40                  45
Leu Gly Ile Ala Leu Phe Lys Leu Met Thr Phe Gln Ile Phe Pro Thr
    50                  55                  60
Unk Thr Ile Val Met Phe Val Val Ala Phe Val Ile Unk Unk Ser Leu
65                  70                  75                  80
Tyr Pro Lys Phe
```

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:685

```
Met Unk Met Ser His Ile Ile Lys Ser Ile Glu Ala Leu Asp Asp Tyr
1               5                  10                  15
Thr Ile Arg Phe Thr Leu Asn Gly Pro Glu Ala Pro Phe Leu Ala Asn
            20                  25                  30
Leu Gly Met Asp Phe Leu Ser Ile Leu Ser Lys Asp Tyr Ala Asp Tyr
        35                  40                  45
Leu Ala Gln Asn Asn Lys Lys Asp Glu Leu Ala Lys Unk Pro Val Gly
    50                  55                  60
Thr Gly Pro Phe Lys Phe Phe Leu Trp Asn Lys Arg
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:685:

(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:685

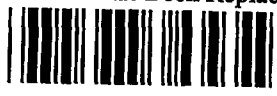
```
Met Unk Met Ser His Ile Ile Lys Ser Ile Glu Ala Leu Asp Asp Tyr
1               5                  10                  15
Thr Ile Arg Phe Thr Leu Asn Gly Pro Glu Ala Pro Phe Leu Ala Asn
            20                  25                  30
Leu Gly Met Asp Phe Leu Ser Ile Leu Ser Lys Asp Tyr Ala Asp Tyr
        35                  40                  45
Leu Ala Gln Asn Asn Lys Lys Asp Glu Leu Ala Lys Unk Pro Val Gly
    50                  55                  60
Thr Gly Pro Phe Lys Phe Phe Leu Trp Asn Lys Arg
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(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:686

```
Leu Met Arg Lys Ile Phe Ser Tyr Ile Ser Lys Val Leu Leu Phe Ile
1               5                  10                  15
Gly Val Val Tyr Ala Glu Pro Asp Ser Lys Val Glu Ala Leu Glu Gly
            20                  25                  30
Arg Lys Gln Glu Ser Ser Leu Asp Lys Lys Ile Arg Gln Glu Leu Lys
        35                  40                  45
Ser Lys Glu Leu Lys Asn Lys Glu Leu Lys Asn Lys Asp Leu Lys Asn
    50                  55                  60
Lys Glu Glu Lys Lys Glu Thr Lys Ala Lys Arg Lys Pro Arg Ala Glu
65                  70                  75                  80
Val His His Gly Asp Ala Lys Asn Pro Thr Pro Lys Ile Thr Pro Pro
                85                  90                  95
Lys Ile Lys Gly Ser Ser Lys Gly Val Gln Asn Gln Gly Val Gln Asn
            100                 105                 110
Asn Ala Pro Lys Pro Glu Glu Lys Asp Thr Thr Pro Gln Ala Thr Glu
        115                 120                 125
Lys Asn Lys Glu Thr Ser Pro Ser Ser Gln Phe Asn Ser Ile Phe Gly
```

```
    130                 135                 140
Asn Pro Asn Asn Ala Thr Asn Asn Thr Leu Glu Asp Lys Val Val Gly
145                 150                 155                 160
Gly Ile Ser Leu Leu Val Asn Gly Ser Pro Ile Thr Leu Tyr Gln Ile
                165                 170                 175
Gln Glu Glu Gln Glu Lys Ser Lys Val Ser Unk Ala Unk Ala Arg Asp
            180                 185                 190
Arg Leu Unk Unk
        195
```

(2) INFORMATION FOR SEQ ID NO:686:

(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:686

```
Leu Met Arg Lys Ile Phe Ser Tyr Ile Ser Lys Val Leu Leu Phe Ile
1               5                   10                  15
Gly Val Val Tyr Ala Glu Pro Asp Ser Lys Val Glu Ala Leu Glu Gly
            20                  25                  30
Arg Lys Gln Glu Ser Ser Leu Asp Lys Lys Ile Arg Gln Glu Leu Lys
        35                  40                  45
Ser Lys Glu Leu Lys Asn Lys Glu Leu Lys Asn Lys Asp Leu Lys Asn
    50                  55                  60
Lys Glu Glu Lys Lys Glu Thr Lys Ala Lys Arg Lys Pro Arg Ala Glu
65                  70                  75                  80
Val His His Gly Asp Ala Lys Asn Pro Thr Pro Lys Ile Thr Pro Pro
                85                  90                  95
Lys Ile Lys Gly Ser Ser Lys Gly Val Gln Asn Gln Gly Val Gln Asn
            100                 105                 110
Asn Ala Pro Lys Pro Glu Glu Lys Asp Thr Thr Pro Gln Ala Thr Glu
        115                 120                 125
Lys Asn Lys Glu Thr Ser Pro Ser Ser Gln Phe Asn Ser Ile Phe Gly
    130                 135                 140
Asn Pro Asn Asn Ala Thr Asn Asn Thr Leu Glu Asp Lys Val Val Gly
145                 150                 155                 160
Gly Ile Ser Leu Leu Val Asn Gly Ser Pro Ile Thr Leu Tyr Gln Ile
                165                 170                 175
Gln Glu Glu Gln Glu Lys Ser Lys Val Ser Unk Ala Unk Ala Arg Asp
            180                 185                 190
Arg Leu Unk Unk
        195
```

(2) INFORMATION FOR SEQ ID NO:687:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

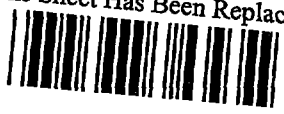
This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687

```
Val Leu Trp Val Leu Tyr Phe Leu Thr Ser Leu Phe Ile Cys Ser Leu
1               5                  10                  15
Ile Val Leu Trp Ser Lys Lys Ser Met Leu Phe Val Asp Asn Ala Asn
            20                  25                  30
Lys Ile Gln Gly Phe His His Ala Arg Thr Pro Arg Ala Gly Gly Leu
        35                  40                  45
Gly Ile Phe Leu Ser Phe Ala Leu Ala Cys Tyr Leu Glu Pro Phe Glu
    50                  55                  60
Met Pro Phe Lys Gly Pro Phe Val Phe Leu Gly Leu Ser Leu Val Phe
65                  70                  75                  80
Leu Ser Gly Phe Leu Glu Asp Ile Asn Leu Ser Leu Ser Pro Lys Ile
                85                  90                  95
Arg Leu Ile Leu Gln Ala Val Gly Val Val Cys Ile Ile Ser Ser Thr
            100                 105                 110
Pro Leu Val Val Ser Asp Phe Ser Pro Leu Phe Ser Leu Pro Tyr Phe
        115                 120                 125
Ile Ala Phe Leu Phe Ala Ile Phe Tyr Ala Gly Gly Tyr Gln
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:688:

(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:688

```
Met Ala Cys Lys Phe Cys Pro Lys Ile Arg Lys Thr Asp Trp Ile Phe
1               5                  10                  15
Ile Leu Ile Ala Ala Leu Gly Phe Tyr Ser Val Asn Lys Leu Gly Tyr
            20                  25                  30
Ala Pro Lys Phe Asn Thr Pro Thr Pro Lys Ser Ser Arg Pro Leu Ser
        35                  40                  45
Arg Pro Ile Glu Lys Pro Asn Asn Met Thr Glu Glu Glu Arg Lys Lys
    50                  55                  60
Arg Phe Ile Glu Leu Gln Lys Ala Cys Leu Leu His Lys Asp Lys Lys
65                  70                  75                  80
Ala Cys Glu Glu Val Phe
```

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...121

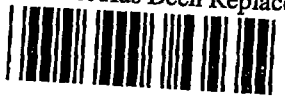
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689

```
Val Asp Ser Ile Leu Ile Asp Glu Ala Arg Thr Pro Leu Ile Ile Ser
1               5                  10                  15
Gly Pro Val Asp Arg Arg Met Glu Asn Tyr Asn Lys Ala Asp Glu Val
            20                  25                  30
Ala Lys Ser Met Gln Val Glu Val Asp Phe Thr Ile Asp Glu Lys Asn
        35                  40                  45
Arg Ala Ile Leu Ile Thr Glu Glu Gly Ile Lys Lys Ala Glu Asn Leu
    50                  55                  60
Phe Gly Val Asp Asn Leu Tyr Lys Ile Glu Asn Ala Ala Leu Ser His
65                  70                  75                  80
His Leu Asp Gln Ala Leu Lys Ala Asn Tyr Leu Phe Phe Ile Asp Lys
                85                  90                  95
Asp Tyr Ile Val Ala Asn Asn Glu Val Val Ile Val Asp Lys Phe Thr
            100                 105                 110
Asp Arg Leu Asn Glu Gly Glu Ala Leu
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:690

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

```
Lys Asp Leu Ala Leu Phe Ala Gly Gly Leu Phe Val Ala Gly Phe Asp
        35                  40                  45
Arg Asn Ala Ile Trp Arg Val Lys Gly Phe Ala
    50                  55
```

(2) INFORMATION FOR SEQ ID NO:691:

(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:691

```
Val Phe Ser Gly Asn Lys Arg Ala Ile Asn Tyr Arg Thr Ile Val Ser
1               5                  10                  15
Ala Phe Val Ile Gln Val Ala Leu Gly Ala Leu Ala Leu Tyr Val Pro
            20                  25                  30
Leu Gly Arg Glu Ile Leu Gln Gly Leu Ala Ser Gly Ile Gln Ser Val
        35                  40                  45
Ile Gly Tyr Gly Tyr Glu Gly Val Arg Phe Leu Phe Gly Asn Leu Ala
    50                  55                  60
Pro Asn Ala Lys Gly Asp Gln Gly Ile Gly Gly Phe Ile Phe Ala Ile
65                  70                  75                  80
Asn Val Leu Ala Ile Ile Ile Phe Phe Ala Ser Leu Ile Ser Leu Leu
                85                  90                  95
Tyr Tyr Leu Lys Ile Met Pro Leu Val Ile Asn Leu Ile Gly Gly Ala
            100                 105                 110
Leu Gln Lys Cys Leu Gly Thr Ser Lys Ala Glu Ser Met Ser Ala Ala
        115                 120                 125
Ala Asn Unk Unk Val Ala His Thr Glu Asp Unk Leu Ser His
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:692:

(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:692

This Sheet Has Been Replaced



```
Met Leu Val Gly Ile Ser Asn Ala Ile Asn Ile Ile Asp Gly Phe Asn
1               5                  10                  15
Gly Leu Ala Ser Gly Ile Cys Ala Ile Ala Leu Leu Val Ile His Tyr
            20                  25                  30
Ile Asp Unk Ser Ser Leu Ser Cys Leu Leu Ala Tyr Met Val Leu Gly
        35                  40                  45
Val Tyr Gly Val Lys Unk Pro Phe Arg Lys Asp Phe Leu Gly Arg Ser
    50                  55                  60
Gly Gly Arg Ile Phe Trp Val Trp Unk Unk Unk Phe Leu Ser Cys Ile
65                  70                  75                  80
```

(2) INFORMATION FOR SEQ ID NO:693:

(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:693

```
Met Lys Arg Ser Ser Val Phe Ser Phe Leu Val Ala Phe Leu Leu Val
1               5                  10                  15
Val Gly Cys Ser His Lys Met Asp Asn Lys Thr Val Ala Gly Asp Val
            20                  25                  30
Ser Thr Lys Ala Val Gln Thr Ala Pro Val Thr Thr Glu Pro Ala Pro
        35                  40                  45
Glu Lys Glu Glu Pro Lys Gln Glu Pro Ala Pro Val Val Glu Glu Lys
    50                  55                  60
Pro Ala Ile Glu Ser Gly Thr Ile Ile Ala Ser Ile Tyr Phe Asp Phe
65                  70                  75                  80
Asp Lys Tyr Glu Ile Lys Glu Ser Asp Gln Glu Thr Leu Asp Glu Ile
                85                  90                  95
Val Gln Lys Ala Lys Glu Asn His Met Gln Val Leu Leu Glu Gly Asn
            100                 105                 110
Thr Asp Glu Phe Gly Ser Ser Glu Tyr Asn Gln Ala Leu Gly Val Lys
        115                 120                 125
Arg Thr Leu Ser Val Lys Asn Ala Leu Val Ile Lys Gly Val Glu Lys
    130                 135                 140
Asp Met Ile Lys Thr Ile Ser Phe Gly Glu Ser Lys Pro Lys Cys Val
145                 150                 155                 160
Gln Lys Thr Arg Glu Cys Tyr Arg Glu Asn Arg Arg Val Asp Val Lys
                165                 170                 175
Leu Val Lys
```

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 179 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:693

```
Met Lys Arg Ser Ser Val Phe Ser Phe Leu Val Ala Phe Leu Leu Val
1               5                  10                  15
Val Gly Cys Ser His Lys Met Asp Asn Lys Thr Val Ala Gly Asp Val
            20                  25                  30
Ser Thr Lys Ala Val Gln Thr Ala Pro Val Thr Thr Glu Pro Ala Pro
        35                  40                  45
Glu Lys Glu Glu Pro Lys Gln Glu Pro Ala Pro Val Val Glu Glu Lys
    50                  55                  60
Pro Ala Ile Glu Ser Gly Thr Ile Ile Ala Ser Ile Tyr Phe Asp Phe
65                  70                  75                  80
Asp Lys Tyr Glu Ile Lys Glu Ser Asp Gln Glu Thr Leu Asp Glu Ile
                85                  90                  95
Val Gln Lys Ala Lys Glu Asn His Met Gln Val Leu Leu Glu Gly Asn
            100                 105                 110
Thr Asp Glu Phe Gly Ser Ser Glu Tyr Asn Gln Ala Leu Gly Val Lys
        115                 120                 125
Arg Thr Leu Ser Val Lys Asn Ala Leu Val Ile Lys Gly Val Glu Lys
    130                 135                 140
Asp Met Ile Lys Thr Ile Ser Phe Gly Glu Ser Lys Pro Lys Cys Val
145                 150                 155                 160
Gln Lys Thr Arg Glu Cys Tyr Arg Glu Asn Arg Arg Val Asp Val Lys
                165                 170                 175
Leu Val Lys
```

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694

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

```
        35                  40                  45
Thr Pro Leu Glu Ala Leu Tyr Arg Glu Leu Leu Glu Glu Ile Gly Thr
    50                  55                  60
Asn Glu Ile Glu Ile Leu Ala Gln Tyr Pro Arg
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:695:

(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:695

```
Val Met Leu Met Ala Ile Phe Thr Pro Tyr Ile Leu Ile Leu Lys Met
1               5                   10                  15
Met Lys Lys Ser Met Ser Leu Phe Ala Asn Met Gly Leu Glu Gln Ile
            20                  25                  30
Phe Cys Asn Arg Asp Ile Lys Asp Leu Asn Asp Phe Val Phe Gly Ile
        35                  40                  45
Glu Val Gly Leu Asp Ser Asn Ala Arg Lys Asn Arg Ser Arg Lys Ala
    50                  55                  60
Met Glu Asn His Leu Ile Gly Leu Phe Val Gln Ala Gln Leu Asn Phe
65                  70                  75                  80
Lys Glu Gln Val Asp Ile Arg Glu Phe Glu Asp Leu Arg Gln Ala Phe
                85                  90                  95
Gly Asn Asp
```

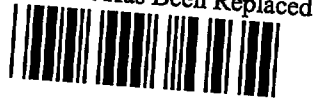
(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696

```
Met Ile Arg Leu Ala Ala Phe Phe Leu Ala Leu Ala Cys Ala Ile Thr
1               5                   10                  15
```

```
Pro Lys Ser Arg Leu Leu Leu Lys Asn Val Leu Leu Asn Pro Thr Arg
            20                  25                  30
Ile Glu Ala Phe Glu Val Leu Lys Lys Met Gly Ala His Ile Glu Tyr
        35                  40                  45
Val Ile Gln Ser Lys Asp Leu Glu Val Ile Gly Asp Ile Tyr Ile Glu
    50                  55                  60
His Ala Pro Leu Lys Ala Ile Ser Ile Asp Gln Asn Ile Ala Ser Leu
65                  70                  75                  80
Ile Asp Glu Ile Pro Ala Leu Ser Ile Ala Met Leu Phe Ala Lys Gly
                85                  90                  95
Lys Ser Met Val Arg Asn Ala Lys Asp Leu Arg Ala Lys Glu Ser Asp
            100                 105                 110
Arg Ile Lys Ala Val Val Ser Asn Phe Lys Ala Leu Gly Ile Glu Cys
        115                 120                 125
Glu Glu Phe Glu Asp Gly Phe Tyr Ile Glu Gly Leu Gly Asp Ala Ser
    130                 135                 140
Gln Leu Lys Gln His Phe Ser Lys Ile Lys Pro Pro Ile Ile Lys Ser
145                 150                 155                 160
Phe Asn Asp His Arg Ile Ala Met Ser Phe Ala Val Leu Thr Leu Ala
                165                 170                 175
Leu Pro Leu Glu Ile Asp Asn Leu Glu Cys Ala Asn Ile Ser Phe Pro
            180                 185                 190
Thr Phe Gln Leu Trp Leu Asn Leu Phe Lys Lys Arg Ser Leu Asn Gly
        195                 200                 205
Asn
```

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697

```
Val Gly Ser Leu Lys Phe Leu Asn Ala Met Gly Val Asp Leu Lys Val
1               5                   10                  15
Lys Glu Ser Ala Asn Ile Met Val Gly Phe Ala Lys Asn Lys Thr Leu
            20                  25                  30
Cys Ala Leu Phe Ile Leu Glu Glu Arg Leu Lys Ala Asn Ala Lys Glu
        35                  40                  45
Val Ile Gln Ala Leu Gln Asn Gln Gly Leu Glu Leu Glu Ile Leu Ser
    50                  55                  60
Gly Asp Asn Glu Ser Ser Val Lys Glu Cys Ala
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698

```
Met Glu Ala Leu Asn Ala Leu Asn Ala Gln Ser Asp Glu Gln Ile Leu
1               5                  10                  15
Cys Glu Gly Tyr Phe Val Leu Leu Gln Ile Leu Glu Pro Met Ile Pro
            20                  25                  30
His Thr Ala Trp Glu Leu Ser Glu Arg Leu Phe Lys Arg Glu Asn Phe
        35                  40                  45
Lys Pro Ile Glu Val Asp Glu Ser Ala Leu Ile Glu Asp Phe Met Thr
    50                  55                  60
Leu Gly Leu Thr Ile Asn Gly Lys Arg Arg Ala Glu Leu Lys Val Asn
65                  70                  75                  80
Ile Asn Ala Ser Lys Glu Glu Ile Ile Ile Leu Ala Lys Lys Glu Leu
                85                  90                  95
Glu Lys Tyr Leu Glu Asn Ala Ser Val Lys Lys Glu Ile Tyr Val Pro
            100                 105                 110
Asn Lys Leu Val Asn Phe Val Thr Ala
        115                 120
```

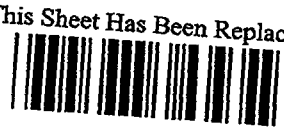
(2) INFORMATION FOR SEQ ID NO:699:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699

```
Met Lys Glu Ser Ile Lys Tyr Leu Leu Glu Ser Val Gly Leu Val Leu
1               5                  10                  15
Leu Met Ser Val Asn Pro Gly Phe Gly Gly Gln Lys Phe Leu Asp Leu
            20                  25                  30
Val Leu Glu Lys Cys Leu Lys Val Lys Glu Leu Ile Lys Arg Tyr Asn
        35                  40                  45
Pro Ser Cys Leu Leu Glu Val Asp Gly Gly Val Asn Asp Lys Asn Ile
    50                  55                  60
Phe Glu Leu Gln Gln Ala Gly Val Asp Val Val Val Ser Gly Ser Tyr
65                  70                  75                  80
Ile Phe Glu Ser Lys Asp Unk Lys Leu Ala Ile Glu Gly Leu Gln Asn
                85                  90                  95
```

Val Arg Gln Pro Leu Ala
100

(2) INFORMATION FOR SEQ ID NO:700:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700

```
Val His Asp Gly Val Leu Gly Trp Val Gly Phe Thr Leu Ile Ala Ser
1               5                  10                  15
Met Tyr His Met Thr Pro Arg Leu Phe Lys Arg Glu Ile Tyr Ser Gly
            20                  25                  30
Arg Leu Val Asp Phe Gln Phe Trp Ile Met Thr Leu Gly Ile Val Leu
        35                  40                  45
Tyr Phe Ser Ser Met Trp Ile Ala Gly Ile Thr Gln Gly Met Met Trp
    50                  55                  60
Arg Asp Val Asp Gln Tyr Gly Asn Leu Thr Tyr Gln Phe Ile Asp Thr
65                  70                  75                  80
Val Lys Ala Leu Ile Pro Tyr Tyr Asn Ile Arg Gly Val Gly Gly Leu
                85                  90                  95
Met Tyr Phe Ile Gly Phe Ile Ile Phe Ala Tyr Asn Ile Phe Met Thr
            100                 105                 110
Ile Thr Ala Gly Lys Lys Leu Glu Arg Glu Pro Asn Tyr Ala Thr Pro
        115                 120                 125
Met Ala Lys
    130
```

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 441 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701

Met Ile Thr Leu Phe Ser Phe Gly Ala Phe Ala Tyr Tyr Phe Val Ser

```
1               5                  10                  15
Ser Gln Ile Ser His Glu Asn Tyr Gln Asn Glu Met Arg His Tyr Gln
            20                  25                  30
Phe Val Thr Thr Ile Asn Glu Ile Leu Asn Asn Tyr Ser Asp Tyr Arg
        35                  40                  45
Ala Ile Glu Asp Tyr Leu Tyr Lys Ile Gly Phe Arg Glu Thr Thr Ile
    50                  55                  60
Glu Asn Leu Glu Lys Val Leu Ala Lys Arg Arg His Gln Leu His His
65                  70                  75                  80
Arg Asn Ile Trp Tyr Ala Glu Val Phe Lys Phe Ser Asp Met Val Phe
                85                  90                  95
Ile Leu Leu Lys Lys Asp Glu His Phe Val Leu Tyr Lys Asp Leu His
            100                 105                 110
Ser Val Ser Tyr Arg Asn Tyr Phe Leu Ala Ile Thr Val Gly Leu Leu
        115                 120                 125
Leu Ile Leu Phe Leu Phe Leu Phe Val Leu Gln Ser Leu Leu Pro Leu
    130                 135                 140
Arg Glu Leu Arg Ser Gln Val Lys Arg Phe Ala Gln Gly Asp Lys Ser
145                 150                 155                 160
Val Ser Cys Lys Ser Lys Gln Lys Asp Glu Ile Gly Asp Leu Ala Asn
                165                 170                 175
Glu Phe Asp Asn Cys Ile Gln Lys Ile Asn Ala Met Asn Glu Ser Arg
            180                 185                 190
Val Leu Phe Leu Arg Ser Ile Met His Glu Leu Arg Thr Pro Ile Thr
        195                 200                 205
Lys Gly Lys Ile Leu Ser Ser Met Leu Lys Glu Glu Leu Ser Cys Lys
    210                 215                 220
Arg Phe Ser Ser Ile Phe Asp His Leu Asn Met Leu Ile Glu Gln Phe
225                 230                 235                 240
Ala Arg Ile Glu Gln Leu Ala Ser Lys Asn Tyr Gly Ser Asn Lys Glu
                245                 250                 255
Lys Phe Leu Met Ser Asp Leu Ile Asp Lys Ile Glu Lys Met Leu Leu
            260                 265                 270
Ile Asp Glu Asp Lys Lys Ser Pro Ile His Val Ser Ser Ser Asn Tyr
        275                 280                 285
Ile Ile Glu Ala Asp Phe Glu Leu Phe Ala Ile Ala Leu Lys Asn Met
    290                 295                 300
Ile Asp Asn Ala Ile Lys Tyr Ser Asp Asp Lys Gln Val Phe Leu Asp
305                 310                 315                 320
Phe Ile Gly Asn Asn Leu Val Val Ser Asn Lys Ser Lys Pro Leu Lys
                325                 330                 335
Glu Asp Phe Glu Lys Tyr Leu Gln Pro Tyr Phe Lys Ser Ser Asn Pro
            340                 345                 350
Ser Gln Ala His Gly Phe Gly Leu Gly Met Tyr Ile Ile Lys Asn Ala
        355                 360                 365
Leu Glu Ala Met Gly Leu Asn Leu Ser Tyr His Tyr Ser Asn Gly Arg
    370                 375                 380
Ile Cys Phe Thr Ile His Asp Cys Val Phe Asn Ser Phe Tyr Asp Leu
385                 390                 395                 400
Glu Ala Asp Asn Glu Glu Leu Pro Pro Pro Glu Asn Leu Arg Glu Val
                405                 410                 415
Lys Gly Met Lys Gly Thr Glu Lys Ala Asn Cys Gly Val Lys Glu Lys
            420                 425                 430
Gln Lys Glu Arg Thr Cys Ser Asn Asp
        435                 440
```

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702

```
Val Leu Leu Leu Ser Arg Met Gly Ile Ala Phe Ala His Ser Ile Phe
1               5                  10                  15
Trp Ser Ile Thr Ala Ser Leu Val Ile Arg Val Ala Pro Arg Asn Lys
            20                  25                  30
Lys Gln Gln Ala Leu Gly Leu Leu Ala Leu Gly Ser Ser Leu Ala Met
        35                  40                  45
Ile Leu Gly Leu Pro Leu Gly Arg Ile Ile Gly Gln Ile Leu Asp Trp
    50                  55                  60
Arg Ser Thr Phe Gly Val Ile Gly Gly Val Ala Thr Leu Ile Met Leu
65                  70                  75                  80
Leu Met Trp Lys Leu Leu Pro His Leu Pro Ser Arg Asn Ala Gly Thr
                85                  90                  95
Leu Ala Ser Val Pro Ile Leu Met Lys Arg Pro Leu Leu Val Gly Ile
            100                 105                 110
Tyr Leu His Val Asn His Gly Tyr Phe Trp Ala Phe His His Leu
        115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:703:

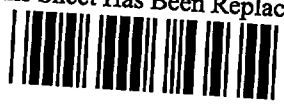
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703

```
Met Gly Thr Leu Ile Glu Lys Trp Phe Gly Phe Ser Gln Ile Arg Glu
1               5                  10                  15
Glu Leu Glu Ala Arg Ile Ser Glu Leu Glu Asp Glu Asn Thr Glu Leu
            20                  25                  30
Leu Arg Glu Arg Glu Tyr Leu Ala Ala Glu Thr Ser Glu Leu Lys Asp
        35                  40                  45
Ala Asn Asp Gln Leu Arg Gln Lys Asn Asp Lys Leu Phe Ile Thr Lys
    50                  55                  60
Asp Lys Leu Thr Lys Glu Asn Thr Glu Leu Phe Ala Glu Asn Glu Ser
65                  70                  75                  80
Leu Ser Val Lys Ile Ser Gly Leu Glu His Ser Asn Asp Gln Leu Trp
                85                  90                  95
Gln Asn Asn Asn Lys Leu Thr Lys Glu Lys Ala Glu Leu Lys Thr Glu
            100                 105                 110
Lys Asp Ile Leu Ala Lys Glu Asn Thr Arg Leu Leu Ala Ala Arg Asp
```

```
        115                 120                 125
Arg Leu Thr Glu Glu Lys Arg Glu Leu Thr Thr Glu Lys Glu Arg Leu
    130                 135                 140
Lys Arg Glu Asn Thr Glu Leu Thr His Lys Ile Thr Glu Leu Thr Lys
145                 150                 155                 160
Glu Asn Lys Ala Leu Thr Thr Glu Asn Asp Lys Leu Asn His Gln Val
                165                 170                 175
Thr Ala Leu Thr Asn Glu Arg Asp Ser Leu Glu Gln Glu Arg Ala Arg
            180                 185                 190
Leu Gln Asp Ala His Gly Phe Leu Glu Lys Arg Cys Thr Asn Leu Glu
        195                 200                 205
Lys Glu Asn Gln Arg Leu Thr Asp Lys Leu Lys Gln Leu Glu Ser Ala
    210                 215                 220
Gln Lys Ser Leu Glu Asn Thr Asn Asn Gln Leu Arg Gln Ala Leu Glu
225                 230                 235                 240
Asn Ser Asn Val Gln Leu Ala Gln Ala Lys Glu Unk Ile Ala Ile Glu
                245                 250                 255
Unk Ser Glu Leu Unk Arg Arg Asn Arg Thr Leu Glu Glu Leu Arg Gly
            260                 265                 270
Tyr Gly Ser Gln Lys Unk Ile Trp Thr Tyr Thr Unk Gly Val
        275                 280                 285
```

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703

```
Met Gly Thr Leu Ile Glu Lys Trp Phe Gly Phe Ser Gln Ile Arg Glu
1               5                   10                  15
Glu Leu Glu Ala Arg Ile Ser Glu Leu Glu Asp Glu Asn Thr Glu Leu
            20                  25                  30
Leu Arg Glu Arg Glu Tyr Leu Ala Ala Glu Thr Ser Glu Leu Lys Asp
        35                  40                  45
Ala Asn Asp Gln Leu Arg Gln Lys Asn Asp Lys Leu Phe Ile Thr Lys
    50                  55                  60
Asp Lys Leu Thr Lys Glu Asn Thr Glu Leu Phe Ala Glu Asn Glu Ser
65                  70                  75                  80
Leu Ser Val Lys Ile Ser Gly Leu Glu His Ser Asn Asp Gln Leu Trp
                85                  90                  95
Gln Asn Asn Asn Lys Leu Thr Lys Glu Lys Ala Glu Leu Lys Thr Glu
            100                 105                 110
Lys Asp Ile Leu Ala Lys Glu Asn Thr Arg Leu Leu Ala Ala Arg Asp
        115                 120                 125
Arg Leu Thr Glu Glu Lys Arg Glu Leu Thr Thr Glu Lys Glu Arg Leu
    130                 135                 140
Lys Arg Glu Asn Thr Glu Leu Thr His Lys Ile Thr Glu Leu Thr Lys
145                 150                 155                 160
Glu Asn Lys Ala Leu Thr Thr Glu Asn Asp Lys Leu Asn His Gln Val
                165                 170                 175
```

```
Thr Ala Leu Thr Asn Glu Arg Asp Ser Leu Glu Gln Glu Arg Ala Arg
            180                 185                 190
Leu Gln Asp Ala His Gly Phe Leu Glu Lys Arg Cys Thr Asn Leu Glu
        195                 200                 205
Lys Glu Asn Gln Arg Leu Thr Asp Lys Leu Lys Gln Leu Glu Ser Ala
    210                 215                 220
Gln Lys Ser Leu Glu Asn Thr Asn Asn Gln Leu Arg Gln Ala Leu Glu
225                 230                 235                 240
Asn Ser Asn Val Gln Leu Ala Gln Ala Lys Glu Unk Ile Ala Ile Glu
                245                 250                 255
Unk Ser Glu Leu Unk Arg Arg Asn Arg Thr Leu Glu Glu Leu Arg Gly
            260                 265                 270
Tyr Gly Ser Gln Lys Unk Ile Trp Thr Tyr Thr Unk Gly Val
        275                 280                 285
```

(2) INFORMATION FOR SEQ ID NO:704:

(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:704

```
Val Leu Arg Lys Leu Leu Gly Lys Asn Cys Ile Glu Thr His Lys Gly
1               5                   10                  15
Val Gly Tyr Arg Leu Thr His Tyr Glu Lys Lys Ser Leu Lys Leu Phe
            20                  25                  30
Leu Gly Thr Tyr Leu Gly Ser Ser Phe Val Leu Met Leu Val Ile Ser
        35                  40                  45
Val Leu Ala Phe Asn Tyr Glu Lys Asn Glu Lys Ile Lys Unk Ile Arg
    50                  55                  60
Met Asp Met Asp Lys Met Ala Ser Lys Ile Ala Ser Glu Ile Ile Gln
65                  70                  75                  80
Leu His Met Gln Thr His Ala Asp Tyr His Asn Ala Leu Asn Ala Leu
                85                  90                  95
Ile Ser Arg Tyr Lys Asp Val Ser Ile Unk Leu Unk Asp Thr
            100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:704:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704

```
Val Leu Arg Lys Leu Leu Gly Lys Asn Cys Ile Glu Thr His Lys Gly
1               5                  10                  15
Val Gly Tyr Arg Leu Thr His Tyr Glu Lys Lys Ser Leu Lys Leu Phe
            20                  25                  30
Leu Gly Thr Tyr Leu Gly Ser Ser Phe Val Leu Met Leu Val Ile Ser
        35                  40                  45
Val Leu Ala Phe Asn Tyr Glu Lys Asn Glu Lys Ile Lys Unk Ile Arg
    50                  55                  60
Met Asp Met Asp Lys Met Ala Ser Lys Ile Ala Ser Glu Ile Ile Gln
65                  70                  75                  80
Leu His Met Gln Thr His Ala Asp Tyr His Asn Ala Leu Asn Ala Leu
                85                  90                  95
Ile Ser Arg Tyr Lys Asp Val Ser Ile Unk Leu Unk Asp Thr
            100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:705:

(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:705

```
Met Arg Ile Ile Ile Arg Leu Leu Ser Phe Lys Met Asn Ala Phe Leu
1               5                  10                  15
Lys Leu Ala Leu Ala Ser Leu Met Gly Gly Leu Trp Tyr Ala Phe Asn
            20                  25                  30
Gly Glu Gly Ser Glu Ile Val Ala Ile Gly Ile Phe Val Leu Ile Leu
        35                  40                  45
Phe Val Phe Phe Ile Arg Pro Val Ser Phe Gln Asp Pro Glu Lys Arg
    50                  55                  60
Glu Glu Tyr Ile Glu Arg Leu Lys Lys Asn His Glu Arg Lys Met Ile
65                  70                  75                  80
Leu Gln Asp Lys Gln Lys Glu Glu Gln Met Arg Leu Tyr Gln Ala Lys
                85                  90                  95
Lys Glu Arg Glu Ser Arg Gln Lys Gln Asp Leu Lys Glu Gln Met Lys
            100                 105                 110
Lys Tyr Ser
        115
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:706:

(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:706

```
Val Arg Ser Cys Lys Gln Ile Phe Asp Lys Gly Leu Lys Pro Tyr Tyr
1               5                  10                  15
Lys His Ser Val Cys Leu Lys Pro Phe Phe Arg Phe Cys Phe Leu Lys
            20                  25                  30
Ile His Ala Tyr Gln Gln Arg Tyr Arg Ala Phe Ala Leu Thr Leu Phe
        35                  40                  45
Ser Cys Lys Phe Phe Asn Ala Cys Lys Ile Phe Ile Pro Ile Ile Asp
    50                  55                  60
Phe Lys Ile Val Phe Ile Pro Ile Leu Lys His Gln Ala Lys Leu Lys
65                  70                  75                  80
Arg Val Ser Asn Ala Tyr
                85
```

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...44

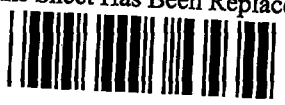
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707

```
Met Cys Gly Met Gly Phe Ile Gly Phe Lys Thr Lys Leu Thr Gln Thr
1               5                  10                  15
Lys Ala Phe Ile Ile Leu Ile Pro Ile Phe Gln Asp Arg Ala Val Lys
            20                  25                  30
Ala Ala Thr Arg Ser Ala Pro Ile Gln Leu Ile Cys
        35                  40
```

(2) INFORMATION FOR SEQ ID NO:708:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 560 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

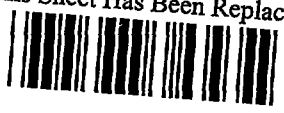
This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708

```
Met Gly Asn Phe Asn Ser Tyr Gly Asp Leu Val Phe Asn Leu Ser His
1               5                  10                  15
Ser Val Ser His Ala Ile Ile Asn Thr Gln Gly Thr Ala Thr Ile Met
            20                  25                  30
Ala Asn Asn Asn Pro Leu Ile Gln Phe Asn Ala Ser Ser Lys Glu Val
        35                  40                  45
Gly Thr Tyr Thr Leu Ile Asp Ser Ala Lys Ala Ile Tyr Tyr Gly Tyr
    50                  55                  60
Asn Asn Gln Ile Thr Gly Gly Ser Ser Leu Asp Asn Tyr Leu Lys Leu
65                  70                  75                  80
Tyr Ala Leu Ile Asp Ile Asn Gly Lys His Met Val Met Thr Asp Asn
                85                  90                  95
Gly Leu Thr Tyr Asn Gly Gln Ala Val Ser Val Lys Asp Gly Gly Leu
            100                 105                 110
Val Val Gly Phe Lys Asp Ser Gln Asn Gln Tyr Ile Tyr Thr Ser Ile
        115                 120                 125
Leu Tyr Asn Lys Val Lys Ile Ala Val Ser Asn Asp Pro Ile Asn Asn
    130                 135                 140
Pro Gln Ala Pro Thr Leu Lys Gln Tyr Ile Ala Gln Ile Gln Gly Val
145                 150                 155                 160
Gln Ser Val Asp Ser Ile Unk Gln Ala Gly Gly Asn Gln Ala Ile Asn
                165                 170                 175
Trp Leu Asn Lys Ile Phe Glu Thr Lys Gly Ser Pro Leu Phe Ala Pro
            180                 185                 190
Tyr Tyr Leu Glu Ser His Ser Thr Lys Asp Leu Thr Thr Ile Ala Gly
        195                 200                 205
Asp Ile Ala Asn Thr Leu Glu Val Ile Ala Asn Pro Asn Phe Lys Asn
    210                 215                 220
Asp Ala Thr Asn Ile Leu Gln Ile Asn Thr Tyr Thr Gln Gln Met Ser
225                 230                 235                 240
Arg Leu Ala Lys Leu Ser Asp Thr Ser Thr Phe Ala Arg Ser Asp Phe
                245                 250                 255
Leu Glu Arg Leu Glu Ala Leu Lys Asn Lys Arg Phe Ala Asp Ala Ile
            260                 265                 270
Pro Asn Ala Met Asp Val Ile Leu Lys Tyr Ser Gln Arg Asn Arg Val
        275                 280                 285
Lys Asn Asn Val Trp Ala Thr Gly Val Gly Gly Ala Ser Phe Ile Ser
    290                 295                 300
Gly Gly Thr Unk Thr Leu Tyr Gly Ile Asn Unk Gly Tyr Asp Arg Phe
305                 310                 315                 320
Ile Lys Gly Val Ile Val Gly Gly Tyr Ala Ala Tyr Gly Tyr Ser Gly
                325                 330                 335
Phe His Ala Asn Ile Thr Gln Ser Gly Ser Ser Asn Val Asn Val Gly
            340                 345                 350
Val Tyr Ser Arg Ala Phe Ile Lys Arg Ser Glu Leu Thr Met Ser Leu
        355                 360                 365
Asn Glu Thr Trp Gly Tyr Asn Lys Thr Phe Ile Asn Ser Tyr Asp Pro
    370                 375                 380
Leu Leu Ser Ile Ile Asn Gln Ser Tyr Arg Tyr Asp Thr Trp Thr Thr
385                 390                 395                 400
Asp Ala Lys Ile Asn Tyr Gly Tyr Asp Phe Met Phe Lys Asp Lys Ser
                405                 410                 415
```

```
Val Ile Phe Lys Pro Gln Val Gly Leu Ser Tyr Tyr Tyr Ile Gly Leu
            420                 425                 430
Ser Gly Leu Arg Gly Ile Met Asp Asp Pro Ile Tyr Asn Gln Phe Arg
        435                 440                 445
Ala Asn Ala Asp Pro Asn Lys Lys Ser Val Leu Thr Ile Asn Phe Ala
    450                 455                 460
Leu Glu Ser Arg His Tyr Phe Asn Lys Asn Ser Tyr Tyr Phe Val Ile
465                 470                 475                 480
Ala Asp Val Gly Arg Asp Leu Phe Ile Asn Ser Met Gly Asp Lys Met
                485                 490                 495
Val Arg Phe Ile Gly Asn Asn Thr Leu Ser Tyr Arg Asp Gly Gly Arg
            500                 505                 510
Tyr Asn Thr Phe Ala Ser Ile Ile Thr Gly Gly Glu Ile Arg Leu Phe
        515                 520                 525
Lys Thr Phe Tyr Val Asn Ala Gly Ile Gly Ala Arg Phe Gly Leu Asp
    530                 535                 540
Tyr Lys Asp Ile Asn Ile Thr Gly Asn Ile Gly Met Unk Unk Unk Phe
545                 550                 555                 560
```

(2) INFORMATION FOR SEQ ID NO:709:

(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:709

```
Leu Met Thr Lys Ser Leu Lys Leu Ile Gln Lys Gly Val Lys Asn Leu
1               5                   10                  15
Tyr Glu Thr Leu Lys Asn Arg Ala Leu Glu His Gln Asp Thr Leu Met
            20                  25                  30
Val Gly Arg Ser His Gly Val Phe Gly Glu Pro Ile Thr Phe Gly Leu
        35                  40                  45
Val Leu Ala Leu Phe Ala Asp Glu Ile Lys Arg His Leu Lys Ala Leu
    50                  55                  60
Asp Leu Thr Met Glu Phe Ile Unk Val Gly Ala Ile Ser Gly Ala Met
65                  70                  75                  80
Gly Asn Phe Ala His Ala Pro Leu Glu Leu Glu Glu Leu Ala Cys Gly
                85                  90                  95
Phe Leu Gly Leu Lys Thr Ala Asn Ile Ser Asn Gln Val Ile Gln Arg
            100                 105                 110
Asp Arg Tyr Ala Gly Leu His Ala Ile Trp Leu Phe
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:709

```
Leu Met Thr Lys Ser Leu Lys Leu Ile Gln Lys Gly Val Lys Asn Leu
1               5                  10                  15
Tyr Glu Thr Leu Lys Asn Arg Ala Leu Glu His Gln Asp Thr Leu Met
            20                  25                  30
Val Gly Arg Ser His Gly Val Phe Gly Glu Pro Ile Thr Phe Gly Leu
        35                  40                  45
Val Leu Ala Leu Phe Ala Asp Glu Ile Lys Arg His Leu Lys Ala Leu
    50                  55                  60
Asp Leu Thr Met Glu Phe Ile Unk Val Gly Ala Ile Ser Gly Ala Met
65                  70                  75                  80
Gly Asn Phe Ala His Ala Pro Leu Glu Leu Glu Glu Leu Ala Cys Gly
                85                  90                  95
Phe Leu Gly Leu Lys Thr Ala Asn Ile Ser Asn Gln Val Ile Gln Arg
            100                 105                 110
Asp Arg Tyr Ala Gly Leu His Ala Ile Trp Leu Phe
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:710

```
Leu Ser Asp Ala Ser Lys Arg Ser Leu Asn Pro Thr Leu Met Met Asn
1               5                  10                  15
Asn Asn Asn Thr Leu Pro Lys Pro Leu Glu Glu Ser Leu Asp Leu Lys
            20                  25                  30
Glu Phe Ile Ala Leu Phe Lys Thr Phe Phe Ala Lys Glu Arg Gly Ser
        35                  40                  45
Ile Ala Leu Glu Asn Asp Leu Lys Gln Ala Phe Thr Tyr Leu Asn Glu
    50                  55                  60
Val Asp Ala Ile Gly Leu Pro Ala Pro Unk Lys Arg Glu Arg Lys Arg
65                  70                  75                  80
Ser Tyr Cys Cys Gln Thr His Gln Ile Arg Asp Ala Pro Phe Arg
                85                  90                  95
```

(2) INFORMATION FOR SEQ ID NO:710:

(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:710

```
Leu Ser Asp Ala Ser Lys Arg Ser Leu Asn Pro Thr Leu Met Met Asn
1               5                  10                  15
Asn Asn Asn Thr Leu Pro Lys Pro Leu Glu Glu Ser Leu Asp Leu Lys
            20                  25                  30
Glu Phe Ile Ala Leu Phe Lys Thr Phe Phe Ala Lys Glu Arg Gly Ser
        35                  40                  45
Ile Ala Leu Glu Asn Asp Leu Lys Gln Ala Phe Thr Tyr Leu Asn Glu
    50                  55                  60
Val Asp Ala Ile Gly Leu Pro Ala Pro Unk Lys Arg Glu Arg Lys Arg
65                  70                  75                  80
Ser Tyr Cys Cys Gln Thr His Gln Ile Arg Asp Ala Pro Phe Arg
                85                  90                  95
```

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711

```
Leu Pro Ile Ile Leu Unk Val Ile Val Met Met Phe Phe Ser Lys Ile
1               5                  10                  15
Val Gly Asp Phe Ile Glu Lys His Tyr Arg Val Lys Thr Leu Ala Phe
            20                  25                  30
Val Phe Leu Leu Val Val Gly Val Phe Leu Phe Leu Glu Gly Leu His
        35                  40                  45
Leu His Ile Asn Lys Asn Tyr Leu Tyr Ala Gly Ile Gly Phe Ala Leu
    50                  55                  60
Leu Ile Glu Cys Leu Unk Ile Phe Ile Glu Lys Lys Met Lys Lys Ser
65                  70                  75                  80
```

(2) INFORMATION FOR SEQ ID NO:711:

(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:711

```
Leu Pro Ile Ile Leu Unk Val Ile Val Met Met Phe Phe Ser Lys Ile
1               5                  10                  15
Val Gly Asp Phe Ile Glu Lys His Tyr Arg Val Lys Thr Leu Ala Phe
            20                  25                  30
Val Phe Leu Leu Val Val Gly Val Phe Leu Phe Leu Glu Gly Leu His
        35                  40                  45
Leu His Ile Asn Lys Asn Tyr Leu Tyr Ala Gly Ile Gly Phe Ala Leu
    50                  55                  60
Leu Ile Glu Cys Leu Unk Ile Phe Ile Glu Lys Lys Met Lys Lys Ser
65                  70                  75                  80
```

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(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:712

```
Met Glu Ser Asn Gln Ser Leu Pro Met Ala Leu Ile Ser Cys Ser Pro
1               5                  10                  15
Asn Ala Lys Gly Ala Asp Ile Lys Gly Tyr Asn Gly Leu Val Gly Glu
            20                  25                  30
Leu Ile Glu Arg Asn Phe Gln Arg Tyr Gly Val Pro Leu Leu Leu Ser
        35                  40                  45
Thr Leu Thr Asn Gly Leu Leu Ile Gly Ile Thr Ser Ala Leu Asn Asn
    50                  55                  60
Arg Gly Asn Lys Glu Glu Val Thr Asn Phe Phe Gly Asp Tyr Leu Leu
65                  70                  75                  80
Leu Gln Leu Met Arg Gln Ser Gly Met Gly Ile Asn Gln Val Val Asn
                85                  90                  95
```

```
Gln Ile Leu Arg Asp Lys Ser Lys Ile Ala Pro Ile Val Val Ile Arg
            100                 105                 110
Glu Gly Ser Arg Val Phe Ile Ser Pro Asn Thr Asp Ile Phe Phe Pro
        115                 120                 125
Ile Pro Arg Glu Asn Glu Val Ile Ala Glu Phe Leu Lys
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...51

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713

```
Val Asn Phe Tyr Leu Ser Pro Lys Asp Tyr His His Tyr His Ala Pro
1               5                   10                  15
Cys Asp Leu Glu Ile Leu Glu Ala Arg Tyr Phe Ala Gly Lys Leu Leu
            20                  25                  30
Pro Val Asn Lys Pro Ser Leu His Lys Lys Gln Asn Leu Phe Val Gly
        35                  40                  45
Asn Glu Arg
    50
```

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(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:714

```
Met Asp Ile Leu Lys Ala Glu His Leu Asn Lys Gln Ile Lys Lys Thr
1               5                   10                  15
Lys Ile Val Ser Asp Val Ser Leu Glu Val Lys Ser Gly Glu Val Val
            20                  25                  30
Gly Leu Leu Gly Pro Asn Gly Ala Gly Lys Thr Thr Thr Phe Tyr Met
        35                  40                  45
Ile Cys Gly Leu Leu Glu Pro Ser Gly Gly Ser Val Tyr Leu Asn Asp
```

```
    50                  55                  60
Val Asp Leu Ala Lys Tyr Pro Leu His Lys Arg Ser Asn Leu Gly Ile
65                  70                  75                  80
Gly Tyr Leu Pro Gln Glu Ser Ser Ile Phe Lys Glu Leu Ser Val Glu
                85                  90                  95
Glu Asn Leu Ala Leu Ala Gly Glu Ser Thr Phe Lys Asn Ser Lys Glu
            100                 105                 110
Ser Glu Glu Lys Met Glu Ser Leu Leu Asp Ala Phe Asn Ile Gln Ala
        115                 120                 125
Ile Arg Glu Arg Lys Gly Met Ser Leu Ser Gly Gly Glu Arg Arg Arg
    130                 135                 140
Val Glu Ile Ala Arg Ala Leu Met Lys Asn Pro Lys Phe Val Leu Leu
145                 150                 155                 160
Asp Glu Pro Phe Ala Gly Val Asp Pro Ile Ala Val Ile Asp Ile Gln
                165                 170                 175
Arg Ile Ile Glu Ser Leu Ile Gly Leu Asn Ile Gly Val Leu Ile Thr
            180                 185                 190
Asp His Asn Val Arg Glu Thr Leu Ser Val Cys His Arg Ala Tyr Val
        195                 200                 205
Ile Lys Ser Gly Thr Leu Leu Ala Ala Gly Thr Leu Met Lys Phe Met
    210                 215                 220
Lys Thr Leu Trp Cys Val Ser Ile Ile
225                 230
```

(2) INFORMATION FOR SEQ ID NO:715:

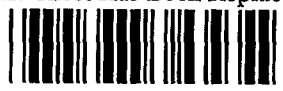
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715

```
Met Ile Lys Ala Arg Phe Lys Lys Arg Leu Leu Gly Ser Arg Gly Ala
1               5                   10                  15
Phe Asp Leu Asn Ile Asp Leu Glu Ile Lys Glu Ala Glu Val Val Ala
            20                  25                  30
Leu Leu Gly Glu Ser Gly Ala Gly Lys Ser Thr Ile Leu Arg Ile Leu
        35                  40                  45
Ala Gly Leu Glu Ala Val Ser Ser Gly Tyr Ile Glu Ala Asn His Ser
    50                  55                  60
Val Trp Leu Asp Thr Gln Lys Lys Ile Phe Leu Lys Pro Gln Gln Arg
65                  70                  75                  80
Lys Ile Gly Phe Val Phe Gln Asp Tyr Ala Leu Phe Pro His Leu Asn
                85                  90                  95
Val Tyr Gln Asn Ile Ala Phe Ala His Pro Lys Asp Lys Asn Lys Ile
            100                 105                 110
His Glu Val Leu Arg Leu Met Arg Leu Glu Asn Leu Ser Gln Gln Lys
        115                 120                 125
Ile Pro Lys Leu Ser Gly Gly Gln Ala Gln Arg Val Ala Leu Ala Arg
    130                 135                 140
Ala Leu Ile Ala Ala Lys Asn Leu Leu Leu Leu Asp Glu Pro Leu Asn
145                 150                 155                 160
```

```
Ala Leu Asp Asn Ala Leu Lys Asn Glu Val Gln Gln Gly Leu Leu Asp
                165                 170                 175
Phe Ile Lys Arg Glu Asn Leu Ser Val Leu Leu Val Ser His Asp Pro
            180                 185                 190
Asn Glu Ile Thr Lys Leu Ala Arg Thr Phe Leu Phe Leu Asn Asn Gly
        195                 200                 205
Val Ile Asp Pro Asn Gln Glu Asn Arg Leu Phe Ser Asn Arg Leu Leu
    210                 215                 220
Val Lys Pro Leu Phe Glu Asp Glu Asn Tyr Cys His Tyr Glu Val Ile
225                 230                 235                 240
Pro Gln Thr Ile Ser Leu Pro Lys Asp Cys Leu Asn Pro Thr Phe Lys
                245                 250                 255
Leu Asp Phe Ile Gln Asn Lys Lys Phe
            260                 265
```

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

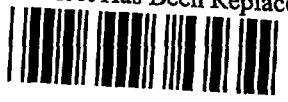
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715

```
Met Ile Lys Ala Arg Phe Lys Lys Arg Leu Leu Gly Ser Arg Gly Ala
1               5                   10                  15
Phe Asp Leu Asn Ile Asp Leu Glu Ile Lys Glu Ala Glu Val Val Ala
            20                  25                  30
Leu Leu Gly Glu Ser Gly Ala Gly Lys Ser Thr Ile Leu Arg Ile Leu
        35                  40                  45
Ala Gly Leu Glu Ala Val Ser Ser Gly Tyr Ile Glu Ala Asn His Ser
    50                  55                  60
Val Trp Leu Asp Thr Gln Lys Lys Ile Phe Leu Lys Pro Gln Gln Arg
65                  70                  75                  80
Lys Ile Gly Phe Val Phe Gln Asp Tyr Ala Leu Phe Pro His Leu Asn
                85                  90                  95
Val Tyr Gln Asn Ile Ala Phe Ala His Pro Lys Asp Lys Asn Lys Ile
            100                 105                 110
His Glu Val Leu Arg Leu Met Arg Leu Glu Asn Leu Ser Gln Gln Lys
        115                 120                 125
Ile Pro Lys Leu Ser Gly Gly Gln Ala Gln Arg Val Ala Leu Ala Arg
    130                 135                 140
Ala Leu Ile Ala Ala Lys Asn Leu Leu Leu Leu Asp Glu Pro Leu Asn
145                 150                 155                 160
Ala Leu Asp Asn Ala Leu Lys Asn Glu Val Gln Gln Gly Leu Leu Asp
                165                 170                 175
Phe Ile Lys Arg Glu Asn Leu Ser Val Leu Leu Val Ser His Asp Pro
            180                 185                 190
Asn Glu Ile Thr Lys Leu Ala Arg Thr Phe Leu Phe Leu Asn Asn Gly
        195                 200                 205
Val Ile Asp Pro Asn Gln Glu Asn Arg Leu Phe Ser Asn Arg Leu Leu
    210                 215                 220
Val Lys Pro Leu Phe Glu Asp Glu Asn Tyr Cys His Tyr Glu Val Ile
```

This Sheet Has Been Replaced



```
225                 230                 235                 240
Pro Gln Thr Ile Ser Leu Pro Lys Asp Cys Leu Asn Pro Thr Phe Lys
                245                 250                 255

Leu Asp Phe Ile Gln Asn Lys Lys Phe
            260                 265
```

(2) INFORMATION FOR SEQ ID NO:716:

(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:716

```
Met Lys Glu Ile Val Thr Ile Glu Asn Val Ser Phe Asn Tyr His Asn
1               5                  10                  15
Arg Ala Ile Phe Lys Asp Phe Asn Leu Ser Ile Gln Glu Gly Asp Phe
            20                  25                  30
Leu Cys Val Leu Gly Glu Ser Gly Ser Gly Lys Ser Thr Leu Leu Gly
        35                  40                  45
Leu Ile Leu Gly Leu Leu Lys Pro Ser Leu Gly Ser Val Lys Ile Phe
    50                  55                  60
Asn Glu Thr Leu Ser Asn Asn Ala Phe Leu Arg Gln Lys Ile Gly Tyr
65                  70                  75                  80
Ile Ala Gln Gly Asn Ser Leu Phe Pro His Leu Asn Ala Leu Gln Asn
                85                  90                  95
Met Thr Phe Cys Leu Asn Leu Gln Gly Ile Asn Lys Gln Ala Ala Gln
            100                 105                 110
Lys Glu Ala Lys Ala Leu Ala Leu Lys Met Gly Leu Asp Glu Ser Leu
        115                 120                 125
Met Asp Lys Phe Pro Asn Glu Leu Ser Gly Gly Gln Ala Lys Glu Trp
    130                 135                 140
Ala Leu Leu Gly Gly Leu Ser Thr Gly Gln Asn Ser Phe Tyr
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:717:

(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

This Sheet Has Been Replaced



(B) LOCATION 1...191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717

```
Met Ile Phe Pro Glu Arg Phe Gln Asn Ala Phe Leu Gly Leu Ser Glu
1               5                  10                  15
Leu Phe Tyr Tyr Ala Ser Ser Leu Ser Phe Tyr Thr Ile Leu Ser Leu
            20                  25                  30
Ser Pro Ile Leu Leu Phe Val Phe Ser Leu Phe Val Ser His Tyr Leu
        35                  40                  45
Gln Ala His Ser Gly Glu Met Glu Ala Leu Ile Phe Pro Asn Ala Pro
    50                  55                  60
Lys Leu Ile Gly Ala Ile Lys Asp Phe Leu Glu Asn Phe Lys Lys Thr
65                  70                  75                  80
Asp Met Thr Leu Gly Thr Leu Glu Glu Val Ser Ile Val Val Ala Leu
                85                  90                  95
Val Leu Phe Cys Glu Asn Tyr Arg Ser Ile Ala Ser Lys Ile Phe Asp
            100                 105                 110
Ala Lys Pro Arg Asp Tyr Ala His Phe Lys Gly Lys Glu Ile Phe Leu
        115                 120                 125
Phe Trp Gly Phe Gly Thr Thr Leu Val Phe Leu Phe Ala Leu Pro Leu
    130                 135                 140
Val Val Phe Phe Asp Ile Lys Ile Gln Val Phe Phe Glu Asp Lys Asp
145                 150                 155                 160
Ser Ser Leu Leu His Val Leu Arg Trp Ile Gly Thr Tyr Ala Phe Phe
                165                 170                 175
Leu Ile Leu Phe Thr Ile Pro Thr Asn Lys Val Phe Lys Leu Lys
            180                 185                 190
```

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:718

```
Met Val Leu Met Ile Phe Thr Ser Ile Leu Lys Ile Ala Leu Lys Val
1               5                  10                  15
Leu Ser Glu Arg Lys Lys Asn Arg Tyr Gly Phe Pro Arg Ile Phe Asp
            20                  25                  30
Val Ala Asp Ile Glu Gln Glu Glu Arg Glu Val Ile Glu Trp Arg Glu
        35                  40                  45
Lys Lys Lys Ala Ser Lys Gln Ser Tyr Lys Gln Asn Leu Gln Ile Asn
    50                  55                  60
Lys Ile Ala Asn Asp Leu Lys Arg Asp Lys Ile Val Asp Lys Arg Thr
65                  70                  75                  80
Ile Leu Ser Val Ile Asp Ala Asp Ile Glu Arg Gly Phe Ile Pro Pro
                85                  90                  95
Lys Asp Leu Leu Lys Gln Leu Glu Lys Ile Ser Ala Ser Leu Ser Lys
            100                 105                 110
Asp Ile Val Ile Thr Ile Lys Gln Val Glu Lys Leu Glu Leu Asn Tyr
```

```
        115                 120                 125
Ala Leu Ile Asp Asn Ile Gln His Asn Thr Leu Asp Asp Thr Leu Asp
    130                 135                 140
Phe Thr Phe Ile Val Gly Asp Ser Leu Ser Val Gln Ser Leu Tyr Val
145                 150                 155                 160
Thr Phe Asn Leu Val Ile Asp Ile Asp Arg Pro Met Ser Glu Gln Phe
                165                 170                 175
Leu Asn Unk Ile Gly Lys Leu Gly Ser Phe Glu Ser Arg Glu Gln Ala
            180                 185                 190
Leu Glu Trp Val Arg Leu Ser Gln Thr Lys Leu Ile Ile Glu Thr Pro
        195                 200                 205
Lys Glu Ala Leu Lys Asn Ala Glu Leu Ser Gln Ile Glu Glu Ile Leu
    210                 215                 220
Thr Gly Cys Ile Phe Asn Gly Ala Tyr Arg Leu Gln Asn Asp Leu Lys
225                 230                 235                 240
Lys Gly Arg
```

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 236 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(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:719

```
Val Ser Glu Val Ala Ser Val Gly Gly Phe Val Lys Asp Tyr Glu Val
1               5                  10                  15
Thr Leu Gln Asn Asp Ser Leu Ile Arg Tyr Asn Leu Ser Leu Glu Gln
            20                  25                  30
Val Ala Asn Ala Ile Lys Asn Ser Asn Asn Asp Thr Gly Gly Gly Val
        35                  40                  45
Ile Leu Glu Asn Gly Phe Glu Lys Ile Ile Arg Ser His Gly Tyr Ile
    50                  55                  60
Gln Ser Leu Asn Asp Leu Glu Glu Ile Val Val Lys Lys Glu Gly Ala
65                  70                  75                  80
Ile Pro Leu Lys Ile Lys Asp Ile Ala Ser Val Arg Leu Ala Pro Lys
                85                  90                  95
Pro Arg Arg Gly Ala Ala Asn Leu Asn Gly Asp Lys Glu Val Val Gly
            100                 105                 110
Gly Ile Val Met Val Arg Tyr His Ala Asp Thr Tyr Lys Val Leu Lys
        115                 120                 125
Ala Ile Lys Glu Lys Ile Ala Thr Leu Gln Ala Ser Asn Pro Asp Val
    130                 135                 140
Lys Ile Thr Ser Val Tyr Asp Arg Ser Glu Leu Ile Glu Lys Gly Ile
145                 150                 155                 160
Asp Asn Leu Ile His Thr Leu Ile Glu Glu Ser Val Ile Val Leu Val
                165                 170                 175
Ile Ile Ala Ile Phe Leu Leu His Phe Arg Ser Ala Leu Val Val Ile
            180                 185                 190
Ile Thr Leu Pro Leu Arg Val Cys Ile Ser Phe Leu Leu Met Ser Tyr
        195                 200                 205
```

```
Phe Asn Ile Glu Ala Ser Ile Met Ser Leu Gly Gly Ile Ala Ile Ala
    210                 215                 220
Ile Gly Ala Met Val Asn Ala Ala Ile Val Met Val
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:720:

(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:720

```
Val Glu Thr Phe Leu Arg Ile Phe Glu Lys Asp Ile Phe Asn Thr Pro
1               5                  10                  15
Tyr Lys Leu Glu Val Ile Asn Ala Thr Glu Gly Gly Ala Arg Ile Lys
            20                  25                  30
Gly Thr Lys Glu Met Pro Phe Lys Glu Val Cys Glu Lys Ile Asp Lys
        35                  40                  45
Ser Lys Pro Lys Pro Pro Ile Asn Leu Ile Tyr Pro Thr Gln Ser Glu
    50                  55                  60
Gln Ala Lys Asn Leu Lys Ile Ala Lys Lys Lys Cys Glu Glu Ile Ile
65                  70                  75                  80
Lys Tyr Ala Asn Glu Lys Lys Thr Gln Val Glu Glu Ala Phe Leu Lys
                85                  90                  95
Val Ala Glu Phe Leu Glu Lys Val Glu Lys Leu His Glu Lys Asn Lys
            100                 105                 110
Leu Glu Glu Leu Asp Phe Glu Glu Leu Glu Asn Leu Ser Ala Glu Ile
        115                 120                 125
Asp Asn Val Lys Glu Leu Phe Asp Asp Lys Arg Phe Asn Ser Tyr Phe
    130                 135                 140
Met Asp Ala Ile Gln Ser Tyr Ile Phe His Gln Glu Leu His Ile Ala
145                 150                 155                 160
Glu Ile Val Cys Lys Lys Thr Ser Asn Glu Asp Gly Ile Lys Gly
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

This Sheet Has Been Replaced



(A) NAME/KEY: misc_feature
(B) LOCATION 1...226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721

```
Met Lys Thr Pro Cys Asn Ala Tyr Phe Leu Lys Thr Pro Pro Lys Asn
1               5                  10                  15
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Phe Leu Leu
            20                  25                  30
Leu Ala Ser Ala Leu Trp Leu Ile Pro Arg Ser Ala Ile Glu Unk Lys
        35                  40                  45
Pro Leu Val Val Ala Thr Lys Pro Ser Ser Glu Gln Tyr Ile Leu Gly
    50                  55                  60
Glu Ile Leu Ser Leu Leu Leu Glu Lys His His Ile Pro Ile Lys Arg
65                  70                  75                  80
Ala Phe Gly Ile Gly Gly Gly Thr Met Asn Ile His Pro Ala Leu Ile
                85                  90                  95
Arg Gly Asp Phe Asp Leu Tyr Val Glu Tyr Thr Gly Thr Ala Trp Val
            100                 105                 110
Asn Thr Leu Lys Asn Pro Leu Thr Gln Lys Val Asp Phe Glu Thr Ile
        115                 120                 125
Lys Lys Arg Tyr Glu Lys Glu Phe Asn Leu Leu Trp Val Gly Leu Leu
    130                 135                 140
Gly Phe Asn Asn Thr Tyr Ser Leu Ala Ile Ser Lys Glu Asp Ala Gln
145                 150                 155                 160
Lys Tyr Ala Ile Glu Thr Phe Ser Asp Leu Ala Phe His Ser Pro Asn
                165                 170                 175
Phe Asp Phe Gly Ala Glu Unk Asp Phe Phe Glu Arg Glu Asp Ala Phe
            180                 185                 190
Lys Gly Leu Ile Lys Ala Tyr Arg Phe His Phe Arg Ser Leu His Glu
        195                 200                 205
Met Unk Ile Asn Leu Arg Tyr Lys Ser Phe Glu Ser Leu Ile Arg Unk
    210                 215                 220
Thr Leu
225
```

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722

```
Val Met Val Tyr Lys Leu Pro Lys His Gln Gln Asn Lys Val Met Ile
1               5                  10                  15
Leu Gly Leu Gly Leu Ala Met Ile Thr Arg Ile Gly Leu Leu Gly Ser
            20                  25                  30
Leu Phe Phe Ile Ser His Leu Gln Lys Pro Leu Phe Ala Ile Ala Gly
        35                  40                  45
Met Ser Phe Ser Trp Arg Asp Val Val Leu Leu Leu Gly Gly Ala Phe
    50                  55                  60
```

```
Leu Ala Phe Lys Ala Leu Val Glu Leu Lys Arg Ala Asp Leu Ser
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:723:

(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:723

```
Val Lys Phe Ser Val Leu Thr Leu Phe Pro Gln Leu Ile Leu Pro Tyr
1               5                  10                  15
Phe Glu Asp Ser Ile Leu Lys Arg Ala Leu Glu Lys Asn Leu Phe Glu
            20                  25                  30
Leu Glu Val Leu Asn Leu Arg Asp Phe Ser Ala Asn Lys Tyr Gln Lys
        35                  40                  45
Ala Unk Ser His Ala His Trp Trp Gly Cys Gly Ala Asn Phe Arg Pro
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:723:

(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:723

```
Val Lys Phe Ser Val Leu Thr Leu Phe Pro Gln Leu Ile Leu Pro Tyr
1               5                  10                  15
Phe Glu Asp Ser Ile Leu Lys Arg Ala Leu Glu Lys Asn Leu Phe Glu
            20                  25                  30
Leu Glu Val Leu Asn Leu Arg Asp Phe Ser Ala Asn Lys Tyr Gln Lys
        35                  40                  45
Ala Unk Ser His Ala His Trp Trp Gly Cys Gly Ala Asn Phe Arg Pro
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:724:

This Sheet Has Been Replaced



(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:724

```
Leu Trp Arg Thr Pro Lys Thr Pro Leu Val Ile Lys Pro Tyr Leu Lys
1               5                  10                  15
Ser Met Ser Asp Ser Glu Ile Phe Ala Unk Unk Cys Val Gly Met Ala
            20                  25                  30
Ser Val Unk Gly Pro Val Leu Ala Gly Tyr Ala Ser Met Gly Ile Pro
        35                  40                  45
Leu Pro Tyr Leu Ile Ala Ala Ser Phe Met Ser Ala Pro Gly Gly Leu
    50                  55                  60
Leu Phe Ala Lys Thr Ile Tyr Pro Gln Asn Glu Thr Ile Ser Ser His
65                  70                  75                  80
Ala Asp Val Ser Ala Glu Glu His Val Asn Ile Ile Glu Ala Unk Ala
                85                  90                  95
Unk Gly Ala Ser Thr Gly Unk His Leu Ala Leu His Val Gly Ala Met
            100                 105                 110
Leu Leu Ala Phe Val Gly Met Val Ala Leu Val Asn Gly Leu Leu Gly
        115                 120                 125
Val Val Gly Gly Phe Leu Gly Met Glu His
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:724:

(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:724

```
Leu Trp Arg Thr Pro Lys Thr Pro Leu Val Ile Lys Pro Tyr Leu Lys
1               5                  10                  15
Ser Met Ser Asp Ser Glu Ile Phe Ala Unk Unk Cys Val Gly Met Ala
            20                  25                  30
Ser Val Unk Gly Pro Val Leu Ala Gly Tyr Ala Ser Met Gly Ile Pro
        35                  40                  45
```

This Sheet Has Been Replaced



```
Leu Pro Tyr Leu Ile Ala Ala Ser Phe Met Ser Ala Pro Gly Gly Leu
    50                  55                  60
Leu Phe Ala Lys Thr Ile Tyr Pro Gln Asn Glu Thr Ile Ser Ser His
65                  70                  75                  80
Ala Asp Val Ser Ala Glu Glu His Val Asn Ile Ile Glu Ala Unk Ala
                85                  90                  95
Unk Gly Ala Ser Thr Gly Unk His Leu Ala Leu His Val Gly Ala Met
            100                 105                 110
Leu Leu Ala Phe Val Gly Met Val Ala Leu Val Asn Gly Leu Leu Gly
        115                 120                 125
Val Val Gly Gly Phe Leu Gly Met Glu His
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:725:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725

```
Met Phe Val Val Phe Ile Glu Gly Phe Gly Leu Ala Ile Ser Leu Cys
1               5                  10                  15
Ala Ala Val Gly Ala Gln Ser Leu Phe Ile Val Glu Arg Gly Met Ala
            20                  25                  30
Arg Asn Tyr Val Phe Leu Ile Cys Ala Leu Cys Phe Met Cys Asp Ile
        35                  40                  45
Val Leu Met Ser Met Gly Val Phe Gly Val Gly Ala Tyr Phe Ala Lys
    50                  55                  60
Asn Leu Tyr Leu Ser Leu Phe Leu Asn Leu Phe Gly Ala Val Phe Thr
65                  70                  75                  80
Gly Phe Tyr Ala Phe Leu Ala Leu Lys Thr Leu Phe Gln Thr Phe Lys
                85                  90                  95
Lys Lys Gln Val Gln Thr Pro Lys Lys Leu Ser Leu Lys Lys Thr Leu
            100                 105                 110
Leu Phe Thr Leu Gly Val Thr Leu Leu Asn Pro Gln Val Tyr Leu Glu
        115                 120                 125
Met Val Phe Leu Ile Gly Ala Ser Ala Met Ser Phe Asn Leu Val Gln
    130                 135                 140
Lys Phe Val Phe Leu Ala Gly Thr Leu Ser Ala Ala Phe Ser Trp Leu
145                 150                 155                 160
Leu Leu Leu Cys Thr Met Ser Leu Arg Tyr Gly Ser Lys Leu Leu Asn
                165                 170                 175
Asn Gln Lys Ile Phe Met Gly Val Asn Leu Phe Val Thr Ala Ile Met
            180                 185                 190
Gly Thr Leu Ser Val Thr Leu Phe Arg Asp Phe Leu Ala Leu Leu Ser
        195                 200                 205
Lys Thr
    210
```

(2) INFORMATION FOR SEQ ID NO:726:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...296

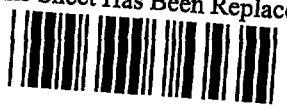
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726

```
Val Lys Pro Lys Ser Met Lys Glu Lys Leu Arg Gly Ala Met Val Asn
1               5                  10                  15
Ile Leu Arg Ile Lys Met Ile Glu Ile Ser Glu Trp Leu Gln Lys Leu
            20                  25                  30
Asp Asp Ala Leu Asp Lys Val Val Ala Lys Lys Glu Pro Glu Ser Phe
        35                  40                  45
Leu Lys Pro Ile Ile Ser Pro Ile Glu Asp Tyr Gln Lys Ser Val Arg
    50                  55                  60
Gln Ile Gln Ala Gln Phe Thr Asp Ala Pro Lys Phe Asn Glu Glu Gly
65                  70                  75                  80
Ala Tyr Pro Gln Phe Leu Ser Cys Gly Leu Leu Gln Val Arg Gly Lys
                85                  90                  95
Asn Gly Ala Asn Met Glu Phe Leu Leu Pro Lys Val Tyr Pro Phe Pro
            100                 105                 110
Pro Lys Ser Leu Tyr Ile Glu His Glu Lys Asp Gly Gln Phe Leu Arg
        115                 120                 125
Glu Met Leu Met Arg Leu Leu Ser Ser Ala Pro Leu Val Gln Leu Glu
    130                 135                 140
Val Ile Leu Ile Asp Ala Leu Ser Leu Gly Gly Ile Phe Asn Leu Ala
145                 150                 155                 160
Arg Arg Leu Leu Asp Lys Asn Asn Asp Phe Ile Tyr Gln Gln Arg Ile
                165                 170                 175
Leu Thr Glu Ser Lys Glu Ile Glu Glu Ala Leu Lys His Leu His Glu
            180                 185                 190
Tyr Leu Lys Val Asn Leu Gln Glu Lys Leu Ala Gly Phe Arg Asp Phe
        195                 200                 205
Val His Tyr Asn Glu Asn Ala Lys Asp Ser Leu Pro Leu Lys Ala Leu
    210                 215                 220
Phe Leu Ser Gly Val Asp Ala Leu Ser Lys Asp Ala Leu Tyr Tyr Leu
225                 230                 235                 240
Glu Lys Ile Met Arg Phe Gly Ser Lys Asn Gly Val Leu Ser Phe Val
                245                 250                 255
Asn Leu Glu Ser Glu Lys Asn Asn Gln Ser Ala Glu Asp Leu Lys Arg
            260                 265                 270
Tyr Ala Glu Phe Phe Lys Asp Arg Thr Ser Phe Glu Unk Leu Lys Tyr
        275                 280                 285
Leu Asn Val Glu Ile Ile Ser Asp
    290                 295
```

(2) INFORMATION FOR SEQ ID NO:727:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...94

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727

```
Val Leu Ile Ser Val Met Ile Gly Gln Asn Gln Val Leu Gly Phe Ile
1               5                  10                  15
Gly Thr Asn Phe Lys Gln Glu Leu Val Val Asp Phe Ile Val Pro Ser
            20                  25                  30
Ala Glu Ile Asn Ile Gly Asn Gln Val Ile Thr Ser Gly Leu Asp Gly
        35                  40                  45
Ile Phe Gly Ala Gly Val Phe Val Gly Glu Val Ser Ser Val Glu Asp
    50                  55                  60
His Tyr Thr Tyr Lys Ser Ala Val Leu Lys Asn Ala Phe Leu Ser Glu
65                  70                  75                  80
Ala Lys Leu Leu Arg His Val Phe Leu Ser Gly Val Lys Asn
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:728:

(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:728

```
Met Glu Ala Gln Leu Arg Phe Thr Gly Val Gly Gly Gln Gly Val Leu
1               5                  10                  15
Leu Ala Gly Glu Ile Leu Ala Glu Ala Lys Ile Val Ser Gly Gly Tyr
            20                  25                  30
Gly Thr Lys Thr Ser Thr Tyr Thr Ser Gln Val Arg Gly Gly Pro Thr
        35                  40                  45
Lys Val Asp Ile Leu Leu Asp Lys Asp Glu Ile Ile Phe Pro Tyr Ala
    50                  55                  60
Lys Glu Gly Glu Ile Asp Phe Met Leu Ser Val Ala Gln Ile Ser Tyr
65                  70                  75                  80
Asn Gln Phe
```

(2) INFORMATION FOR SEQ ID NO:729:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729

```
Met Gln Ala Trp Val Asp Lys Pro Val Leu Leu Glu Pro Asp Ser Asn
1               5                  10                  15
Ala Gln Tyr Ala Ala Val Ile Glu Ile Asp Val Ala Glu Ile Thr Glu
            20                  25                  30
Pro Ile Leu Ala Cys Pro Asn Asp Pro Asp Asp Val Ala Thr Leu Ser
        35                  40                  45
Glu Val Leu Ala Asp Thr Thr Gly Lys Arg Pro His Ala Ile Asp Glu
    50                  55                  60
Val Phe Ile Gly Ser Cys Met Thr Asn Ile Gly His Phe Arg Ala Phe
65                  70                  75                  80
Gly Glu Ile Val Lys Asn Ala Pro Pro Ser Gln Ala Arg Leu Trp Val
                85                  90                  95
Val Pro Pro Ser Lys Met Asp Glu Gln Glu Leu Ile Asn Glu Gly Tyr
            100                 105                 110
Tyr Ala Ile Phe Gly Ala Ala Gly Ala Arg Thr Glu Val Pro Gly Cys
        115                 120                 125
Ser Leu Cys Met Gly Asn Gln Ala Arg Val Arg Asp Asn Ala Val Val
    130                 135                 140
Phe Ser Thr Ser Thr Arg Asn Phe Asp Asn Arg Met Gly Arg Gly Ala
145                 150                 155                 160
Lys Val Tyr Leu Gly Ser Ala Glu Leu Gly Ala Ala Cys Ala Leu Leu
                165                 170                 175
Gly Arg Ile Pro Thr Lys Glu Glu Tyr Met Asn Leu Val Ser Glu Lys
            180                 185                 190
Leu Glu Ser Gln Lys Asp Lys Ile Tyr Arg Ser
        195                 200
```

(2) INFORMATION FOR SEQ ID NO:730:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 220 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730

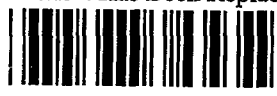
This Sheet Has Been Replaced



```
Val Gly Asn Ala Gly Val Ala Leu Ala Gly Leu Met Ser Asp Glu Ile
1               5                  10                  15
Tyr Leu Cys Ala Leu Asp Cys Ala Tyr Ile Lys Gly Phe Lys Lys His
            20                  25                  30
Ala Gln Asn Ser Tyr Tyr Gly Asp Glu Lys Glu Ile Asp Thr Ser Ser
        35                  40                  45
Leu Ile Ser Val Glu Gly Asn Val Glu Gly Tyr Glu Thr Phe Ser Asp
    50                  55                  60
Ser Leu Phe Leu Leu Ser Lys Glu Arg Ile Glu Glu Ala Leu His Tyr
65                  70                  75                  80
Tyr Gln Pro Lys Lys Val Tyr Asn Leu Ser Tyr Gly Ala Lys Ile Lys
                85                  90                  95
His Ala Val Ser Leu Asn His Ser Gln Val Lys Leu Lys Gln Ile Asn
            100                 105                 110
Lys Gln Asp Ala Ile Val Arg Ile Lys Ser Met Phe Ser Pro Arg Ser
        115                 120                 125
Asn His Ala Lys Asp Leu Lys Asn Leu Gln Lys Asn Leu Ile Arg Phe
    130                 135                 140
Lys Glu Asp Phe Phe Thr His Leu Asn Thr Pro Cys Lys Thr Lys Gln
145                 150                 155                 160
Glu Ala Phe Glu Trp Val Asp Ser Leu Ser Gly Phe Cys Gln Thr Ala
                165                 170                 175
Ser Ala Lys Thr Pro Thr Ile Gly Ile Leu Phe Glu Gly Ser Val Ala
            180                 185                 190
His Ile Leu Gln Ser Val Leu Ile Val Ser Leu His Leu Lys Glu Asn
        195                 200                 205
Glu Leu Thr Leu Leu Ser Asn Ser Leu Lys Thr Pro
    210                 215                 220
```

(2) INFORMATION FOR SEQ ID NO:731:

This Sheet Has Been Replaced



(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:731

```
Val Met Asn Phe Phe Val Gly Gly Leu Ser Ile Val Cys Asn Val Val
1               5                  10                  15
Val Ile Thr Tyr Ser Ala Leu His Pro Thr Ala Pro Val Glu Gly Ala
            20                  25                  30
Glu Asp Ile Val Gln Val Ser His His Leu Thr Ser Phe Tyr Gly Pro
        35                  40                  45
Ala Thr Gly Leu Leu Phe Gly Phe Thr Tyr Leu Tyr Ala Ala Ile Asn
    50                  55                  60
His Thr Phe Gly Leu Asp Trp Arg Pro Tyr Ser Trp Tyr Ser Leu Phe
65                  70                  75                  80
Val Ala Ile Asn Thr Val Pro Ala Ala Ile Leu Ser His Tyr Ser Asp
                85                  90                  95
Met Leu Asp Asp His Lys Val Leu Gly Ile Thr Glu Gly Asp Trp Trp
            100                 105                 110
Ala Ile Ile Unk
```

115

(2) INFORMATION FOR SEQ ID NO:731:

(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:731

```
Val Met Asn Phe Phe Val Gly Gly Leu Ser Ile Val Cys Asn Val Val
1               5                  10                  15
Val Ile Thr Tyr Ser Ala Leu His Pro Thr Ala Pro Val Glu Gly Ala
            20                  25                  30
Glu Asp Ile Val Gln Val Ser His His Leu Thr Ser Phe Tyr Gly Pro
        35                  40                  45
Ala Thr Gly Leu Leu Phe Gly Phe Thr Tyr Leu Tyr Ala Ala Ile Asn
    50                  55                  60
His Thr Phe Gly Leu Asp Trp Arg Pro Tyr Ser Trp Tyr Ser Leu Phe
65                  70                  75                  80
Val Ala Ile Asn Thr Val Pro Ala Ala Ile Leu Ser His Tyr Ser Asp
                85                  90                  95
Met Leu Asp Asp His Lys Val Leu Gly Ile Thr Glu Gly Asp Trp Trp
            100                 105                 110
Ala Ile Ile Unk
        115
```

(2) INFORMATION FOR SEQ ID NO:732:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732

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

```
Val Gln Asn Thr Pro Lys Asn Leu Pro Pro Ile Gln Leu Arg Leu Asp
        35                  40                  45
Gln Ala Tyr Glu Asp Leu Ile Lys Met Leu Asp Asn Met Gly Lys Ser
    50                  55                  60
Thr Gln Tyr Glu Phe Pro Lys Ile Lys Glu Ile Leu Glu Gln Ser Glu
65                  70                  75                  80
Glu Glu Trp Leu Gly Val Ala His Glu Glu Cys Val Ala Leu Val Met
                85                  90                  95
Leu Ile Ser Pro Lys Ala Ser Ile Glu Asn Ser Pro Ile Tyr Lys Asn
            100                 105                 110
Cys Tyr Glu Ala Tyr Val Lys Gln Arg Ile His Asp Leu Tyr Asp Phe
        115                 120                 125
Tyr Ile Glu Gly Lys Lys Val Lys Arg Lys Ile Lys Lys Ala His Glu
    130                 135                 140
His Glu Met Ala Leu Asn Lys Ser Gln Pro Leu Lys Lys Glu Pro Pro
145                 150                 155                 160
Lys Ser Glu Asn Lys Lys Gly Leu Thr Lys Pro Ser Leu Lys Asp Ala
                165                 170                 175
Lys Ile Pro Lys Gly Tyr Tyr Leu Gln Ile Gly Ala Phe Leu Asn Ser
            180                 185                 190
Pro Ser Lys Asp Phe Leu Gln Thr Leu Lys Thr Phe Pro His Gln Met
        195                 200                 205
Glu Glu Lys Asp Ser Leu Thr His Tyr Leu Ile Gly Pro Tyr Lys Thr
    210                 215                 220
Lys Glu Glu Ala Leu Lys Gln Leu Glu Asn Ala Ala Lys Ser Phe Lys
225                 230                 235                 240
Asn Lys Pro Ala Leu Val Glu Lys
                245
```

(2) INFORMATION FOR SEQ ID NO:733:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733

```
Met Gln Glu Ile Leu Ile Pro Leu Lys Glu Lys Ser Tyr Lys Val Phe
1               5                   10                  15
Leu Gly Glu Leu Pro Glu Ile Lys Leu Lys Gln Lys Ala Leu Ile Ile
            20                  25                  30
Ser Asp Ser Ile Val Ala Gly Leu His Leu Pro Tyr Leu Leu Glu Arg
        35                  40                  45
Leu Asn Ala Leu Glu Val Arg Val Cys Val Ile Glu Ser Gly Glu Lys
    50                  55                  60
Tyr Lys Asn Phe His Ser Leu Glu Arg Ile Leu Asn Asn Ala Phe Glu
65                  70                  75                  80
Met Gln Leu Asn Arg His Ser Leu Met Ile Ala Leu Gly Gly Gly Val
                85                  90                  95
Ile Ser Asp Met Val Gly Phe Ala Ser Ser Ile Tyr Phe Arg Gly Ile
            100                 105                 110
Asp Phe Ile Asn Ile Pro Tyr Asp Phe Thr Arg Ser Ser Gly Cys Glu
```

```
        115                 120                 125
Arg Gly Gly Glu Asn Arg Asp Gln His Ala Leu Trp Gln Glu Pro Asn
    130                 135                 140
Arg Ile Val Pro Pro Ala
145                 150
```

(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

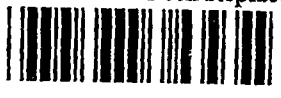
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734

```
Val Leu Leu Gly Lys His Ser Gly Ala Gly Leu Leu Ser Ala Leu Unk
1               5                  10                  15
Ala Leu Ser Phe Gly Ser Gly Val Val Ser Ile Gln Ala Leu Glu Cys
            20                  25                  30
Glu Ile Thr Ser Asn Asn Lys Pro Leu Glu Leu Val Phe Cys Glu Asn
        35                  40                  45
Phe Pro Lys Lys Leu Ser Ala Phe Ala Leu Gly Met Gly Leu Glu Asn
    50                  55                  60
Ile Pro Lys Asp Phe Lys Lys Trp Leu Glu Leu Ala Pro Cys Val Leu
65                  70                  75                  80
Asp Ala Gly Val Phe Tyr His Lys Glu Val Leu Gln Ala Leu Glu Lys
                85                  90                  95
Glu Val Ile Leu Thr Pro His Pro Lys Glu Phe Leu Ser Leu Leu Lys
            100                 105                 110
Ser Val Gly Ile Asn Ile Ser Met Leu Glu Leu Leu Asp Asn Lys Leu
        115                 120                 125
Glu Ile Ala Arg Asp Phe Ser Gln Lys Tyr Pro Lys Val Val Leu Leu
    130                 135                 140
Leu Lys Gly Ala Asn Thr Leu Ile Ala His Gln Gly Arg Val Phe Ile
145                 150                 155                 160
Asn Asn Leu Gly Ser Val Ala Leu Ala Lys Ala Gly Ser Gly Asp Val
                165                 170                 175
Leu Ala Gly Leu Ile Val Ser Leu Leu Ser Gln Asn Tyr Thr Pro Leu
            180                 185                 190
Unk Ala Ala Ile Asn Ala Ser Leu Ala His Ala Leu Ala Gly Leu Unk
        195                 200                 205
Phe Lys Asn Unk Unk Ala Leu Thr Pro Unk Asp Leu Ile Glu Lys Unk
    210                 215                 220
Lys Arg Leu
225
```

This Sheet Has Been Replaced



(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

```
Val Leu Leu Gly Lys His Ser Gly Ala Gly Leu Leu Ser Ala Leu Unk
1               5                  10                  15
Ala Leu Ser Phe Gly Ser Gly Val Val Ser Ile Gln Ala Leu Glu Cys
            20                  25                  30
Glu Ile Thr Ser Asn Asn Lys Pro Leu Glu Leu Val Phe Cys Glu Asn
        35                  40                  45
Phe Pro Lys Lys Leu Ser Ala Phe Ala Leu Gly Met Gly Leu Glu Asn
    50                  55                  60
Ile Pro Lys Asp Phe Lys Lys Trp Leu Glu Leu Ala Pro Cys Val Leu
65                  70                  75                  80
Asp Ala Gly Val Phe Tyr His Lys Glu Val Leu Gln Ala Leu Glu Lys
                85                  90                  95
Glu Val Ile Leu Thr Pro His Pro Lys Glu Phe Leu Ser Leu Leu Lys
            100                 105                 110
Ser Val Gly Ile Asn Ile Ser Met Leu Glu Leu Leu Asp Asn Lys Leu
        115                 120                 125
Glu Ile Ala Arg Asp Phe Ser Gln Lys Tyr Pro Lys Val Val Leu Leu
    130                 135                 140
Leu Lys Gly Ala Asn Thr Leu Ile Ala His Gln Gly Arg Val Phe Ile
145                 150                 155                 160
Asn Asn Leu Gly Ser Val Ala Leu Ala Lys Ala Gly Ser Gly Asp Val
                165                 170                 175
Leu Ala Gly Leu Ile Val Ser Leu Leu Ser Gln Asn Tyr Thr Pro Leu
            180                 185                 190
Unk Ala Ala Ile Asn Ala Ser Leu Ala His Ala Leu Ala Gly Leu Unk
        195                 200                 205
Phe Lys Asn Unk Unk Ala Leu Thr Pro Unk Asp Leu Ile Glu Lys Unk
    210                 215                 220
Lys Arg Leu
225
```

(2) INFORMATION FOR SEQ ID NO:735:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:735

```
Met Arg Ile Leu His Tyr Gly Gly Glu Leu Pro Cys Asp Cys Pro Lys
1               5                  10                  15
Arg Ile Ala Gly Leu Asp Phe Ala Leu Lys Ile Leu Thr Asn Ile Thr
            20                  25                  30
Ser Asp His Leu Asp Phe His Gln Asn Ile Glu Asn Tyr Arg Asp Ala
        35                  40                  45
Lys Asn Ser Phe Phe Lys Asp Glu Gly Leu Lys Val Ile Asn Arg Asp
    50                  55                  60
Glu Thr Asn Ala Leu Phe Asn Pro Ile Asn Ala Arg Thr Tyr Ala Leu
65                  70                  75                  80
Asp Lys Lys Ala His Leu Asn Val Gln Ala Phe Ser Leu Asn Pro Ser
                85                  90                  95
Ile Ser Ala Ser Leu Cys Tyr Gln His Asp Leu Arg Asp Pro Asn Leu
            100                 105                 110
Lys Glu Thr Ala Leu Ile His Ser Pro Leu Leu Gly Arg Tyr Asn Leu
        115                 120                 125
Tyr Asn Ile Leu Ala Gly Val Leu Gly Val Lys Leu Leu Thr Gln Leu
    130                 135                 140
Pro Leu Glu Thr Ile Ala Pro Leu Leu Glu Asn Phe Tyr Gly Val Lys
145                 150                 155                 160
Gly Arg Leu Glu Ile Val His Ser Lys Pro Leu Val Val Val Asp Phe
                165                 170                 175
Ala His Thr Thr Asp Gly Met Gln Gln Val Phe
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:736:

(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:736

```
Val Ser Ile Lys Glu Glu Ser Gln Thr Leu Ala Asp Ile Thr Phe Gln
1               5                  10                  15
Asn Tyr Phe Arg Met Phe Ser Lys Leu Ser Gly Met Thr Gly Thr Ala
            20                  25                  30
Gln Thr Glu Ala Thr Glu Phe Leu Glu Ile Tyr Asn Leu Glu Val Val
        35                  40                  45
Ser Ile Pro Thr Asn Leu Ala Ile Lys Arg Lys Asp Leu Asn Asp Leu
    50                  55                  60
Ile Tyr Lys Ser Glu Lys Glu Lys Phe Asp Ala Val Ile Leu Lys Ile
65                  70                  75                  80
Lys Glu Leu His Asp Lys Gly Gln Pro Val Leu Val Gly Thr Ala Ser
                85                  90                  95
Ile Glu Lys Ser Glu Thr Leu His Ala Leu Leu Lys Lys Glu Arg Ile
            100                 105                 110
Pro His Thr Val Leu Asn Ala Lys Gln His Thr Lys Glu Ala Glu Ile
        115                 120                 125
Ile Lys Asp Ala Gly Leu Lys Gly Ala Val Thr Ile Ala Thr Asn Met
    130                 135                 140
```

This Sheet Has Been Replaced



```
Ala Gly Arg Gly Val Asp Ile Lys Leu Thr Asp Glu Val Lys Glu Leu
145                 150                 155                 160
Gly Gly Leu Tyr Ile Ile Gly Thr Glu Arg His Glu Ser Arg Arg Ile
                165                 170                 175
Asp Asn Gln Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp Pro Gly Val
            180                 185                 190
Ser Gln Phe Tyr Leu Ser
        195
```

(2) INFORMATION FOR SEQ ID NO:737:

(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

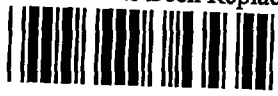
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737

```
Val Val Ala Asp Glu Val Arg Lys Leu Ala Glu Lys Thr Gln Lys Ala
1               5                   10                  15
Thr Lys Glu Ile Ala Val Val Val Lys Ser Met Gln Gln Glu Ala Asn
            20                  25                  30
Asp Ile Gln Thr Asn Thr His Asp Ile Asn Ser Ile Val Gly Ser Ile
        35                  40                  45
Lys Gly Asp Val Glu Glu Leu Lys Ser Thr Val Lys Asn Asn Met Ile
    50                  55                  60
Val Ala Gln Ala Ala Lys Tyr Thr Ile Tyr Asn Ile Asn Asn Arg Val
65                  70                  75                  80
Phe Cys Gly Unk Ala Lys Leu Asp His Val Val Phe Lys Asn Asn Leu
                85                  90                  95
Tyr Gly Met Val Unk Leu Val Ser Ile Pro Leu Thr Leu Pro Ala His
            100                 105                 110
Lys Ser Unk Arg Leu Gly Lys Trp Tyr Tyr Glu Gly Ala Gly Lys Glu
        115                 120                 125
Asn Phe Ala Asn Thr Ser Gly Tyr Arg Ala Leu Glu Ser His His Ala
    130                 135                 140
Ser Val His Ala Glu Ala Asn Asp Leu Val Lys Ala Val Gln Glu Asp
145                 150                 155                 160
His Val Thr Asp Ser Lys Tyr Leu Glu His Lys Val His Leu Met Glu
                165                 170                 175
Asp Ser Ala Lys His Val Lys Glu Asn Ile Asp Lys Met Phe Tyr Glu
            180                 185                 190
Lys Gln Asp Glu Leu Asn Lys Ile Ile Glu Lys Ile Gln Lys Gly Glu
        195                 200                 205
```

(2) INFORMATION FOR SEQ ID NO:738:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:738

```
Met Asn Thr Ser Lys Lys Leu Gly Asn Pro Leu Leu Phe Leu His Asp
1               5                  10                  15
Asn Lys Ile Leu Leu Phe Val Val Gly Val Ser Met Gly Gly Trp Ala
            20                  25                  30
Thr Ser Lys Ile Tyr Gln Phe Glu Ser Ala Leu Glu Pro Ile His Phe
        35                  40                  45
Lys Phe Ala Arg Lys Leu Ser Leu Ser Pro Phe Leu Asn Leu Ser His
    50                  55                  60
Leu Val Arg Asn Lys Pro Leu Asn Thr Thr Asp Gly Gly Phe Met Leu
65                  70                  75                  80
Pro Leu Tyr His Glu Leu Ala Thr Gln Tyr Pro Leu Leu Leu Lys Phe
                85                  90                  95
Asp Gln Gln Asn Asn Pro Arg Glu Leu Leu Arg Pro Asn Thr Leu Asn
            100                 105                 110
His Gln Leu Gln Pro Ser Leu Thr Pro Phe Lys Asp Cys Ala Val Met
        115                 120                 125
Ala Phe Arg Asn His Ser Phe Lys Asp Ser Leu Met Leu Glu Thr Cys
    130                 135                 140
Lys Thr Pro Thr Asp Trp Gln Lys Pro Ile Ser Thr Asn Leu Lys Asn
145                 150                 155                 160
Leu Asp Asp Ser Leu Asn Leu Leu Asn Leu Asn Gly Ile Leu Tyr Leu
                165                 170                 175
Ile His Asn Pro Ser Asp Leu Ser Leu Arg Arg Lys Glu Leu Trp Leu
            180                 185                 190
Ser Lys Leu Glu Asn Gln Gln Leu Ile
        195                 200
```

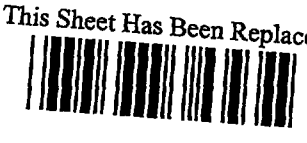
(2) INFORMATION FOR SEQ ID NO:739:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739

```
Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
1               5                  10                  15
Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
            20                  25                  30
```

```
Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
        35                  40                  45
Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
    50                  55                  60
Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
65                  70                  75                  80
Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
                85                  90                  95
Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
            100                 105                 110
Asp Gly Met Thr Val Arg Glu Leu Ser Arg Trp Cys His Asn His
        115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:740:

(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:740

```
Val Asn Val Gly Val Pro Phe Ser Tyr Gln Val Ser Ala Thr Phe Gln
1               5                   10                  15
Asn Ser Arg Leu Ser Ser Leu Leu Glu Thr Leu Lys Lys Ser Phe Leu
            20                  25                  30
Glu Lys Pro Leu Ile Glu Ser Ser Ala Asn Lys Ile Ala Asp Ile Phe
        35                  40                  45
Ser Lys Ala Val Leu Phe Leu Ala Phe Val Ser Phe Leu Leu Trp Gln
    50                  55                  60
Phe Gly Leu Gly Gly Asn Phe Glu Lys Ser Phe Asn Gly Val Tyr
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:741:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...49

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741

This Sheet Has Been Replaced



```
Met Leu Met Val Asn Gly Tyr Gln Ile Thr Met His Lys Gly Tyr Lys
1               5                  10                  15
Val Gly Phe Phe Thr Ser Gly Tyr Asn Pro Asp Phe Ala Gln Thr Ile
            20                  25                  30
Gln Asn Arg Ser Tyr Leu Met Ser Ser Tyr Glu Leu Ser Phe Leu Arg
        35                  40                  45
Asn
```

(2) INFORMATION FOR SEQ ID NO:742:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 412 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742

```
Met Val Gln Phe Gln Asn Thr Leu Ile Lys Phe His Ala Leu Ser Phe
1               5                  10                  15
Lys Asn Ala Asn Leu Ile Tyr Asn Ala Lys Leu Asn Lys Thr Cys Tyr
            20                  25                  30
Lys Glu Asn Ser Asn Thr Ile Ile Leu Arg Ile Lys Met Leu Thr Gln
        35                  40                  45
Glu Asp Val Leu Asn Ala Leu Lys Thr Ile Ile Tyr Pro Asn Phe Glu
    50                  55                  60
Lys Asp Ile Val Ser Phe Gly Phe Val Lys Asn Ile Thr Leu His Asp
65                  70                  75                  80
Asn Gln Leu Gly Leu Leu Ile Glu Ile Pro Ser Ser Ser Glu Glu Thr
                85                  90                  95
Ser Ala Ile Leu Arg Glu Asn Ile Ser Lys Ala Met Gln Glu Lys Gly
            100                 105                 110
Val Lys Ala Leu Asn Leu Asp Ile Lys Thr Pro Pro Lys Pro Gln Ala
        115                 120                 125
Pro Lys Pro Thr Thr Lys Asn Leu Ala Lys Asn Ile Lys His Val Val
    130                 135                 140
Met Ile Ser Ser Gly Lys Gly Gly Val Gly Lys Ser Thr Thr Ser Val
145                 150                 155                 160
Asn Leu Ser Ile Ala Leu Ala Asn Leu Asn Gln Lys Val Gly Leu Leu
                165                 170                 175
Asp Ala Asp Val Tyr Gly Pro Asn Ile Pro Arg Met Met Gly Leu Gln
            180                 185                 190
Asn Ala Asp Val Ile Met Asp Pro Ser Gly Lys Lys Leu Ile Pro Leu
        195                 200                 205
Lys Ala Phe Gly Val Ser Val Met Ser Met Gly Leu Leu Tyr Asp Glu
    210                 215                 220
Gly Gln Ser Leu Ile Trp Arg Gly Pro Met Leu Met Arg Ala Ile Glu
225                 230                 235                 240
Gln Met Leu Ser Asp Ile Ile Trp Gly Asp Leu Asp Val Leu Val Val
                245                 250                 255
Asp Met Pro Pro Arg Asn Arg Arg Cys Ala Ala His Ala Ala Gln Ala
            260                 265                 270
```

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

(2) INFORMATION FOR SEQ ID NO:743:

This Sheet Has Been Replaced



(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:743

```
Met Gly Val Val Ile Gly Glu Thr Thr Glu Ile Gly Asp Asp Val Thr
1               5                   10                  15
Ile Tyr His Gly Val Thr Leu Gly Gly Thr Gly Lys Phe Lys Gly Lys
            20                  25                  30
Arg His Pro Thr Leu Gly Asn Arg Val Val Val Gly Ala Gly Ala Lys
        35                  40                  45
Val Leu Gly Ala Ile Cys Val Gly Asp Asp Val Arg Ile Gly Ala Asn
    50                  55                  60
Ala Val Val Leu Ser Asp Leu Pro Thr Gly Ser Thr Ala Val Gly Ala
65                  70                  75                  80
Lys Ala Lys Thr Ile Thr Lys Asp Arg
                85
```

(2) INFORMATION FOR SEQ ID NO:744:

(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:744

```
Met Leu Ser Phe Ile Ser Ala Phe Asp Lys Arg Gly Val Ser Ile Arg
1               5                  10                  15
Leu Leu Thr Ala Leu Leu Leu Leu Phe Ser Leu Gly Leu Ala Lys Asp
            20                  25                  30
Leu Glu Ile Gln Thr Phe Val Ala Lys Tyr Leu Ser Lys Asn Gln Lys
        35                  40                  45
Ile Gln Ala Leu Gln Glu Gln Ile Asp Ala Leu Asp Ser Gln Glu Lys
    50                  55                  60
Val Val Ser Lys Trp Asp Asn Pro Ile Leu Tyr Leu Gly Tyr Asn Asn
65                  70                  75                  80
Ala Asn Val Ser Asp Phe Phe Arg Leu Asp Ser Thr Leu Met Gln Asn
                85                  90                  95
Met Ser Leu Gly Leu Ser Gln Lys Val Asp Leu Asn Gly Lys Lys Leu
            100                 105                 110
Thr Gln Ser Lys Met Ile Asn Leu Glu Lys Gln Lys Lys Ile Leu Glu
        115                 120                 125
Leu Lys Lys Thr Lys Gln Gln Leu Val Ile Asn Leu Met Ile Asn Gly
    130                 135                 140
Ile Glu Asn Tyr Lys Asn Gln Gln Glu Ile Glu Leu Leu Asn Thr Ala
145                 150                 155                 160
Ile Lys Asn Leu Glu Asn Thr Leu Tyr Gln Ala Asn His Ser Ser Ser
                165                 170                 175
Pro Asp Leu Ile Glu Ile Asp Lys Leu Glu Asn Leu Lys Ile Ala Asn
            180                 185                 190
```

(2) INFORMATION FOR SEQ ID NO:745:

This Sheet Has Been Replaced



(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:745

```
Val Unk Leu Tyr Leu Ala Leu Thr Leu Ser Leu Gly Ile Ala Met Leu
1               5                  10                  15
Leu Val Glu Met Leu Ile Gly Asn Leu Gly Lys Lys Asp Val Val Ser
            20                  25                  30
Asn Tyr Gln Ile Leu Asp Pro Lys Arg Lys Lys Tyr Tyr Pro Phe Thr
        35                  40                  45
Ser Phe Phe Ile Leu Gly Gly Pro Leu Ile Leu Ser Phe Tyr Ala Val
    50                  55                  60
Val Leu Gly Trp Val Leu Tyr Tyr Leu Phe Val Val Thr Phe Asp Leu
65                  70                  75                  80
```

```
Pro Lys Asp Leu Unk Gln Ala Lys Met Gln Phe Unk Met Leu Gln Asn
                85                  90                  95
Gly Ser Leu Ile Trp Pro Val Ile Asp Phe Ser Ala Cys
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:745:

(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:745

```
Val Unk Leu Tyr Leu Ala Leu Thr Leu Ser Leu Gly Ile Ala Met Leu
1               5                  10                  15
Leu Val Glu Met Leu Ile Gly Asn Leu Gly Lys Lys Asp Val Val Ser
            20                  25                  30
Asn Tyr Gln Ile Leu Asp Pro Lys Arg Lys Lys Tyr Tyr Pro Phe Thr
        35                  40                  45
Ser Phe Phe Ile Leu Gly Gly Pro Leu Ile Leu Ser Phe Tyr Ala Val
    50                  55                  60
Val Leu Gly Trp Val Leu Tyr Tyr Leu Phe Val Val Thr Phe Asp Leu
65                  70                  75                  80
Pro Lys Asp Leu Unk Gln Ala Lys Met Gln Phe Unk Met Leu Gln Asn
                85                  90                  95
Gly Ser Leu Ile Trp Pro Val Ile Asp Phe Ser Ala Cys
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:746:

This Sheet Has Been Replaced



(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

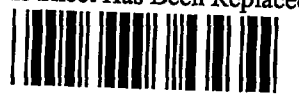
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746

```
Val Pro Ala Val Gly Gly Ala Leu Ile Trp Unk Unk Ile Unk Ile Tyr
1               5                  10                  15
Glu Leu Tyr His Gly Unk Val Asn Glu Unk Ile Phe Unk Val Leu Tyr
```

```
            20                  25                  30
Ser Ile Leu Leu Ile Gly Val Leu Ile Asp Ser Val Ile Lys Pro Ile
        35                  40                  45
Leu Ile Val Phe Ile Lys Lys Arg Ile Phe Lys Thr Thr Leu Lys Ile
    50                  55                  60
Asn Glu Ile Leu Ile Phe Phe Ser Met Ile Ala Gly Ile Ser Gln Phe
65                  70                  75                  80
Gly Phe Trp Gly Ile Ile Val Gly Pro Thr Ile Thr Ala Phe Phe Ile
                85                  90                  95
Ala Leu Leu Arg Leu Tyr Glu Asn Tyr Phe Ile Gln Lys Glu Gln Lys
            100                 105                 110
Thr Cys Glu Cys
        115
```

(2) INFORMATION FOR SEQ ID NO:747:

This Sheet Has Been Replaced



(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:747

```
Val Val Val Ile Ile Leu Val Val Val Ile Ile Gln Asn Ser Ser Ser
1               5                   10                  15
Leu Lys Glu Glu Arg Glu Gln Glu Arg Ala Ile Lys Pro Asp Thr Lys
            20                  25                  30
Asn Asn Ser Phe Asn Glu Thr Asn Pro Thr Glu Glu Lys Lys Leu Glu
        35                  40                  45
Pro Thr Pro Lys Leu Glu Glu Lys His Lys Glu Gln Asp Lys Gln Gly
    50                  55                  60
Lys Glu Ala Ile Lys Glu Asn Pro Asn Thr Ile Tyr Ile Ile Pro Lys
65                  70                  75                  80
Arg Asp Ile Trp Val Glu Val Ile Asp Leu Asp Glu Lys Lys Asn Ser
                85                  90                  95
Phe Gln Lys Val Phe Lys Lys Ser Tyr Pro Leu Glu Ala Lys Asn His
            100                 105                 110
Arg Leu Leu Leu Arg Phe Gly His Gly His Leu Ile Leu Lys Asn Asn
        115                 120                 125
His Gln Glu Gln Asp Tyr Asn Asp Ser Lys Thr Arg Arg Phe Leu Tyr
    130                 135                 140
Glu Pro Asn Lys Gly Leu Thr Leu Ile Asn Glu Ala Gln Tyr Lys Ala
145                 150                 155                 160
Leu Gln Gln
```

(2) INFORMATION FOR SEQ ID NO:748:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748

```
Met Asp Glu Ile Tyr Gln Ile Ala Lys Asn Lys Thr Leu Ile Val Ile
1               5                  10                  15
Ala His Arg Leu Ser Thr Ile Glu Arg Cys Glu Val Ile Ile Asp Met
            20                  25                  30
Ser Gln His Lys Asp Asn Leu Gly
        35                  40
```

(2) INFORMATION FOR SEQ ID NO:749:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749

```
Val Ala Gly Ser Phe Ile Ile Ala Leu Phe Ser Val Leu Ala Asp Gln
1               5                  10                  15
Phe Val Ser Val Phe Gln His Glu Asn Ala Leu Gln Arg Leu Phe Ser
            20                  25                  30
Gln Asn Ala Thr Gln Lys Gln Lys Lys Lys Ser Leu Cys
        35                  40                  45
```

(2) INFORMATION FOR SEQ ID NO:750:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:750

```
Met Val Ala Leu Ser Asn Ala Leu Ser Arg Val Phe Gly Ser Val Ala
1               5                  10                  15
Gly Tyr Lys Phe Pro Ser Phe Ile Gln Lys Ser Ile Asn Ala Leu Tyr
            20                  25                  30
Val Lys Ile Phe Lys Ile Asp Leu Ser Glu Phe Glu Pro Leu Glu Asn
        35                  40                  45
Tyr Lys Ser Leu Asn Ala Leu Phe Met Arg Ser Leu Lys Lys Glu Arg
    50                  55                  60
Pro Phe Asp Lys Ala Pro Ile Phe Ala Leu Arg Leu Ala Met Ala Leu
65                  70                  75                  80
Ile Thr Glu Cys Ala Phe Leu Asp Asn Asp Ser Ala Leu Gln Ile Lys
                85                  90                  95
Gly Met Pro Tyr Lys Ala His Glu Leu Val Gly Glu Ile Asn Pro Leu
            100                 105                 110
Ser Pro Leu Phe Ser Met
        115
```

(2) INFORMATION FOR SEQ ID NO:751:

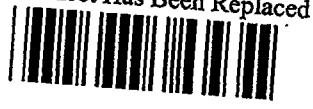
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751

```
Met Ala Val Leu Lys Lys Met Ile Gly Leu Val Ala Val Leu Ser Val
1               5                  10                  15
Leu Leu Ala Arg Asp Asn Pro Phe Glu Pro Glu Ile Asn Ser Lys Asn
            20                  25                  30
Leu Gln Gly Gly Phe Ser Gly Ile Tyr Asp Asp Tyr Leu Lys Glu Ile
        35                  40                  45
His Val Asp Leu Pro Thr Ser Ala Arg Ile Leu Lys Lys Ile Thr Leu
    50                  55                  60
Thr Tyr Gln Asp Ile Asp Gly Ser Ile His Ser Lys Val Val Gly Ile
65                  70                  75                  80
Asp Lys Ser Ile Asp Trp His Tyr Pro Leu Lys Leu Ser Gln His Thr
                85                  90                  95
Leu Asn Gln Asp Ala Phe Glu Lys Arg Tyr Gln Ile Gln Asp Phe Asp
            100                 105                 110
Phe Leu Met Ala Asn Asn Thr Met Ile Leu Arg Ser Pro Tyr Lys Ile
        115                 120                 125
Leu Arg Ser Phe Val Leu Val Asn Pro Tyr Arg Ile Val Leu Asp Thr
    130                 135                 140
Gln Lys Gly Pro Leu Asp Ile Tyr Gln Asn Met Asp Leu Asn Gln Lys
145                 150                 155                 160
Phe Phe Ser His Ile Lys Val Gly Thr His Lys Asp Tyr Tyr Arg Ile
                165                 170                 175
```

```
Thr Leu Ile Leu Asp Gly Lys Tyr Arg Tyr Leu Leu Glu Glu Lys Asn
            180                 185                 190
Gly Ala Tyr Glu Leu Lys Leu Lys
        195                 200
```

(2) INFORMATION FOR SEQ ID NO:752:

This Sheet Has Been Replaced



(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:752

```
Met Gly Gly Phe Thr Ser Ile Trp His Trp Val Ile Val Leu Leu Val
1               5                  10                  15
Ile Val Leu Leu Phe Gly Ala Lys Lys Ile Pro Glu Leu Ala Lys Gly
            20                  25                  30
Leu Gly Ser Gly Ile Lys Asn Phe Lys Lys Ala Val Lys Asp Asp Glu
        35                  40                  45
Glu Glu Ala Lys Asn Glu Leu Lys Thr Leu Asp Ala Gln Ala Thr Gln
    50                  55                  60
Thr Lys Val His Glu Thr Ser Glu Ile Lys Ser Lys Gln Glu Ser
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:753:

(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

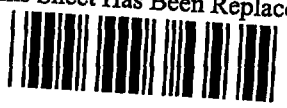
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753

```
Leu Thr Thr Lys Ala Cys Trp Leu Leu Arg Val Cys Cys Tyr Arg Ser
1               5                  10                  15
Leu Asn Ile Thr Ile Lys Asp Arg Thr Met Lys Thr Asn Gly His Phe
            20                  25                  30
Lys Asp Phe Ala Trp Lys Lys Cys Phe Leu Gly Ala Ser Val Val Ala
        35                  40                  45
Leu Leu Val Gly Cys Ser Pro His Ile Ile Glu Thr Asn Glu Val Ala
```

```
    50                  55                  60
Leu Lys Leu Asn Tyr His Pro Ala Ser Glu Lys Val Gln Ala Leu Asp
65                  70                  75                  80
Glu Lys Ile Leu Leu Leu Arg Pro Ala Phe Gln Tyr Ser Unk Asn Ile
                85                  90                  95
Cys
```

(2) INFORMATION FOR SEQ ID NO:753:

This Sheet Has Been Replaced



(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:753

```
Leu Thr Thr Lys Ala Cys Trp Leu Leu Arg Val Cys Cys Tyr Arg Ser
1               5                  10                  15
Leu Asn Ile Thr Ile Lys Asp Arg Thr Met Lys Thr Asn Gly His Phe
            20                  25                  30
Lys Asp Phe Ala Trp Lys Lys Cys Phe Leu Gly Ala Ser Val Val Ala
        35                  40                  45
Leu Leu Val Gly Cys Ser Pro His Ile Ile Glu Thr Asn Glu Val Ala
    50                  55                  60
Leu Lys Leu Asn Tyr His Pro Ala Ser Glu Lys Val Gln Ala Leu Asp
65                  70                  75                  80
Glu Lys Ile Leu Leu Leu Arg Pro Ala Phe Gln Tyr Ser Unk Asn Ile
                85                  90                  95
Cys
```

(2) INFORMATION FOR SEQ ID NO:754:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

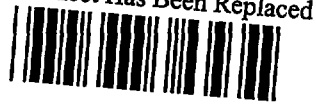
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754

```
Leu Ser Glu Trp Gln Thr Phe Cys Leu Lys Asp Leu Gly Lys Ile Val
1               5                  10                  15
Gly Gly Ala Thr Pro Pro Thr Asn Asn Pro Lys Asn Tyr Gly Asn Lys
            20                  25                  30
Ile Ala Trp Ile Thr Pro Lys Asp Leu Ser Thr Leu Gln Gly Arg Tyr
        35                  40                  45
Ile Lys Lys Gly Ser Arg Ser Ile Ser Arg Leu Gly Phe Lys Ser Cys
    50                  55                  60
Ser Cys Val Leu Leu Pro Lys His Ala Ile Leu Phe Ser Ser Arg Ala
65                  70                  75                  80
Pro Ile Gly Tyr Val Ala Ile Ala Glu Lys Arg Leu Cys Thr Asn Gln
                85                  90                  95
Gly Phe Lys Ser Ile Ile Pro Asn Lys Lys Ile Tyr Phe Glu Phe Leu
            100                 105                 110
Tyr Tyr Leu Leu Lys Tyr Tyr Lys Asp Asn Ile Ser Asn Ile Gly Gly
        115                 120                 125
Gly Thr Thr Phe Lys Glu Val Ser Gly Ala Thr Leu Gly Ser Ile Pro
    130                 135                 140
Ser
145
```

(2) INFORMATION FOR SEQ ID NO:754:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754

```
Leu Ser Glu Trp Gln Thr Phe Cys Leu Lys Asp Leu Gly Lys Ile Val
1               5                  10                  15
Gly Gly Ala Thr Pro Pro Thr Asn Asn Pro Lys Asn Tyr Gly Asn Lys
            20                  25                  30
Ile Ala Trp Ile Thr Pro Lys Asp Leu Ser Thr Leu Gln Gly Arg Tyr
        35                  40                  45
Ile Lys Lys Gly Ser Arg Ser Ile Ser Arg Leu Gly Phe Lys Ser Cys
    50                  55                  60
Ser Cys Val Leu Leu Pro Lys His Ala Ile Leu Phe Ser Ser Arg Ala
65                  70                  75                  80
Pro Ile Gly Tyr Val Ala Ile Ala Glu Lys Arg Leu Cys Thr Asn Gln
                85                  90                  95
Gly Phe Lys Ser Ile Ile Pro Asn Lys Lys Ile Tyr Phe Glu Phe Leu
            100                 105                 110
Tyr Tyr Leu Leu Lys Tyr Tyr Lys Asp Asn Ile Ser Asn Ile Gly Gly
        115                 120                 125
Gly Thr Thr Phe Lys Glu Val Ser Gly Ala Thr Leu Gly Ser Ile Pro
    130                 135                 140
Ser
145
```

(2) INFORMATION FOR SEQ ID NO:755:

(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:755

```
Val Arg Leu Asn Ala Ala Val Val Val Asp Gly Lys Tyr Lys Ile Ala
1               5                  10                  15
Leu Glu Asp Gly Ala Asn Ala Leu Glu Tyr Glu Pro Leu Ser Asp Glu
            20                  25                  30
Unk Unk Lys Lys Ile Asn Unk Leu Val Lys Gln Ala Ile Gly Asp Asn
        35                  40                  45
Gln Asn Arg Gly Asp Asp Val Ala Val Ser Asn Phe Glu Phe Asn Pro
    50                  55                  60
Met Val Pro Met Ile Asp Asn Ala Thr Leu Ser Glu Lys Ile Ile Tyr
65                  70                  75                  80
Lys Thr Gln Lys Ile Leu Gly Leu Phe Met Phe Leu Ile Lys Val Tyr
                85                  90                  95
Leu Val Phe Ile Val Leu Phe Ile Phe Tyr Lys Lys Val Ile Val Pro
            100                 105                 110
Phe Ser Glu Arg Met Leu Glu Val Val Pro Asp Glu Asp Lys Glu Val
        115                 120                 125
Lys Ser Met Phe Glu Glu Met Asn Glu Glu Glu Asp Glu Leu Asn Lys
    130                 135                 140
Leu Gly Asp Leu Arg Lys Lys Val Glu Asp Gln Leu Gly Leu Asn Ala
145                 150                 155                 160
Ser Phe Ser Glu Glu Glu Val Arg Tyr Glu Ile Ile Leu Glu Lys Ile
                165                 170                 175
Arg Gly Thr Leu Lys Glu Arg Pro Asp Glu Ile Ala Thr Leu Phe Lys
            180                 185                 190
Leu Leu Ile Lys Asp Glu Ile Ser Ser Asp Ser Ala Lys Gly
        195                 200                 205
```

(2) INFORMATION FOR SEQ ID NO:756:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 98 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:756

```
Val Cys Phe Ile Leu Pro Phe Cys Leu Gly Val Leu Gly Thr Gln Ile
1               5                  10                  15
Phe Lys Gln Glu Thr Pro Arg Gln Leu Pro Ile Val Val Val Asp Leu
            20                  25                  30
Asp Lys Thr Thr Thr Ser His Gln Val Ala Phe Glu Leu Gly Ala Thr
        35                  40                  45
Ser Ala Val Glu Ile Lys Tyr Gln Val Thr Ser Leu Ser Glu Ala Lys
    50                  55                  60
Arg Phe Leu Asn Ser Ala Glu Val Tyr Gly Ala Leu Ile Leu Pro Lys
65                  70                  75                  80
Asp Leu Glu Arg Lys Ile Lys Met Gly Arg Lys Val Unk Phe Ala Leu
                85                  90                  95
Leu Leu
```

(2) INFORMATION FOR SEQ ID NO:757:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757

```
Met Lys Gly Leu Trp Leu Val Ile Ser Leu Val Phe Val Gly Phe Leu
1               5                  10                  15
Trp Ala Asn Glu Ser Tyr Val Phe Asn Asn Ser Lys Gly Arg Leu Thr
            20                  25                  30
Glu Lys Ser Val Ala Phe Ile Glu Gly Val Ser Lys Glu Leu Tyr Leu
        35                  40                  45
Lys Thr Gly Val Arg Phe Ala Ile Asp Met Thr Asp Phe Glu Lys Asn
    50                  55                  60
Pro Ile Ala Leu Ala Asn Lys Lys Glu Arg Gln Ser Tyr Gln Glu Gly
65                  70                  75                  80
Phe Leu Lys Gln Leu Lys Pro Pro Phe Val Val Phe Phe Phe Tyr His
                85                  90                  95
Asp Ala Gln Lys Ile Glu Leu Val Ala Asn Pro Lys Asp Leu Leu Asp
            100                 105                 110
Thr Asp Lys Ile Phe Phe Glu Lys Ile Ala Pro Leu Leu Pro Thr Asn
        115                 120                 125
Ala Lys Glu Tyr Thr Pro Gln Arg Ile Ser Ala Met Leu Ile Asn Gly
    130                 135                 140
Tyr Ser Val Ala Val Asp Ala Leu Ala Glu Lys Tyr His Val Asn Ile
145                 150                 155                 160
Thr Gln Asn Phe Ser Ala Pro Lys Gly Val Thr Phe Val Lys Val Val
                165                 170                 175
Ile Tyr Ile Leu Leu Leu Thr Leu Leu Gly Ala Phe Leu Gly Leu Tyr
            180                 185                 190
Phe Phe Lys Lys Ser
        195
```

(2) INFORMATION FOR SEQ ID NO:758:

(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:758

```
Leu Val Gln Ile Val Val Val Phe Tyr Gly Leu Pro Ala Leu Gly Val
1               5                  10                  15
Tyr Met Asp Pro Ile Pro Ala Gly Ile Ile Ala Phe Ser Phe Asn Val
            20                  25                  30
Gly Ala Tyr Ala Ser Glu Thr Leu Arg Ala Ser Phe Leu Ser Val Pro
        35                  40                  45
Lys Asp Gln Trp Asp Ser Ser Leu Ser Leu Gly Leu Asn Tyr Leu Gln
    50                  55                  60
Thr Phe Trp His Val Ile Phe Phe Gln Ala Leu Lys Val Ala Thr Pro
65                  70                  75                  80
Ser Leu Ser Asn Thr Phe Ile Ser Leu Phe Lys Glu Thr Ser Leu Ala
                85                  90                  95
Ser Val Val Thr Ile Ala Glu Unk Phe Arg Ile Ala Gln Gln Lys Unk
            100                 105                 110
Asn Val Ser Tyr Asp Phe Unk Pro Ile Tyr Leu Glu Unk Ala Leu Ile
        115                 120                 125
Tyr Trp Leu Phe Cys Leu Val Leu Glu Val Ile Gln Lys Arg Val Glu
    130                 135                 140
Lys Ile Leu Asn
145
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:758:

(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:758

```
Leu Val Gln Ile Val Val Val Phe Tyr Gly Leu Pro Ala Leu Gly Val
1               5                  10                  15
```

```
Tyr Met Asp Pro Ile Pro Ala Gly Ile Ile Ala Phe Ser Phe Asn Val
            20                  25                  30
Gly Ala Tyr Ala Ser Glu Thr Leu Arg Ala Ser Phe Leu Ser Val Pro
        35                  40                  45
Lys Asp Gln Trp Asp Ser Ser Leu Ser Leu Gly Leu Asn Tyr Leu Gln
    50                  55                  60
Thr Phe Trp His Val Ile Phe Phe Gln Ala Leu Lys Val Ala Thr Pro
65                  70                  75                  80
Ser Leu Ser Asn Thr Phe Ile Ser Leu Phe Lys Glu Thr Ser Leu Ala
                85                  90                  95
Ser Val Val Thr Ile Ala Glu Unk Phe Arg Ile Ala Gln Gln Lys Unk
            100                 105                 110
Asn Val Ser Tyr Asp Phe Unk Pro Ile Tyr Leu Glu Unk Ala Leu Ile
        115                 120                 125
Tyr Trp Leu Phe Cys Leu Val Leu Glu Val Ile Gln Lys Arg Val Glu
    130                 135                 140
Lys Ile Leu Asn
145
```

(2) INFORMATION FOR SEQ ID NO:759:

(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:759

```
Met Cys Ser Lys Lys Ile Arg Asn Leu Ile Leu Cys Phe Gly Phe Ile
1               5                   10                  15
Leu Ser Leu Cys Ala Glu Glu Asn Ile Thr Lys Glu Asn Met Thr Glu
            20                  25                  30
Thr Asn Thr Thr Glu Glu Asn Thr Pro Lys Asp Ala Pro Ile Leu Leu
        35                  40                  45
Glu Glu Lys Arg Ala Gln Thr Leu Glu Leu Lys Glu Glu Asn Glu Val
    50                  55                  60
Ala Lys Lys Ile
65
```

(2) INFORMATION FOR SEQ ID NO:760:

This Sheet Has Been Replaced



(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:760

```
Val Val Ala Asp Glu Val Arg Asn Leu Ala Gly Arg Thr Gln Lys Ser
1               5                  10                  15
Leu Ala Glu Ile Asn Ser Thr Ile Met Val Ile Val Gln Glu Ile Asn
            20                  25                  30
Asp Val Ser Ser Gln Met Asn Leu Asn Ser Gln Lys Met Glu Arg Leu
        35                  40                  45
Ser Asp Met Ser Lys Ser Val Gln Glu Thr Tyr Glu Lys Met Ser Ser
    50                  55                  60
Asn Leu Ser Ser Val Val Leu Asp Ser Asn Gln Ser Met Asp Asp Tyr
65                  70                  75                  80
Ala Lys Ser Gly His Gln Ile Glu Ala Met Val Ser Asp Phe Ala Glu
                85                  90                  95
Val Glu Lys Val Ala Ser Lys Thr Leu Ala Asp Ser Ser Asp Ile Leu
            100                 105                 110
Asn Ile Ala Thr His Val Ser Gly Thr Thr Met Asn Leu Unk Lys Gln
        115                 120                 125
Val Asn Leu Phe Lys Thr
    130
```

(2) INFORMATION FOR SEQ ID NO:760:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760

```
Val Val Ala Asp Glu Val Arg Asn Leu Ala Gly Arg Thr Gln Lys Ser
1               5                  10                  15
Leu Ala Glu Ile Asn Ser Thr Ile Met Val Ile Val Gln Glu Ile Asn
            20                  25                  30
Asp Val Ser Ser Gln Met Asn Leu Asn Ser Gln Lys Met Glu Arg Leu
        35                  40                  45
Ser Asp Met Ser Lys Ser Val Gln Glu Thr Tyr Glu Lys Met Ser Ser
    50                  55                  60
Asn Leu Ser Ser Val Val Leu Asp Ser Asn Gln Ser Met Asp Asp Tyr
65                  70                  75                  80
Ala Lys Ser Gly His Gln Ile Glu Ala Met Val Ser Asp Phe Ala Glu
                85                  90                  95
Val Glu Lys Val Ala Ser Lys Thr Leu Ala Asp Ser Ser Asp Ile Leu
            100                 105                 110
Asn Ile Ala Thr His Val Ser Gly Thr Thr Met Asn Leu Unk Lys Gln
        115                 120                 125
Val Asn Leu Phe Lys Thr
    130
```

(2) INFORMATION FOR SEQ ID NO:761:

(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:761

```
Val Leu Lys Thr Leu Ser Ile Arg Leu Val Ile Leu Leu Asn Cys Ser
1               5                  10                  15
Leu Ala Thr Asn Ala Cys Ser Gly Val Gln Lys Leu Arg Asp Glu Ser
            20                  25                  30
His Arg Tyr Ala Ile Asn Phe His Arg Ser Thr Lys Leu Lys Asn Met
        35                  40                  45
Lys Gln Ile Ala Leu Leu Lys Glu Lys Gly Ile Gly Glu Ala Ser Val
    50                  55                  60
Lys Lys Leu Leu Asp Tyr Phe Gly Ser Phe Glu Ala Ile Glu Lys Ala
65                  70                  75                  80
Ser Asp Gln Glu Lys Asn Ala Val Leu Lys Lys Arg Lys
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

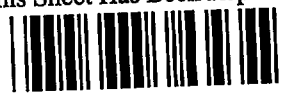
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762

```
Val Gly Ile Ile Arg Gly Ile Ile His Arg Pro Glu Leu Ile Leu Leu
1               5                  10                  15
Asp Glu Pro Phe Ser Ala Leu Asp Ser Leu Asn Arg Lys Asn Leu Gln
            20                  25                  30
Asp Leu Ile Lys Glu Ile His Gln Asn Ser Cys Ala Thr Phe Ile Met
        35                  40                  45
Val Thr His Asp Glu Asn Glu Ala Gln Lys Leu Ala Thr Lys Thr Leu
    50                  55                  60
Glu Ile Lys Ala Leu Lys Gln Glu Gln
```

This Sheet Has Been Replaced



65 70

(2) INFORMATION FOR SEQ ID NO:763:

(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

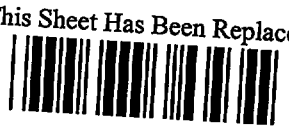
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763

```
Val Ile Phe Ile Ala Thr Ala Asn Asn Ile Asp Arg Ile Pro Ala Pro
1               5                  10                  15
Leu Arg Asp Arg Met Glu Phe Ile Ser Val Ser Ser Tyr Thr Pro Ser
            20                  25                  30
Glu Lys Glu Glu Ile Ala Lys Asn Tyr Leu Ile Pro Gln Glu Leu Glu
        35                  40                  45
Lys His Ala Leu Lys Pro Ser Glu Val Asp Ile Ser His Glu Cys Leu
    50                  55                  60
Lys Leu Ile Ile Glu Lys Tyr Thr Arg Glu Ala Gly Val Arg Asp Leu
65                  70                  75                  80
Arg Arg Gln Ile Ala Thr Ile Met Arg Lys Ala Ala Leu Lys Tyr Leu
                85                  90                  95
Glu Asp Asn Pro His Lys Lys Gly Arg Thr Lys Lys Ser Glu Asp Lys
            100                 105                 110
Asp Lys Lys Gly Gly Asn Glu Glu Asn Glu Lys Arg Gly Glu Ser Lys
        115                 120                 125
Asp Phe Cys Val Ser Ile Thr Pro Asp Asn Leu Lys Glu Tyr Leu Glu
    130                 135                 140
Arg Met Val Phe Glu Ile Unk Pro Ile Asp Glu Glu Asn Lys Ile Gly
145                 150                 155                 160
Ile Val Asn Gly Leu Ala Trp Thr Pro Val Gly Gly Asp Val Leu Lys
                165                 170                 175
Ile Glu Ala Val Lys Ile Arg Gly Lys Gly Glu Leu Lys Leu Thr Gly
            180                 185                 190
Ser Leu Gly Asp Val Met Lys Glu Ser Ala Ile Ile Ala Phe Ser Val
        195                 200                 205
Val Lys Val Leu Leu Asp Asn Glu Thr Leu Lys Val Pro Lys Ile Pro
    210                 215                 220
Ser Glu Thr Asp Ala Glu Asn Unk Lys Lys Lys Lys Val Leu Lys Val
225                 230                 235                 240
Unk Asn Ala Tyr Asp Leu His Leu His Val Pro Lys Gly Leu Arg Leu
                245                 250                 255
Lys Thr Ala Arg Ala Leu Gly Ser Leu Trp Arg Ala
            260                 265
```

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764

```
Met Glu Phe Met Lys Lys Phe Val Ala Leu Gly Leu Leu Ser Ala Val
1               5                  10                  15
Leu Ser Ser Ser Leu Leu Ala Glu Gly Asp Gly Val Tyr Ile Gly Thr
            20                  25                  30
Asn Tyr Gln Leu Gly Gln Ala Arg Leu Asn Ser Asn Ile Tyr Asn Thr
        35                  40                  45
Gly Asp Cys Thr Gly Ser Val Val Gly Cys Pro Pro Gly Leu Thr Ala
    50                  55                  60
Asn Lys His Asn Pro Gly Gly Thr Asn Ile Asn Trp His Ser Lys Tyr
65                  70                  75                  80
Ala Asn Gly Ala Leu Asn Gly Phe Gly Leu Asn Val Gly Tyr Lys Lys
                85                  90                  95
Phe Phe Gln Phe Lys Ser Leu Asp Met Thr Ser Lys Trp Phe Gly Phe
            100                 105                 110
Arg Val Tyr Gly Leu Phe Asp Tyr Gly His Ala Asp Leu Gly Lys Gln
        115                 120                 125
Val Tyr Ala Pro Asn Lys Ile Gln Leu Asp Met Val Ser Trp Gly Val
    130                 135                 140
Gly Ser Asp Leu Leu Ala Asp Ile Ile Asp Lys Asp Asn Ala Ser Phe
145                 150                 155                 160
Gly Ile Phe Gly Gly Val Ala Ile Gly Gly Asn Thr Trp Lys Ser Ser
                165                 170                 175
Ala Ala Asn Tyr Trp Lys Glu Gln Ile Ile Glu Ala Lys Gly Pro Asp
            180                 185                 190
Val Cys Thr Pro Thr Tyr Cys Asn Pro Asn Ala Pro Tyr Ser Thr Asn
        195                 200                 205
Thr Ser Thr Val Ala Phe Gln Val Trp Leu Asn Phe Gly Val Arg Ala
    210                 215                 220
Asn Ile Tyr Lys His Asn Gly Val Glu Phe Gly Val Arg Val Pro Leu
225                 230                 235                 240
Leu Ile Asn Lys Phe Leu Ser Ala Gly Pro Asn Ala Thr Asn Leu Tyr
                245                 250                 255
Tyr His Leu Lys Arg Asp Tyr Ser Leu Tyr Leu Gly Tyr Asn Tyr Thr
            260                 265                 270
Phe
```

(2) INFORMATION FOR SEQ ID NO:764:

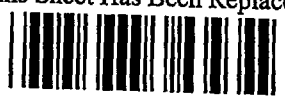
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764

```
Met Glu Phe Met Lys Lys Phe Val Ala Leu Gly Leu Leu Ser Ala Val
1               5                  10                  15
Leu Ser Ser Ser Leu Leu Ala Glu Gly Asp Gly Val Tyr Ile Gly Thr
            20                  25                  30
Asn Tyr Gln Leu Gly Gln Ala Arg Leu Asn Ser Asn Ile Tyr Asn Thr
        35                  40                  45
Gly Asp Cys Thr Gly Ser Val Val Gly Cys Pro Pro Gly Leu Thr Ala
    50                  55                  60
Asn Lys His Asn Pro Gly Gly Thr Asn Ile Asn Trp His Ser Lys Tyr
65                  70                  75                  80
Ala Asn Gly Ala Leu Asn Gly Phe Gly Leu Asn Val Gly Tyr Lys Lys
                85                  90                  95
Phe Phe Gln Phe Lys Ser Leu Asp Met Thr Ser Lys Trp Phe Gly Phe
            100                 105                 110
Arg Val Tyr Gly Leu Phe Asp Tyr Gly His Ala Asp Leu Gly Lys Gln
        115                 120                 125
Val Tyr Ala Pro Asn Lys Ile Gln Leu Asp Met Val Ser Trp Gly Val
    130                 135                 140
Gly Ser Asp Leu Leu Ala Asp Ile Ile Asp Lys Asp Asn Ala Ser Phe
145                 150                 155                 160
Gly Ile Phe Gly Gly Val Ala Ile Gly Gly Asn Thr Trp Lys Ser Ser
                165                 170                 175
Ala Ala Asn Tyr Trp Lys Glu Gln Ile Ile Glu Ala Lys Gly Pro Asp
            180                 185                 190
Val Cys Thr Pro Thr Tyr Cys Asn Pro Asn Ala Pro Tyr Ser Thr Asn
        195                 200                 205
Thr Ser Thr Val Ala Phe Gln Val Trp Leu Asn Phe Gly Val Arg Ala
    210                 215                 220
Asn Ile Tyr Lys His Asn Gly Val Glu Phe Gly Val Arg Val Pro Leu
225                 230                 235                 240
Leu Ile Asn Lys Phe Leu Ser Ala Gly Pro Asn Ala Thr Asn Leu Tyr
                245                 250                 255
Tyr His Leu Lys Arg Asp Tyr Ser Leu Tyr Leu Gly Tyr Asn Tyr Thr
            260                 265                 270
Phe
```

(2) INFORMATION FOR SEQ ID NO:765:

(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

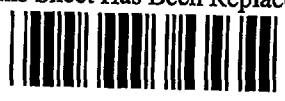
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765

```
Met Asn Tyr Asp Asn Tyr Trp Asp Glu Asp Lys Pro Glu Leu Asn Ile
1               5                  10                  15
Thr Pro Leu Val Asp Val Met Leu Val Leu Leu Ala Ile Leu Met Val
            20                  25                  30
Thr Thr Pro Thr Leu Thr Tyr Lys Glu Glu Ile Ala Leu Pro Ser Gly
        35                  40                  45
Ser Lys Thr Ala Arg Ala Thr Gln Asp Lys Val Ile Glu Ile Arg Met
    50                  55                  60
Asp Lys Asp Ala Lys Ile Tyr Ile Asp Ser Gln Thr Tyr Glu Tyr Unk
65                  70                  75                  80
Ser Phe Pro Asp Thr Phe Asn Leu Leu Ser Lys Lys Tyr Asp Lys Asp
                85                  90                  95
Thr Arg Val Ser Ile Arg Ala Asp Lys Arg Leu Thr Tyr Asp Lys Val
            100                 105                 110
Ile Tyr Leu Leu Lys Thr Ile Lys Glu Ala Gly Phe Leu Lys Val Ser
        115                 120                 125
Leu Ile Thr Ser Pro
    130
```

(2) INFORMATION FOR SEQ ID NO:765:

This Sheet Has Been Replaced



(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:765

```
Met Asn Tyr Asp Asn Tyr Trp Asp Glu Asp Lys Pro Glu Leu Asn Ile
1               5                  10                  15
Thr Pro Leu Val Asp Val Met Leu Val Leu Leu Ala Ile Leu Met Val
            20                  25                  30
Thr Thr Pro Thr Leu Thr Tyr Lys Glu Glu Ile Ala Leu Pro Ser Gly
        35                  40                  45
Ser Lys Thr Ala Arg Ala Thr Gln Asp Lys Val Ile Glu Ile Arg Met
    50                  55                  60
Asp Lys Asp Ala Lys Ile Tyr Ile Asp Ser Gln Thr Tyr Glu Tyr Unk
65                  70                  75                  80
Ser Phe Pro Asp Thr Phe Asn Leu Leu Ser Lys Lys Tyr Asp Lys Asp
                85                  90                  95
Thr Arg Val Ser Ile Arg Ala Asp Lys Arg Leu Thr Tyr Asp Lys Val
            100                 105                 110
Ile Tyr Leu Leu Lys Thr Ile Lys Glu Ala Gly Phe Leu Lys Val Ser
        115                 120                 125
Leu Ile Thr Ser Pro
    130
```

(2) INFORMATION FOR SEQ ID NO:766:

(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:766

```
Met Pro Pro Thr Unk Pro Gln Ala Ser Ile Leu Arg Leu Thr Leu Lys
1               5                  10                  15
Asn Pro Leu Unk Unk Leu Ser Arg Tyr Ser Leu Cys Leu Leu Lys Lys
            20                  25                  30
Thr Arg Leu Gln Thr Thr Ser Asn Ser Ala Pro Lys Ala Cys Leu Ile
        35                  40                  45
Ala Gly Leu Leu Lys Lys Ser Lys Pro Phe Ile Leu Asn Thr Leu Lys
    50                  55                  60
Ile Arg Ser Leu Leu Lys Pro
65                  70
```

(2) INFORMATION FOR SEQ ID NO:766:

This Sheet Has Been Replaced



(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:766

```
Met Pro Pro Thr Unk Pro Gln Ala Ser Ile Leu Arg Leu Thr Leu Lys
1               5                  10                  15
Asn Pro Leu Unk Unk Leu Ser Arg Tyr Ser Leu Cys Leu Leu Lys Lys
            20                  25                  30
Thr Arg Leu Gln Thr Thr Ser Asn Ser Ala Pro Lys Ala Cys Leu Ile
        35                  40                  45
Ala Gly Leu Leu Lys Lys Ser Lys Pro Phe Ile Leu Asn Thr Leu Lys
    50                  55                  60
Ile Arg Ser Leu Leu Lys Pro
65                  70
```

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:767

```
Met Gly Cys Ser Phe Ile Phe Lys Lys Val Arg Val Tyr Ser Lys Met
1               5                  10                  15
Leu Val Ala Leu Gly Leu Ser Ser Val Leu Ile Gly Cys Ala Met Asn
            20                  25                  30
Pro Ser Ala Glu Thr Lys Lys Pro Asn Asp Ala Lys Asn Gln Gln Pro
        35                  40                  45
Val Gln Thr His Glu Arg Met Thr Thr Ser Ser Glu His Val Thr Pro
    50                  55                  60
Leu Asp Phe Asn Tyr Pro Val His Ile Val Gln Ala Pro Gln Asn His
65                  70                  75                  80
His Val Val Gly Ile Leu Met Pro Arg Ile Gln Val Ser Asp Asn Leu
                85                  90                  95
Lys Pro Tyr Ile Asp Lys Phe Gln Asp Ala Leu Ile Asn Gln Ile Gln
            100                 105                 110
Thr Ile Phe Glu Lys Arg Gly Tyr Gln Val Leu Arg Phe Gln Asp Glu
        115                 120                 125
Lys Ala Leu Asn Val Gln Asp Lys Lys Lys Ile Phe Ser Val Leu Asp
    130                 135                 140
Leu Lys Gly
145
```

(2) INFORMATION FOR SEQ ID NO:768:

(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:768

```
Met Asp Arg Lys Leu Leu Arg Leu Tyr Gln Pro Leu Asn Ala Tyr Ser
1               5                  10                  15
Tyr Asn Ser Asp Ser Leu Phe Leu Tyr Asp Phe Ser Arg Pro Phe Ile
            20                  25                  30
Lys Asn Ser Gly Ala Ile Leu Asp Ile Gly Ser Gly Cys Gly Val Leu
        35                  40                  45
Gly Leu Leu Cys Ala Arg Asp Asn Pro Leu Ala Ser Val His Leu Val
    50                  55                  60
Glu Lys Asp Ser Lys Met Ala Phe Cys Ser Gln Lys Asn Ala Leu Lys
```

```
65                  70                  75                  80
Phe Pro Asn Ala Gln Val Phe Glu Ser Asp Phe Leu Asp Phe Asn Pro
                85                  90                  95
Pro Ile Leu Tyr Asp Ala Ile Val Cys Asn Pro Pro Phe Tyr Ala Leu
            100                 105                 110
Gly Ser Ile Lys Ser Gln Ile Lys Gly His Ala Arg His Gln Ser Glu
        115                 120                 125
Leu Asp Phe Ala Ser Leu Val Ala Lys Val Lys Lys Cys Leu Lys Pro
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:769:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...47

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769

```
Met Leu Ser Ala Leu Val Met Leu Pro Phe Met Glu Val Phe Tyr Tyr
1               5                   10                  15
Phe Asn Phe Pro Leu Trp Leu Asn Leu Phe Leu Gly Gln Thr Ile Gly
            20                  25                  30
Ala Val Ile Phe Phe Lys Leu Asp Lys Leu Ile Phe Ser Lys Lys
        35                  40                  45
```

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

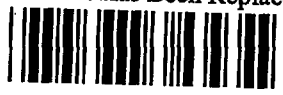
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770

```
Met Asn Thr Ile Ile Arg Tyr Ala Ser Leu Trp Gly Leu Cys Ile Thr
1               5                   10                  15
Leu Thr Leu Ala Gln Thr Pro Ser Lys Thr Pro Asp Glu Ile Lys Gln
            20                  25                  30
Ile Leu Asn Asn Tyr Ser His Lys Asn Leu Lys Leu Ile Asp Unk Pro
        35                  40                  45
```

This Sheet Has Been Replaced



This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:772:

(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:772

```
Met Gln Tyr Ala Asn Ala Tyr Gln Ala Tyr Gln His Asn Arg Val Ser
1               5                  10                  15
Val Glu Ser Pro Ala Lys Leu Ile Glu Met Leu Tyr Glu Gly Ile Leu
            20                  25                  30
Arg Phe Ser Ser Gln Ala Lys Arg Cys Ile Glu Asn Glu Asp Ile Glu
        35                  40                  45
Lys Lys Ile Tyr Tyr Ile Asn Arg Val Thr Asp Ile Phe Thr Glu Leu
    50                  55                  60
Leu Asn Ile Leu Asp Tyr Glu Lys Gly Gly Unk Val Ala Val Tyr Leu
65                  70                  75                  80
Thr Gly Leu Tyr Thr His Gln Ile Lys Val Leu Thr Gln Ala Asn Val
                85                  90                  95
Glu
```

(2) INFORMATION FOR SEQ ID NO:773:

(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:773

```
Met Met Phe Asp Asn Thr Leu Ile Asn Leu Phe Glu Thr Ala Pro Leu
1               5                  10                  15
Leu Thr Ser Leu Leu Ala Gly Ile Leu Thr Phe Leu Ser Pro Cys Val
            20                  25                  30
Leu Pro Leu Ile Pro Ala Tyr Met Ser Tyr Ile Ser Gln Ile Ser Leu
        35                  40                  45
```

```
Thr Ser Ser Leu Unk Ala Thr Pro Gly Phe Unk Pro Ser Pro Lys Glu
    50                  55                  60
Thr Ala Thr Thr Ile Asn Gln Glu Ile Ala Lys Tyr His Glu Lys Ser
65                  70                  75                  80
Asp Lys Ala Ala Leu Gly Leu Tyr Glu Leu Leu Lys Gly Ala Thr Thr
                85                  90                  95
Asn Leu Ser Leu Gln Ala Gln Glu Leu Ser Val Lys Gln Ala Met Glu
            100                 105                 110
Glu Pro His His Arg Gln Ser Asp Val Phe Ala Tyr Phe Glu Arg Glu
        115                 120                 125
Leu
```

(2) INFORMATION FOR SEQ ID NO:771:

This Sheet Has Been Replaced



(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

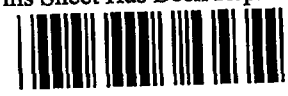
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771

```
Met Val Leu Phe Leu Ser Ile Phe Lys Lys Ser Phe Asn Asp Phe Leu
1               5                   10                  15
Ser Ala Arg Met Leu Leu Ile Asn Leu Gly Pro Ile Leu Leu Ser Leu
            20                  25                  30
Ala Phe Phe Gly Ala Ile Phe Tyr Tyr Asn Gly Gly Ser Ile Val Asn
        35                  40                  45
Tyr Cys Gln Thr Leu Leu Pro Gln Ser Leu Asn Asp Tyr Ala His Ser
    50                  55                  60
Gln Gly Phe Phe Ala Gly Val Phe Ala Trp Val Phe Lys Ala Leu Val
65                  70                  75                  80
Tyr Phe Leu Ile Phe Trp Ile Val Ile Leu Leu Ser Leu Val Ile Asn
                85                  90                  95
Ile Phe Ala Ser Ile Phe Tyr Thr Pro Leu Val Val Ser Tyr Leu His
            100                 105                 110
Gln Lys Tyr Tyr Pro His Val Val Leu Glu Glu Phe Gly Ser Ile Leu
        115                 120                 125
Phe Ser Ile Lys Tyr Phe Leu Lys Ser Leu Thr Phe Met Leu Leu Phe
    130                 135                 140
Leu Ala Val Leu Thr Pro Leu Tyr Phe Ile Pro Phe Ile Gly Val Phe
145                 150                 155                 160
Gly Val Phe Phe Ser Ile Val Pro His Phe His Phe Phe Lys Asn Thr
                165                 170                 175
Met Ser Leu Asp Ile Ala Ser Met Ile Phe Asn His Gln Ser Tyr Gln
            180                 185                 190
Asn Leu Leu Lys Gln His Arg Leu Lys His Tyr Arg Phe Ser Phe Phe
        195                 200                 205
Cys Tyr Leu Phe Ser Leu Ile Pro Phe Phe Asn Phe Phe Ala Thr Leu
    210                 215                 220
Leu Gln Thr Leu Lys Leu Thr His Tyr Ile Phe Ile Phe Lys Glu Lys
225                 230                 235                 240
Glu Cys
```

```
Glu Asp Ile Lys Asp Gly Lys Ala Lys Arg Val Ser Val Phe Leu Lys
    50                  55                  60
Ser Leu Met Phe Val Val Gly Phe Ser Leu Val Phe Leu Gly Val Gly
65                  70                  75                  80
Met Ser Met Ala Lys Leu Ile His Ser Phe Ser Phe Ser Trp Val Asn
                85                  90                  95
Tyr Ile Ala Gly Gly Ile Val Ile Leu Phe Gly Leu His Phe Leu Gly
            100                 105                 110
Val Phe Arg Phe Ala Phe Leu Tyr Lys Thr Gln Ser Val Gly Leu Ala
        115                 120                 125
Ser Lys Ser Asn Ser Met Gln Arg Phe Thr Pro Phe Phe Leu Ala
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:774:

This Sheet Has Been Replaced



(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:774

```
Met Pro Val Ile Arg Val Leu Val Met Leu Ala Thr Met Met Met Lys
1               5                  10                  15
Leu Val Lys Thr Ala Lys Glu Lys Lys Val Phe Lys Asn Val Gly Ile
            20                  25                  30
Ser Ile Met Gly Ile Ala Phe Trp Glu Ala Ile Lys Asp Ser Ile Lys
        35                  40                  45
Lys Gln Ile Lys Lys Ser Asp Trp Ile Cys Gly Asn Val Lys Thr Ala
    50                  55                  60
Asp Asp Tyr Leu Lys Thr His Pro Asn Ser Trp Phe Asn Ser Ala Ile
65                  70                  75                  80
Gly Val Thr Ala Ile Thr Ala Met Leu Met Asn Val Cys Phe Ala Asp
                85                  90                  95
Asp Gln Ser Lys Lys Glu Val Ala Gln Ala Gln Lys Glu Ala Glu Asn
            100                 105                 110
Ala Arg Asp Arg Ala Asn Lys Ser Gly Ile Glu Leu Glu Gln Glu Glu
        115                 120                 125
Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Glu Gln Glu Lys Gln Lys
    130                 135                 140
Thr Glu Gln Glu Lys Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Glu
145                 150                 155                 160
Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln Ile Lys
                165                 170                 175
Val Glu Gln Glu Gln Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Asn
            180                 185                 190
Asn Thr Gln Lys Asp Leu Val Asn Lys Ala Glu Gln Asn Cys Gln Glu
        195                 200                 205
Asn His Asn Gln Phe Phe Ile Lys Asn
    210                 215
```

(2) INFORMATION FOR SEQ ID NO:774:

This Sheet Has Been Replaced



(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:774

```
Met Pro Val Ile Arg Val Leu Val Met Leu Ala Thr Met Met Met Lys
1               5                  10                  15
Leu Val Lys Thr Ala Lys Glu Lys Lys Val Phe Lys Asn Val Gly Ile
            20                  25                  30
Ser Ile Met Gly Ile Ala Phe Trp Glu Ala Ile Lys Asp Ser Ile Lys
        35                  40                  45
Lys Gln Ile Lys Lys Ser Asp Trp Ile Cys Gly Asn Val Lys Thr Ala
    50                  55                  60
Asp Asp Tyr Leu Lys Thr His Pro Asn Ser Trp Phe Asn Ser Ala Ile
65                  70                  75                  80
Gly Val Thr Ala Ile Thr Ala Met Leu Met Asn Val Cys Phe Ala Asp
                85                  90                  95
Asp Gln Ser Lys Lys Glu Val Ala Gln Ala Gln Lys Glu Ala Glu Asn
            100                 105                 110
Ala Arg Asp Arg Ala Asn Lys Ser Gly Ile Glu Leu Glu Gln Glu Glu
        115                 120                 125
Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Glu Gln Glu Lys Gln Lys
    130                 135                 140
Thr Glu Gln Glu Lys Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Glu
145                 150                 155                 160
Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln Ile Lys
                165                 170                 175
Val Glu Gln Glu Gln Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Asn
            180                 185                 190
Asn Thr Gln Lys Asp Leu Val Asn Lys Ala Glu Gln Asn Cys Gln Glu
        195                 200                 205
Asn His Asn Gln Phe Phe Ile Lys Asn
    210                 215
```

(2) INFORMATION FOR SEQ ID NO:775:

(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:775

```
Val Leu Val Val Gly Lys Pro Asn Glu Ser Tyr Ala Asp Thr His Ala
1               5                  10                  15
Arg Ile Glu His Phe Ile Lys Leu Val Asp Phe Lys Gly Glu Ile Val
            20                  25                  30
Phe Ile Asn Glu Asp Asn Ser Ser Val Glu Ala Tyr Glu Asn Leu Glu
        35                  40                  45
His Leu Gly Lys Lys Asn Lys Arg Ile Ala Thr Lys Asp Gly Arg Leu
    50                  55                  60
Asp Ser Leu Ser Ala Cys Arg Ile Leu Glu Arg Tyr Cys Gln Gln Val
65                  70                  75                  80
Leu Lys Lys Gly
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:776:

(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:776

```
Met Val Ile Ser Gly His Phe Thr Thr Tyr Ser Tyr Ile Glu Pro Phe
1               5                  10                  15
Ile Ile Gln Ile Ser Gln Phe Ser Pro Asp Ile Thr Thr Leu Met Leu
            20                  25                  30
Phe Val Phe Gly Leu Ala Gly Val Val Gly Ser Phe Leu Phe Gly Arg
        35                  40                  45
Leu Tyr Ala Lys Asn Ser Arg Lys Phe Ile Ala Phe Ala Met Val Leu
    50                  55                  60
Val Ile Cys Pro Gln Pro Leu Ala Phe Cys Val
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:776:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

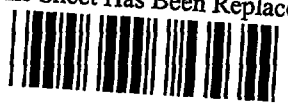
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

This Sheet Has Been Replaced



(A) NAME/KEY: misc_feature
(B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776

```
Met Val Ile Ser Gly His Phe Thr Thr Tyr Ser Tyr Ile Glu Pro Phe
1               5                  10                  15
Ile Ile Gln Ile Ser Gln Phe Ser Pro Asp Ile Thr Thr Leu Met Leu
            20                  25                  30
Phe Val Phe Gly Leu Ala Gly Val Val Gly Ser Phe Leu Phe Gly Arg
        35                  40                  45
Leu Tyr Ala Lys Asn Ser Arg Lys Phe Ile Ala Phe Ala Met Val Leu
    50                  55                  60
Val Ile Cys Pro Gln Pro Leu Ala Phe Cys Val
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:777:

(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:777

```
Met Arg Ile Leu Ile Leu Lys Asn Lys Pro Pro Thr Leu Arg Ser Lys
1               5                  10                  15
Ala Leu Thr Arg Ser Trp Gly Ile Asn Phe Ser Leu Lys Asn Thr Leu
            20                  25                  30
Ala Tyr Ala Phe Met Gly Phe Phe Asp Tyr Ala His Ala Asn Ser Ile
        35                  40                  45
Lys Leu Lys Asn Pro Asn Tyr Asn Ser Glu Ala Ala Gln Val Ala Ser
    50                  55                  60
Gln Ile Leu Gly Lys Gln Glu Ile Asn Arg Leu Thr Asn Ile Ala Asp
65                  70                  75                  80
Pro Arg Thr Phe Glu Pro Asn Met Leu Thr Tyr Gly Gly Ala Met Asp
                85                  90                  95
Val Met Val Asn Val Ile Asn Asn Gly Ile Met Ser Leu Gly Ala Phe
            100                 105                 110
Gly Gly Ile Gln Leu Ala Gly Asn Ser Trp Leu Met Ala Unk Pro Ser
        115                 120                 125
Phe Glu Gly Ile Leu Gly Glu Gln Ala Leu Val Ser Arg Lys Pro Leu
    130                 135                 140
Leu Ser Asn Phe Tyr Ser Met Trp Gly Leu Ala
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:778

```
Met Lys Ser Thr Arg Ile Gly Ser Lys Ile Val Met Met Val Cys Ala
1               5                  10                  15
Val Val Ile Val Ile Ser Ala Val Met Gly Val Ile Ile Ser Tyr Lys
            20                  25                  30
Val Glu Ser Val Leu Gln Ser Gln Ala Thr Glu Leu Leu Gln Lys Lys
        35                  40                  45
Ala Gln Leu Val Ser Phe Lys Ile Gln Gly Ile Met Lys Arg Ile Phe
    50                  55                  60
Met Gly Ala Asn Thr Leu Glu Arg Phe Leu Ser Asp Glu Asn Gly Ala
65                  70                  75                  80
Ile Asn Asp Thr Leu Lys Arg Arg Met Leu Ser Glu Phe Leu Leu Ala
                85                  90                  95
Asn Pro His Val Leu Leu Val Ser Ala Ile Tyr Thr Asn Asn Asn Glu
            100                 105                 110
Arg Met Ile Thr Ala Met Asn Met Asp Ser Lys Ile Ala Tyr Pro Asn
        115                 120                 125
Thr Ala Leu Asn Glu Asn Met Thr Unk Pro Ile His Ser Leu Lys Ser
    130                 135                 140
Ile Thr Arg Ser Unk Pro Tyr Tyr Lys Glu Val Asn Unk Unk Lys Ile
145                 150                 155                 160
Tyr Unk Unk Unk Ile Thr Leu Pro Leu Unk Unk Lys Asn Unk Asn Unk
                165                 170                 175
Ile Unk Unk Leu Asn Phe Unk Leu Asn Ile Asp Unk Phe Leu Tyr Unk
            180                 185                 190
```

(2) INFORMATION FOR SEQ ID NO:778:

(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:778

```
Met Lys Ser Thr Arg Ile Gly Ser Lys Ile Val Met Met Val Cys Ala
1               5                  10                  15
Val Val Ile Val Ile Ser Ala Val Met Gly Val Ile Ile Ser Tyr Lys
            20                  25                  30
Val Glu Ser Val Leu Gln Ser Gln Ala Thr Glu Leu Leu Gln Lys Lys
```

```
        35                  40                  45
Ala Gln Leu Val Ser Phe Lys Ile Gln Gly Ile Met Lys Arg Ile Phe
    50                  55                  60
Met Gly Ala Asn Thr Leu Glu Arg Phe Leu Ser Asp Glu Asn Gly Ala
65                  70                  75                  80
Ile Asn Asp Thr Leu Lys Arg Arg Met Leu Ser Glu Phe Leu Leu Ala
                85                  90                  95
Asn Pro His Val Leu Leu Val Ser Ala Ile Tyr Thr Asn Asn Asn Glu
            100                 105                 110
Arg Met Ile Thr Ala Met Asn Met Asp Ser Lys Ile Ala Tyr Pro Asn
        115                 120                 125
Thr Ala Leu Asn Glu Asn Met Thr Unk Pro Ile His Ser Leu Lys Ser
    130                 135                 140
Ile Thr Arg Ser Unk Pro Tyr Tyr Lys Glu Val Asn Unk Unk Lys Ile
145                 150                 155                 160
Tyr Unk Unk Unk Ile Thr Leu Pro Leu Unk Unk Lys Asn Unk Asn Unk
                165                 170                 175
Ile Unk Unk Leu Asn Phe Unk Leu Asn Ile Asp Unk Phe Leu Tyr Unk
            180                 185                 190
```

(2) INFORMATION FOR SEQ ID NO:779:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 171 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

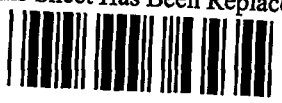
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779

```
Met Asn Val Lys Lys Lys Glu Lys Pro Gln Ser Gly Lys Ile Asp Arg
1               5                   10                  15
Val Asp Cys Leu Glu Lys Leu Gly Lys Glu Asn Thr Thr Phe Leu Ser
            20                  25                  30
Ser Ile Ala Met Gly Ser Ile Gly Gln Leu Ala Ile Pro Ile Pro Gly
        35                  40                  45
Val Gly Val Leu Ile Gly Gly Phe Val Gly Gly Val Met Ser Lys Thr
    50                  55                  60
Phe Tyr Asp Val Ser Leu Thr Ile Phe Lys Glu Ala Lys Leu Ala Arg
65                  70                  75                  80
Gln Arg Arg Ile Glu Ile Glu Lys Glu Cys Arg Glu Ser Ile Arg Gln
                85                  90                  95
Leu Glu Met Tyr Gln Asn Gln Phe Asn Glu Val Phe Glu Arg Tyr Phe
            100                 105                 110
His Gly Thr Ile Lys Phe Phe Asn Glu Ser Phe Asp Glu Leu Glu Arg
        115                 120                 125
Ala Leu Cys Ala Gly Asp Ala Asp Leu Ala Ile Ala Val Asn Asn Lys
    130                 135                 140
Ile Gln Glu Gly Met Gly Gln Glu Leu Leu Phe Asp Asn Lys Gln Glu
145                 150                 155                 160
Cys Trp Glu Phe Ile Thr Ser Arg Lys Glu Gly
                165                 170
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:780:

(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:780

```
Met Trp Pro Unk Lys Leu Phe Leu Lys Pro Leu Lys Glu Thr Ser Leu
1               5                  10                  15
Ala Leu Val Gly Val Ala Lys Asn Ile Lys Ile Val Ala Leu Lys Ala
            20                  25                  30
Gly Leu Lys Arg Ala Tyr Leu Pro Asn Arg Ser Leu Ile Phe Phe Leu
        35                  40                  45
Ile Lys Arg Tyr Leu Arg Phe Asp Lys Ser Gln Pro Phe Ile Ser Ile
    50                  55                  60
Thr Ala Leu Leu Ala Phe Phe Gly Val Ala Val Gly Val Met Val Leu
65                  70                  75                  80
Ile Val Ala Met Ala Ile Met Asn Gly Met Ser Lys Glu Phe Glu Lys
                85                  90                  95
Lys Leu Phe Val Met Asn Tyr Pro Leu Thr Leu Tyr Thr Thr Ser Pro
            100                 105                 110
Tyr Gly Ile Ser Glu Glu Val Val Gln Ala Leu Glu Lys Lys Phe Pro
        115                 120                 125
Asn Leu Pro Phe Ser Unk Pro Ile Cys Lys Pro Lys Ala
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:781:

(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

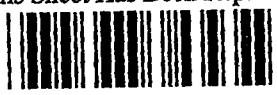
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781

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

```
        35                  40                  45
Ser Arg His Ala Gln Gly Trp Lys Arg Glu Thr Leu Pro Cys Ala Leu
    50                  55                  60
Ser Phe Gln Asn Ala Leu
65                  70
```

(2) INFORMATION FOR SEQ ID NO:782:

This Sheet Has Been Replaced



(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:782

```
Val His His Leu Unk Arg Leu Leu Asp Ser Gly Ser Glu Arg Cys Ile
1               5                  10                  15
Gly Cys Gly Leu Cys Glu Lys Ile Cys Thr Ser Asn Cys Ile Arg Ile
            20                  25                  30
Ile Thr His Lys Gly Glu Asp Asn Arg Lys Lys Ile Asp Ser Tyr Thr
        35                  40                  45
Ile Asn Leu Gly Arg Cys Ile Tyr Cys Gly Leu Cys Ala Glu Val Cys
    50                  55                  60
Pro Glu Leu Ala Ile Val Met Gly Asn Arg Phe Glu Asn Ala Ser Thr
65                  70                  75                  80
Gln Arg Ser Gln Tyr Gly Ser Lys Ser Glu Phe Leu Thr Ser Glu Gln
                85                  90                  95
Asp Ala Lys Asn Cys Ser His Ala Glu Phe Leu Gly Phe Gly Ala Val
            100                 105                 110
Ser Pro Asn Tyr Asn Glu Arg Met Gln Ala Thr Pro Leu Asp Tyr Val
        115                 120                 125
Gln Glu Pro Ser Lys Glu Glu Ser Lys Glu Glu Phe Unk Thr Ser Pro
    130                 135                 140
Glu Ser His Lys Gly Asp Glu Asn Val
145                 150
```

(2) INFORMATION FOR SEQ ID NO:783:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature

(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783

```
Met Ala Ile Trp Gly Trp Cys Phe Leu Phe Leu Ser Ser Leu Met Trp
1               5                  10                  15
Gly Ser Ser Met His Glu Leu Val Leu Arg Ser Gln Ala Leu Gly Phe
            20                  25                  30
Glu Thr Arg Leu Val Gln Cys Asp Leu Ser Phe Ser Tyr Glu Arg Phe
        35                  40                  45
Ile Ser Lys Thr Lys Arg Ser Leu Ala Val Leu Glu Glu Phe Asp Trp
    50                  55                  60
Leu Asn Ser Gly Phe Asp Phe Ser Arg Leu Asn Val Glu Asn Asp Thr
65                  70                  75                  80
Leu Glu Leu Leu Lys Ala Leu Tyr Phe Lys Leu Glu Lys Leu Glu Ser
                85                  90                  95
Leu Leu Leu Lys Glu Asn Leu Leu Glu Leu Glu Gln Lys Asp Arg Ile
            100                 105                 110
Ile Ala Leu Gly His Gly Leu Val Cys Leu Lys Lys Gln Ser Leu Ile
        115                 120                 125
Ala Pro Gln Thr Tyr Tyr Gly Arg Cys Val Leu Glu Gly Lys Ile Leu
    130                 135                 140
Ala Phe Phe Gly Val Ala Arg Asp Lys Asp Phe Leu Glu Ile Thr Arg
145                 150                 155                 160
Met His Ala Leu Asp Ile Lys Arg Tyr Asp Ser Phe Ile Val Asp Ser
                165                 170                 175
Glu Arg Lys Gly Leu Lys Leu
            180
```

(2) INFORMATION FOR SEQ ID NO:784:

This Sheet Has Been Replaced



(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

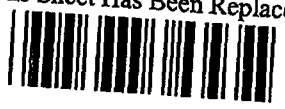
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784

```
Met Pro Glu Asn Ser Lys Leu Gln Pro Ala Lys Leu Gly Lys Asn Phe
1               5                  10                  15
Asp Pro Val Asp His Ser Asn Arg Asn Phe Phe Phe Ser Leu Ile Leu
            20                  25                  30
Ser Val Leu Leu His Trp Leu Ile Tyr Phe Leu Phe Glu His Arg Glu
        35                  40                  45
Asp Phe Phe Pro Ser Lys Pro Lys Leu Val Lys Leu Asn Pro Glu Asn
    50                  55                  60
Leu Leu Val
65
```

(2) INFORMATION FOR SEQ ID NO:785:

(i) SEQUENCE CHARACTERISTICS:

This Sheet Has Been Replaced



(A) LENGTH: 253 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(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:785

```
Met Ala Tyr Lys Tyr Asp Arg Asp Leu Glu Phe Leu Lys Gln Leu Glu
1               5                  10                  15
Ser Ser Asp Leu Asp Leu Phe Glu Val Leu Val Phe Gly Lys Asp
            20                  25                  30
Gly Glu Lys Arg His Asn Glu Lys Leu Thr Ser Ser Ile Glu Tyr Lys
        35                  40                  45
Arg His Gly Asp Asp Tyr Ala Lys Tyr Ala Glu Arg Ile Ala Glu Glu
    50                  55                  60
Leu Gln Tyr Tyr Gly Ser Asn Ser Phe Ala Ser Phe Ile Lys Gly Glu
65                  70                  75                  80
Gly Val Leu Tyr Lys Glu Ile Leu Cys Asp Val Cys Asp Lys Leu Lys
                85                  90                  95
Val Asn Tyr Asn Lys Lys Thr Glu Thr Thr Leu Ile Glu Gln Asn Met
            100                 105                 110
Leu Ser Lys Ile Leu Glu Arg Ser Leu Glu Glu Met Asp Asp Glu Glu
        115                 120                 125
Val Lys Glu Met Cys Asp Glu Leu Ser Ile Lys Asn Thr Asp Asn Leu
    130                 135                 140
Asn Arg Gln Ala Leu Ser Ala Ala Thr Leu Thr Leu Phe Lys Met Gly
145                 150                 155                 160
Gly Phe Lys Ser Tyr Gln Leu Ala Val Ile Val Ala Asn Ala Val Ala
                165                 170                 175
Lys Thr Ile Leu Gly Arg Gly Leu Ser Leu Ala Gly Asn Gln Val Leu
            180                 185                 190
Thr Arg Thr Leu Ser Phe Leu Thr Gly Pro Val Gly Trp Ile Ile Thr
        195                 200                 205
Gly Val Trp Thr Ala Ile Asp Ile Ala Gly Pro Ala Tyr Arg Val Thr
    210                 215                 220
Ile Pro Ala Cys Ile Val Val Ala Thr Leu Arg Leu Lys Thr Gln Gln
225                 230                 235                 240
Ala Asn Glu Asp Lys Lys Ser Leu Gln Ile Glu Ser Val
                245                 250
```

(2) INFORMATION FOR SEQ ID NO:785:

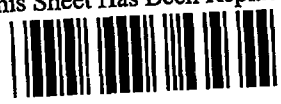
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785

```
Met Ala Tyr Lys Tyr Asp Arg Asp Leu Glu Phe Leu Lys Gln Leu Glu
1               5                  10                  15
Ser Ser Asp Leu Leu Asp Leu Phe Glu Val Leu Val Phe Gly Lys Asp
            20                  25                  30
Gly Glu Lys Arg His Asn Glu Lys Leu Thr Ser Ser Ile Glu Tyr Lys
        35                  40                  45
Arg His Gly Asp Asp Tyr Ala Lys Tyr Ala Glu Arg Ile Ala Glu Glu
    50                  55                  60
Leu Gln Tyr Tyr Gly Ser Asn Ser Phe Ala Ser Phe Ile Lys Gly Glu
65                  70                  75                  80
Gly Val Leu Tyr Lys Glu Ile Leu Cys Asp Val Cys Asp Lys Leu Lys
                85                  90                  95
Val Asn Tyr Asn Lys Lys Thr Glu Thr Thr Leu Ile Glu Gln Asn Met
            100                 105                 110
Leu Ser Lys Ile Leu Glu Arg Ser Leu Glu Glu Met Asp Asp Glu Glu
        115                 120                 125
Val Lys Glu Met Cys Asp Glu Leu Ser Ile Lys Asn Thr Asp Asn Leu
    130                 135                 140
Asn Arg Gln Ala Leu Ser Ala Ala Thr Leu Thr Leu Phe Lys Met Gly
145                 150                 155                 160
Gly Phe Lys Ser Tyr Gln Leu Ala Val Ile Val Ala Asn Ala Val Ala
                165                 170                 175
Lys Thr Ile Leu Gly Arg Gly Leu Ser Leu Ala Gly Asn Gln Val Leu
            180                 185                 190
Thr Arg Thr Leu Ser Phe Leu Thr Gly Pro Val Gly Trp Ile Ile Thr
        195                 200                 205
Gly Val Trp Thr Ala Ile Asp Ile Ala Gly Pro Ala Tyr Arg Val Thr
    210                 215                 220
Ile Pro Ala Cys Ile Val Val Ala Thr Leu Arg Leu Lys Thr Gln Gln
225                 230                 235                 240
Ala Asn Glu Asp Lys Lys Ser Leu Gln Ile Glu Ser Val
                245                 250
```

(2) INFORMATION FOR SEQ ID NO:786:

(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

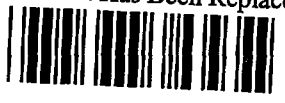
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786

```
Val Phe Leu Val Gln Ser Trp Ala Leu Ser Leu Lys Ile Asp Ser Leu
1               5                  10                  15
Phe Ser Leu Phe Ser Val Gly Lys Ile Pro Ser Gly Ser Lys Asp Pro
            20                  25                  30
Phe Ala Leu Arg Arg Leu Ser Phe Gly Leu Leu Lys Ile Ile Ala His
```

```
        35                  40                  45
Tyr Gly Leu Glu Phe Asp Leu Lys Ala Asp Leu Lys Asn Leu Phe Glu
    50                  55                  60
Lys Val Gly Val Tyr Gln Ser Phe Asp Leu Glu Val Leu Glu Lys Phe
65                  70                  75                  80
Leu Leu Glu Arg Phe His Asn Leu Ile Asp Cys Asn Leu Ser Ile Ile
                85                  90                  95
Arg Ser Val Leu Asn Thr Asn Glu Arg Asp Ile Val Lys Ile Ile Gln
            100                 105                 110
Lys Val Lys Ala Leu Lys Arg Phe Leu Asp Asn Pro Lys Asn Ala Gln
        115                 120                 125
Lys Lys Glu Leu Leu Phe Ser Ala Phe Lys Arg Leu Ala Asn Ile Asn
    130                 135                 140
Lys Asp Arg Asn Pro Asn Glu Ser Ser Gly Phe Ser Thr Ser Leu Phe
145                 150                 155                 160
Lys Glu Leu Gln Glu His Ala Leu Phe Glu Ala Phe Asn
                165                 170
```

(2) INFORMATION FOR SEQ ID NO:787:

This Sheet Has Been Replaced



(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

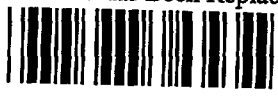
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787

```
Met Ser Leu Ala Pro Ser Val Met Ala Gly Phe Leu Phe Cys Ala Gly
1               5                  10                  15
Ser Cys Ser Leu Arg Phe Pro Asn Tyr Ser Lys Ile Ile Ser Ile Asp
            20                  25                  30
Val Asp Thr Val Phe Leu Gly Asp Val Ala Ser Ala Tyr Phe Ala Leu
        35                  40                  45
Asp Asn Glu Pro Thr Lys Leu Leu Gly Met Val Arg Asp Thr Phe Ser
    50                  55                  60
His Leu Pro Phe Glu Ala Phe Cys Asp Phe Cys Glu Arg Thr Cys Lys
65                  70                  75                  80
Asn Phe Lys Ile Asp Leu Leu Arg Phe Ser Gln Asn Glu Leu Lys Arg
                85                  90                  95
Ile His Gln Gly Phe Asn Met Gly Phe Leu Val Ala Asn Leu Asp Leu
            100                 105                 110
Trp Arg Glu Asn Gly Phe Glu Lys Ile Ala Leu Glu Phe Leu Lys Thr
        115                 120                 125
Arg Gly Lys Asp Leu Phe Tyr Pro Glu Gln Cys Leu Ile Asn Met Val
    130                 135                 140
Phe Leu Glu Arg Ile Leu Glu Leu Pro Ile His Tyr Asn Cys Tyr Ser
145                 150                 155                 160
Asp Phe Phe Lys Glu His Tyr Pro Lys Ser Ile Ile Met Leu His Phe
                165                 170                 175
Ile Lys Tyr Lys Pro Trp Arg Ser Val Ser Ser Leu Asn Gly Arg Leu
            180                 185                 190
Ile Cys Tyr Glu Ala Glu Ala Ser Phe Trp Leu Ala Asn Leu Phe Cys
        195                 200                 205
```

```
Thr Pro Phe Lys Asn Asp Phe Phe Lys Glu Arg Leu Glu Met Ala Lys
    210                 215                 220
Asp Gln Gln Met Gln Ser Phe Lys Thr His Ile Arg Ser Lys Thr Ile
225                 230                 235                 240
Arg Asp Tyr Phe Tyr Phe Arg Ile Lys Asn Ile Leu Lys Lys Val Phe
                245                 250                 255
Glu Leu Ser
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:788:

(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:788

```
Leu Leu Leu Phe Ile Val Val Ile Thr Ser Leu Val Lys Asn Thr Ile
1               5                   10                  15
Pro Asn Ile Trp Leu Thr Lys Ile Leu Tyr Met Ala Ile Leu Leu Cys
            20                  25                  30
Ala Ile Ala His Ser Val Gly Unk Ile Leu Arg Trp Tyr Val Ser Gly
        35                  40                  45
His Ser Pro Trp Ser Asn Ala Tyr Glu Ser Met Phe Tyr Ile Ala Trp
    50                  55                  60
Ala Ser Val Ile Ala Gly Phe Val Leu Arg Unk Lys Leu Ala Leu Ser
65                  70                  75                  80
Ala Ser Ser Phe Leu Ala Gly Ile Ala Leu Phe Val Ala His Leu Gly
                85                  90                  95
Phe Met Asp Pro Gln Ile Gly Pro Leu Val Pro Val Leu Lys Ser Tyr
            100                 105                 110
Trp Leu Asn Ile His Val Ser Val Ile Thr Ala Ser Tyr Gly Phe Leu
        115                 120                 125
Gly Leu Cys Phe Val Leu Gly Ile Leu Ser Leu Val Leu Phe Ile Leu
    130                 135                 140
Arg Lys Gln Gly Arg Phe Asn Leu Asp Lys Thr Ile Leu Ser Ile Ser
145                 150                 155                 160
Ala Ile Asn Glu Met Ser Met Ile Leu Gly Leu Phe Met Leu Thr Ala
                165                 170                 175
Gly Asn Phe Leu Gly Gly Val Trp Ala Asn Glu Ser Trp Gly Arg Tyr
            180                 185                 190
Trp Gly Trp Asp Pro Lys Glu Thr Trp Ala Leu Ile Ser Ile Cys Val
        195                 200                 205
Tyr Ala Leu Ile Leu His Leu Arg Phe Leu Gly Ser Gln Asn Trp Pro
    210                 215                 220
Phe Ile Leu Ala Ser Ser Ser Val Leu Gly Phe Tyr Ser Val Leu Met
225                 230                 235                 240
Thr Leu Phe Trp Arg Glu Leu Leu Pro Phe Trp Leu Ala Gln Leu Cys
                245                 250                 255
Arg Arg Unk Ser Phe Ala Asp Pro Tyr Phe Phe Ile Leu Phe Gly Ser
            260                 265                 270
Asp Thr Phe Arg Ser Arg Ile Leu Ala Tyr Phe Lys Arg His Leu Ser
```

275 280 285
Leu Pro Lys Leu Val
290

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:788:

(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:788

Leu Leu Leu Phe Ile Val Val Ile Thr Ser Leu Val Lys Asn Thr Ile
1 5 10 15
Pro Asn Ile Trp Leu Thr Lys Ile Leu Tyr Met Ala Ile Leu Leu Cys
20 25 30
Ala Ile Ala His Ser Val Gly Unk Ile Leu Arg Trp Tyr Val Ser Gly
35 40 45
His Ser Pro Trp Ser Asn Ala Tyr Glu Ser Met Phe Tyr Ile Ala Trp
50 55 60
Ala Ser Val Ile Ala Gly Phe Val Leu Arg Unk Lys Leu Ala Leu Ser
65 70 75 80
Ala Ser Ser Phe Leu Ala Gly Ile Ala Leu Phe Val Ala His Leu Gly
85 90 95
Phe Met Asp Pro Gln Ile Gly Pro Leu Val Pro Val Leu Lys Ser Tyr
100 105 110
Trp Leu Asn Ile His Val Ser Val Ile Thr Ala Ser Tyr Gly Phe Leu
115 120 125
Gly Leu Cys Phe Val Leu Gly Ile Leu Ser Leu Val Leu Phe Ile Leu
130 135 140
Arg Lys Gln Gly Arg Phe Asn Leu Asp Lys Thr Ile Leu Ser Ile Ser
145 150 155 160
Ala Ile Asn Glu Met Ser Met Ile Leu Gly Leu Phe Met Leu Thr Ala
165 170 175
Gly Asn Phe Leu Gly Gly Val Trp Ala Asn Glu Ser Trp Gly Arg Tyr
180 185 190
Trp Gly Trp Asp Pro Lys Glu Thr Trp Ala Leu Ile Ser Ile Cys Val
195 200 205
Tyr Ala Leu Ile Leu His Leu Arg Phe Leu Gly Ser Gln Asn Trp Pro
210 215 220
Phe Ile Leu Ala Ser Ser Ser Val Leu Gly Phe Tyr Ser Val Leu Met
225 230 235 240
Thr Leu Phe Trp Arg Glu Leu Leu Pro Phe Trp Leu Ala Gln Leu Cys
245 250 255
Arg Arg Unk Ser Phe Ala Asp Pro Tyr Phe Phe Ile Leu Phe Gly Ser
260 265 270
Asp Thr Phe Arg Ser Arg Ile Leu Ala Tyr Phe Lys Arg His Leu Ser
275 280 285
Leu Pro Lys Leu Val
290

(2) INFORMATION FOR SEQ ID NO:789:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 194 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:789

```
Val Ile Val Cys Ser Ala Ala Gly Leu Ser His Phe Phe Gly Phe Ser
1               5                  10                  15
Met Ser Leu Gly Ala Phe Ile Val Gly Met Ala Ile Ser Lys Ser Arg
            20                  25                  30
Tyr Lys Ile Asn Val Gln Glu Glu Phe Ala Gln Leu Lys Asn Leu Phe
        35                  40                  45
Leu Ala Leu Phe Phe Ile Thr Ile Gly Met Gln Ile Asn Val Ser Phe
    50                  55                  60
Phe Met Glu Lys Phe Phe Val Val Ile Phe Leu Leu Ile Leu Val Met
65                  70                  75                  80
Ser Phe Lys Thr Phe Ile Ile Tyr Ala Leu Leu Arg Phe Phe Arg Asp
                85                  90                  95
Ala Lys Thr Ala Ile Lys Thr Ala Leu Ser Leu Ala Gln Ile Gly Glu
            100                 105                 110
Phe Ser Phe Val Ile Phe Leu Asn Ser Gly Ser His Gln Leu Phe Asn
        115                 120                 125
Leu Gln Glu Lys Lys Gly Ile Leu Gly Phe Leu His Gln Lys Asn Ile
    130                 135                 140
Leu Asn Ile Ala Gln Asn Asp Ile His Gln Leu Leu Ile Leu Met Val
145                 150                 155                 160
Val Phe Ser Met Leu Ala Thr Pro Phe Ile Leu Lys Tyr Leu Glu Ser
                165                 170                 175
Ile Ala Gln Phe Ile Leu His Gln Lys Ser Gln Glu Asn Glu Pro Ala
            180                 185                 190
Lys Lys
```

(2) INFORMATION FOR SEQ ID NO:790:

(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

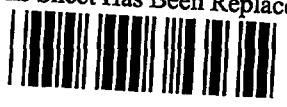
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790

```
Met Phe Tyr Leu Ile Asn Thr Gly Val Pro His Leu Val Gly Phe Val
1               5                  10                  15
Lys Asn Lys Gly Leu Leu Asn Ser Leu Asn Thr Leu Glu Leu Arg Ala
            20                  25                  30
Leu Arg His Glu Phe Asn Ala Asn Ile Asn Ile Ala Phe Ile Glu Asn
        35                  40                  45
Lys Glu Thr Ile Phe Leu Gln Thr Tyr Glu Arg Gly Val Glu Asp Phe
    50                  55                  60
Thr Leu Ala Cys Gly Thr Gly Met Ala Ala Val Phe Ile Ala Ala Arg
65                  70                  75                  80
Leu Phe His Asn Thr Pro Lys Lys Ala Thr Leu Ile Pro Lys Ser Asn
                85                  90                  95
Glu Phe Leu Glu Leu Ser Leu Lys Asn Asp Gly Ile Phe Tyr Lys Gly
            100                 105                 110
Val Ala Arg Tyr Ile Gly Met Ser Val Leu Gly Met Gly Val Phe Lys
        115                 120                 125
Asn Gly Cys Phe
    130
```

(2) INFORMATION FOR SEQ ID NO:791:

This Sheet Has Been Replaced



(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:791

```
Met Ile Lys Ala Ile Asp Ile Ser His Asp Phe Glu Lys Pro Leu Tyr
1               5                  10                  15
Asn Gly Val Asn Leu Arg Ile Lys Pro Lys Glu Ser Met Glu Ile Leu
            20                  25                  30
Gly Val Ser Gly Ser Gly Lys Ser Thr Leu Ile Ser His Leu Ala Thr
        35                  40                  45
Met Leu Lys Pro Asp Ser Gly Thr Val Ser Leu Leu Glu His Gln Asp
    50                  55                  60
Ile Tyr Ala Leu Asn Ser Lys Lys Leu Leu Glu Leu Arg Arg Leu Lys
65                  70                  75                  80
Val Gly Ile Val Phe Gln Ser His Tyr Leu Phe Lys Gly Phe Ser Ala
                85                  90                  95
Leu Glu Asn Leu Gln Val Ala Ser Ile Leu Ala Lys Gln Glu Ile Asn
            100                 105                 110
His Ser Leu Leu Glu Gln Leu Gly Ile Ala His Thr Leu Lys Gln Gly
        115                 120                 125
Val Gly Glu Leu Ser Gly Gly Gln Gln Gln Arg Leu Ser Ile Ala Arg
    130                 135                 140
Val Leu Ser Lys Lys Pro Gln Ile Ile Ile Ala Asp Glu Pro Thr Gly
145                 150                 155                 160
Asn Leu Asp Thr Thr Ser Ala Asn Gln Val Ile Ser Met Leu Gln Asn
                165                 170                 175
```

```
Tyr Ile Thr Glu Asn Glu Gly Ala Leu Val Leu Ala Thr His Asp Glu
            180                 185                 190
His Leu Ala Phe Thr Cys Ser Gln Val Tyr Arg Leu Glu Lys Glu Ser
        195                 200                 205
Leu Ile Lys Glu Lys
    210
```

(2) INFORMATION FOR SEQ ID NO:792:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...47

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792

```
Met Leu Asp Lys Arg Ile Lys Thr Leu Leu Leu Phe Phe Gly Leu Asn
1               5                   10                  15
Met Val Cys Leu Ser Val Ser Phe Thr Asn Lys Pro His Leu Cys Phe
            20                  25                  30
Trp Phe Leu Val Leu Gly Cys Tyr Leu Val Tyr Glu Trp Gln Lys
        35                  40                  45
```

(2) INFORMATION FOR SEQ ID NO:793:

(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:793

```
Val Glu Met Ile His Thr Gln Asp Tyr Ile Lys Met Glu Glu Ala Ala
1               5                   10                  15
Thr Glu Ala Ile Lys Arg Lys Glu Ser Ser Ile Tyr Leu Gly Met Asp
            20                  25                  30
Ile Leu Lys Asn Gly Ala Asp Ala Leu Ile Ser Ala Gly His Ser Gly
        35                  40                  45
Ala Thr Met Gly Leu Ala Thr Leu Arg Leu Gly Arg Ile Lys Gly Val
    50                  55                  60
Glu Arg Pro Ala Ile Cys Thr Leu Met Pro Ser Val Gly Lys Arg Pro
```

```
65                  70                  75                  80
Ser Val Leu Leu Asp Ala Gly Ala Asn Thr Asp Cys Lys Pro Glu Tyr
                85                  90                  95
Leu Ile Asp Phe Ala Leu Met Gly Tyr Glu Tyr Ala Lys Ser Val Leu
            100                 105                 110
His Tyr Asp Ser Pro Lys Val Gly Leu Leu Ser Asn Gly Glu Glu Asp
        115                 120                 125
Ile Lys Gly Gly Ile Arg Ser Leu Lys Lys Arg Ile Lys Cys
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:793:

(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:793

```
Val Glu Met Ile His Thr Gln Asp Tyr Ile Lys Met Glu Glu Ala Ala
1               5                   10                  15
Thr Glu Ala Ile Lys Arg Lys Glu Ser Ser Ile Tyr Leu Gly Met Asp
            20                  25                  30
Ile Leu Lys Asn Gly Ala Asp Ala Leu Ile Ser Ala Gly His Ser Gly
        35                  40                  45
Ala Thr Met Gly Leu Ala Thr Leu Arg Leu Gly Arg Ile Lys Gly Val
    50                  55                  60
Glu Arg Pro Ala Ile Cys Thr Leu Met Pro Ser Val Gly Lys Arg Pro
65                  70                  75                  80
Ser Val Leu Leu Asp Ala Gly Ala Asn Thr Asp Cys Lys Pro Glu Tyr
                85                  90                  95
Leu Ile Asp Phe Ala Leu Met Gly Tyr Glu Tyr Ala Lys Ser Val Leu
            100                 105                 110
His Tyr Asp Ser Pro Lys Val Gly Leu Leu Ser Asn Gly Glu Glu Asp
        115                 120                 125
Ile Lys Gly Gly Ile Arg Ser Leu Lys Lys Arg Ile Lys Cys
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:794:

(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

This Sheet Has Been Replaced

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...59

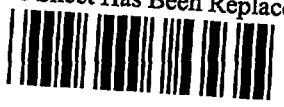
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794

```
Met Lys Thr Ile Lys Asn Gly Ile Met Ile Gly Thr Leu Gly Ala Leu
1               5                  10                  15
Leu Leu Ser Gly Cys Ser Ser Phe Asp Ala Gln Arg Phe Ala Cys Leu
            20                  25                  30
Pro Lys Asp His Ser Ser Lys Asp Ala Ser Thr Lys Lys Glu Ala Gln
        35                  40                  45
Tyr Ile Pro Lys Gly Phe Phe Asp Pro Tyr Ser Ser Asn Leu Asn His
    50                  55                  60
Trp Asp Ser Thr Phe
65
```

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:795

```
Met Leu Glu Ile Lys Asn Leu Asn Cys Val Leu Asn Ser His Phe Ser
1               5                  10                  15
Leu Gln Asn Ile Asn Ile Ser Leu Ser Tyr Ser Glu Arg Val Ala Ile
            20                  25                  30
Val Gly Glu Ser Gly Ser Gly Lys Ser Ser Ile Ala Asn Leu Val Met
        35                  40                  45
Arg Leu Asn Pro Arg Phe Lys Ser His Asn Gly Glu Ile Leu Phe Glu
    50                  55                  60
Thr Thr Asn Leu Leu Lys Glu Ser Glu Ala Phe Unk Gln His Leu Arg
65                  70                  75                  80
Gly Asn Ile Ile Ala Tyr Ile Ala Gln Asp Pro Leu Ser Ser Leu Asn
                85                  90                  95
Pro Leu His Lys Ile Gly Lys Gln Met Ser Glu Ala Tyr Phe Leu His
            100                 105                 110
His Lys Asn Ala Ser Gln Val Ser Leu Asn Glu Gln Val Leu Asn Val
        115                 120                 125
Met Lys Gln Val Gln Leu Asp Glu Asn Phe Trp Asn Val Ser Leu Met
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795

```
Met Leu Glu Ile Lys Asn Leu Asn Cys Val Leu Asn Ser His Phe Ser
1               5                  10                  15
Leu Gln Asn Ile Asn Ile Ser Leu Ser Tyr Ser Glu Arg Val Ala Ile
            20                  25                  30
Val Gly Glu Ser Gly Ser Gly Lys Ser Ser Ile Ala Asn Leu Val Met
        35                  40                  45
Arg Leu Asn Pro Arg Phe Lys Ser His Asn Gly Glu Ile Leu Phe Glu
    50                  55                  60
Thr Thr Asn Leu Leu Lys Glu Ser Glu Ala Phe Unk Gln His Leu Arg
65                  70                  75                  80
Gly Asn Ile Ile Ala Tyr Ile Ala Gln Asp Pro Leu Ser Ser Leu Asn
                85                  90                  95
Pro Leu His Lys Ile Gly Lys Gln Met Ser Glu Ala Tyr Phe Leu His
            100                 105                 110
His Lys Asn Ala Ser Gln Val Ser Leu Asn Glu Gln Val Leu Asn Val
        115                 120                 125
Met Lys Gln Val Gln Leu Asp Glu Asn Phe Trp Asn Val Ser Leu Met
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:796:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 190 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796

```
Met Glu Leu Ile Leu Gly Ser Gln Ser Ser Ala Arg Ala Asn Leu Leu
1               5                  10                  15
Lys Glu His Gly Ile Lys Phe Glu Gln Lys Ala Leu Tyr Phe Asp Glu
            20                  25                  30
Glu Ser Leu Lys Thr Thr Asp Pro Arg Glu Phe Val Tyr Leu Ala Cys
        35                  40                  45
Lys Gly Lys Leu Glu Lys Ala Lys Glu Leu Leu Ala Asn Asn Cys Ala
    50                  55                  60
Ile Val Val Ala Asp Ser Val Val Ser Val Gly Asn Arg Met Gln Arg
65                  70                  75                  80
Lys Ala Lys Asn Lys Arg Glu Ala Leu Glu Phe Leu Lys Arg Gln Asn
                85                  90                  95
```

```
Gly Asn Glu Ile Glu Val Leu Thr Cys Ser Ala Leu Ile Ser Pro Val
            100                 105                 110
Leu Glu Trp Leu Asp Leu Ser Val Phe Arg Ala Arg Leu Lys Ala Phe
        115                 120                 125
Asp Cys Ser Glu Ile Glu Lys Tyr Leu Glu Ser Gly Leu Trp Gln Gly
    130                 135                 140
Ser Ala Gly Cys Val Arg Leu Glu Asp Phe His Lys Pro Tyr Ile Lys
145                 150                 155                 160
Ser Ser Ser Lys Asn Leu Ser Val Gly Leu Gly Leu Asn Val Glu Gly
                165                 170                 175
Leu Leu Gly Ala Leu Lys Leu Gly Val Lys Leu Ser Leu Leu
            180                 185                 190
```

(2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:797

```
Met Asn Tyr Lys Val Ala Ser Ala Arg Asn Ile Ala Thr Leu Leu Phe
1               5                   10                  15
Leu Phe Phe Ser Gln Ser Glu Ala Phe Asp Leu Gly Lys Ile Ala Lys
            20                  25                  30
Ile Lys Ala Gly Ala Glu Ser Phe Ser Lys Val Gly Phe Asn Asn Lys
        35                  40                  45
Pro Ile Asn Unk Asn Lys Gly Ile Tyr Pro Thr Glu Thr Phe Met Thr
    50                  55                  60
Ile Asn Gly Leu His Ala Gly Gly Phe Tyr Gly Ala Leu Ala Gln Lys
65                  70                  75                  80
Arg Tyr Gly
```

(2) INFORMATION FOR SEQ ID NO:797:

(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:797

```
Met Asn Tyr Lys Val Ala Ser Ala Arg Asn Ile Ala Thr Leu Leu Phe
1               5                  10                  15
Leu Phe Phe Ser Gln Ser Glu Ala Phe Asp Leu Gly Lys Ile Ala Lys
            20                  25                  30
Ile Lys Ala Gly Ala Glu Ser Phe Ser Lys Val Gly Phe Asn Asn Lys
        35                  40                  45
Pro Ile Asn Unk Asn Lys Gly Ile Tyr Pro Thr Glu Thr Phe Met Thr
    50                  55                  60
Ile Asn Gly Leu His Ala Gly Gly Phe Tyr Gly Ala Leu Ala Gln Lys
65                  70                  75                  80
Arg Tyr Gly
```

(2) INFORMATION FOR SEQ ID NO:798:

(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:798

```
Met Leu Ile Leu Gly His Pro Leu Ile Pro Ser Ala Arg Phe Val Phe
1               5                  10                  15
Ile Lys Asn Thr Asp Ala Ile His Ser Ser Ala Asn Asn Asp Ile Val
            20                  25                  30
Cys Phe Glu Ala Asn Pro Lys Asn Leu Glu Leu Ala Gln Tyr Cys Cys
        35                  40                  45
Glu Asn Gly Val His Phe Ser Val Ile Phe Leu Ser His Lys Ile Glu
    50                  55                  60
Thr Asp Thr Phe Phe Leu Phe Asn Ala Phe Lys Pro Leu Tyr Cys Ile
65                  70                  75                  80
Phe Lys Asp Ile Lys Gln Ala Ile Leu Ala Gln Gln His Ala Thr Asn
                85                  90                  95
Tyr Leu Leu Asp Ser Lys Ile Leu Phe Ser Met Asp Phe Asn Asp Thr
            100                 105                 110
Glu Ser Trp Glu Ile Cys Ala Lys Asn Gln Ile Asp Gly Val Ile Ser
        115                 120                 125
Lys Asp Ser Leu Leu Leu Lys
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:799:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

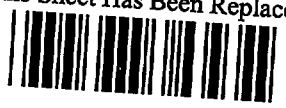
This Sheet Has Been Replaced



(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799

```
Met Lys Lys Arg Leu Asn Ile Gly Leu Val Gly Leu Gly Cys Val Gly
1               5                  10                  15
Ser Thr Val Ala Lys Ile Leu Gln Glu Asn Gln Glu Ile Ile Lys Asp
            20                  25                  30
Arg Ala Gly Val Glu Ile Lys Ile Lys Lys Ala Val Val Arg Asp Val
        35                  40                  45
Lys Lys His Lys Gly Tyr Ala Phe Glu Ile Ser Asp Asp Leu Glu Ser
    50                  55                  60
Val Ile Glu Asp Lys Gly Ile Asp Ile Val Val Glu Leu Met Gly Gly
65                  70                  75                  80
Val Glu Ala Pro Tyr Leu Leu Ala Lys Lys Thr Leu Ala Lys Gln Lys
                85                  90                  95
Ala Phe Val Thr Ala Asn Lys Ala Met Leu Ala Tyr His Arg Tyr Glu
            100                 105                 110
Leu Glu Gln Ile Ala Lys Asn Thr Pro Ile Gly Phe Glu Ala Ser Val
        115                 120                 125
Cys Gly Gly Ile Pro Ile Ile Lys Ala Leu Lys Asp Gly Leu Ser Ala
    130                 135                 140
Asn His Ile Leu Ser Phe Lys Gly Ile Leu Asn Gly Thr Ser Asn Tyr
145                 150                 155                 160
Ile Leu Ser Gln Met Phe Lys Asn Gln Ala Ser Phe Lys Asp Ala Leu
                165                 170                 175
Lys Asp Ala Gln His Leu Gly Tyr Ala Glu Leu Asn Pro Glu Phe Asp
            180                 185                 190
Ile Lys Gly Ile Asp Ala Ala His Lys Leu Leu Ile Leu Ala Ser Leu
        195                 200                 205
Ala Tyr Gly Ile Asp Ala Lys Leu Glu Glu Ile Leu Ile Glu Gly Ile
    210                 215                 220
Glu Lys Ile Glu Pro Asp Asp Met Glu Phe Ala Lys Glu Phe Gly Tyr
225                 230                 235                 240
Ser Ile Lys Leu Leu Gly Ile Ala Lys Lys His Gln Gly Leu His
                245                 250                 255
```

(2) INFORMATION FOR SEQ ID NO:800:

(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

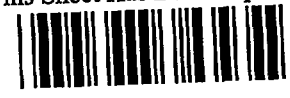
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800

```
Met Gln Glu Lys Arg Leu Lys Ala Ile Gln Asn Lys Ile Ala Ser Trp
1               5                  10                  15
Ile Lys Glu Ile Glu Ser Gly Phe Ile Asp Ala Leu Phe Ser Lys Ile
            20                  25                  30
Gly Pro Ser Lys Met Leu Arg Ser Lys Leu Met Leu Ala Leu Leu Asp
        35                  40                  45
Glu Lys Thr Asp Ala Ile Leu Leu Asp Lys Ala Leu Asn Leu Cys Ala
    50                  55                  60
Ile Val Glu Met Ile Gln Thr Ala Ser Leu Leu His Asp Asp Val Ile
65                  70                  75                  80
Asp Lys Ala Thr Met Arg Arg Lys Leu Pro Ser Ile Asn Ala Leu Phe
                85                  90                  95
Gly Asn Phe Asn Ala Val Met Leu Gly Asp Val Phe Tyr Ser Lys Ala
            100                 105                 110
Phe Phe Glu Leu Ser Lys Met Gly Glu Ser Ile Ala Gln Ala Leu Ser
        115                 120                 125
Asn Ala Val Leu Arg Leu Ser Arg Gly Glu Ile Glu Asp Val Phe Val
    130                 135                 140
Gly Glu Cys Phe Asn Ser Asp Lys Gln Lys Tyr Trp Arg Ile Leu Glu
145                 150                 155                 160
Asp Lys Thr Ala His Phe Ile Glu Ala Ser Leu Lys Ser Met Ala Ile
                165                 170                 175
Leu Leu Asn Lys Asp Ala Lys Met Tyr Ala Asp Phe Gly Leu His Phe
            180                 185                 190
Gly Met Ala Phe Gln Ile Ile Asp Asp Leu Leu Asp Ile Thr Gln Asp
        195                 200                 205
Ala Asn Thr Leu Gly Lys Pro Asn Phe Ser Asp Phe Lys Glu Gly Lys
    210                 215                 220
Thr Thr Leu Pro Tyr Leu Leu Leu Tyr Glu Lys Leu Asn Gln His Glu
225                 230                 235                 240
Gln Gly Phe
```

(2) INFORMATION FOR SEQ ID NO:801:

This Sheet Has Been Replaced



(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:801

```
Met Leu Gly Lys Lys Asn Glu Glu Val Leu Ile Asp Glu Asn Leu Val
1               5                  10                  15
Gly Gly Val Ile Ala Leu Asp Arg Leu Ala Lys Leu Asn Lys Ala Asn
            20                  25                  30
Arg Thr Phe Lys Arg Ala Phe Tyr Leu Ser Met Val Leu Asn Val Ala
        35                  40                  45
Ala Val Thr Ser Ile Val Met Met Met Pro Leu Lys Lys Thr Asp Ile
    50                  55                  60
Phe Val Tyr Gly Ile Asp Arg Tyr Thr Gly Glu Phe Lys Ile Val Lys
65                  70                  75                  80
```

SUBSTITUTE SHEET (RULE 26)

```
Arg Ser Asp Ala Arg Gln Ile Val Asn Ser Glu Ala Val Val Asp Ser
                85                  90                  95
Ala Thr Ser Lys Phe Val Ser Leu Leu Phe Gly Tyr Ser Lys Asn Ser
            100                 105                 110
Leu Arg Asp Arg Lys Asp Gln Leu Met Gln Tyr Cys Asp Val Ser Phe
        115                 120                 125
Gln Thr Gln Ala Met Arg Met Phe Asn Glu Asn Ile Arg Gln Phe Val
    130                 135                 140
Asp Lys Val Arg Ala Glu Ala Ile Ile Ser Ser Asn Ile Gln Arg Glu
145                 150                 155                 160
Lys Val Lys Asn Ser Pro Leu Thr Arg Leu Thr Phe Phe Ile Thr Ile
                165                 170                 175
Lys Ile Thr Pro Asp Thr Met Glu Asn Tyr Glu Tyr Ile Thr Lys Lys
            180                 185                 190
Gln Val Thr Ile Tyr Tyr Asp Phe Ala Arg Gly Asn Ser Ser Gln Glu
        195                 200                 205
Asn Leu Ile Ile Asn Pro Phe Gly Phe Lys Val Phe Asp Ile Gln Ile
    210                 215                 220
Thr Asp Leu Gln Asn Glu Gln Thr Val Ser Glu Ile Leu Arg Lys Ile
225                 230                 235                 240
Lys Glu Val Glu Ser Lys Asn Lys Ala Leu Asn Lys
                245                 250
```

(2) INFORMATION FOR SEQ ID NO:802:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 165 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

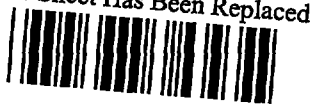
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802

```
Met Arg Ala Ile Ala Ile Val Leu Ala Arg Ser Ser Ser Lys Arg Ile
1               5                   10                  15
Lys Asn Lys Asn Met Ile Asp Phe Phe Asn Lys Pro Met Leu Ala Tyr
            20                  25                  30
Pro Ile Glu Thr Ala Leu Asn Ser Lys Leu Phe Glu Lys Val Phe Ile
        35                  40                  45
Ser Ser Asp Ser Met Glu Tyr Val Asn Leu Ala Lys Asn Tyr Gly Ala
    50                  55                  60
Ser Phe Leu Asn Leu Arg Pro Lys Asn Leu Ala Asp Asp Arg Ala Thr
65                  70                  75                  80
Thr Leu Glu Val Met Ala Tyr His Met Lys Glu Leu Glu Leu Lys Asp
                85                  90                  95
Glu Asp Ile Ala Cys Cys Leu Tyr Gly Val Ser Val Phe Leu Gln Glu
            100                 105                 110
Lys His Leu Gln Asn Ala Phe Glu Thr Leu Lys Gln Asn Gln Asn Thr
        115                 120                 125
Asp Tyr Val Phe Thr Cys Ser Pro Phe Ser Ala Ser Pro Ile Val Leu
    130                 135                 140
Leu Ala Leu Lys Thr Ala Phe Lys Trp Leu Leu Lys Ser Ile Gln Thr
145                 150                 155                 160
Arg Ala Arg Lys Ile
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:803:

This Sheet Has Been Replaced



(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:803

```
Met Ser Asn Gln Ala Ser His Leu Asp Asn Phe Met Asn Ala Lys Asn
1               5                  10                  15
Pro Lys Ser Phe Phe Asp Asn Lys Gly Asn Thr Lys Phe Ile Ala Ile
            20                  25                  30
Thr Ser Gly Lys Gly Gly Val Gly Lys Ser Asn Ile Ser Ala Asn Leu
        35                  40                  45
Ala Tyr Ser Leu Tyr Lys Lys Gly Tyr Lys Val Gly Val Phe Asp Ala
    50                  55                  60
Asn Ile Gly Leu Ala Asn Leu Asp Val Ile Phe Gly Val Lys Thr Gln
65                  70                  75                  80
Lys Asn Ile Leu His Asp Leu Lys Gly Glu Asp Lys Leu Lys Glu Ile
                85                  90                  95
Ile Cys Glu Ile Glu Pro Gly Leu Cys Leu Ile Pro Gly Asp Ser Gly
            100                 105                 110
Glu Glu Ile Leu Lys Tyr Ile Ser Glu Ala Glu Asp Phe Asp Ser Phe
        115                 120                 125
Leu Asp Glu Glu Gly Val Leu Ser Ala Leu Ile Tyr Ile Leu Ile Asn
    130                 135                 140
Thr Phe Ser Lys Asn Leu Gly Pro Leu Ser Gln Thr Phe Leu Asn Phe
145                 150                 155                 160
Gln Ser Phe Leu Phe Ile Phe Ile Gln Ser Pro
                165                 170
```

(2) INFORMATION FOR SEQ ID NO:804:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804

```
Met Gln His Leu Val Leu Ile Gly Phe Met Gly Ser Gly Lys Ser Ser
1               5                  10                  15
Leu Ala Gln Glu Leu Gly Leu Ala Leu Lys Leu Glu Val Leu Asp Thr
            20                  25                  30
Asp Met Ile Ile Ser Glu Arg Val Gly Leu Ser Val Arg Gly Ile Phe
        35                  40                  45
Glu Glu Leu Gly Glu Asp Asn Phe Arg Met Phe Glu Lys Ile
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:805:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805

```
Met Ser Ile Lys Glu Asn Leu Glu Gln Val Arg Asn Glu Phe Lys Ser
1               5                  10                  15
Asp Glu Lys Leu Leu Glu Gly Ala Phe Arg Leu Glu Lys Phe Phe Lys
            20                  25                  30
Arg Tyr Lys Trp Val Leu Leu Phe Ile Val Val Ala Phe Ile Ala Tyr
        35                  40                  45
Leu Gly Asp Thr Lys Leu Gln Asp Tyr Lys His Glu Gln Thr Arg Glu
    50                  55                  60
Arg Ile Thr Gln Ile Tyr Asn Glu Val Leu Glu Ser Pro Asn Asn Ile
65                  70                  75                  80
Ala Leu Gln Lys Arg Leu Lys Glu Val Ala Pro Glu Leu Tyr Asp Leu
                85                  90                  95
Tyr Gln Phe Ala Arg Ala Ser Glu Arg Asn Asp Ala Asn Glu Phe Lys
            100                 105                 110
Arg Leu Ser Gln Ser Ser Asn Glu Ile Val Lys Ala Phe Ala Lys Tyr
        115                 120                 125
Ser Tyr Ala Ser Leu Ser Arg Asp Lys Asn Leu Leu Glu Lys Ser Pro
    130                 135                 140
Ile Leu Lys Glu Met Ser Ala Leu Gln Glu Val Asn Leu Leu Tyr Glu
145                 150                 155                 160
Glu Asn Ser Lys Asp Ala Ile Lys Lys Ala His Gln Ser Leu Ser Thr
                165                 170                 175
Ile Pro Leu Ser Ser Ser Leu Tyr Ala Ile Ile Ser Val Leu Lys His
            180                 185                 190
Tyr Gly Met Leu Glu Asp Ile
        195
```

(2) INFORMATION FOR SEQ ID NO:806:

(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:806

```
Met Asp Ala Leu Glu Ile Thr Gln Lys Leu Ile Ser Tyr Pro Thr Ile
1               5                  10                  15
Thr Pro Lys Glu Cys Gly Ile Phe Glu Tyr Ile Lys Ser Leu Phe Pro
            20                  25                  30
Ala Phe Lys Thr Leu Glu Cys Glu Lys Asn Gly Val Lys Asn Leu Phe
        35                  40                  45
Leu Tyr Arg Ile Phe Asn Pro Leu Lys Lys His Ala Glu Lys Glu His
    50                  55                  60
Ala Lys Glu Lys His Val Lys Glu Asn Val Unk Pro Leu His Phe Cys
65                  70                  75                  80
Unk Ala Gly His Ile Unk Val Val Pro Pro Gly Unk Unk Unk Unk Unk
                85                  90                  95
Asp Ser Phe Unk Unk Ile Ile Lys Glu Gly Phe Leu Tyr Gly Arg Gly
            100                 105                 110
Ala Gln Asp Met Lys Gly Gly Val Gly Unk Phe Unk Arg Cys Unk Unk
        115                 120                 125
Lys Phe
    130
```

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:806

```
Met Asp Ala Leu Glu Ile Thr Gln Lys Leu Ile Ser Tyr Pro Thr Ile
1               5                  10                  15
Thr Pro Lys Glu Cys Gly Ile Phe Glu Tyr Ile Lys Ser Leu Phe Pro
            20                  25                  30
Ala Phe Lys Thr Leu Glu Cys Glu Lys Asn Gly Val Lys Asn Leu Phe
        35                  40                  45
Leu Tyr Arg Ile Phe Asn Pro Leu Lys Lys His Ala Glu Lys Glu His
    50                  55                  60
Ala Lys Glu Lys His Val Lys Glu Asn Val Unk Pro Leu His Phe Cys
65                  70                  75                  80
```

```
Unk Ala Gly His Ile Unk Val Val Pro Pro Gly Unk Unk Unk Unk Unk
                85                  90                  95
Asp Ser Phe Unk Unk Ile Ile Lys Glu Gly Phe Leu Tyr Gly Arg Gly
            100                 105                 110
Ala Gln Asp Met Lys Gly Gly Val Gly Unk Phe Unk Arg Cys Unk Unk
        115                 120                 125
Lys Phe
    130
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:807:

(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:807

```
Val His Phe Asn Gln Val Val Leu Pro Lys Gly Val Gly Ala Ile Leu
1               5                  10                  15
Val Ala Pro Lys Gly Pro Gly Ser Ala Leu Arg Glu Glu Tyr Leu Lys
            20                  25                  30
Asn Arg Gly Leu Tyr His Leu Ile Ala Ile Glu Gln Glu Ser Ser Ile
        35                  40                  45
His Asn Ala Lys Ala Val Ala Leu Ser Tyr Ala Lys Ala Met Gly Gly
    50                  55                  60
Gly Arg Met Gly Val Leu Glu Thr Ser Phe Lys Glu Glu Cys Glu Ser
65                  70                  75                  80
Asp Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Leu Glu Val Asp
                85                  90                  95
Arg Lys Asn Gly Val
            100
```

(2) INFORMATION FOR SEQ ID NO:808:

(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

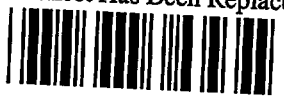
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808

```
Met Lys Lys Phe Phe Ser Gln Ser Leu Leu Ala Leu Ile Ile Ser Met
1               5                  10                  15
Asn Ala Val Ser Gly Met Asp Gly Asn Gly Val Phe Leu Gly Ala Gly
            20                  25                  30
Tyr Leu Gln Gly Gln Ala Gln Met His Ala Asp Ile Asn Ser Gln Lys
        35                  40                  45
Gln Ala Thr Asn Ala Thr Ile Lys Gly Phe Asp Ala Leu Leu Gly Tyr
    50                  55                  60
Gln Phe Phe Phe Glu Lys His Phe Gly Leu Arg Leu Tyr Gly Val Phe
65                  70                  75                  80
```

(2) INFORMATION FOR SEQ ID NO:809:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809

```
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 Unk Ile Ser Ser Asn Glu Leu
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 Unk 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 Ala Ile Ala Trp Leu
        435                 440                 445
```

(2) INFORMATION FOR SEQ ID NO:810:

This Sheet Has Been Replaced



(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

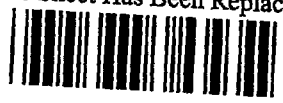
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810

```
Met Asn Asp Thr Thr Glu His His Gly Ser Asn Pro Leu Asn Ala Pro
1               5                   10                  15
Pro Pro Ser Asn Ser Gln Ser Asn Asp Leu Leu Asn Leu Leu Asp Ser
            20                  25                  30
Leu Tyr Pro Lys Gly Ser Leu Gly Glu Gln Arg Phe His Glu Ala Leu
        35                  40                  45
Lys Asn Gln Glu Glu Leu Lys Asn Ile Leu Ile Glu Ile Glu Lys Leu
    50                  55                  60
Pro Gln Glu Lys Arg Tyr Glu Leu Leu Met Gln Ile Gly Gln Ala Lys
65                  70                  75                  80
Gln Arg Ile Met Glu Ala Tyr Ala His Ser Phe Leu Gly Tyr Ile Gly
                85                  90                  95
Gly Leu Glu His Leu Leu Gly Leu Cys Met Gly Gly Ile Phe Val Leu
            100                 105                 110
Phe Ala Ile Tyr Phe Val Phe Leu Arg Thr Ser Lys Asn Thr Glu Leu
        115                 120                 125
Val Glu Ser Leu Lys Thr Lys Leu Lys Leu Gln Tyr Phe Tyr Tyr Ala
    130                 135                 140
Phe Gly Val Gly Ala Val Leu Phe Phe Gly Leu Glu Thr Ile Arg Ser
```

```
145                 150                 155                 160
Ile Tyr Glu Leu Tyr Ile Leu Gly Ile Gly Ser Thr Asn Asp Lys Val
                165                 170                 175
Leu Phe Val Leu Lys Asn Ile Cys Phe Ile Gly Met Gly Tyr Leu Ile
            180                 185                 190
Tyr Lys Val Ile Lys Val Ile Gly Ile Lys Asn Phe Ile Asn Gly Leu
        195                 200                 205
Phe Ala Ser Lys Lys Gln Gly Gly Ala Glu
    210                 215
```

(2) INFORMATION FOR SEQ ID NO:811:

This Sheet Has Been Replaced



(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:811

```
Met Met Asp Lys Val Gly Phe Lys Ser Gln Gly Ile Phe Val Met Asp
1               5                   10                  15
Ala Ser Lys Arg Asp Gly Arg Leu Asn Ala Tyr Phe Gly Gly Leu Gly
            20                  25                  30
Lys Asn Lys Arg Val Val Leu Phe Asp Thr Leu Ile Ser Lys Val Gly
        35                  40                  45
Thr Glu Unk Leu Leu Ala Ile Leu Gly His Glu Leu Gly His Phe Lys
    50                  55                  60
Asn Lys Asp Leu Leu Lys Asn Leu Gly Ile Met Gly Gly Leu Leu Ala
65                  70                  75                  80
Leu Val Phe Ala Leu Ile Ala His Leu Pro Pro Leu Val Phe Glu Gly
                85                  90                  95
Phe Asn Val Ser Gln Thr Pro Ala Ser Leu Ile Thr Ile Leu Leu Leu
            100                 105                 110
Phe Leu Pro Val Phe Ser Phe Tyr Ala Met Pro Leu Ile Gly Phe Phe
        115                 120                 125
Ser Arg Lys Asn Glu Tyr Asn Ala Asp Lys Phe Gly Ala Ser Leu Ser
    130                 135                 140
Ser Lys Glu Thr Leu Ala Lys Ala Leu Val Ser Ile Val Asn Glu Asn
145                 150                 155                 160
Lys Ala Phe Pro Tyr Ser His Pro Phe Tyr Val Phe Leu His Phe Thr
                165                 170                 175
His Pro Pro Leu Leu Glu Arg Leu Lys Ala Leu Asp Tyr Glu Ile Glu
            180                 185                 190
```

(2) INFORMATION FOR SEQ ID NO:812:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced

(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:812

```
Met Ile Leu Ser Ile Glu Ser Ser Cys Asp Asp Ser Ser Leu Ala Leu
1               5                  10                  15
Thr Arg Ile Glu Asp Ala Lys Leu Ile Ala His Phe Lys Ile Ser Gln
            20                  25                  30
Glu Lys His His Ser Ser Tyr Gly Gly Val Val Pro Glu Ile Ala Ser
        35                  40                  45
Arg Leu His Ala Glu Asn Leu Pro Leu Leu Leu Glu Arg Val Lys Ile
    50                  55                  60
Ser Leu Asn Lys Asp Phe Ser Lys Ile Lys Ala Ile Ala Ile Thr Asn
65                  70                  75                  80
Gln Pro Gly Leu Ser Val Thr Leu Ile Glu Gly Leu Met Met Ala Lys
                85                  90                  95
Ala Leu Ser Leu Ser Leu Asn Leu Pro Leu Ile Leu Glu Asp His Leu
            100                 105                 110
Arg Gly His Val Tyr Ser Leu Phe Ile Asn Glu Lys Gln Thr Arg Met
        115                 120                 125
Pro Leu Ser Val Leu Leu Val Ser Gly Gly His Ser Leu Ile Leu Glu
    130                 135                 140
Ala Arg Asp Tyr Glu Asp Ile Lys Ile Val Ala Thr Ser Leu Asp Asp
145                 150                 155                 160
Ser Phe Gly Glu Ser Phe Asp Lys Val Ser Lys Met Leu Asp Leu Gly
                165                 170                 175
Tyr Pro Gly Gly Pro Ile Val Glu Lys Leu Ala Leu Asp Tyr Ala His
            180                 185                 190
Pro Asn Glu Pro Leu Met Phe Pro Ile Pro Leu Lys Asn Ser Pro Asn
        195                 200                 205
Leu Ala Phe Ser Phe Ser Gly Leu Lys Asn Ala Val Arg Leu Glu Val
    210                 215                 220
Glu Lys Asn Ala His Asn Leu Asn Asp Glu Val Lys Gln Lys Ile Gly
225                 230                 235                 240
Tyr His Phe Gln Ser Ala Ala Ile Glu His Leu Ile Gln Gln Thr Lys
                245                 250                 255
Arg Tyr Phe Lys Ile Lys Arg Pro Lys Ile Phe Gly Ile Val Gly Gly
            260                 265                 270
Ala Ser Gln Asn Leu Ala Leu Arg Lys Ala Phe Glu Asp Leu Cys Ala
        275                 280                 285
Glu Phe Asp Cys Glu Leu Val Leu Ala Pro Leu Glu Phe Cys Ser Asp
    290                 295                 300
Asn Ala Ala Met Ile Gly Arg Ser Ser Leu Glu Ala Tyr Gln Lys Lys
305                 310                 315                 320
Arg Phe Ile Pro Leu Glu Lys Ala Asp Ile Ser Pro Arg Thr Leu Leu
                325                 330                 335
Lys Asn Phe Glu
            340
```

(2) INFORMATION FOR SEQ ID NO:812:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812

```
Met Ile Leu Ser Ile Glu Ser Ser Cys Asp Asp Ser Ser Leu Ala Leu
1               5                  10                  15
Thr Arg Ile Glu Asp Ala Lys Leu Ile Ala His Phe Lys Ile Ser Gln
            20                  25                  30
Glu Lys His His Ser Ser Tyr Gly Gly Val Val Pro Glu Ile Ala Ser
        35                  40                  45
Arg Leu His Ala Glu Asn Leu Pro Leu Leu Leu Glu Arg Val Lys Ile
    50                  55                  60
Ser Leu Asn Lys Asp Phe Ser Lys Ile Lys Ala Ile Ala Ile Thr Asn
65                  70                  75                  80
Gln Pro Gly Leu Ser Val Thr Leu Ile Glu Gly Leu Met Met Ala Lys
                85                  90                  95
Ala Leu Ser Leu Ser Leu Asn Leu Pro Leu Ile Leu Glu Asp His Leu
            100                 105                 110
Arg Gly His Val Tyr Ser Leu Phe Ile Asn Glu Lys Gln Thr Arg Met
        115                 120                 125
Pro Leu Ser Val Leu Leu Val Ser Gly Gly His Ser Leu Ile Leu Glu
    130                 135                 140
Ala Arg Asp Tyr Glu Asp Ile Lys Ile Val Ala Thr Ser Leu Asp Asp
145                 150                 155                 160
Ser Phe Gly Glu Ser Phe Asp Lys Val Ser Lys Met Leu Asp Leu Gly
                165                 170                 175
Tyr Pro Gly Gly Pro Ile Val Glu Lys Leu Ala Leu Asp Tyr Ala His
            180                 185                 190
Pro Asn Glu Pro Leu Met Phe Pro Ile Pro Leu Lys Asn Ser Pro Asn
        195                 200                 205
Leu Ala Phe Ser Phe Ser Gly Leu Lys Asn Ala Val Arg Leu Glu Val
    210                 215                 220
Glu Lys Asn Ala His Asn Leu Asn Asp Glu Val Lys Gln Lys Ile Gly
225                 230                 235                 240
Tyr His Phe Gln Ser Ala Ala Ile Glu His Leu Ile Gln Gln Thr Lys
                245                 250                 255
Arg Tyr Phe Lys Ile Lys Arg Pro Lys Ile Phe Gly Ile Val Gly Gly
            260                 265                 270
Ala Ser Gln Asn Leu Ala Leu Arg Lys Ala Phe Glu Asp Leu Cys Ala
        275                 280                 285
Glu Phe Asp Cys Glu Leu Val Leu Ala Pro Leu Glu Phe Cys Ser Asp
    290                 295                 300
Asn Ala Ala Met Ile Gly Arg Ser Ser Leu Glu Ala Tyr Gln Lys Lys
305                 310                 315                 320
Arg Phe Ile Pro Leu Glu Lys Ala Asp Ile Ser Pro Arg Thr Leu Leu
                325                 330                 335
Lys Asn Phe Glu
            340
```

(2) INFORMATION FOR SEQ ID NO:813:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:813

```
Met Asn Ile Tyr Gln Lys Asn Leu Gln Ala Leu Phe Lys Lys Asp Pro
1               5                  10                  15
Leu Leu Phe Ala Lys Leu Lys Ala Ile Lys Glu Asn Lys Lys Tyr Glu
            20                  25                  30
Val Phe Leu Gly Asn Asp Ser Ala Asn Phe Asn Leu Leu Asp Lys Glu
        35                  40                  45
Thr Asn Thr Pro Leu Phe Glu Lys Ser Pro Leu Asp Ser Ser Leu Glu
    50                  55                  60
Leu Tyr Lys Asn Ser Glu Ile His Met Leu Tyr Pro Tyr Leu Tyr Tyr
65                  70                  75                  80
Phe Gly Leu Gly Asn Gly Val Phe Tyr Arg Leu Leu Leu Gly Asn Glu
                85                  90                  95
Asn Leu Lys Arg Leu Val Val Ile Glu Pro Glu Ile Glu Val Ile Phe
            100                 105                 110
Ile Val Leu Asn Leu Leu Asp Phe Ser Thr Glu Ile Leu Glu Asn Arg
        115                 120                 125
Leu Ile Leu Leu His Ala Ser Phe Cys Asn Tyr Asn Met Ile Ala Ser
    130                 135                 140
Leu Phe Asp Met Asp Lys Lys Ser Arg Leu Tyr Ala Arg Met Tyr Asp
145                 150                 155                 160
Leu Lys Leu Phe Asn Ala Tyr Tyr Glu Arg Tyr Ser His Gln Met Ile
                165                 170                 175
Glu Ile Asn Gln His Phe Thr Arg Ala Leu Glu His Gly Ala Ile Ser
            180                 185                 190
Val Gly Asn Asp Ala Lys Ala His Ser
        195                 200
```

(2) INFORMATION FOR SEQ ID NO:814:

(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:814

```
Met Lys Lys Ile Ile Leu Ala Cys Leu Val Ala Phe Val Gly Ala Asn
1               5                  10                  15
Leu Ser Ala Glu Pro Lys Trp Tyr Ser Lys Ala Tyr Asn Lys Thr Asn
```

```
            20                  25                  30
Ala Gln Lys Gly Tyr Leu Tyr Gly Ser Gly Ser Ala Thr Ser Lys Glu
        35                  40                  45
Ala Ser Lys Gln Lys Ala Leu Ala Asp Leu Val Ala Ser Ile Ser Val
    50                  55                  60
Val Val Asn Ser Gln Ile His Ile Gln Lys Ser Arg Val Asp Asn Lys
65                  70                  75                  80
Leu Lys Ser Ser Asp Ser Gln Thr Ile Asn Leu Lys Thr Asp Asp Leu
                85                  90                  95
Glu Leu Asn Asn Val Glu Ile Val Asn Gln Glu Ala Gln Lys Gly Ile
            100                 105                 110
Tyr Tyr Thr Arg Val Arg Asn Gln Ser Lys Leu Val Phe Ala Gly Phe
        115                 120                 125
Lys Gly
    130
```

(2) INFORMATION FOR SEQ ID NO:815:

This Sheet Has Been Replaced



(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:815

```
Met Lys Ile Gln Thr Ile Ser Thr Leu Val Leu Thr Ile Ile Met Val
1               5                   10                  15
Ile Gln Lys Met Ile Val Gly Lys Ile Ser Pro His Lys Thr Ala Glu
            20                  25                  30
Glu Phe Thr Asn Leu Met Leu Asn Met Ile Ala Val Leu Asp Ser Gln
        35                  40                  45
Ser Trp Gly Asp Ala Ile Leu Asn Ala Pro Phe Glu Phe Thr Asn Ser
    50                  55                  60
Pro Thr Asp Cys Asp Asn Asp Pro Ser Lys Cys Val Asn Pro Gly Thr
65                  70                  75                  80
Asn Gly Leu Val Asn Ser Lys Val Asp Gln Lys Tyr Val Leu Asn Lys
                85                  90                  95
Gln Asp Ile Val Asn Lys Phe Lys Asn Lys Ala Asp Leu Asp Val Ile
            100                 105                 110
Val Leu Lys Asp Ser Gly Val Val Gly Unk Unk Asn Gly Tyr Gly Asn
        115                 120                 125
Asp Gly Glu Tyr Gly Thr Leu Gly Val Unk Ala Tyr Ala Leu Gly Ser
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:816:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816

```
Val Val Ile Arg Leu Val Leu Asn Met Leu Thr Cys Gln Ile Ser Tyr
1               5                  10                  15
Ile Arg Ile Ser Tyr Leu Val Ser Val Ser Asp Phe Val Ile Cys Lys
            20                  25                  30
Glu Arg Phe Met Asp Glu Ile Lys Thr Leu Leu Val Asp Phe Phe Pro
        35                  40                  45
Gln Ala Lys His Phe Gly Ile Ile Leu Ile Lys Ala Ile Val Val Phe
    50                  55                  60
Cys Ile Gly Phe Tyr Phe Ser Phe Phe Leu Arg Asn Lys Thr Met Lys
65                  70                  75                  80
Leu Leu Ser Lys Lys Asp Glu Ile Leu Ala Asn Phe Val Ala Gln Val
                85                  90                  95
Thr Phe Ile Leu Ile Leu Ile Ile Thr Thr Ile Ile Ala Leu Ser Thr
            100                 105                 110
Leu Gly Val Gln Thr Thr Ser Ile Ile Thr Val Leu Gly Thr Val Gly
        115                 120                 125
Ile Ala Val Ala Leu Ala Leu Lys Asp Tyr Leu Ser Ser Ile Ala Gly
    130                 135                 140
Gly Ile Ile Leu Ile Ile Leu His Pro Phe Lys Lys Gly Asp Ile Ile
145                 150                 155                 160
Glu Ile Ser Gly Leu Glu Gly Lys Val Glu Ala Leu Asn Phe Phe Asn
                165                 170                 175
Thr Ser Leu Arg Leu His Asp Gly Arg Leu Ala Val Leu Pro Asn Arg
            180                 185                 190
Ser Val Ala Asn Ser Asn Ile Ile Asn Ser Asn Asn Thr Ala Cys Arg
        195                 200                 205
Arg Ile Glu Trp Val Cys Gly Val Gly Tyr Gly Ser Asp Ile Glu Leu
    210                 215                 220
Val His Lys Thr Ile Lys Asp Val Ile Asp Gly Met Glu Lys Ile Asp
225                 230                 235                 240
Lys Asn Met Pro Thr Phe Ile Gly Ile Thr Asp Phe Gly Gln Ser Ser
                245                 250                 255
Leu Asn Phe Thr Ile Arg Val Trp Ala Lys Ile Glu Asp Gly Ile Phe
            260                 265                 270
Asn Val Arg Ser Glu Leu Ile Glu Arg Ile Lys Asn Ala Leu Asp Ala
        275                 280                 285
Asn Arg Ile Glu Ile Pro Phe Asn Lys Leu Asp Ile Ser Ile Asn Lys
    290                 295                 300
Gln Asp Ser Ser Lys
305
```

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817

```
Met Lys Asn Phe Ser Pro Leu Tyr Cys Leu Lys Unk Leu Lys Lys Arg
1               5                  10                  15
His Leu Ile Ala Leu Ser Leu Pro Leu Leu Ser Tyr Ala Asn Gly Phe
            20                  25                  30
Lys Ile Gln Glu Gln Ser Leu Asn Gly Thr Ala Leu Gly Ser Ala Tyr
        35                  40                  45
Val Ala Gly Ala Arg Gly Ala Asp Ala Ser Phe Tyr Asn Pro Ala Asn
    50                  55                  60
Met Gly Phe Thr Asn Asp Trp Gly Glu Asn Arg Ser Glu Phe Glu Met
65                  70                  75                  80
Thr Thr Thr Val Ile Asn Ile Pro Thr Phe Ser Phe Lys Val Pro Thr
                85                  90                  95
Thr Asn Gln Unk Leu Tyr Ser Val Thr Ser Leu Glu Ile Asp Lys Ser
            100                 105                 110
Gln Gln Asn Ile Leu Gly Ile Ile Asn Thr Ile Gly Leu Gly Asn Ile
        115                 120                 125
Leu Lys Ala Leu Gly Asn Thr Ala Ala Thr Asn Gly Leu Ser Gln Ala
    130                 135                 140
Ile Asn Arg Val Gln Gly Leu Met Asn Leu Thr Asn Gln Lys Val Val
145                 150                 155                 160
Thr Leu Ala Ser
```

(2) INFORMATION FOR SEQ ID NO:818:

(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:818

```
Met Cys Leu Ala Ile Pro Ser Lys Val Ile Ala Ile Asn Asp Asn Val
1               5                  10                  15
Ala Leu Leu Glu Thr Leu Gly Val Gln Arg Glu Ala Ser Leu Asp Leu
            20                  25                  30
Met Gly Glu Ser Val Lys Val Gly Asp Tyr Val Leu Leu His Ile Gly
        35                  40                  45
Tyr Val Met Ser Lys Asp
    50
```

(2) INFORMATION FOR SEQ ID NO:819:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1..202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819

```
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 Asn 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
Ala Asn Ala Glu Gln Thr Glu Phe Tyr Tyr
        195                 200
```

(2) INFORMATION FOR SEQ ID NO:820:

(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:820

```
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 Unk Unk
            100                 105                 110
Lys Thr Unk Unk Lys Thr Trp Gly Ile Met Pro Leu Ala Met Lys Ser
        115                 120                 125
Thr 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:820:

This Sheet Has Been Replaced



(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:820

```
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 Unk Unk
            100                 105                 110
Lys Thr Unk Unk Lys Thr Trp Gly Ile Met Pro Leu Ala Met Lys Ser
        115                 120                 125
Thr 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

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:821:

(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:821

```
Val Val Ser Gly Val Val Ile Ile Ile Val Phe Phe Val Pro Ile Leu
1               5                  10                  15
Thr Leu Gln Gly Leu Glu Gly Lys Met Phe Arg Pro Leu Ala Gln Ser
            20                  25                  30
Ile Val Tyr Ala Leu Leu Gly Thr Leu Val Leu Ser Ile Thr Ile Ile
        35                  40                  45
Pro Val Val Ser Ser Leu Val Leu Lys Ala Thr Pro His Ser Glu Thr
    50                  55                  60
Phe Leu Thr Arg Phe Leu Asn Arg Ile Tyr Ala Pro Leu Leu Glu Phe
65                  70                  75                  80
Phe Val His Asn Pro Lys Lys Val Ile Leu Gly Ala Phe Val Phe Leu
                85                  90                  95
Ile Ala Ser Leu Ser Leu Phe Pro Phe Val Gly Lys Asn Phe Met Pro
            100                 105                 110
Ala Leu Asp Glu Gly Asp Val Val Leu Ser Val Glu Thr Thr Pro Ser
        115                 120                 125
Ile Ser Leu Asp Gln Ser Lys Asp Leu Met Leu Asn Ile Glu Ser Ala
    130                 135                 140
Ile Lys Lys His Val Lys Glu Val Lys Ser Ile Val Ala Arg Thr Gly
145                 150                 155                 160
Ser Asp Glu Leu Gly Leu Asp Leu Gly Gly Leu Asn Gln Thr Asp Thr
                165                 170                 175
Phe Ile Ser Phe Ile Pro Lys Lys Glu Trp
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:822:

(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:

This Sheet Has Been Replaced



(A) NAME/KEY: misc_feature
(B) LOCATION 1...72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822

```
Val Gly Tyr Ile Pro Unk Glu Lys Ile Val Gly Ile Ser Ala Ile Ala
1               5                  10                  15
Lys Leu Ile Glu Ile Tyr Ser Lys Arg Leu Gln Ile Gln Glu Arg Leu
            20                  25                  30
Thr Thr Gln Ile Ala Glu Thr Phe Asp Glu Ile Ile Glu Pro Arg Gly
        35                  40                  45
Val Ile Val Val Cys Glu Ala Lys Pro Leu Val His Glu His Ala Arg
    50                  55                  60
Gly Ala Lys Ala Lys Cys Asp His
65                  70
```

(2) INFORMATION FOR SEQ ID NO:823:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823

```
Leu Asp Pro Phe Ser His Lys Glu Asn Phe Leu Ala Val Glu Thr Phe
1               5                  10                  15
Lys Met Leu Gly Lys Thr Glu Ser Lys Asp Asn Leu Asn Trp Met Ile
            20                  25                  30
Ala Leu Ile Ile Glu Lys Asp Lys Val Tyr Glu Gln Val Gly Ser Val
        35                  40                  45
Arg Phe Val Val Val Val Ala Ser Ala Ile Met Val Leu Ala Leu Ile
    50                  55                  60
Ile Ala Ile Thr Leu Leu Met Arg Ala Ile Val Ser Asn Arg Leu Glu
65                  70                  75                  80
Val Val Ser Ser Thr Leu Ser His Phe Phe Lys Leu Leu Asn Asn Gln
                85                  90                  95
Unk His Ser Ser Unk Unk Lys Leu Val Unk Ala Arg Ser Asn Asp Glu
            100                 105                 110
Leu Gly Arg Unk Gln Thr Unk Asp Unk
        115                 120
```

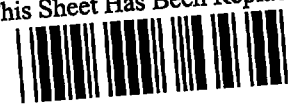
(2) INFORMATION FOR SEQ ID NO:823:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823

```
Leu Asp Pro Phe Ser His Lys Glu Asn Phe Leu Ala Val Glu Thr Phe
1               5                  10                  15
Lys Met Leu Gly Lys Thr Glu Ser Lys Asp Asn Leu Asn Trp Met Ile
            20                  25                  30
Ala Leu Ile Ile Glu Lys Asp Lys Val Tyr Glu Gln Val Gly Ser Val
        35                  40                  45
Arg Phe Val Val Val Val Ala Ser Ala Ile Met Val Leu Ala Leu Ile
    50                  55                  60
Ile Ala Ile Thr Leu Leu Met Arg Ala Ile Val Ser Asn Arg Leu Glu
65                  70                  75                  80
Val Val Ser Ser Thr Leu Ser His Phe Phe Lys Leu Leu Asn Asn Gln
                85                  90                  95
Unk His Ser Ser Unk Unk Lys Leu Val Unk Ala Arg Ser Asn Asp Glu
            100                 105                 110
Leu Gly Arg Unk Gln Thr Unk Asp Unk
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:824:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824

```
Val Ala Leu Val Phe Asp Ser Leu Ile Glu Asn Lys Lys
1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:825:

(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:825

```
Met Lys Lys Ile Gly Leu Ser Leu Cys Leu Val Leu Ser Leu Gly Phe
1               5                  10                  15
Leu Lys Ala His Glu Val Ser Ala Glu Glu Ile Ala Asp Ile Phe Tyr
            20                  25                  30
Lys Leu Asn Ala Lys Glu Pro Lys Met Lys Ile Asn His Thr Lys Gly
        35                  40                  45
Phe Cys Ala Lys Gly Val Phe Leu Pro Asn Pro Gln Ala Arg Glu Asp
    50                  55                  60
Leu Glu Val Pro Leu Leu Asn Glu Lys Glu Ile Pro Ala Ser Val Arg
65                  70                  75                  80
Tyr Ser Leu Gly Gly Val Val Asp Trp Thr Ile Lys Ala Arg Leu Gly
                85                  90                  95
Glu Trp Arg
```

(2) INFORMATION FOR SEQ ID NO:826:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:826

```
Val Ile Lys Pro His Ser Val Gly Leu Val Arg Ile Gly Ile Cys Leu
1               5                  10                  15
Ser Leu Glu Val Gly Tyr Glu Leu Gln Val Arg Thr Arg Ser Gly Leu
            20                  25                  30
Ala Leu Asn His Gln Val Met Val Leu Asn Unk Pro Gly Thr Val Asp
        35                  40                  45
Asn Asp Tyr Arg Gly Glu Ile Lys Val Ile Leu Ala Asn Leu Ser Asp
    50                  55                  60
Lys Asp Phe Lys Val Gln Val
65                  70
```

(2) INFORMATION FOR SEQ ID NO:827:

(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

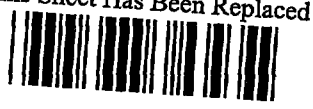
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827

```
Met Glu Phe Tyr Gln Val Tyr Asp Pro Leu Gly His Ile Trp Leu Ser
1               5                  10                  15
Ala Leu Val Ala Leu Ser Pro Ile Ala Leu Phe Phe Ile Ser Leu Ile
            20                  25                  30
Val Phe Lys Leu Lys Gly Tyr Ser Ala Gly Phe Leu Ser Leu Ala Leu
        35                  40                  45
Ser Ile Leu Ile Ala Leu Phe Val Tyr Lys Met Pro Val Gln Met Val
    50                  55                  60
Ser Ala Ser Phe Phe Tyr Gly Phe Leu Tyr Gly Leu Trp Pro Ile Ala
65                  70                  75                  80
Trp Ile Val Ile Ala Ala Ile Phe Leu Tyr Asn Leu Ser Val Lys Ser
                85                  90                  95
Gly Tyr Phe Glu Ile Leu Lys Glu Ser Ile Leu Ser Leu Thr Pro Asp
            100                 105                 110
His Arg Ile Leu Val Ile Leu Ile Gly Phe Cys Phe Gly Ser Phe Leu
        115                 120                 125
Unk Gly Ala Unk Gly Phe Gly Gly Pro Val Ala Ile Thr Ala Ala Ile
    130                 135                 140
Leu Val Ala Leu Gly
145
```

(2) INFORMATION FOR SEQ ID NO:827:

This Sheet Has Been Replaced



(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

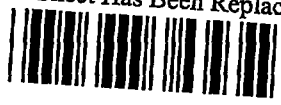
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827

```
Met Glu Phe Tyr Gln Val Tyr Asp Pro Leu Gly His Ile Trp Leu Ser
1               5                  10                  15
Ala Leu Val Ala Leu Ser Pro Ile Ala Leu Phe Phe Ile Ser Leu Ile
            20                  25                  30
Val Phe Lys Leu Lys Gly Tyr Ser Ala Gly Phe Leu Ser Leu Ala Leu
        35                  40                  45
Ser Ile Leu Ile Ala Leu Phe Val Tyr Lys Met Pro Val Gln Met Val
    50                  55                  60
Ser Ala Ser Phe Phe Tyr Gly Phe Leu Tyr Gly Leu Trp Pro Ile Ala
65                  70                  75                  80
Trp Ile Val Ile Ala Ala Ile Phe Leu Tyr Asn Leu Ser Val Lys Ser
                85                  90                  95
Gly Tyr Phe Glu Ile Leu Lys Glu Ser Ile Leu Ser Leu Thr Pro Asp
```

```
            100                 105                 110
His Arg Ile Leu Val Ile Leu Ile Gly Phe Cys Phe Gly Ser Phe Leu
        115                 120                 125
Unk Gly Ala Unk Gly Phe Gly Gly Pro Val Ala Ile Thr Ala Ala Ile
    130                 135                 140
Leu Val Ala Leu Gly
145
```

(2) INFORMATION FOR SEQ ID NO:828:

This Sheet Has Been Replaced



(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:828

```
Met Glu Ile Ile Leu Leu Ile Val Ala Ala Val Val Leu Phe Tyr Phe
1               5                  10                  15
Tyr Asn Thr Leu Lys Glu Tyr Leu Lys Asn Pro Leu Asn Pro Lys Thr
            20                  25                  30
Lys Thr Glu Glu Tyr Asp Leu Lys Asn Asp Pro Tyr Leu Leu Val Gln
        35                  40                  45
Ser Ser Pro Leu Asp Lys Phe Lys Gln Thr Gln Ile Gly Ala Tyr Met
    50                  55                  60
Arg Leu Leu Lys Phe Leu Asp Ile Gln Lys Asn Ala Leu Asp Asn Ala
65                  70                  75                  80
Leu Arg Thr Leu Phe Ile His Glu Leu Glu Gln Pro Leu Asn Ser Glu
                85                  90                  95
Gln Gln Asn Leu Ala Lys Glu Leu Leu Asn Glu Pro Val Asp Lys Lys
            100                 105                 110
Glu Asn Phe Glu Ser Leu Cys Gln Glu Ile Ala Asp His Thr His Gly
        115                 120                 125
Glu Tyr Thr Lys Arg Leu Lys Leu Val Glu Phe Leu Met Leu Leu Ala
    130                 135                 140
Tyr Ala Asp Gly Ile Leu Asp Ser Lys Glu Lys Glu Leu Phe Leu Asp
145                 150                 155                 160
Val Gly Ala Phe Leu Gln Ile Asp Asn Gln Asp Phe Asn Glu Leu Tyr
                165                 170                 175
Asp Asn Phe Glu His Phe Asn Ser Ile Glu Ile Pro Met Ser Leu Glu
            180                 185                 190
Glu Ala Lys Asn Leu Phe Glu Ile Gln Thr His Thr Thr Met Gln Asp
        195                 200                 205
Leu Glu Lys Lys Ala Leu Asp Leu Ser Ala Pro Tyr Tyr His Lys Met
    210                 215                 220
Asn Asp Asn Lys Arg Tyr Ser Glu Gln Asp Phe Ile Ser Leu Lys Lys
225                 230                 235                 240
Ile Ala Leu Ala Ser Gln Leu Leu Glu Asn Asp Leu Lys Asp Ser
                245                 250                 255
```

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829

```
Met Glu Val Glu His Gly Lys Ile Glu Thr Thr Leu Ser Leu Gly Ala
1               5                  10                  15
Ser His Leu Glu Val Ile Lys Met Met Leu Leu Glu Ser Leu Pro Ser
            20                  25                  30
Leu Val Asn Asn Ile Thr Ile Thr Leu Ile Ser Leu Ile Gly Tyr Ser
        35                  40                  45
Ala Lys Ala Gly Ala Leu Gly Ala Gly Gly Leu Gly Asp Leu Ala Ile
    50                  55                  60
Arg Ile Gly Tyr Gln Ser Tyr Arg Gly Asp Val Leu Phe Tyr Ala Val
65                  70                  75                  80
Val Val Ile Ile Val Leu Val Gln Ile Ile Gln Ser Ala Gly Asp Tyr
                85                  90                  95
Val Val Lys Arg Leu Arg Lys Asn Lys Tyr
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 527 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830

```
Met Asn Glu Ile Asp Lys Ser Val Asp Ile Gly Phe Leu Arg Ile Leu
1               5                  10                  15
Asp Val Ile Lys Lys Val Lys Thr Pro Lys Gly Gly Ile Glu Val Leu
            20                  25                  30
Arg Thr Leu Ile Asp Phe Thr Pro Lys Ile Glu Asn Ala Leu Asn Leu
        35                  40                  45
Ala Thr Lys Ser His Lys Gly Gln Tyr Arg Lys Ser Gly Glu Pro Tyr
    50                  55                  60
Ile Val His Pro Ile Cys Val Ala Ser Val Val Ala Phe Cys Gly Gly
65                  70                  75                  80
Asp Glu Ala Met Val Cys Ala Ala Leu Leu His Asp Val Val Glu Asp
```

This Sheet Has Been Replaced

```
                85                  90                  95
Thr Pro Cys Glu Ile Glu Thr Ile Glu Arg Glu Phe Gly Gln Asp Val
            100                 105                 110
Ala Asn Leu Val Asp Ala Leu Thr Lys Ile Thr Glu Ile Arg Lys Glu
        115                 120                 125
Glu Leu Gly Val Ser Ser Gln Asp Pro Arg Met Val Val Ser Ala Leu
    130                 135                 140
Thr Phe Arg Lys Ile Leu Ile Ser Ala Ile Gln Asp Pro Arg Ala Leu
145                 150                 155                 160
Val Val Lys Ile Ser Asp Arg Leu His Asn Met Leu Thr Leu Asp Ala
                165                 170                 175
Leu Pro His Asp Lys Gln Val Arg Ile Ser Lys Glu Thr Leu Ala Val
            180                 185                 190
Tyr Ala Pro Ile Ala Ser Arg Leu Gly Met Ser Ser Ile Lys Asn Glu
        195                 200                 205
Leu Glu Asp Lys Ser Phe Tyr Tyr Ile Tyr Pro Glu Glu Tyr Lys Asn
    210                 215                 220
Ile Lys Glu Tyr Leu His Lys Asn Lys Gln Ser Leu Leu Leu Lys Leu
225                 230                 235                 240
Asn Ala Phe Ala Ser Lys Leu Glu Lys Lys Leu Phe Asp Ser Gly Phe
                245                 250                 255
Ser His Ser Asp Phe Lys Leu Val Thr Arg Val Lys Arg Pro Tyr Ser
            260                 265                 270
Ile Tyr Leu Lys Met Gln Arg Lys Gly Ala Val Asn Ile Asp Glu Ile
        275                 280                 285
Leu Asp Leu Leu Ala Ile Arg Ile Leu Leu Lys Asn Pro Ile Asp Cys
    290                 295                 300
Tyr Lys Val Leu Gly Ile Ile His Leu Asn Phe Lys Pro Ile Val Ser
305                 310                 315                 320
Arg Phe Lys Asp Tyr Ile Ala Leu Pro Lys Glu Asn Gly Tyr Lys Thr
                325                 330                 335
Ile His Thr Thr Ile Phe Asp Glu Ser Ser Val Tyr Glu Val Gln Ile
            340                 345                 350
Arg Thr Phe Asp Met His Met Gly Ala Glu Tyr Gly Asn Ser Ala His
        355                 360                 365
Trp Lys Tyr Lys Ala Gly Gly Val Asp His Glu Glu His His Glu Gly
    370                 375                 380
Met Arg Trp Leu Gln Asn Phe Lys Tyr His Asp Ser Asp Leu Lys Asn
385                 390                 395                 400
Asp Pro Lys Glu Phe Tyr Glu Leu Ala Lys Asn Asp Leu Tyr Arg Glu
                405                 410                 415
Asp Ile Val Val Phe Ser Pro His Gly Asp Thr Tyr Thr Leu Pro Val
            420                 425                 430
Gly Ala Ile Ala Leu Asp Phe Ala Tyr Met Val His Ser Asp Leu Gly
        435                 440                 445
Asp Lys Ala Thr Asp Ala Tyr Ile Asn Ser Lys Lys Ala Leu Leu Asn
    450                 455                 460
Gln Glu Leu Arg Ser Gly Asp Val Val Lys Ile Ile Lys Gly Asp Lys
465                 470                 475                 480
Val Ile Pro Arg Phe Ile Trp Met Asp Gln Leu Lys Thr Ser Lys Ala
                485                 490                 495
Lys Asn His Leu Arg Ile Gln Arg Arg Asn Arg Leu Lys Glu Ile Asp
            500                 505                 510
Thr Lys Ser Met Ile Asn Ile Leu Ala Thr Phe Phe Trp Ala Leu
        515                 520                 525
```

(2) INFORMATION FOR SEQ ID NO:831:

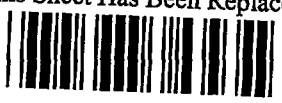
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(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:831

```
Val Val Val Val Glu Asn Ile Lys Asp Ala Val Pro Leu Ala Gln Ser
1               5                  10                  15
Leu Ile Unk Gly Gly Ile Pro Ile Ile Glu Val Thr Leu Arg Ser Asn
            20                  25                  30
Cys Ala Leu Glu Ala Ile Glu Leu Ile Ala Lys Asn Val Pro Lys Met
        35                  40                  45
Arg Val Gly Ala Gly Thr Ile Leu Asn Leu Thr Gln Leu Glu Gln Ala
    50                  55                  60
Gln Asn Arg Gly Ala Glu Phe Leu Ile Ser Pro Gly Leu Thr Ile Lys
65                  70                  75                  80
Leu Leu Glu His Ala Lys Lys Lys Asp Met Pro Leu Ile Pro Gly Val
                85                  90                  95
Ser Ser Ser Ser Glu Val Met Gln Ala Leu Glu Leu Gly Tyr Asn Ala
            100                 105                 110
Leu Lys Phe Phe Pro Ala Glu Tyr Cys Gly Gly Arg
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:832:

(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:832

```
Val Glu Lys Ile Lys Pro Tyr Ala Pro Lys Asp Ser Pro Leu Ile Asp
1               5                  10                  15
Tyr Ser Ser Leu Val Arg Asn Val Gln Ser Thr Leu Lys Gly Thr Ser
            20                  25                  30
Phe Glu Thr Leu Ile Asn Gly Val Trp Glu Ser Phe Glu Thr Lys Val
        35                  40                  45
Leu Gly Glu Phe Asn Ala Tyr Asn Ile Ala Ser Ala Ile Leu Thr Ala
    50                  55                  60
Lys His Leu Gly Leu Glu Thr Glu Arg Ile Lys Arg Leu Val Phe Glu
65                  70                  75                  80
Leu Lys Pro Ile Asn His Arg Leu Gln Leu Leu Glu Ala Asn Gln Lys
                85                  90                  95
Ile Ile Ile Asp Asp Asn Phe Asn Gly Asn Leu Lys Gly Met
            100                 105                 110
```

This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:833:

(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:833

```
Met Lys Arg Ile Leu Val Ser Leu Ala Val Leu Ser His Ser Ala His
1               5                  10                  15
Ala Val Lys Thr His Asn Leu Glu Arg Val Glu Ala Ser Gly Val Ala
            20                  25                  30
Asn Asp Lys Glu Ala Pro Leu Ser Trp Arg Ser Lys Glu Val Arg Asn
        35                  40                  45
Tyr Met Gly Ser Arg Thr Val Ile Ser Asn Lys Gln Leu Thr Lys Ser
    50                  55                  60
Ala Asn Gln Ser Ile Glu Glu Ala Leu Gln Asn Val Pro Gly Val His
65                  70                  75                  80
Ile Arg Asn Ser Thr Gly Ile Gly Ala Val Pro Ser Ile Ser Ile Arg
                85                  90                  95
Gly Phe Gly Ala Gly Gly Pro Gly His Ser Asn Thr Gly Met Ile Leu
            100                 105                 110
Val Asn Gly Ile Pro Ile Tyr Val Ala Pro Tyr Val Glu Ile Gly Thr
        115                 120                 125
Val Ile Phe Pro Val Thr Phe Gln Ser Val Asp Arg Ile Ser Val Thr
    130                 135                 140
Lys Gly Gly Glu Ser Val Arg Tyr Gly Pro Asn Ala Phe Gly Gly Val
145                 150                 155                 160
Ile Asn Ile Ile Thr Lys Gly Ile Pro Thr Asn Trp Glu Ser Gln Val
                165                 170                 175
Ser Glu Arg Thr Thr Phe Trp Gly Lys Ser Glu Asn Gly Gly Phe Phe
            180                 185                 190
Asn Gln Asn Ser Lys Asn Ile Asp Lys Ser Leu Val Asn Asn Met Leu
        195                 200                 205
Phe Asn Thr Tyr Leu Arg Thr Gly Gly Met Met Asn Lys His Phe Gly
    210                 215                 220
Ile Gln Ala Gln Val Asn Trp Leu Lys Gly Gln Gly Phe Arg Tyr Asn
225                 230                 235                 240
Ser Pro Thr Asp Ile Gln Asn Tyr Met Leu Asp Ser Leu Tyr Gln Ile
                245                 250                 255
Asn Asp Ser Asn Lys Ile Thr Ala Phe Phe Gln Tyr Tyr Ser Tyr Phe
            260                 265                 270
Leu Thr Asp Pro Gly Ser Leu Gly Ile Ala Ala Tyr Asn Gln Asn Arg
        275                 280                 285
Phe Gln Asn Asn Arg Pro Asn Asn Asp Lys Ser Gly Arg Ala Lys Arg
    290                 295                 300
Trp Gly Ala Val Tyr Gln Asn Phe Phe Gly Asp Thr Asp Arg Val Gly
305                 310                 315                 320
Gly Gly Phe His Phe
                325
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:833:

(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

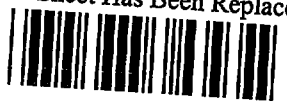
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833

```
Met Lys Arg Ile Leu Val Ser Leu Ala Val Leu Ser His Ser Ala His
1               5                  10                  15
Ala Val Lys Thr His Asn Leu Glu Arg Val Glu Ala Ser Gly Val Ala
            20                  25                  30
Asn Asp Lys Glu Ala Pro Leu Ser Trp Arg Ser Lys Glu Val Arg Asn
        35                  40                  45
Tyr Met Gly Ser Arg Thr Val Ile Ser Asn Lys Gln Leu Thr Lys Ser
    50                  55                  60
Ala Asn Gln Ser Ile Glu Glu Ala Leu Gln Asn Val Pro Gly Val His
65                  70                  75                  80
Ile Arg Asn Ser Thr Gly Ile Gly Ala Val Pro Ser Ile Ser Ile Arg
                85                  90                  95
Gly Phe Gly Ala Gly Gly Pro Gly His Ser Asn Thr Gly Met Ile Leu
            100                 105                 110
Val Asn Gly Ile Pro Ile Tyr Val Ala Pro Tyr Val Glu Ile Gly Thr
        115                 120                 125
Val Ile Phe Pro Val Thr Phe Gln Ser Val Asp Arg Ile Ser Val Thr
    130                 135                 140
Lys Gly Gly Glu Ser Val Arg Tyr Gly Pro Asn Ala Phe Gly Gly Val
145                 150                 155                 160
Ile Asn Ile Ile Thr Lys Gly Ile Pro Thr Asn Trp Glu Ser Gln Val
                165                 170                 175
Ser Glu Arg Thr Thr Phe Trp Gly Lys Ser Glu Asn Gly Gly Phe Phe
            180                 185                 190
Asn Gln Asn Ser Lys Asn Ile Asp Lys Ser Leu Val Asn Asn Met Leu
        195                 200                 205
Phe Asn Thr Tyr Leu Arg Thr Gly Gly Met Met Asn Lys His Phe Gly
    210                 215                 220
Ile Gln Ala Gln Val Asn Trp Leu Lys Gly Gln Gly Phe Arg Tyr Asn
225                 230                 235                 240
Ser Pro Thr Asp Ile Gln Asn Tyr Met Leu Asp Ser Leu Tyr Gln Ile
                245                 250                 255
Asn Asp Ser Asn Lys Ile Thr Ala Phe Phe Gln Tyr Tyr Ser Tyr Phe
            260                 265                 270
Leu Thr Asp Pro Gly Ser Leu Gly Ile Ala Ala Tyr Asn Gln Asn Arg
        275                 280                 285
Phe Gln Asn Asn Arg Pro Asn Asn Asp Lys Ser Gly Arg Ala Lys Arg
    290                 295                 300
Trp Gly Ala Val Tyr Gln Asn Phe Phe Gly Asp Thr Asp Arg Val Gly
305                 310                 315                 320
Gly Gly Phe His Phe
                325
```

(2) INFORMATION FOR SEQ ID NO:834:

This Sheet Has Been Replaced



(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:834

```
Leu Arg Ser Ile Ser Arg Ile Lys Met Leu Ser Val Tyr Glu Lys Gly
1               5                  10                  15
Asn Ala Leu Asp Lys Arg Val Leu Glu Glu Trp Leu Leu Ser Glu Asp
            20                  25                  30
Ile Leu Met Glu Asn Ala Ala Met Ala Leu Glu Arg Ala Val Leu Gln
        35                  40                  45
Asn Ala Ser Leu Gly Ala Lys Val Ile Ile Leu Cys Gly Ser Gly Asp
    50                  55                  60
Asn Gly Gly Asp Gly Tyr Thr Leu Ala Arg Arg Leu Val Gly Arg Phe
65                  70                  75                  80
Lys Thr Leu Val Phe Glu Met Lys Leu Ala Lys Ser Pro Met Cys Gln
                85                  90                  95
Leu Gln Lys Glu Arg Ala Lys Lys Val Gly Val Val Ile Lys Ala Trp
            100                 105                 110
Glu Glu Lys Asn Glu Asp Leu Glu Cys Asp Val Leu Val Asp Cys Val
        115                 120                 125
Val Gly Ser Ala Phe Lys Gly Gly Leu Glu Pro Phe Leu Asp Phe Glu
    130                 135                 140
Ser Leu Ser Gln Lys Ala Arg Phe Lys Ile Ala Cys Asp Ile Pro Ser
145                 150                 155                 160
Gly Ile Asp Ser Lys Gly Arg Val Asp Lys Arg Ala Phe Lys Unk Gly
                165                 170                 175
Tyr Arg Leu Ser Ala Trp Ala Leu Phe Lys Ser Cys Leu Leu Ser Unk
            180                 185                 190
Lys Unk Lys Unk Tyr Ile Unk Unk Leu Lys Unk Unk His Leu Unk Val
        195                 200                 205
Phe Asn Gln Ile Tyr Glu Ile Pro Thr Unk Thr Phe Leu Leu Glu Lys
    210                 215                 220
Unk Asp Leu Lys Leu Pro Leu Arg Asp Arg Lys Lys Arg Ser Gln Arg
225                 230                 235                 240
Arg Leu Arg Ala Cys Ala Cys Ala Phe Gly Gln Ala
                245                 250
```

(2) INFORMATION FOR SEQ ID NO:834:

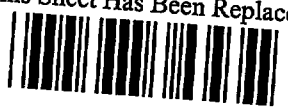
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

This Sheet Has Been Replaced



(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834

```
Leu Arg Ser Ile Ser Arg Ile Lys Met Leu Ser Val Tyr Glu Lys Gly
1               5                  10                  15
Asn Ala Leu Asp Lys Arg Val Leu Glu Glu Trp Leu Leu Ser Glu Asp
            20                  25                  30
Ile Leu Met Glu Asn Ala Ala Met Ala Leu Glu Arg Ala Val Leu Gln
        35                  40                  45
Asn Ala Ser Leu Gly Ala Lys Val Ile Ile Leu Cys Gly Ser Gly Asp
    50                  55                  60
Asn Gly Gly Asp Gly Tyr Thr Leu Ala Arg Arg Leu Val Gly Arg Phe
65                  70                  75                  80
Lys Thr Leu Val Phe Glu Met Lys Leu Ala Lys Ser Pro Met Cys Gln
                85                  90                  95
Leu Gln Lys Glu Arg Ala Lys Lys Val Gly Val Val Ile Lys Ala Trp
            100                 105                 110
Glu Glu Lys Asn Glu Asp Leu Glu Cys Asp Val Leu Val Asp Cys Val
        115                 120                 125
Val Gly Ser Ala Phe Lys Gly Gly Leu Glu Pro Phe Leu Asp Phe Glu
    130                 135                 140
Ser Leu Ser Gln Lys Ala Arg Phe Lys Ile Ala Cys Asp Ile Pro Ser
145                 150                 155                 160
Gly Ile Asp Ser Lys Gly Arg Val Asp Lys Arg Ala Phe Lys Unk Gly
                165                 170                 175
Tyr Arg Leu Ser Ala Trp Ala Leu Phe Lys Ser Cys Leu Leu Ser Unk
            180                 185                 190
Lys Unk Lys Unk Tyr Ile Unk Unk Leu Lys Unk Unk His Leu Unk Val
        195                 200                 205
Phe Asn Gln Ile Tyr Glu Ile Pro Thr Unk Thr Phe Leu Leu Glu Lys
    210                 215                 220
Unk Asp Leu Lys Leu Pro Leu Arg Asp Arg Lys Lys Arg Ser Gln Arg
225                 230                 235                 240
Arg Leu Arg Ala Cys Ala Cys Ala Phe Gly Gln Ala
                245                 250
```

(2) INFORMATION FOR SEQ ID NO:835:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 597 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835

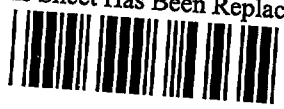
```
Met Ser Asn Gln Glu Tyr Thr Phe Gln Thr Glu Ile Asn Gln Leu Leu
1               5                  10                  15
Asp Leu Met Ile His Ser Leu Tyr Ser Asn Lys Glu Ile Phe Leu Arg
```

```
            20                  25                  30
Glu Leu Ile Ser Asn Ala Ser Asp Ala Leu Asp Lys Leu Asn Tyr Leu
        35                  40                  45
Met Leu Thr Asp Glu Lys Leu Lys Gly Leu Asn Thr Thr Pro Ser Ile
    50                  55                  60
His Leu Ser Phe Asp Ser Gln Lys Lys Thr Leu Thr Ile Lys Asp Asn
65                  70                  75                  80
Gly Ile Gly Met Asp Lys Ser Asp Leu Ile Glu His Leu Gly Thr Ile
                85                  90                  95
Ala Lys Ser Gly Thr Lys Ser Phe Leu Ser Ala Leu Ser Gly Asp Lys
            100                 105                 110
Lys Lys Asp Ser Ala Leu Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser
        115                 120                 125
Ala Phe Met Val Ala Ser Lys Ile Val Val Gln Thr Lys Lys Val Thr
    130                 135                 140
Ser His Gln Ala Tyr Ala Trp Val Ser Asp Gly Lys Gly Lys Phe Glu
145                 150                 155                 160
Ile Ser Glu Cys Val Lys Glu Glu Gln Gly Thr Glu Ile Thr Leu Phe
                165                 170                 175
Leu Lys Glu Glu Asp Ser His Phe Ala Ser Arg Trp Glu Ile Asp Ser
            180                 185                 190
Val Val Lys Lys Tyr Ser Glu His Ile Pro Phe Pro Ile Phe Leu Thr
        195                 200                 205
Tyr Thr Asp Thr Lys Phe Glu Gly Glu Gly Asp Asn Lys Lys Glu Val
    210                 215                 220
Lys Glu Glu Lys Cys Asp Gln Ile Asn Gln Ala Ser Ala Leu Trp Lys
225                 230                 235                 240
Met Asn Lys Ser Glu Leu Lys Glu Lys Asp Tyr Lys Asp Phe Tyr Gln
                245                 250                 255
Ser Phe Ala His Asp Asn Ser Glu Pro Leu Ser Tyr Ile His Asn Lys
            260                 265                 270
Val Glu Gly Ser Leu Glu Tyr Thr Thr Leu Phe Tyr Ile Pro Ser Lys
        275                 280                 285
Ala Pro Phe Asp Leu Phe Arg Val Asp Tyr Lys Ser Gly Val Lys Leu
    290                 295                 300
Tyr Val Lys Arg Val Phe Ile Thr Asp Asp Asp Lys Glu Leu Leu Pro
305                 310                 315                 320
Ser Tyr Leu Arg Phe Val Lys Gly Val Ile Asp Ser Glu Asp Leu Pro
                325                 330                 335
Leu Asn Val Ser Arg Glu Ile Leu Gln Gln Asn Lys Ile Leu Ala Asn
            340                 345                 350
Ile Arg Ser Ala Ser Val Lys Lys Ile Leu Ser Glu Ile Glu Arg Leu
        355                 360                 365
Ser Lys Asp Asn Lys Asn Tyr His Lys Phe Tyr Glu Pro Phe Gly Lys
    370                 375                 380
Val Leu Lys Glu Gly Leu Tyr Gly Asp Phe Glu Asn Lys Glu Lys Leu
385                 390                 395                 400
Leu Glu Leu Leu Arg Phe Tyr Ser Lys Asp Lys Gly Glu Trp Ile Ser
                405                 410                 415
Leu Lys Glu Tyr Lys Glu Asn Leu Lys Glu Asn Gln Lys Ser Ile Tyr
            420                 425                 430
Tyr Leu Leu Gly Glu Asn Leu Asp Leu Leu Lys Ala Ser Pro Leu Leu
        435                 440                 445
Glu Lys Tyr Ala Gln Lys Gly Tyr Asp Val Leu Leu Leu Ser Asp Glu
    450                 455                 460
Ile Asp Ala Phe Val Met Pro Gly Val Asn Glu Tyr Asp Lys Thr Pro
465                 470                 475                 480
Phe Arg Asp Ala Ser His Ser Glu Ser Leu Lys Glu Leu Gly Leu Ala
                485                 490                 495
Glu Ile His Asp Glu Val Lys Asp Gln Phe Lys Asp Leu Ile Lys Ala
            500                 505                 510
Phe Glu Glu Asn Leu Lys Asp Glu Ile Lys Gly Val Glu Leu Ser Gly
        515                 520                 525
His Leu Thr Ser Ala Val Ala Leu Ile Gly Asp Glu Pro Asn Ala Met
    530                 535                 540
```

```
Met Ala Asn Trp Met Arg Gln Met Gly Gln Ser Val Pro Glu Ser Lys
545                 550                 555                 560
Lys Thr Leu Glu Leu Asn Pro Asn His Ala Ile Leu Gln Lys Leu Leu
                565                 570                 575
Lys Cys Glu Asp Lys Glu Gln Leu Ser Ala Phe Ile Trp Leu Leu Tyr
            580                 585                 590
Asp Gly Arg Ser Phe
        595
```

(2) INFORMATION FOR SEQ ID NO:836:

This Sheet Has Been Replaced



(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:836

```
Val Asn Leu Gly Ala Tyr Tyr Thr Pro Pro Tyr Leu Val Asp Cys Ala
1               5                   10                  15
Tyr Lys Leu Leu Lys Lys His Val Gly Ile Glu Asn Tyr Thr Leu Leu
            20                  25                  30
Asp Thr Ala Cys Gly Asn Lys Glu Phe Leu Lys Leu His His Pro Lys
        35                  40                  45
Lys Ile Gly Ala Asp Ile Asp Pro Lys Cys Asp Ala Leu Ile Ile Asn
    50                  55                  60
Ala Leu Ala Asn Pro Lys Arg Glu Asn Tyr Gly Ile Ser Gln Asp Glu
65                  70                  75                  80
Pro Leu Ile Ile Val Gly Asn Pro Pro Tyr Asn Asp Arg Thr Ser Phe
                85                  90                  95
Ile Lys Gln Asp Ile Lys Asn Lys Asp Phe Ile Phe Glu Ile Asp Asn
            100                 105                 110
Asp Leu Lys Ser Arg Asp Leu Gly Ile Ser Phe Leu Lys Ser Phe Ala
        115                 120                 125
Ile Leu Lys Pro Ala Phe Ile Cys Val Leu His Pro Leu Ser Tyr Leu
    130                 135                 140
Ile Lys Glu Ala Asn Phe Lys Gln Phe Lys Ala Ile
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:837:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837

```
Met Lys Ser Ile Leu Leu Phe Ile Ile Phe Val Val Cys Gln Leu Glu
1               5                  10                  15
Gly Lys Lys Phe Ser Gln Asp Asn Phe Lys Val Asp Tyr Asn Tyr Tyr
            20                  25                  30
Leu Arg Lys Gln Asp Leu His Ile Ile Lys Thr Gln Asn Asp Leu Ser
        35                  40                  45
Asn Ala Trp Tyr Leu Pro Pro Gln Lys Ala Pro Lys Glu His Ser Trp
    50                  55                  60
Val Asp Phe Ala Lys Lys Tyr Leu Asn Met Met Asp Tyr Leu Gly Thr
65                  70                  75                  80
Tyr Phe Leu Pro Phe Tyr His Ser Phe Thr Pro Ile Phe Gln Trp Tyr
                85                  90                  95
His Pro Asn Ile Asn Pro Tyr Lys Arg Asn Glu Phe Lys Phe Gln Ile
            100                 105                 110
Ser Phe Arg Val Pro Val Phe Arg His Ile Leu Trp Thr Lys Gly Thr
        115                 120                 125
Leu Tyr Leu Asp Tyr Thr Gln Thr Asn Trp Phe Gln Ile Tyr Asn Asp
    130                 135                 140
Pro Gln Ser Ala Pro Met Arg Met Ile Lys Phe His Ala
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:838:

(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:838

```
Met Gly Leu Met Gly Val Ser Gln Gly Leu Pro Asn Thr Thr Ser Lys
1               5                  10                  15
Phe Gly Ile Glu Phe Asp Ser Leu Ala Asp Val Val Ala Phe Gly Val
            20                  25                  30
Ala Pro Ser Leu Ile Thr Tyr Phe Tyr Val Gly Tyr Asn Phe Gly Arg
        35                  40                  45
Ile Gly Met Ala Val Ser Ala Leu Phe Val Ile Phe Gly Ala Ile Arg
    50                  55                  60
Leu Ala Arg Phe Asn Ile Ser Thr Asn Thr Ser Asp Pro Tyr Ser Phe
65                  70                  75                  80
Ile Gly Ile Pro Ile Pro Ala Ala Ala Val Leu Val Val Leu Cys Val
                85                  90                  95
Leu Leu Asp Asn Lys Tyr His Phe Leu Glu Gly Asn Thr Glu Lys Leu
            100                 105                 110
Phe Leu Gly Phe Ile Val Leu Leu Gly Val Leu Met Val Ser Asn Ile
        115                 120                 125
```

```
Arg Tyr Pro Asn Phe Lys Lys Val Lys Trp Asn Leu Lys Leu Phe Ile
    130                 135                 140
Leu Val Leu Ile Phe Leu Ser Leu Val Phe Val Arg Pro Leu Glu Ala
145                 150                 155                 160
Leu Ser Val Phe Met Gly Leu Tyr Leu Ile Tyr Gly Ile Ile Arg Trp
                165                 170                 175
Ile Phe Leu Met Val Lys Ile Thr Phe Asn Lys Asn Lys Ser Ala
            180                 185                 190
```

(2) INFORMATION FOR SEQ ID NO:839:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(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:839

```
Met Ile Gly Val Tyr Pro Asn Tyr Ser Lys Lys Gln Leu Lys Arg Pro
1               5                   10                  15
Leu Val Ile Phe Val Ser Arg Glu Leu Ala Leu Ala Asn Gly Ile Leu
            20                  25                  30
Thr Asp Ala Tyr Asp Ile Glu Ala Asn Leu Tyr Met Asn Ala Arg Ile
        35                  40                  45
Val Met Unk Asn Asn Lys Arg Lys His Tyr Glu Gln Arg Val Asn Leu
    50                  55                  60
His Phe Unk Arg Ser Leu Gly Unk Val Phe Asp His Arg Ser Asn His
65                  70                  75                  80
Val Leu Cys Asp Glu Lys Asp Leu Leu Arg
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:840:

(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:840

```
Val Lys Ile Thr Ile Met Ile Lys Asp Phe Asn His Tyr Cys Arg Lys
```

```
1               5                   10                  15
Ile Thr Arg Gly Phe Val Lys Ile Pro Thr Lys Lys Gln Gly Ala Lys
            20                  25                  30
Lys Met Lys Lys Ala Gly Phe Leu Phe Leu Ala Ala Met Ala Ile Ile
        35                  40                  45
Val Val Ser Leu Asn Ala Lys Asp Pro Asn Val Leu Arg Lys Ile Val
    50                  55                  60
Phe Glu Lys Cys Leu Pro Asn Tyr Glu Lys Asn Gln Asn Pro Ser Pro
65                  70                  75                  80
Cys Ile Glu Val Lys Pro Asp Ala Gly Tyr Val Val Leu Lys Asp Ile
                85                  90                  95
Asn Gly Pro Leu Gln Tyr Leu Leu Met Pro Thr Thr His Ile Ser Gly
            100                 105                 110
Ile Glu Asn Pro Leu Leu Leu Asp Pro Ser Thr Pro Asn Phe Phe Tyr
        115                 120                 125
Leu Ser Trp Gln Ala Arg Asp Phe Met Ser Unk Lys Tyr Gly Lys Pro
    130                 135                 140
Ile Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn Ser Lys Lys Gly Arg
145                 150                 155                 160
Ser Gln Asn His Phe His Ile His Ile Ser Cys Ile Ser Leu Asp Val
                165                 170                 175
Arg Lys Gln Leu Asp Asn Asn Leu Lys Asn Ile Asn Ser Arg Trp Ser
            180                 185                 190
Pro Leu Ser Gly Gly Leu Asn Gly His Lys Tyr Leu Ala Arg Arg Val
        195                 200                 205
Thr Glu Ser Glu Leu Ala Gln Lys Ser Pro Phe Val Met Leu Ala Lys
    210                 215                 220
Glu Val Pro Asn Ala His Lys Arg Met Gly Asp Tyr Gly Leu Ala Val
225                 230                 235                 240
Val Gln Gln Ser Asp Asn Ser Phe Val Leu Leu Ala Thr Gln Phe Asn
                245                 250                 255
Pro Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu Ile Gln Asp His Glu
            260                 265                 270
Cys Ala Ile Leu Arg
        275
```

(2) INFORMATION FOR SEQ ID NO:841:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841

```
Val Leu Thr Ser Gly Asp Met Ile Thr Cys Pro Tyr Cys Gly Arg Ile
1               5                   10                  15
Leu Tyr Ala Glu Ser Thr His Glu Ser Asn Ala Gln Pro Pro Lys Glu
            20                  25                  30
Ser Gln Pro Lys Glu Ser Gln Glu Glu Ser Gln Glu Glu Ser Gln Glu
        35                  40                  45
Glu Ser Gln Glu Ala Val Arg Leu Ile Val
    50                  55
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:842:

(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:842

```
Met Ala Leu Asp Lys Arg Ile Trp Met His Phe Asp Leu Leu Pro Phe
1               5                  10                  15
Val Phe Ile Ile Pro Leu Leu Val Val Ser Phe Leu Leu Ile Phe Glu
            20                  25                  30
Ser Ser Ala Val Leu Ser Leu Lys Gln Gly Val Tyr Tyr Ala Ile Gly
        35                  40                  45
Phe Leu Leu Phe Trp Val Val Phe Phe Ile Pro Phe Arg Lys Leu Asp
    50                  55                  60
Arg Trp Leu Phe Ala Leu Tyr Trp Ala Cys Val Ile Leu Leu Ala Leu
65                  70                  75                  80
Val Asp Phe Met Gly Ser Ser Lys Leu Gly Ala Gln Arg Trp Leu Val
                85                  90                  95
Ile Pro Phe Thr Ser Ile Thr Leu Gln Pro Ser Glu Pro Val Lys Asn
            100                 105                 110
Arg Unk Ser Phe Ile Val Gly Ala Phe Unk Unk Asn Unk Pro Asp Unk
        115                 120                 125
Leu Leu Arg Ala Met Ile Gly Ala Cys Phe
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:842:

(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

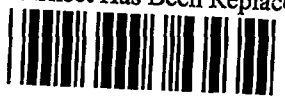
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842

```
Met Ala Leu Asp Lys Arg Ile Trp Met His Phe Asp Leu Leu Pro Phe
1               5                  10                  15
Val Phe Ile Ile Pro Leu Leu Val Val Ser Phe Leu Leu Ile Phe Glu
```

```
            20                  25                  30
Ser Ser Ala Val Leu Ser Leu Lys Gln Gly Val Tyr Tyr Ala Ile Gly
        35                  40                  45
Phe Leu Leu Phe Trp Val Val Phe Phe Ile Pro Phe Arg Lys Leu Asp
    50                  55                  60
Arg Trp Leu Phe Ala Leu Tyr Trp Ala Cys Val Ile Leu Leu Ala Leu
65                  70                  75                  80
Val Asp Phe Met Gly Ser Ser Lys Leu Gly Ala Gln Arg Trp Leu Val
                85                  90                  95
Ile Pro Phe Thr Ser Ile Thr Leu Gln Pro Ser Glu Pro Val Lys Asn
            100                 105                 110
Arg Unk Ser Phe Ile Val Gly Ala Phe Unk Unk Asn Unk Pro Asp Unk
        115                 120                 125
Leu Leu Arg Ala Met Ile Gly Ala Cys Phe
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:843:

This Sheet Has Been Replaced



(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

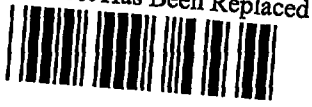
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843

```
Met Lys Leu Asn Asp Pro Phe Thr Ser Pro Asn Lys Ala Lys Lys Glu
1               5                  10                  15
Leu Ser Pro Lys Gly Phe Arg Gly Gly Leu Glu Ser Glu Ile Leu Leu
            20                  25                  30
Gly Phe Val Leu Gln Lys Glu Arg Val Phe Leu His Thr His Glu His
        35                  40                  45
Leu Glu Leu Ser His Glu Glu Glu Thr Arg Phe Phe Glu Leu Val Gly
    50                  55                  60
Lys Arg Leu Asn Asp Cys Pro Ile Glu Tyr Leu Leu Gly Ser Cys Asp
65                  70                  75                  80
Phe Tyr Gly Arg Ser Phe Phe Val Asn Glu His Val Leu Ile Pro Arg
                85                  90                  95
Pro Glu Thr Glu Ile Leu Val Gln Lys Ala Leu Asn Ile Ile Ser Gln
            100                 105                 110
Tyr His Leu Lys Glu Ile Gly Glu Ile Gly Ile Gly Ser Gly Cys Val
        115                 120                 125
Ser Val Ser Leu Ala Leu Glu Asn Pro Asn Leu Ser Ile Tyr Ala Ser
    130                 135                 140
Asp Ile Ser Pro Lys Ala Leu Glu Val Ala Leu Lys Asn Ile Glu Arg
145                 150                 155                 160
Phe Cys Leu Lys Glu Arg Val Phe Leu Lys Gln Thr Arg Leu Trp Asp
                165                 170                 175
His Met Pro Thr Ile Glu Met Leu Val Ser Asn Pro Pro Tyr Ile Ala
            180                 185                 190
Arg Asn Tyr Pro Leu Glu Lys Ser Val Leu Lys Glu Pro His Glu Ala
        195                 200                 205
Leu Phe Gly Gly Val Lys Gly Asp Glu Ile Leu Lys Glu Ile Val Phe
    210                 215                 220
```

```
Leu Ala Ala Lys Leu Lys Ile Pro Phe Leu Val Cys Glu Met Gly Tyr
225                 230                 235                 240
Asp Gln Leu Lys Ser Leu Lys Glu Cys Leu Glu Phe Cys Gly Tyr Asp
                245                 250                 255
Ala Glu Phe Tyr Lys Asp Leu Ser Gly Phe Asp Arg Gly Phe Val Gly
            260                 265                 270
Val Leu Lys Ser Phe Leu Arg
        275
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...36

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844

```
Met Ile Ser Phe Ile Gly Phe Glu Cys Ser Ala Leu Lys Val Phe Leu
1               5                   10                  15
Thr Phe Gly Tyr Ile Val Phe Lys Unk Trp His Tyr Ser Ala Ile Arg
            20                  25                  30
Leu Ile Val Ile
        35
```

(2) INFORMATION FOR SEQ ID NO:845:

(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

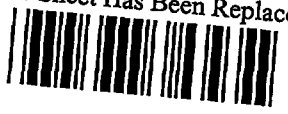
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845

```
Val Ile Gln Ser His Pro Lys Gln Thr Leu Ile Glu Asp Glu Asn Tyr
1               5                   10                  15
Phe Tyr Ala Asn Lys Gly Leu Tyr Lys Thr Asn Lys Glu Ala Phe Leu
            20                  25                  30
Arg Val Tyr Lys Ile Pro Glu Ser Met Pro Ile Glu Lys Arg Glu Ser
        35                  40                  45
Leu Ser Lys Val Ser Lys Ile Phe Leu Ala Leu Leu Phe Phe Ile Ser
```

```
    50                  55                  60
Ser Met Leu Phe Gly Ile Phe Trp Arg Leu Pro Lys Arg Leu Asp Thr
65                  70                  75                  80
Lys Met Ser Leu Glu Ser Ala His Lys Asn Glu Leu Glu Asn Ala Phe
                85                  90                  95
Gln Arg Tyr Asp Ala Leu Gly Val Arg Phe Glu Asp Ile Ala Gly Val
            100                 105                 110
Asn Glu Val Lys Glu Glu Leu Leu Glu Val Ile Asp Tyr Leu Lys Lys
        115                 120                 125
Pro
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:846:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846

```
Met Phe Val Val Lys Met Val Leu Gly Phe Leu Ile Leu Leu Ser Pro
1               5                   10                  15
Leu Cys Ala Thr Gly Leu Asp Ile Ser Gln Thr Asp Ile Ile Glu Arg
            20                  25                  30
Ser Leu Asn Phe Leu Leu Phe Val Gly Ile Leu Trp Tyr Phe Leu Ala
        35                  40                  45
Lys Arg Leu Arg Ser Phe Leu His Ser Lys Ser Leu Glu Ile Ser Lys
    50                  55                  60
Arg Leu Glu Glu Ile Gln Ala Gln Leu Lys Val Ser Lys Glu His Lys
65                  70                  75                  80
Lys Lys Leu Leu Lys Glu Leu Glu Gln Ala Lys Glu Lys Ala Glu Leu
                85                  90                  95
Ile Ile Ser Asp Ala Asn Lys Glu Ala Leu His Asp His Ala Lys Ile
            100                 105                 110
Arg Ile Thr Asn Gln Asn Gly Cys Gly Lys Phe Asp Gln Lys Phe
        115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:847:

(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:847

```
Met Arg Val Leu Glu Trp Lys Tyr Trp Leu Asn Thr Asp Lys Trp Asp
1               5                  10                  15
Thr Pro Thr Asn Lys Pro Pro Gln Thr Phe Lys Ile Gln Ile Phe Lys
            20                  25                  30
Ile Gln Ile Gly Ile Ile Asn Asn Phe Asn His Leu Ile Lys Gly Ser
        35                  40                  45
Ser Met Lys Asn Ala Phe Lys Ala Phe Ala Leu Leu Ile Val Phe Phe
    50                  55                  60
Ser Asn Ala Leu Leu Ala Gln Asp Leu Lys Ile Ala Ala Ala Ala Asn
65                  70                  75                  80
Leu Thr Arg Ala Leu Lys Ala Leu Val Lys Glu Phe Gln Lys Glu His
                85                  90                  95
Pro Lys Asp Ala Ile Asn Ile Ser Phe Asn Ser Ser Gly Lys Leu Tyr
            100                 105                 110
Ala Gln Ile Ala Gln Asn Ala Pro Phe Asp Leu Phe Ile Ser Ala Asp
        115                 120                 125
Ile Ala Arg Pro Lys Lys Leu Tyr Asp Glu Lys Ile Thr Pro Phe Lys
    130                 135                 140
Glu Glu Val Tyr Ala Lys Gly Val Leu Val Leu Trp Ser Glu Asn Leu
145                 150                 155                 160
Lys Met Asp Ser Leu Glu Ile Leu Lys Asp Pro Lys Ile Lys Arg Ile
                165                 170                 175
Ala Met Ala Asn Pro Lys Leu Ala Pro Tyr Gly Lys Ala Ser Met Glu
            180                 185                 190
Val Leu Asp Arg Leu Lys Leu Thr Pro Ser Leu Lys Ser Lys Ile Ile
        195                 200                 205
Tyr Gly Ala Ser Ile Ser Gln Ala His Gln Phe Ile Ala Thr Lys Asn
    210                 215                 220
Ala Gln Ile Gly Phe Gly Ala Leu Ser Leu Ile Asp Lys Lys Asp Lys
225                 230                 235                 240
Asn Leu Ser Tyr Phe Ile Ile Asp Lys Thr Leu Tyr Asn Pro Ile Glu
                245                 250                 255
Gln Ala Leu Ile Ile Thr Lys Asn Gly Ala Asn Asn Pro Leu Ala Lys
            260                 265                 270
Val Phe Lys Asp
        275
```

(2) INFORMATION FOR SEQ ID NO:848:

This Sheet Has Been Replaced



(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:848

```
Val Ala Leu Leu Glu Pro Ser Val Met Tyr Leu Thr Glu Lys Tyr Gln
```

```
1               5                   10                  15
Tyr Ser Arg Phe Lys Val Thr Trp Gly Leu Val Ala Leu Ile Phe Val
            20                  25                  30
Val Gly Val Val Leu Ile Phe Ser Leu His Lys Asp Tyr Lys Asp Tyr
        35                  40                  45
Leu Thr Phe Phe Glu Lys Ser Leu Phe Asp Trp Leu Asp Phe Ala Ser
    50                  55                  60
Ser Thr Ile Ile Unk Pro Leu Gly Gly Met Unk Thr Phe Ile Phe Met
65                  70                  75                  80
Gly Trp Val Leu Lys Lys Glu Lys Leu Arg Leu Leu Ser Ala His Phe
                85                  90                  95
Leu Gly Pro Lys Leu Phe Ala Thr Trp Tyr Phe Leu Leu Lys Tyr Ile
            100                 105                 110
Thr Pro Leu Ile Val Phe Ser Ile Trp Leu Ser Lys Ile Tyr
        115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:849:

This Sheet Has Been Replaced



(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

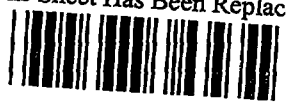
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849

```
Val Gly Leu Met Lys Ile Arg Phe Met Gly Arg Ser Val Phe Val Gly
1               5                   10                  15
Asp Leu Glu Arg Ile Glu Glu Val Ala Arg Phe Glu Glu Phe Trp Leu
            20                  25                  30
Leu Gly Gly Gln Lys Ala Ile Lys Glu Pro Arg Arg Leu Val Leu Glu
        35                  40                  45
Ile Ala Leu Lys His Gln Leu Asn Lys Leu Leu Lys Arg Val Gln Lys
    50                  55                  60
His Phe Lys Glu Asp Glu Leu Gly Ile Phe Lys Gln Met His Asp Lys
65                  70                  75                  80
Lys Ile Gln Ser Val Ala Thr Asn Ser Ile Gly Arg Leu Phe Asp Ile
                85                  90                  95
Val Ala Phe Ser Leu Gly Val Val Gly Thr Ile Ser Phe Glu Ala Glu
            100                 105                 110
Ser Gly Gln Val Leu Glu Asn Leu Ala Leu Gln Ser Asp Glu Ile Ala
        115                 120                 125
Phe Tyr Pro Phe Glu Ile Lys Asn Ser Val Val Arg Leu Lys Glu Phe
    130                 135                 140
Tyr Gln Ala Phe Glu Lys Asp Leu Gly Val Leu Glu Pro Lys Arg Ile
145                 150                 155                 160
Ala Lys Lys Phe Phe Asn Ser Leu Val Glu Ile Ile Thr Ala Leu Ile
                165                 170                 175
Ala Pro Phe Lys Gly His Val Val Val Cys Ser Gly Gly Val Phe Cys
            180                 185                 190
Asn Gln Leu Leu Cys Glu Gln Leu Ala Lys Arg Leu Lys Lys Leu Gln
        195                 200                 205
Arg Glu Tyr Phe Phe His Lys His Phe Pro Pro Asn Asp Arg Ser Ile
    210                 215                 220
```

```
Pro Val Gly Gln Ala Leu Met Ala Tyr Phe Asn Pro Thr Ile Ile Lys
225                 230                 235                 240
Lys Gly
```

(2) INFORMATION FOR SEQ ID NO:850:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850

```
Val Ser Asp Ser Asn Ala Leu Lys Glu Val Phe Leu Asn Ile Ser Ala
1               5                  10                  15
Lys Glu Asp His Cys Asp Val Leu Ile Asn Ser Ala Gly Tyr Gly Val
            20                  25                  30
Phe Gly Ser Val Glu Asp Thr Pro Ile Glu Glu Val Lys Lys Gln Phe
        35                  40                  45
Ser Val Asn Phe Phe Ala Leu Cys Glu Val Val Gln Leu Cys Leu Pro
    50                  55                  60
Leu Leu Lys Asn Lys Pro Tyr Ser Lys Ile Phe Asn Leu Ser Ser Ile
65                  70                  75                  80
Ala Gly Arg Val Ser Met Leu Phe Leu Gly His Tyr Ser Ala Ser Lys
                85                  90                  95
His Ala Leu Glu Ala Tyr Ser Asp Ala Leu Arg Leu Glu Leu Lys Pro
            100                 105                 110
Phe Asn Val Gln Val Cys Leu Ile Glu Pro Gly Pro Val Lys Ser Asn
        115                 120                 125
Trp Glu Lys Thr Ala Phe Glu Asn Asp Glu Arg Lys Asp Ser Val Tyr
    130                 135                 140
Ala Leu Glu Val Asn Ala Ala
145                 150
```

(2) INFORMATION FOR SEQ ID NO:851:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

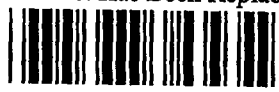
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851

```
Val Ile Val Ala Trp Leu Phe Arg Phe Lys Ser Ile Ala Phe Ser Ile
1               5                  10                  15
Leu Ile Thr Leu Leu Val Ile Leu Val Asp Ile Trp Val Tyr Ser Asp
            20                  25                  30
Val Arg Gln Phe Leu Leu Asp Thr Ser Ser Ser Phe Ile Trp Leu Leu
        35                  40                  45
Ile Ala Leu Leu Ile Lys Trp Gly Val Ile Val Ile Ser Ala Arg Lys
    50                  55                  60
Cys Tyr Gln Phe Ser Gln Lys Met Phe Ala Leu Ile Gln Arg Lys Arg
65                  70                  75                  80
Gln Ile Arg Glu Asn Leu Lys Asn Arg Ser Asn Arg Lys Asp Ala Lys
                85                  90                  95
Asn Phe Glu Lys Leu Ser Asn Ile Ala Glu Glu Ile Ile Ser Lys Lys
            100                 105                 110
Gln Glu Glu Ser His His Lys Glu Asp Ser Asn Asp Glu Asn His Lys
        115                 120                 125
Asp Lys Leu Ser Asn Ile Thr Glu Glu Met Ile Leu Lys Lys Gln Glu
    130                 135                 140
Glu Leu Lys Ala Arg Lys Asp Lys Gly Asp
145                 150
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:852:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...326

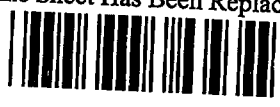
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852

```
Val Leu Met Ala Leu Unk Asp Lys Arg Tyr Gly Leu Glu Ala Gly Ile
1               5                  10                  15
Lys Tyr Phe Thr Met Gly Ala Met Ala Ser Ala Phe Phe Ala Met Gly
            20                  25                  30
Ala Met Ala Phe Tyr Leu Leu Thr Gly Ser Leu Asn Leu Glu Val Ile
        35                  40                  45
Thr Leu Tyr Leu His Thr Glu Gly Ile Thr Asn Pro Met Leu Phe Ala
    50                  55                  60
Met Gly Thr Ile Phe Leu Ile Gly Ala Ile Gly Phe Lys Val Ser Leu
65                  70                  75                  80
Val Pro Phe His Thr Trp Met Pro Asp Val Tyr Glu Gly Asn Asn Pro
                85                  90                  95
Val Phe Ala Ser Tyr Ile Ser Ile Val Pro Lys Ile Ala Gly Phe Val
            100                 105                 110
Val Ala Thr Arg Leu Phe Gly Ala Phe Ile Asp Thr His Thr Ala Trp
        115                 120                 125
Val Glu Asp Ile Phe Tyr Val Leu Ile Leu Met Thr Ile Thr Ile Pro
    130                 135                 140
Asn Phe Ile Ala Leu Trp Gln Glu Asp Val Lys Arg Met Leu Ala Tyr
145                 150                 155                 160
```

```
Ser Ser Ile Ser His Ser Gly Phe Ala Leu Ala Cys Val Phe Ile His
                165                 170                 175
Thr Glu Asp Ser Gln Gln Ala Met Phe Val Tyr Trp Phe Met Phe Ala
            180                 185                 190
Phe Thr Tyr Ile Gly Ala Phe Gly Leu Leu Trp Leu Leu Lys Ser Arg
        195                 200                 205
Glu Lys Thr Trp Asp Glu Arg Tyr Asp His Pro Tyr Ser Lys Phe Asn
    210                 215                 220
Gly Leu Ile Lys Thr His Pro Leu Val Ala Ile Leu Gly Ala Ile Phe
225                 230                 235                 240
Val Phe Gly Leu Ala Gly Ile Pro Pro Phe Ser Val Phe Trp Gly Lys
                245                 250                 255
Phe Leu Ala Val Glu Ser Ala Leu Glu Ser Asn His Ile Leu Leu Ala
            260                 265                 270
Val Val Met Leu Val Asn Ser Ala Val Ala Ala Phe Tyr Tyr Phe Arg
        275                 280                 285
Trp Leu Val Ala Met Phe Phe Asn Lys Pro Leu Gln Thr Gln Ser Tyr
    290                 295                 300
Ala Lys Thr Ile Phe Thr Pro Lys Thr Pro Pro Cys Pro Phe Met Arg
305                 310                 315                 320
Ser Leu Leu Pro Trp Arg
                325
```

(2) INFORMATION FOR SEQ ID NO:852:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...326

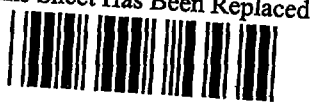
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852

```
Val Leu Met Ala Leu Unk Asp Lys Arg Tyr Gly Leu Glu Ala Gly Ile
1               5                   10                  15
Lys Tyr Phe Thr Met Gly Ala Met Ala Ser Ala Phe Phe Ala Met Gly
            20                  25                  30
Ala Met Ala Phe Tyr Leu Leu Thr Gly Ser Leu Asn Leu Glu Val Ile
        35                  40                  45
Thr Leu Tyr Leu His Thr Glu Gly Ile Thr Asn Pro Met Leu Phe Ala
    50                  55                  60
Met Gly Thr Ile Phe Leu Ile Gly Ala Ile Gly Phe Lys Val Ser Leu
65                  70                  75                  80
Val Pro Phe His Thr Trp Met Pro Asp Val Tyr Glu Gly Asn Asn Pro
                85                  90                  95
Val Phe Ala Ser Tyr Ile Ser Ile Val Pro Lys Ile Ala Gly Phe Val
            100                 105                 110
Val Ala Thr Arg Leu Phe Gly Ala Phe Ile Asp Thr His Thr Ala Trp
        115                 120                 125
Val Glu Asp Ile Phe Tyr Val Leu Ile Leu Met Thr Ile Thr Ile Pro
    130                 135                 140
Asn Phe Ile Ala Leu Trp Gln Glu Asp Val Lys Arg Met Leu Ala Tyr
145                 150                 155                 160
Ser Ser Ile Ser His Ser Gly Phe Ala Leu Ala Cys Val Phe Ile His
```

```
                165                 170                 175
Thr Glu Asp Ser Gln Gln Ala Met Phe Val Tyr Trp Phe Met Phe Ala
            180                 185                 190
Phe Thr Tyr Ile Gly Ala Phe Gly Leu Leu Trp Leu Leu Lys Ser Arg
        195                 200                 205
Glu Lys Thr Trp Asp Glu Arg Tyr Asp His Pro Tyr Ser Lys Phe Asn
    210                 215                 220
Gly Leu Ile Lys Thr His Pro Leu Val Ala Ile Leu Gly Ala Ile Phe
225                 230                 235                 240
Val Phe Gly Leu Ala Gly Ile Pro Pro Phe Ser Val Phe Trp Gly Lys
                245                 250                 255
Phe Leu Ala Val Glu Ser Ala Leu Glu Ser Asn His Ile Leu Leu Ala
            260                 265                 270
Val Val Met Leu Val Asn Ser Ala Val Ala Ala Phe Tyr Tyr Phe Arg
        275                 280                 285
Trp Leu Val Ala Met Phe Phe Asn Lys Pro Leu Gln Thr Gln Ser Tyr
    290                 295                 300
Ala Lys Thr Ile Phe Thr Pro Lys Thr Pro Pro Cys Pro Phe Met Arg
305                 310                 315                 320
Ser Leu Leu Pro Trp Arg
                325
```

(2) INFORMATION FOR SEQ ID NO:853:

This Sheet Has Been Replaced



(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:853

```
Met Asn Tyr Pro Asn Leu Pro Asn Ser Ala Leu Unk Ile Ser Glu Gln
1                   5                   10                  15
Pro Glu Val Lys Glu Ile Thr Asn Glu Leu Leu Lys Gln Leu Gln Asn
            20                  25                  30
Ala Leu Arg Ser Asn Ala His Phe Ser Glu Gln Val Glu Leu Ser Leu
        35                  40                  45
Lys Cys Ile Val Arg Ile Leu Glu Val Leu Leu Ser Leu Asp Phe Phe
    50                  55                  60
Lys Asn Ala Asn Glu Ile Asp Ser Ser Leu Arg Asn Ser Ile Glu Trp
65                  70                  75                  80
Leu Thr Asn Ala Gly Glu Ser Leu Lys Leu Lys Met Lys Glu Tyr Glu
                85                  90                  95
Arg Phe Phe Ser Glu Phe Asn Thr Ser Met His Ala Asn Glu Gln Glu
            100                 105                 110
Val Thr Asn Thr Leu Asn Ala Asn Ala Glu Asn Ile Lys Ser Unk Ile
        115                 120                 125
Lys Unk Leu Glu Asn Gln Leu Ile Glu Thr Thr Thr Arg Leu Leu Thr
    130                 135                 140
Ser Tyr Gln Ile Phe Leu Asn Gln Ala Arg Asp Asn Ala Asn Asn Gln
145                 150                 155                 160
Ile Thr Lys Asn Lys Thr Unk Ser Leu Glu Ala Ile Thr Gln Ala Lys
                165                 170                 175
```

Asn Asn Ser

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854

```
Met Ile Asn Ser Lys Lys Ser Leu Lys Lys Gly Leu Arg Gly Phe Phe
1               5                  10                  15
Lys Ile Leu Lys Asp Arg Asn Gly Ala His Phe Ser Cys Gly Ala Thr
            20                  25                  30
Ser Gly Phe Gly Leu Glu Ile Ala Lys Ala Phe Leu Gln Lys Asn His
        35                  40                  45
Val Val Phe Gly Thr Gly Arg Arg Gln Glu Asn Leu Gln Lys Leu Gln
    50                  55                  60
Leu Ala Tyr Pro Lys Arg Phe Ile Pro Leu Cys Phe Asp Leu Gln Asn
65                  70                  75                  80
Lys Pro Glu Thr Lys Arg Ala Ile Glu Thr Ile Phe Ser Met Thr Asp
                85                  90                  95
Arg Ile Asp Ala Leu Ile Asn Asn Ala Gly Leu Ala Leu Gly Leu Asn
            100                 105                 110
Lys Ala Tyr Glu Cys Glu Leu Asp Asp Trp Glu Val Met Ile Asp Thr
        115                 120                 125
Asn Ile Lys Gly Leu Leu His Leu Thr Arg Leu Ile Leu Pro Ser Met
    130                 135                 140
Ile Glu His Asp Gln Gly Thr Ile Ile Asn Leu Gly Ser Ile Ala Gly
145                 150                 155                 160
Thr Tyr Ala Tyr Pro Gly Gly Unk Val Tyr Gly Ala Ser Lys Ala Unk
                165                 170                 175
Val Lys Gln Unk Ser Unk Asn Leu Arg Ala Asp Val Ala Gly Thr Asn
            180                 185                 190
Thr Arg Gly Arg Arg Trp Asn Pro Gly Cys Val Ala Lys Pro Lys Val
        195                 200                 205
Ser Arg Val Arg Gly Lys Gly Asp Lys Pro Lys Pro Lys Ser Gly Tyr
    210                 215                 220
Glu Lys His Pro Leu Pro Gln Thr Thr Arg Gln Gly Leu Thr Ser Gly
225                 230                 235                 240
```

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854

```
Met Ile Asn Ser Lys Lys Ser Leu Lys Lys Gly Leu Arg Gly Phe Phe
1               5                  10                  15
Lys Ile Leu Lys Asp Arg Asn Gly Ala His Phe Ser Cys Gly Ala Thr
            20                  25                  30
Ser Gly Phe Gly Leu Glu Ile Ala Lys Ala Phe Leu Gln Lys Asn His
        35                  40                  45
Val Val Phe Gly Thr Gly Arg Arg Gln Glu Asn Leu Gln Lys Leu Gln
    50                  55                  60
Leu Ala Tyr Pro Lys Arg Phe Ile Pro Leu Cys Phe Asp Leu Gln Asn
65                  70                  75                  80
Lys Pro Glu Thr Lys Arg Ala Ile Glu Thr Ile Phe Ser Met Thr Asp
                85                  90                  95
Arg Ile Asp Ala Leu Ile Asn Asn Ala Gly Leu Ala Leu Gly Leu Asn
            100                 105                 110
Lys Ala Tyr Glu Cys Glu Leu Asp Asp Trp Glu Val Met Ile Asp Thr
        115                 120                 125
Asn Ile Lys Gly Leu Leu His Leu Thr Arg Leu Ile Leu Pro Ser Met
    130                 135                 140
Ile Glu His Asp Gln Gly Thr Ile Ile Asn Leu Gly Ser Ile Ala Gly
145                 150                 155                 160
Thr Tyr Ala Tyr Pro Gly Gly Unk Val Tyr Gly Ala Ser Lys Ala Unk
                165                 170                 175
Val Lys Gln Unk Ser Unk Asn Leu Arg Ala Asp Val Ala Gly Thr Asn
            180                 185                 190
Thr Arg Gly Arg Arg Trp Asn Pro Gly Cys Val Ala Lys Pro Lys Val
        195                 200                 205
Ser Arg Val Arg Gly Lys Gly Asp Lys Pro Lys Pro Lys Ser Gly Tyr
    210                 215                 220
Glu Lys His Pro Leu Pro Gln Thr Thr Arg Gln Gly Leu Thr Ser Gly
225                 230                 235                 240
```

(2) INFORMATION FOR SEQ ID NO:855:

(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

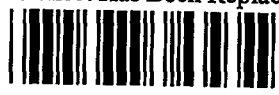
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855

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

```
Ser Ala Tyr Glu Pro Ile Ser Gly Ser Gln Lys Pro Ile Val Gly Gln
            20                  25                  30
Ala Leu Leu Leu Leu Ala Ile Leu Ile Leu Leu Asp Leu Ser Phe His
        35                  40                  45
His Gln Ile Ile Leu Phe Val Asp His Ser Leu Lys Ala Val Pro Leu
    50                  55                  60
Gly Arg Phe Val Phe Glu Pro Glu Leu Ala Lys Asn Ile Val Lys Ala
65                  70                  75                  80
Phe Ser His Leu Phe Val Ile Gly Phe Ser Met Ala Phe Pro Ile Leu
                85                  90                  95
Cys Leu Val Leu Leu Ser Asp Ile Ile Phe Gly Met Ile Met Lys Thr
            100                 105                 110
His Pro Gln Phe Asn Leu Leu Ala Ile Gly Phe Pro Val Lys Ile Ala
        115                 120                 125
Ile Gly Phe Val Gly Ile Ile Leu Ile Ala Ser Ala Ile Met Gly Arg
    130                 135                 140
Phe Lys Glu Glu Ile Ser Leu Ala Phe Ser Val Ile Ser Lys Ile Phe
145                 150                 155                 160
```

(2) INFORMATION FOR SEQ ID NO:856:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...94

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856

```
Met Tyr Gly Val Lys Glu Ile Lys Asp Lys Ile Asp Lys Gln Leu His
1               5                   10                  15
Asn Asn Asp His Leu Phe Glu Gly Leu Phe Gly Glu Lys Glu Asp Leu
            20                  25                  30
Lys Lys Leu Val Ser Met Phe Gly Gln Leu Arg Phe Gln Lys Arg Trp
        35                  40                  45
Ser Gln Thr Pro Arg Val Pro Gln Thr Ser Val Leu Gly His Thr Leu
    50                  55                  60
Cys Val Ala Ile Met Gly Tyr Leu Leu Ser Phe Asp Leu Lys Ala Cys
65                  70                  75                  80
Lys Ser Met Arg Ile Asn His Phe Leu Gly Gly Leu Phe Pro
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:857:

(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:857

```
Met Thr Leu Asp Asp Leu Leu Gly Gly Ser Leu Asp Pro His Cys Phe
1               5                  10                  15
Cys Lys Pro Leu Ile Lys Thr Lys Lys Asp Gln Glu Arg Leu Leu Ser
            20                  25                  30
Leu Ala Leu Lys Ala His Pro Lys Ile Ser Phe Gly Lys Asp Ser Ala
        35                  40                  45
Pro His Phe Ile Ser Lys Lys His Ser Ala Asn Ile Pro Ala Gly Ile
    50                  55                  60
Phe Ser Ala Pro Ile Leu Leu Pro Ala Leu Cys Glu Leu Phe Glu Lys
65                  70                  75                  80
His Asn Ala Leu Glu Asn Leu Gln Ala Phe Ile Ser Asp Asn Ala Lys
                85                  90                  95
Lys Ile Tyr Ala Leu Asp Asn Leu Pro Ser Lys Lys Ala His Leu Ser
            100                 105                 110
Lys Lys Pro Phe Ile Val Pro Thr His Thr Leu Cys Leu Asn Glu Lys
        115                 120                 125
Ile Ala Ile Leu Arg Gly Gly Glu Thr Leu Ser Trp Asn Leu Gln Glu
    130                 135                 140
Ile Ala
145
```

(2) INFORMATION FOR SEQ ID NO:858:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858

```
Val Ser Gly Val Val Leu Ser Lys Phe Asp Ser Asp Ser Lys Gly Gly
1               5                  10                  15
Ile Ala Leu Gly Ile Thr Tyr Gln Leu Gly Leu Pro Leu Arg Phe Ile
            20                  25                  30
Gly Ser Gly Glu Lys Ile Pro Asp Leu Asp Val Phe Met Pro Glu Arg
        35                  40                  45
Ile Val Gly Arg Leu Met Gly Ala Gly Asp Ile Ile Ser Leu Ala Glu
    50                  55                  60
Lys Thr Ala Ser Val Leu Asn Pro Asn Glu Ala Lys Asp Leu Ser Lys
65                  70                  75                  80
Lys Leu Lys Lys Gly Gln Phe Thr Phe Asn Asp Phe Leu Asn Gln Ile
                85                  90                  95
Glu Lys Val Lys Lys Leu Gly Ser Met Ser Ser Leu Ile Ser Met Ile
            100                 105                 110
```

```
Pro Gly Leu Gly Asn Met Ala Ser Ala Leu Lys Asp Thr Asp Leu Glu
        115                 120                 125
Ser Ser Leu Glu Val Lys Lys Ile Lys Ala Met Val Asn Ser Met Thr
    130                 135                 140
Lys Lys Glu Arg Glu Asn Pro Glu Ile Leu Asn Gly Ser Arg Arg Lys
145                 150                 155                 160
Arg Ile Ala Leu Gly Unk Gly Leu Glu Unk Unk Glu Ile Asn Arg Ile
                165                 170                 175
Ile Lys Arg Phe Asp Gln Ala Ser Lys Met Ala Lys Arg Leu Thr Asn
            180                 185                 190
Lys Lys Gly Ile Ser Asp Leu Met Asn Leu Unk Unk
        195                 200
```

(2) INFORMATION FOR SEQ ID NO:858:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...204

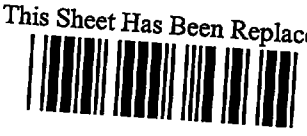
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858

```
Val Ser Gly Val Val Leu Ser Lys Phe Asp Ser Asp Ser Lys Gly Gly
1               5                   10                  15
Ile Ala Leu Gly Ile Thr Tyr Gln Leu Gly Leu Pro Leu Arg Phe Ile
            20                  25                  30
Gly Ser Gly Glu Lys Ile Pro Asp Leu Asp Val Phe Met Pro Glu Arg
        35                  40                  45
Ile Val Gly Arg Leu Met Gly Ala Gly Asp Ile Ile Ser Leu Ala Glu
    50                  55                  60
Lys Thr Ala Ser Val Leu Asn Pro Asn Glu Ala Lys Asp Leu Ser Lys
65                  70                  75                  80
Lys Leu Lys Lys Gly Gln Phe Thr Phe Asn Asp Phe Leu Asn Gln Ile
                85                  90                  95
Glu Lys Val Lys Lys Leu Gly Ser Met Ser Ser Leu Ile Ser Met Ile
            100                 105                 110
Pro Gly Leu Gly Asn Met Ala Ser Ala Leu Lys Asp Thr Asp Leu Glu
        115                 120                 125
Ser Ser Leu Glu Val Lys Lys Ile Lys Ala Met Val Asn Ser Met Thr
    130                 135                 140
Lys Lys Glu Arg Glu Asn Pro Glu Ile Leu Asn Gly Ser Arg Arg Lys
145                 150                 155                 160
Arg Ile Ala Leu Gly Unk Gly Leu Glu Unk Unk Glu Ile Asn Arg Ile
                165                 170                 175
Ile Lys Arg Phe Asp Gln Ala Ser Lys Met Ala Lys Arg Leu Thr Asn
            180                 185                 190
Lys Lys Gly Ile Ser Asp Leu Met Asn Leu Unk Unk
        195                 200
```

(2) INFORMATION FOR SEQ ID NO:859:

(i) SEQUENCE CHARACTERISTICS:

This Sheet Has Been Replaced



(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:859

```
Met Gly Val Leu Gly Met Phe Ala Phe Phe Ser Trp Val Phe Leu Phe
1               5                  10                  15
Lys His Asn Leu Ser His Lys Ile Arg Leu Tyr His Glu Lys Lys Asp
            20                  25                  30
Phe Asp Lys Leu Leu Lys Gln Ile Leu Ser Gln Asp Thr Gln Lys Thr
        35                  40                  45
Phe Leu Lys Thr Lys Phe Lys Ser Asp Leu Ala Lys Asn Leu Ser Gln
    50                  55                  60
Ile Leu Ala Arg Tyr Asp Leu Lys Ala Asp Leu Asn Thr Pro Asn Ser
65                  70                  75                  80
Gly Cys Glu Lys Val Asp Asn Leu Phe Lys His Tyr His Asn Ile Glu
                85                  90                  95
Asn Asn Thr Leu Glu Pro Lys Asp His Ala Lys His Ser Leu Ala Tyr
            100                 105                 110
Glu His Ala Tyr Phe Ser Lys Arg Leu Lys Ala Phe Ile His Asn Asp
        115                 120                 125
Leu Lys Asn Ala Phe Glu Val Leu Thr Asn Ala Gln Ile Pro Leu Glu
    130                 135                 140
Leu Arg Arg Tyr Ala Tyr Arg Asn Arg Pro Lys Arg Gln Gln Lys Arg
145                 150                 155                 160
Gly Phe Lys Gly Cys Glu Cys Asp Ala Arg Gly Phe Gly
                165                 170
```

(2) INFORMATION FOR SEQ ID NO:860:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:860

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

```
Asn Ile His Ala Val Lys Leu Val Gly Glu Gly Glu Gly Ile Pro Lys
        35                  40                  45
Phe Leu Thr Asn Asn Ile Phe Thr Lys Val Phe Tyr Glu Ile Leu Lys
    50                  55                  60
Lys His Gly Asn Asp Gly Ser Phe Lys Phe Leu Leu His Asn Lys Val
65                  70                  75                  80
Pro Ile Thr Arg Gly Met Gly Ser Ser Ser Ala Met Ile Val Gly Ala
                85                  90                  95
Val Ala Ser Ala Phe Ala Phe Leu Gly Phe Ala Phe Asp Arg Glu Asn
            100                 105                 110
Ile Leu Asn Thr Ala Leu Ile Tyr Glu Asn His Pro Asp Asn Ile Thr
        115                 120                 125
Pro Ala Val Phe Gly Gly Tyr Asn Ala Ala Phe Val Glu Lys Lys Lys
    130                 135                 140
Val Ile Ser Leu Lys Thr Lys Ile Pro Ser Phe Leu Lys Ala Val Met
145                 150                 155                 160
Val Ile Pro Asn Arg Val Ile Ser Thr Lys Gln Ser Arg His Leu Cys
                165                 170                 175
Pro Ser Val Thr Ala Cys Lys Lys Ala Cys Leu Thr Phe Arg Met Arg
            180                 185                 190
Val
```

(2) INFORMATION FOR SEQ ID NO:861:

(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:861

```
Val Ala Lys Asn Leu Val Ala Ser Gly Val Cys Asp Lys Ala Thr Val
1               5                   10                  15
Gln Leu Ala Tyr Ala Ile Gly Val Ile Glu Pro Val Ser Ile Tyr Val
            20                  25                  30
Asn Thr His Asn Thr Ser Lys His Ser Ser Ala Glu Leu Glu Lys Cys
        35                  40                  45
Val Lys Ser Val Phe Lys Leu Thr Pro Lys Gly Ile Ile Glu Ser Leu
    50                  55                  60
Asp Leu Leu Arg Pro Ile Tyr Ser Leu Thr Ser Ala Tyr Gly His Phe
65                  70                  75                  80
Gly Arg Glu Leu Glu Glu Phe Thr Trp Glu Lys Thr Asn Lys Val Glu
                85                  90                  95
Glu Ile Lys Ala Phe Phe Lys Arg
            100
```

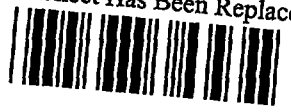
(2) INFORMATION FOR SEQ ID NO:862:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 amino acids
(B) TYPE: amino acid

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

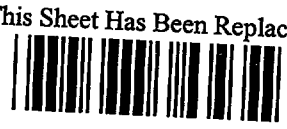
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862

```
Val Arg Leu Phe Arg Phe Val Gly Trp Tyr Tyr Phe Lys Tyr Phe Leu
1               5                  10                  15
Ile Val Leu Leu Ala Leu Glu Leu Phe Phe Val Gly Ile Asp Ser Leu
            20                  25                  30
Lys Tyr Ala Asp Lys Met Pro Asp Ser Ala Asn Met Ile Ile Leu Phe
        35                  40                  45
Phe Thr Tyr Asp Ile Leu Phe Ala Leu Asn Tyr Thr Leu Pro Ile Ser
    50                  55                  60
Leu Leu Leu Ala Met Val Leu Phe Tyr Ile Thr Phe Ile Lys Ser Asn
65                  70                  75                  80
Gln Tyr Thr Ala Leu Leu Ser Ile Gly Phe Ser Lys Cys Gln Ile Leu
                85                  90                  95
Ser Pro Ile Phe Leu Ile Ser Leu Phe Phe Thr Ala Val Tyr Val Gly
            100                 105                 110
Leu Asn Ala Thr Pro Phe Val Tyr Met Glu Glu Lys Thr Gln Asn Leu
        115                 120                 125
Ile Tyr Lys Asp Asn Ser Leu Ser Val Ser Glu His Leu Leu Val Lys
    130                 135                 140
Tyr Asn Asp Asp Tyr Val Tyr Phe Asp Lys Ile Asn Pro Leu Leu Gln
145                 150                 155                 160
Lys Ala Gln Asn Ile Lys Val Phe Arg Leu Lys Asp Lys Thr Leu Glu
                165                 170                 175
Ser Tyr Ala Glu Ala Lys Glu Ala Phe Phe Glu Asp Lys Tyr Trp Ile
            180                 185                 190
Leu His Asp Thr Thr Ile Tyr Glu Met Pro Leu Ser Phe Glu Leu Gly
        195                 200                 205
Ala Asn Ala Leu Asn Thr Thr His Leu Glu Thr Phe Lys Thr Leu Lys
    210                 215                 220
Asn Phe Arg Pro Lys Val Leu Asp Thr Ile Tyr Gln Asn Lys Pro Ala
225                 230                 235                 240
Val Ser Ile Thr Asp Ala Leu Leu Ser Leu His Ala Leu Val Arg Gln
                245                 250                 255
Asn Ala Asp Thr Lys Lys Val Arg Ser Phe Leu Tyr Val Phe Ala Ile
            260                 265                 270
Leu Pro Phe Phe Val Pro Phe Leu Ser Val Leu Ile Ala Tyr Phe Ser
        275                 280                 285
Pro Ser Leu Ala Arg Tyr Glu Asn Leu Ala Leu Leu Gly Leu Lys Phe
    290                 295                 300
Ile Ile Ile Thr Leu Val Val Trp Gly Leu Phe Phe Ala Leu Gly Lys
305                 310                 315                 320
Phe Ser Ile Ser Gly Ile Leu Ile Pro Glu Ile Gly Val Leu Ser Pro
                325                 330                 335
Phe Phe Val Phe Leu Ala Leu Ser Leu Trp Tyr Phe Lys Lys Leu Asn
            340                 345                 350
Lys Arg Leu
        355
```

(2) INFORMATION FOR SEQ ID NO:863:

This Sheet Has Been Replaced



(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:863

```
Val Glu Lys Ala His Pro Asp Val Phe Asn Leu Leu Leu Gln Val Leu
1               5                  10                  15
Asp Glu Gly His Leu Thr Asp Ser Lys Gly Val Arg Val Asp Phe Lys
            20                  25                  30
Asn Thr Ile Leu Ile Leu Thr Ser Asn Val Ala Ser Gly Ala Leu Leu
        35                  40                  45
Glu Glu Asp Leu Ser Glu Ala Asp Lys Gln Lys Ala Ile Lys Glu Ser
    50                  55                  60
Leu Arg Gln Phe Phe Lys Pro Glu Phe Leu Asn Arg Leu Asp Glu Ile
65                  70                  75                  80
Ile Ser Phe Asn Ala Leu Asp Ser His Ala Ile Ile
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:863:

(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:863

```
Val Glu Lys Ala His Pro Asp Val Phe Asn Leu Leu Leu Gln Val Leu
1               5                  10                  15
Asp Glu Gly His Leu Thr Asp Ser Lys Gly Val Arg Val Asp Phe Lys
            20                  25                  30
Asn Thr Ile Leu Ile Leu Thr Ser Asn Val Ala Ser Gly Ala Leu Leu
        35                  40                  45
Glu Glu Asp Leu Ser Glu Ala Asp Lys Gln Lys Ala Ile Lys Glu Ser
    50                  55                  60
Leu Arg Gln Phe Phe Lys Pro Glu Phe Leu Asn Arg Leu Asp Glu Ile
65                  70                  75                  80
Ile Ser Phe Asn Ala Leu Asp Ser His Ala Ile Ile
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:864:

This Sheet Has Been Replaced



(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:864

```
Leu Val Phe Leu Asp Arg Arg Leu Ile Val Met Val Thr Asp Ser Lys
1               5                  10                  15
Gly Ser Arg Tyr Ile Asn Val His Ile Leu Phe Arg Gln Ile Ser Leu
            20                  25                  30
Tyr Ala Leu Leu Ser Val Val Gly Ser Leu Leu Phe Leu Gly Val Ser
        35                  40                  45
Leu Leu Val Leu Asn Lys Glu Ile Lys Asn Ile Glu Lys Gln His Ala
    50                  55                  60
Leu Unk Thr Lys Glu Phe Glu Lys Lys Arg Glu Thr Asn Glu Unk Leu
65                  70                  75                  80
Ser Unk
```

(2) INFORMATION FOR SEQ ID NO:864:

(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:864

```
Leu Val Phe Leu Asp Arg Arg Leu Ile Val Met Val Thr Asp Ser Lys
1               5                  10                  15
Gly Ser Arg Tyr Ile Asn Val His Ile Leu Phe Arg Gln Ile Ser Leu
            20                  25                  30
Tyr Ala Leu Leu Ser Val Val Gly Ser Leu Leu Phe Leu Gly Val Ser
        35                  40                  45
Leu Leu Val Leu Asn Lys Glu Ile Lys Asn Ile Glu Lys Gln His Ala
    50                  55                  60
Leu Unk Thr Lys Glu Phe Glu Lys Lys Arg Glu Thr Asn Glu Unk Leu
65                  70                  75                  80
```

Ser Unk

(2) INFORMATION FOR SEQ ID NO:865:

This Sheet Has Been Replaced



(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:865

```
Leu Ser Leu Met Unk Val Leu Asn Ala Lys Glu Cys Val Unk Pro Ile
1               5                  10                  15
Thr Arg Ser Val Lys Tyr His Gln Gln Ser Ala Glu Ile Arg Ala Leu
            20                  25                  30
Gln Leu Gln Ser Tyr Lys Met Ala Lys Met Ala Leu Asp Asn Asn Leu
        35                  40                  45
Lys Leu Val Lys Asp Lys Lys Pro Ala Val Ile Leu Asp Leu Asp Glu
    50                  55                  60
Thr Val Leu Asn Thr Phe Asp Tyr Ala Gly Tyr Leu Val Lys Asn Cys
65                  70                  75                  80
Ile Lys Tyr Thr Pro Glu Thr Trp Asp Lys Phe Glu Lys Glu Gly Ser
                85                  90                  95
Leu Thr Leu Ile Pro Gly Ala Leu Asp Phe Leu Glu Tyr Ala Asn Ser
            100                 105                 110
Lys Gly Val Lys Ile Phe Tyr Ile Ser Asn Arg Thr Gln Lys Asn Lys
        115                 120                 125
Ala Phe Thr Leu Lys Thr Leu Lys Ser Phe Lys Leu Pro Gln Val Ser
    130                 135                 140
Glu Glu Ser Val Leu Leu Lys Glu Lys Gly Lys Pro Lys Ala Val Arg
145                 150                 155                 160
Arg Glu Leu Val Ala Lys Asp Tyr Ala Ile Val Leu Gln Val Gly Asp
                165                 170                 175
Thr Leu His Asp Phe Asp Ala Ile Phe Ala Lys Asp Ala Lys Asn Ser
            180                 185                 190
Gln Glu Gln Gln Ala Lys Val Leu Gln Asn Ala Gln Lys Phe Gly Thr
        195                 200                 205
Glu Trp Ile Ile Leu Pro Asn Ser Leu Tyr Gly Thr Trp Glu Asp Gly
    210                 215                 220
Pro Ile Lys Ala Trp Gln Asn Lys Lys
225                 230
```

(2) INFORMATION FOR SEQ ID NO:865:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(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:865

```
Leu Ser Leu Met Unk Val Leu Asn Ala Lys Glu Cys Val Unk Pro Ile
1               5                  10                  15
Thr Arg Ser Val Lys Tyr His Gln Gln Ser Ala Glu Ile Arg Ala Leu
            20                  25                  30
Gln Leu Gln Ser Tyr Lys Met Ala Lys Met Ala Leu Asp Asn Asn Leu
        35                  40                  45
Lys Leu Val Lys Asp Lys Lys Pro Ala Val Ile Leu Asp Leu Asp Glu
    50                  55                  60
Thr Val Leu Asn Thr Phe Asp Tyr Ala Gly Tyr Leu Val Lys Asn Cys
65                  70                  75                  80
Ile Lys Tyr Thr Pro Glu Thr Trp Asp Lys Phe Glu Lys Glu Gly Ser
                85                  90                  95
Leu Thr Leu Ile Pro Gly Ala Leu Asp Phe Leu Glu Tyr Ala Asn Ser
            100                 105                 110
Lys Gly Val Lys Ile Phe Tyr Ile Ser Asn Arg Thr Gln Lys Asn Lys
        115                 120                 125
Ala Phe Thr Leu Lys Thr Leu Lys Ser Phe Lys Leu Pro Gln Val Ser
    130                 135                 140
Glu Glu Ser Val Leu Leu Lys Glu Lys Gly Lys Pro Lys Ala Val Arg
145                 150                 155                 160
Arg Glu Leu Val Ala Lys Asp Tyr Ala Ile Val Leu Gln Val Gly Asp
                165                 170                 175
Thr Leu His Asp Phe Asp Ala Ile Phe Ala Lys Asp Ala Lys Asn Ser
            180                 185                 190
Gln Glu Gln Gln Ala Lys Val Leu Gln Asn Ala Gln Lys Phe Gly Thr
        195                 200                 205
Glu Trp Ile Ile Leu Pro Asn Ser Leu Tyr Gly Thr Trp Glu Asp Gly
    210                 215                 220
Pro Ile Lys Ala Trp Gln Asn Lys Lys
225                 230
```

(2) INFORMATION FOR SEQ ID NO:866:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866

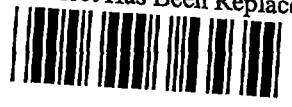
```
Met Ile Tyr Gly Val Leu Asp Gly Leu Phe Leu Ala Ile Leu Gln Ala
1               5                  10                  15
```

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

(2) INFORMATION FOR SEQ ID NO:867:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:867

```
Met Leu Ala Ala Gly Leu Thr Leu Pro Glu Phe Gly Cys Tyr Leu Ser
1               5                   10                  15
His Tyr Leu Leu Trp Lys Glu Cys Val Lys Leu Asp Gln Pro Val Val
            20                  25                  30
Ile Leu Glu Asp Asp Val Thr Leu Glu Ser His Phe Met Gln Ala Leu
        35                  40                  45
Glu Asp Cys Leu Lys Ser Pro Phe Asp Phe Val Arg Leu Tyr Gly Cys
    50                  55                  60
Tyr Trp Tyr Tyr Gln Arg Asp Lys Ile Pro Cys Phe Ala Gln Arg Ile
65                  70                  75                  80
Cys Ile Ser Ser Leu
                85
```

(2) INFORMATION FOR SEQ ID NO:867:

(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

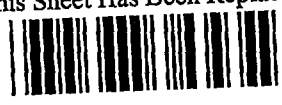
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867

```
Met Leu Ala Ala Gly Leu Thr Leu Pro Glu Phe Gly Cys Tyr Leu Ser
1               5                  10                  15
His Tyr Leu Leu Trp Lys Glu Cys Val Lys Leu Asp Gln Pro Val Val
            20                  25                  30
Ile Leu Glu Asp Asp Val Thr Leu Glu Ser His Phe Met Gln Ala Leu
        35                  40                  45
Glu Asp Cys Leu Lys Ser Pro Phe Asp Phe Val Arg Leu Tyr Gly Cys
    50                  55                  60
Tyr Trp Tyr Tyr Gln Arg Asp Lys Ile Pro Cys Phe Ala Gln Arg Ile
65                  70                  75                  80
Cys Ile Ser Ser Leu
                85
```

(2) INFORMATION FOR SEQ ID NO:868:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 289 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

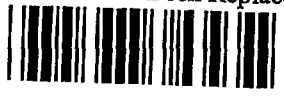
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...289

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868

```
Met Leu Ala Phe Leu Lys Thr Pro Arg Asn Ser Ala Phe Ala Leu Gly
1               5                  10                  15
Ile Phe Val Gly Ala Leu Leu Phe Tyr Trp Cys Ala Leu Arg Leu Ser
            20                  25                  30
His Ser Asp Phe Thr Tyr Leu Leu Pro Leu Ile Ile Val Leu Val Ala
        35                  40                  45
Leu Val Tyr Gly Val Leu Phe Tyr Leu Leu Leu Tyr Phe Glu Asn Pro
    50                  55                  60
Tyr Phe Arg Leu Leu Ser Phe Leu Gly Ser Ser Phe Ile His Pro Phe
65                  70                  75                  80
Gly Phe Asp Trp Leu Val Pro Asp Ser Phe Phe Ser Tyr Ser Val Phe
                85                  90                  95
```

```
Arg Val Asp Lys Leu Ser Leu Gly Leu Ile Phe Leu Ala Cys Ile Phe
            100                 105                 110
Leu Ser Ala Gln Asn Leu Lys Lys Tyr Arg Met Ile Gly Val Leu Leu
        115                 120                 125
Leu Leu Gly Ala Leu Asp Phe His Phe Phe Lys Ile Ser Asp Leu Lys
    130                 135                 140
Glu Val Gly Asn Ile Glu Leu Val Ser Thr Arg Thr Pro Gln Asp Leu
145                 150                 155                 160
Lys Phe Asp Ser Asn Tyr Leu Asn Asn Ile Glu Asn Asn Ile Leu Lys
                165                 170                 175
Glu Ile Lys Leu Ala Gln Ser Lys Gln Lys Thr Leu Ile Val Phe Pro
            180                 185                 190
Glu Thr Ala Tyr Pro Ile Ala Leu Glu Asn Ser Pro Phe Lys Thr Gln
        195                 200                 205
Leu Glu Asp Leu Ser Asp Lys Ile Ala Ile Leu Ile Gly Thr Leu Arg
    210                 215                 220
Ala Gln Gly Tyr Ser Leu Tyr Asn Ser Ser Phe Leu Phe Ser Lys Lys
225                 230                 235                 240
Ser Val Gln Ile Ala Asp Lys Val Ile Leu Ala Pro Phe Gly Glu Ile
                245                 250                 255
Met Pro Leu Pro Glu Phe Leu Gln Lys Pro Leu Glu Lys Leu Phe Phe
            260                 265                 270
Ala Arg Ala Leu Ile Tyr Thr Ala Thr Leu Pro Ile Ser Ala Ile Leu
        275                 280                 285
His
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:869:

(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:869

```
Met Asn Asp Pro Lys His Val Val Tyr Val Trp Leu Asp Ala Leu Leu
1               5                   10                  15
Asn Tyr Ala Ser Ala Leu Gly Tyr Leu Asn Gly Leu Asp Asn Lys Met
            20                  25                  30
Ala His Phe Glu Arg Ala Arg His Ile Val Gly Lys Asp Ile Leu Arg
        35                  40                  45
Phe His Ala Ile Tyr Trp Pro Ala Phe Leu Met Ser Leu Asn Leu Pro
    50                  55                  60
Leu Phe Lys Gln Leu Cys Val His Gly Trp Trp Thr Ile Glu Gly Val
65                  70                  75                  80
Lys Met Ser Lys Ser Leu Gly Asn Val Leu Asp Ala Gln Lys Leu Ala
                85                  90                  95
Met Glu Tyr Gly Ile Glu Glu Leu Arg Tyr Phe Leu Leu Arg Glu Val
            100                 105                 110
Pro Phe Gly Gln Asp Gly Asp Phe Ser Lys Lys Ala Leu Val Glu Arg
        115                 120                 125
Ile Asn Ala Asn Leu Asn Asn Asp Leu Gly Asn Leu Leu Asn Arg Leu
```

```
    130                 135                 140
Leu Gly Met Ala Lys Lys Tyr Phe Asn Tyr Ser Leu Lys Ser Thr Lys
145                 150                 155                 160
Ile Thr Ala Tyr Tyr Pro Lys Glu Leu Glu Lys Ala His Gln Ile Leu
                165                 170                 175
Asp Asn Ala Asn Ser Phe Val Pro Lys Met Gln Leu His Lys Ala Leu
            180                 185                 190
Glu Glu Leu Phe Asn Ile Tyr Asp Phe Leu Asn Lys Leu Ile Ala Lys
        195                 200                 205
Glu Glu Pro Trp Val Leu His Lys Asn Asn Glu Ser Glu Lys Leu Glu
    210                 215                 220
Ala Leu Leu Ser Leu Ile Ala Asn Thr Leu Leu Gln Ser Ser Phe Leu
225                 230                 235                 240
Leu Tyr Ala Phe Met Pro Lys Ser Ala Met Lys Leu Ala Ser Ala Phe
                245                 250                 255
Arg Val Glu Ile Thr Pro Asn Asn Tyr Glu Arg Phe Phe Lys Ala Lys
            260                 265                 270
Lys Leu Gln Asp Met Val Leu Gln Asp Thr Glu Pro Leu Phe Ser Lys
        275                 280                 285
Ile Glu Lys Ile Glu Lys Ile Glu Lys Ile Glu Lys Ile Glu Lys Ile
    290                 295                 300
Glu Lys Gly Glu Glu Ala Leu Ala Glu Lys Ala Glu Lys Lys Glu Lys
305                 310                 315                 320
Glu Lys Ala Pro Pro Thr Gln Glu Asn Tyr Ile Ser Ile Glu Asp Phe
                325                 330                 335
Lys Lys Val Glu Ile Lys Val Gly Leu Ile Lys Glu Ala Gln Arg Ile
            340                 345                 350
Glu Lys Ser Asn Lys Leu Leu Arg Leu Lys Val Asp Leu Gly Glu Asn
        355                 360                 365
Arg Leu Arg Gln Ile Ile Ser Gly Ile Ala Leu Asp Tyr Glu Pro Glu
    370                 375                 380
Ser Leu Val Gly Gln Met Val Cys Val Val Ala Asn Leu Lys Pro Ala
385                 390                 395                 400
Lys Leu Met Gly Glu Met Ser Glu Gly Met Ile Leu Ala Val Arg Asp
                405                 410                 415
Asn Asp Asn Leu Ala Leu Ile Ser Pro Thr Arg Glu Lys Ile Ala Gly
            420                 425                 430
Ser Leu Ile Ser
        435
```

(2) INFORMATION FOR SEQ ID NO:870:

This Sheet Has Been Replaced



(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:870

```
Met Lys Arg Pro Ile Ser Lys Leu Lys Gln Asn Phe Leu Gln Phe Lys
1               5                   10                  15
His Ser Phe Asn Lys His Leu Asp Lys Tyr Ser Leu Tyr Tyr Arg Leu
            20                  25                  30
```

```
Phe Asn Ile Ser Ser Ile Val Ile Gly Phe Leu Ile Ala Leu Phe Ser
        35                  40                  45
Tyr Gly Ala Gly Val Ile Leu Val Tyr Pro Ile Leu Phe Leu Phe Ala
    50                  55                  60
Leu Ile Ile Lys Pro Ser Phe Phe Tyr Tyr Thr Thr Tyr Leu Leu Leu
65                  70                  75                  80
Leu Val Ser Leu Ser Ile Ile Ser Lys Tyr Tyr Leu Leu Ser His Ala
                85                  90                  95
Asn Phe Thr Met Lys Leu Ile Met Leu Met Thr Gln Trp Gln Asn Trp
            100                 105                 110
Phe Leu
```

(2) INFORMATION FOR SEQ ID NO:871:

(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

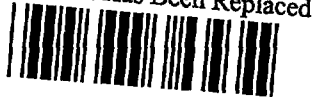
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871

```
Met Gly Phe Glu Lys Ser Ile Leu Asp Asn Leu Asn Gly Ala Gln Lys
1               5                   10                  15
Ile Val 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 Glu Phe
                165                 170
```

(2) INFORMATION FOR SEQ ID NO:872:

This Sheet Has Been Replaced



(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:872

```
Leu Ile Ala Leu Arg Val Thr Ala Trp Lys Val Unk Ala Met Lys Arg
1               5                  10                  15
Leu His Leu Ser Val Lys Asp Ala Glu Asn Phe Asp Ala Ile Leu Arg
            20                  25                  30
Glu Arg Pro Phe Phe Lys Asp Leu Ile Glu Phe Met Val Ser Gly Pro
        35                  40                  45
Val Val Val Met Val Leu Glu Gly Lys Asp Ala Val Ala Lys Asn Arg
    50                  55                  60
Glu Leu Met Gly Ala Thr Asp Pro Lys Leu Ala Gln Lys Gly Thr Ile
65                  70                  75                  80
Arg Ala Asp Phe Ala Glu Ser Ile Asp Ala Asn Ala Val His Gly Ser
                85                  90                  95
Asp Ser Leu Glu Asn Ala His Asn Glu Ile Ala Phe Phe Phe Ala Ala
            100                 105                 110
Arg Glu Phe
        115
```

(2) INFORMATION FOR SEQ ID NO:872:

This Sheet Has Been Replaced



(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:872

```
Leu Ile Ala Leu Arg Val Thr Ala Trp Lys Val Unk Ala Met Lys Arg
1               5                  10                  15
Leu His Leu Ser Val Lys Asp Ala Glu Asn Phe Asp Ala Ile Leu Arg
            20                  25                  30
Glu Arg Pro Phe Phe Lys Asp Leu Ile Glu Phe Met Val Ser Gly Pro
        35                  40                  45
Val Val Val Met Val Leu Glu Gly Lys Asp Ala Val Ala Lys Asn Arg
    50                  55                  60
Glu Leu Met Gly Ala Thr Asp Pro Lys Leu Ala Gln Lys Gly Thr Ile
65                  70                  75                  80
Arg Ala Asp Phe Ala Glu Ser Ile Asp Ala Asn Ala Val His Gly Ser
                85                  90                  95
Asp Ser Leu Glu Asn Ala His Asn Glu Ile Ala Phe Phe Phe Ala Ala
            100                 105                 110
```

Arg Glu Phe
115

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:873:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873

```
Val Phe Thr Tyr Ser Leu Gly Gln Val Phe Phe Ser Leu Ser Ile Gly
1               5                  10                  15
Leu Gly Ile Asn Ile Thr Tyr Ala Ala Val Thr Asp Lys Thr Gln Asn
            20                  25                  30
Leu Leu Lys Ser Thr Ile Trp Val Val Leu Ser Gly Ile Leu Ile Ser
        35                  40                  45
Leu Val Unk Gly Leu Met Ile Phe Thr Phe Val Phe Glu Tyr Gly Ala
    50                  55                  60
Asn Val Ser Gln Gly Thr Gly Leu Ile Phe Thr Ser Leu Pro Val Val
65                  70                  75                  80
Phe Gly Gln Met Gly Ala Ile Gly Val Pro Cys Phe Asn Ser Phe Leu
                85                  90                  95
Ala Arg Ala Arg Phe Cys Trp His His Phe Tyr Gly Gly Phe Ile Arg
            100                 105                 110
Ala Lys Arg Asp Val Ser Tyr Arg Lys Val Ser Ile Leu Ser Phe
        115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:874:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...150

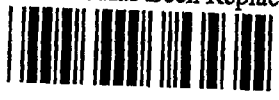
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874

```
Met Lys Pro Leu His Phe Ser His Leu Asp Arg Glu Gln Ser Gly Asp
1               5                  10                  15
Val Gly Phe Ile Ile Lys Asn Leu Ile Phe Leu Gly Val Phe Ser Leu
```

```
            20                  25                  30
Leu Gly Trp Leu Asn Thr Glu Tyr Phe Leu Trp Pro Ser Met Leu Glu
        35                  40                  45
Leu Lys Lys Ile Leu Leu Glu Glu Asn Arg Lys Lys Ser Val Leu Glu
    50                  55                  60
Tyr Ala Gln Arg His Phe Glu Thr Ala Leu Ala Asn Tyr Arg Asn Gln
65                  70                  75                  80
Lys Glu Thr Ser Glu Ser Leu Leu Lys Ile Phe Asn Asp Glu Glu Ser
                85                  90                  95
Arg Arg Ile Leu Glu Lys Ile Leu Lys Lys Cys Phe Asp Ala Tyr Lys
            100                 105                 110
Ile Lys Pro Leu Leu Ser Gln Asn Pro Ser Gln Lys Thr Gln Phe Phe
        115                 120                 125
Ile Met Ala Arg Ala Ser Glu Leu Glu Lys Thr Tyr Leu Phe Phe Thr
    130                 135                 140
Leu Ile Asn Lys Tyr Leu
145                 150
```

(2) INFORMATION FOR SEQ ID NO:875:

is Sheet Has Been Replaced



(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:875

```
Met Asn Ala Leu Lys Arg Ala Cys Leu Arg Leu Met Gly Glu Thr Asn
1               5                   10                  15
Thr Asp Asp Leu Unk Pro Unk Ser Asp Ala Phe Thr Arg Ser Asp Ile
            20                  25                  30
Pro Leu His Ala Lys Ala Met Leu Lys Asn Arg Ile Glu Asn Tyr Glu
        35                  40                  45
Gln Arg Ile Glu Ala Ile Lys Thr Lys Gly Val Pro Val Ala Tyr Val
    50                  55                  60
Gly Asp Val Val Gly Thr Gly Ser Ser Arg Lys Ser Ala Thr Asn Ser
65                  70                  75                  80
Ile Met Trp His Phe Gly Lys Asp Ile Pro Phe Val Pro Asn Lys Arg
                85                  90                  95
Ser Gly Gly Ile Val Ile Gly Gly Val Ile Ala Pro Ile Phe Phe Ala
            100                 105                 110
Thr Cys Glu Asp Ser Gly Ala Leu Pro Ile Val Ala Asp Val Lys Asp
        115                 120                 125
Leu Lys Glu Gly Asp Ile Ile Lys Ile Tyr Pro Tyr Lys Gly Glu Ile
    130                 135                 140
Thr Leu Asn Asp Lys Val Val Ser Thr Phe Lys Leu Glu Pro Glu Thr
145                 150                 155                 160
Leu Leu Asp Glu Val Arg Ala Ser Gly Arg Ile Pro Leu Ile Ile Gly
                165                 170                 175
Arg Gly Leu Thr Asn Lys Ala Arg Lys Phe Leu Gly Arg Arg Ile Gly
            180                 185                 190
Ser Val Gln Lys Thr Phe Arg Pro Ser Ser Ala Leu Arg Leu His Phe
        195                 200                 205
```

Ala

(2) INFORMATION FOR SEQ ID NO:876:

(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:876

```
Met Leu Ser Ala His Gln Pro Phe Lys Asn Tyr Pro Asp Leu Ile Lys
1               5                  10                  15
Lys Glu Leu Gln Glu His Asn Ala Tyr Ala Ser Val Ala Ser Gly Val
            20                  25                  30
Pro Ala Met Cys Asp Gly Ile Thr Gln Gly Tyr Glu Gly Met Glu Leu
        35                  40                  45
Ser Leu Phe Ser Arg Asp Val Ile Ala Leu Ser Thr Unk Val Gly Leu
    50                  55                  60
Ser His Asn Val Phe Asp Gly Ala Phe Phe Leu Gly Val Cys Asp Lys
65                  70                  75                  80
Ile Val Pro Gly Leu Leu Ile Gly Ala Leu Ser Phe Gly Asn Leu Ala
                85                  90                  95
Ser Val Phe Val Pro Ser Gly Pro Met Val Ser Gly Ile Glu Asn Tyr
            100                 105                 110
Lys Lys Ala Lys Ala Arg Gln Asp Phe Ala Met Gly Lys Ile Asn Arg
        115                 120                 125
Glu Glu Leu Leu Lys Val Glu Met Gln Ser Tyr His Asp Val Gly Thr
    130                 135                 140
Cys Thr Phe Tyr Gly Thr Ala Asn Ser Asn Gln Met Met Met Glu Phe
145                 150                 155                 160
Met Gly Leu His Val Ala Asn Ser Ser Phe Ile Asn Pro Asn Asn Pro
                165                 170                 175
Leu Arg Lys Val Leu Val Glu Glu Ser Ala Lys Arg Leu Ala Ser Gly
            180                 185                 190
Lys Val Leu Pro Leu Ala Lys Leu Ile Asp Glu Lys Ser Ile Leu Asn
        195                 200                 205
Ala Leu Ile Gly Leu Met Ala Thr Gly Gly Ser Thr Asn His Thr Leu
    210                 215                 220
His Leu Ile Ala Ile Ala Asp Leu Val Gly
225                 230
```

(2) INFORMATION FOR SEQ ID NO:877:

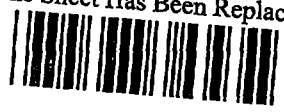
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

his Sheet Has Been Replaced



This Sheet Has Been Replaced



(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

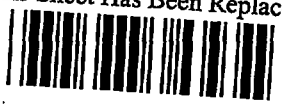
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877

```
Leu Met Trp Leu Lys Thr Leu Thr Leu Gln Thr Leu Asn Thr Asp Lys
1               5                  10                  15
Ala Leu Gln Glu Phe Ser Lys Thr Met Glu Ala Phe Lys Thr Lys Leu
            20                  25                  30
Ile Gln Ser Ala Asn Asp Val His Ser Glu Thr Ser Arg Ala Ala Ile
        35                  40                  45
Ala Asn Asp Leu Glu Arg Leu Lys Glu His Met Ile Asn Val Ala Asn
    50                  55                  60
Thr Ser Ile Gly Gly Glu Phe Leu Phe Gly Gly Ser Lys Val Asp Arg
65                  70                  75                  80
Pro Pro Ile Asp Ser Asn Gly Lys Tyr His Gly Asn Gly Glu Asp Leu
                85                  90                  95
Asn Ala Leu Ile Ser Ser Asp Asn Leu Val Pro Tyr Asn Ile Ser Gly
            100                 105                 110
Gln Asp Leu Phe Leu Gly Thr Asp Lys Asp Lys His Lys Leu Ile Thr
        115                 120                 125
Thr Asn Ile Lys Leu Leu Asn Gln Asn Lys Leu Unk Pro Asp Val Met
    130                 135                 140
Asp Ala Leu Glu His Ser Ser Leu Pro Glu Glu Val Phe Ile Lys Pro
145                 150                 155                 160
Ser Asp Thr Leu Arg Glu Leu Ile Gly Asp Asn Asp Lys Asn Pro Thr
                165                 170                 175
Asn Asp Pro Lys Glu Phe Phe Tyr Leu Gln Gly Ile Arg Pro Asp Gly
            180                 185                 190
Ser Ser Phe Lys Glu Lys Phe Ala Leu Asp Lys Ala Tyr Gln Asn Gln
        195                 200                 205
Glu Ser Ala Thr Lys Val Ser Asp Leu Leu Asp Lys Ile Gly His Ala
    210                 215                 220
Tyr Gly Asn Thr Ser Gln Asn Lys Val Val Asp Val Ser Leu Asn Asn
225                 230                 235                 240
Trp Gly Gln Ile Glu Ile Lys Asn Leu Thr Pro Gly Ser Glu Asn Leu
                245                 250                 255
Asp Phe His Leu Ile Ser Ser Asp Gly Asp Phe Asp Asp Leu Asp Ala
            260                 265                 270
Leu Arg Ser Ser Gly Lys Arg Val Thr Glu Tyr Val Lys Ser Ala Phe
        275                 280                 285
Val Thr Asp Arg Ser Leu Ser Gln Val Lys Ala Val Pro Asn Met Tyr
    290                 295                 300
Asn Pro Lys Val Leu Glu Ile Pro Ser Val Phe Val Thr Lys Asp Asn
305                 310                 315                 320
Val Leu Ala Asn Lys Asn Thr Lys Leu Ser Glu Ile Phe Gly Asp Lys
                325                 330                 335
Val Glu Thr Leu Lys Ile Asn Ala Ser Arg Leu Gly Asp Glu Ser Ala
            340                 345                 350
Ile Lys Ile Pro Asn Leu Pro Ile Asn Leu Asp Ile Pro Ile Leu Leu
        355                 360                 365
Asp Val Lys Asn Ser Thr Ile Lys Asp Leu Lys Asp Ala Ile Lys Glu
    370                 375                 380
Arg Phe Asn Asn Glu Gly Gly Cys Gly Asn
385                 390
```

(2) INFORMATION FOR SEQ ID NO:877:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...394

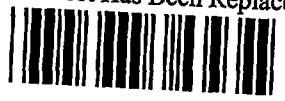
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877

```
Leu Met Trp Leu Lys Thr Leu Thr Leu Gln Thr Leu Asn Thr Asp Lys
1               5                  10                  15
Ala Leu Gln Glu Phe Ser Lys Thr Met Glu Ala Phe Lys Thr Lys Leu
            20                  25                  30
Ile Gln Ser Ala Asn Asp Val His Ser Glu Thr Ser Arg Ala Ala Ile
        35                  40                  45
Ala Asn Asp Leu Glu Arg Leu Lys Glu His Met Ile Asn Val Ala Asn
    50                  55                  60
Thr Ser Ile Gly Gly Glu Phe Leu Phe Gly Gly Ser Lys Val Asp Arg
65                  70                  75                  80
Pro Pro Ile Asp Ser Asn Gly Lys Tyr His Gly Asn Gly Glu Asp Leu
                85                  90                  95
Asn Ala Leu Ile Ser Ser Asp Asn Leu Val Pro Tyr Asn Ile Ser Gly
            100                 105                 110
Gln Asp Leu Phe Leu Gly Thr Asp Lys Asp Lys His Lys Leu Ile Thr
        115                 120                 125
Thr Asn Ile Lys Leu Leu Asn Gln Asn Lys Leu Unk Pro Asp Val Met
    130                 135                 140
Asp Ala Leu Glu His Ser Ser Leu Pro Glu Glu Val Phe Ile Lys Pro
145                 150                 155                 160
Ser Asp Thr Leu Arg Glu Leu Ile Gly Asp Asn Asp Lys Asn Pro Thr
                165                 170                 175
Asn Asp Pro Lys Glu Phe Phe Tyr Leu Gln Gly Ile Arg Pro Asp Gly
            180                 185                 190
Ser Ser Phe Lys Glu Lys Phe Ala Leu Asp Lys Ala Tyr Gln Asn Gln
        195                 200                 205
Glu Ser Ala Thr Lys Val Ser Asp Leu Leu Asp Lys Ile Gly His Ala
    210                 215                 220
Tyr Gly Asn Thr Ser Gln Asn Lys Val Val Asp Val Ser Leu Asn Asn
225                 230                 235                 240
Trp Gly Gln Ile Glu Ile Lys Asn Leu Thr Pro Gly Ser Glu Asn Leu
                245                 250                 255
Asp Phe His Leu Ile Ser Ser Asp Gly Asp Phe Asp Asp Leu Asp Ala
            260                 265                 270
Leu Arg Ser Ser Gly Lys Arg Val Thr Glu Tyr Val Lys Ser Ala Phe
        275                 280                 285
Val Thr Asp Arg Ser Leu Ser Gln Val Lys Ala Val Pro Asn Met Tyr
    290                 295                 300
Asn Pro Lys Val Leu Glu Ile Pro Ser Val Phe Val Thr Lys Asp Asn
305                 310                 315                 320
Val Leu Ala Asn Lys Asn Thr Lys Leu Ser Glu Ile Phe Gly Asp Lys
                325                 330                 335
Val Glu Thr Leu Lys Ile Asn Ala Ser Arg Leu Gly Asp Glu Ser Ala
            340                 345                 350
Ile Lys Ile Pro Asn Leu Pro Ile Asn Leu Asp Ile Pro Ile Leu Leu
        355                 360                 365
Asp Val Lys Asn Ser Thr Ile Lys Asp Leu Lys Asp Ala Ile Lys Glu
```

370 375 380
Arg Phe Asn Asn Glu Gly Gly Cys Gly Asn
385 390

(2) INFORMATION FOR SEQ ID NO:878:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878

Leu Lys Ala Leu Asn Asp Cys Met Val Phe Phe His Lys Lys Ile Ile
1 5 10 15
Leu Asn Phe Ile Tyr Ser Leu Met Val Ala Phe Leu Phe His Leu Ser
20 25 30
Tyr Gly Val Leu Leu Lys Ala Asp Gly Met Ala Lys Lys Gln Thr Leu
35 40 45
Leu Val Gly Glu Arg Leu Val Trp Asp Lys Leu Thr Leu Leu Gly Phe
50 55 60
Leu Glu Lys Asn His Ile Pro Gln Lys Leu Tyr Tyr Asn Leu Ser Ser
65 70 75 80
Gln Asp Lys Glu Leu Ser Ala Glu Ile Gln Ser Asn Val Thr Tyr Tyr
85 90 95
Unk Phe Lys Arg Cys Lys
100

(2) INFORMATION FOR SEQ ID NO:878:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...102

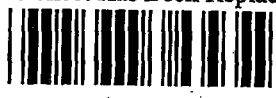
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878

Leu Lys Ala Leu Asn Asp Cys Met Val Phe Phe His Lys Lys Ile Ile
1 5 10 15
Leu Asn Phe Ile Tyr Ser Leu Met Val Ala Phe Leu Phe His Leu Ser
20 25 30

```
Tyr Gly Val Leu Leu Lys Ala Asp Gly Met Ala Lys Lys Gln Thr Leu
        35                  40                  45
Leu Val Gly Glu Arg Leu Val Trp Asp Lys Leu Thr Leu Leu Gly Phe
    50                  55                  60
Leu Glu Lys Asn His Ile Pro Gln Lys Leu Tyr Tyr Asn Leu Ser Ser
65                  70                  75                  80
Gln Asp Lys Glu Leu Ser Ala Glu Ile Gln Ser Asn Val Thr Tyr Tyr
                85                  90                  95
Unk Phe Lys Arg Cys Lys
            100
```

(2) INFORMATION FOR SEQ ID NO:879:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879

```
Met Lys Phe Leu Lys Phe Phe Ala Ser Ser Val Thr Leu Asp Glu Lys
1               5                   10                  15
Phe Leu Met Phe Leu Leu Cys Asn Ala Leu Ser Asn Ala Tyr Lys Asn
            20                  25                  30
Ser Asp Leu Phe Ser Phe Ser Lys Gly Phe Leu Gly Ala Phe Leu Ile
        35                  40                  45
Gly Phe Val Val Tyr Tyr Gly Cys Ala Leu Ile Pro Lys Lys Arg Leu
    50                  55                  60
Lys Tyr Ser Leu Glu Trp Leu Phe Ile Gly Ser Gly Ile Ile Phe Ser
65                  70                  75                  80
Val Ala Glu Ile Phe Thr Leu Phe Met Phe Lys Met Pro Phe Ser Lys
                85                  90                  95
Gly Leu Ile Asp Thr Leu Leu Ala Thr Asn Ser Ser Glu Thr Met Ala
            100                 105                 110
Phe Ile Lys Ser Tyr Lys Asn Tyr Leu Leu Tyr Tyr Ala Leu Ile Leu
        115                 120                 125
Ile Ala Leu Leu Ile Ala Ile Lys Ile Ile Arg Phe Arg Ala Leu Val
    130                 135                 140
Pro Gly Val Ile Ala Ser Val Leu Gly Leu Ser Ile Leu Thr Ile Gly
145                 150                 155                 160
Ser Val Arg Asn Ile Lys His Leu Thr Lys Asn Asp Ala Ile Leu Lys
                165                 170                 175
Arg Ser Leu Phe Ser Leu Ser Leu Ala Arg Gly Phe Tyr Ser Ala Tyr
            180                 185                 190
Leu Ser Leu Phe Asp Arg Gln Gln Ala Ile Lys Phe Tyr Ser Phe Leu
        195                 200                 205
Asn Asn Leu Tyr Leu Pro Ser Asp Tyr Leu Ser Ser Thr Gly Asp Ile
    210                 215                 220
Ser Asn Val Val Leu Val Ile Ala Lys Ala Arg Ala Glu Ile Ser Cys
225                 230                 235                 240
Asn Ser Met Ala Ile Ala Phe Leu Ile Ile Pro Tyr Thr Ser Glu Leu
                245                 250                 255
Ala Asn Glu Arg Glu Arg Glu Arg Glu
```

260 265

(2) INFORMATION FOR SEQ ID NO:880:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880

```
Met Lys Phe Phe Leu Leu Lys Lys Phe Ser Unk Phe Leu Asn Thr Gln
1               5                  10                  15
Thr His Phe Asn Leu Lys Arg Leu Asn Ala Ser Ser Phe Leu Leu Glu
            20                  25                  30
Thr Phe Ser Lys Glu Lys His Ala Phe Val Val Asp Leu Ser Ala Pro
        35                  40                  45
Tyr Ile Gly Leu Ser Lys Lys Pro Pro Glu Ser Val Leu Lys Asn Thr
    50                  55                  60
Leu Ala Leu Asp Phe Cys Leu Asn Lys Phe Thr Lys Asn Ala Lys Ile
65                  70                  75                  80
Leu Gln Ala Asn Val Ile Asp Asn Asp Arg Ile Leu Glu Ile Lys Gly
                85                  90                  95
Ala Lys Asp Leu Ala Tyr Lys Ser Glu Thr Phe Ile Leu Arg Leu Glu
            100                 105                 110
Met Ile Pro Lys Lys Ala Asn Leu Met Ile Leu Asp Gln Glu Lys Cys
        115                 120                 125
Val Ile Glu Ala Phe Arg Phe Asn Asp Arg Val Ala Lys Asn Asp Ile
    130                 135                 140
Leu Gly Ala Leu Pro Pro Asn Ile Tyr Glu His Gln Glu Glu Asp Leu
145                 150                 155                 160
Asp Phe Lys Gly Leu Leu Asp Ile Leu Glu Lys Asp Phe Leu Ser Tyr
                165                 170                 175
Gln His Lys Glu Leu Glu His Lys Lys Asn Gln Ile Ile Lys Arg Leu
            180                 185                 190
Asn Ala Gln Lys Glu Arg Leu Lys Glu Lys Leu Glu Lys Leu Glu Asp
        195                 200                 205
Pro Lys Thr Leu Gln Leu Glu Ala Lys Glu Leu Gln Thr Gln Ala Ser
    210                 215                 220
Leu Leu Leu Thr Tyr Gln His Leu Ile Asn Arg Arg Glu Asn Arg Val
225                 230                 235                 240
Ile Leu Lys Asp Phe Glu Asp Lys Glu Cys Met Ile Glu Ile Asp Lys
                245                 250                 255
Ser Met Pro Leu Asn Ala Phe Ile Asn Lys Lys Phe Thr Leu Ser Lys
            260                 265                 270
Lys Lys Lys Gln Lys Ser Gln Phe Leu Tyr Leu Glu Glu Glu Asn Leu
        275                 280                 285
Lys Glu Lys Ile Ala Phe Lys Glu Asn Gln Ile Asn Tyr Val Arg Asp
    290                 295                 300
Ala Ala Glu Glu Ser Val Leu Glu Met Phe Met Pro Val Lys Asn Ser
305                 310                 315                 320
Lys Ile Lys Arg Pro Met Asn Gly Tyr Glu Val Leu Tyr Tyr Lys Asp
                325                 330                 335
```

Unk Lys Unk Gly Leu Gly Lys Thr Lys Lys Arg Ile Ser Ser Phe Tyr
340 345 350
Lys Thr Gln Unk Arg Met Ile Unk Gly Cys Unk
355 360

(2) INFORMATION FOR SEQ ID NO:880:

(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:880

Met Lys Phe Phe Leu Leu Lys Lys Phe Ser Unk Phe Leu Asn Thr Gln
1 5 10 15
Thr His Phe Asn Leu Lys Arg Leu Asn Ala Ser Ser Phe Leu Leu Glu
20 25 30
Thr Phe Ser Lys Glu Lys His Ala Phe Val Val Asp Leu Ser Ala Pro
35 40 45
Tyr Ile Gly Leu Ser Lys Lys Pro Pro Glu Ser Val Leu Lys Asn Thr
50 55 60
Leu Ala Leu Asp Phe Cys Leu Asn Lys Phe Thr Lys Asn Ala Lys Ile
65 70 75 80
Leu Gln Ala Asn Val Ile Asp Asn Asp Arg Ile Leu Glu Ile Lys Gly
85 90 95
Ala Lys Asp Leu Ala Tyr Lys Ser Glu Thr Phe Ile Leu Arg Leu Glu
100 105 110
Met Ile Pro Lys Lys Ala Asn Leu Met Ile Leu Asp Gln Glu Lys Cys
115 120 125
Val Ile Glu Ala Phe Arg Phe Asn Asp Arg Val Ala Lys Asn Asp Ile
130 135 140
Leu Gly Ala Leu Pro Pro Asn Ile Tyr Glu His Gln Glu Glu Asp Leu
145 150 155 160
Asp Phe Lys Gly Leu Leu Asp Ile Leu Glu Lys Asp Phe Leu Ser Tyr
165 170 175
Gln His Lys Glu Leu Glu His Lys Lys Asn Gln Ile Ile Lys Arg Leu
180 185 190
Asn Ala Gln Lys Glu Arg Leu Lys Glu Lys Leu Glu Lys Leu Glu Asp
195 200 205
Pro Lys Thr Leu Gln Leu Glu Ala Lys Glu Leu Gln Thr Gln Ala Ser
210 215 220
Leu Leu Leu Thr Tyr Gln His Leu Ile Asn Arg Arg Glu Asn Arg Val
225 230 235 240
Ile Leu Lys Asp Phe Glu Asp Lys Glu Cys Met Ile Glu Ile Asp Lys
245 250 255
Ser Met Pro Leu Asn Ala Phe Ile Asn Lys Lys Phe Thr Leu Ser Lys
260 265 270
Lys Lys Lys Gln Lys Ser Gln Phe Leu Tyr Leu Glu Glu Glu Asn Leu
275 280 285
Lys Glu Lys Ile Ala Phe Lys Glu Asn Gln Ile Asn Tyr Val Arg Asp
290 295 300
Ala Ala Glu Glu Ser Val Leu Glu Met Phe Met Pro Val Lys Asn Ser

This Sheet Has Been Replaced

```
305                 310                 315                 320
Lys Ile Lys Arg Pro Met Asn Gly Tyr Glu Val Leu Tyr Tyr Lys Asp
                325                 330                 335
Unk Lys Unk Gly Leu Gly Lys Thr Lys Lys Arg Ile Ser Ser Phe Tyr
            340                 345                 350
Lys Thr Gln Unk Arg Met Ile Unk Gly Cys Unk
        355                 360
```

(2) INFORMATION FOR SEQ ID NO:995:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 822 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...822

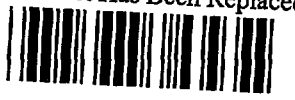
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995

```
GACGCACGTA GTTTCTTTTT AAGATTGGTA GCTATGGCAT TATGTTTGAT CTTAATTAAT      60
AGTAGAGGAG TAGCGATGGG ATACGCAAGC AAATTAGCTT TAAAGATTTG TTTGGTAGGT     120
TTATGTTTAT TTAGCACCCT TGGTGACGAA CACCTTGAGC AAAAAGGGAA TTATATTTAT     180
AAGGGAGAGG AGGCTTATAA TAATAAGGAA TATGAGCGAG CGGCTTCTTT TTATAAGAGC     240
GCTATTAAAA ATGGTGAGTC GCTTGCTTAT ATTCTTTTAG GGATCATGTA TGAAAATGGT     300
AGGGGTGTAC CTAAAGATTA CAAGAAAGCG GTTGAATATT TCCAAAAAGC TGTTGATAAC     360
GATATACCTA GAGGGTATAA CAATTTGGGC GTGATGTATA AAGAGGGTAA GGGAGTTCCT     420
AAAGATGAAA AGAAAGCGGT GGAATATTTT AGAATAGCTA CAGAGAAAGG TTATACTAAC     480
GCTTATATCA ACTTAGGCAT CATGTATATG GAGGGCAGGG GAGTTCCAAG TAACTATGCG     540
AAAGCGACAG AATGTTTTAG AAAAGCGATG CATAAGGGCA ATGTGGAAGC TTATATTCTC     600
CTAGGGGATA TTTATTATAG CGGGAATGAT CAATTGGGTA TTGAGCCGGA CAAAGATAAG     660
GCTGTTGTCT ATTATAAAAT GGCGGCCGAT GTGAGTTCTT CTAGAGCTTA TGAAGGGTTG     720
TCAGAGCCTT ACCGGTATGG GTTAGGCGTG GAAAAAGATA AAAAAAAGGC TGAAGAATAC     780
ATGCAAAAAG CATGCGATTT TGACATTGAT AAAAATTGTA AG                        822
```

(2) INFORMATION FOR SEQ ID NO:996:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:996

```
ACGATGAAAA ATACATCGTC ATCAACGACT TTAACAATGA ATGACACCAT TGCCGCTATC      60
GCTACCCCTT TAGGCAAGGG AGCGATTAGC ATCATTAAAA TCAGCGGCCA TAACGCCCTA     120
AACATCCTCA AACAACTCAC CCAAAAACAA GACTTCACCC CCAGATACGC TTACGTGTGC     180
GACATTTTTT CTGATGGCGT TTTATTGGAC AAAGCGTTAG TGATTTATTT CAAAGCCCCC     240
TATAGTTTCA CCGGTGAAGA TGTGTGCGAA ATCCAATGCC ATGGAAGCCC CCTTTTAGCG     300
CAAAATATCC TTCAAGCTTG CTTGAATTTA GGGGCTAGGC TCGCTAAAGC GGGGGAATTT     360
AGCAAAAAAG CCTTTTTAAA CCATAAAATG GATTTGAGCG AGATTGAAGC GAGCGTTCAG     420
CTCATCCTTT GTGAAGATGA AAGCGTT                                         447
```

(2) INFORMATION FOR SEQ ID NO:997:

(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:997

```
AATCTAATTT ATCGGAGCTC ACAAAGGAGC GCAGCCGCTT GCGTGGTGCG TTTGAATAAA      60
GAGCCGATGA TTGAATACTT GAAATCCAAT ATCAAGCTCA TTGATGAGAT GATTGCAAGC     120
GGTTATGAAG ACAAAGAGAC TTTGAAAAAA CGCAGAGATG CGATGCAAGC TTGGGTGGAT     180
AAGCCGGTAT TGTTAGAGCC AGATAGTAAC GCCCAATACG CCGCTGTCAT TGAAATTGAT     240
GTGGCAGAAA TCACGGAGCC TATTTTGGCA TGCCCTAATG ACCCTGATGA CGTCGCTACT     300
TTGAGCGAAG TTTTAGCGGA TACGACCGGC AAAAGACCCC ACGCTATTGA TGAAGTGTTT     360
ATTGGCTCTT GCATGACGAA TATTGGGCAT TTCAGAGCCT TTGGTGAAAT CGTTAAAAAC     420
GCCCCTCCCA GTCAAGCACG CCTTTGGGTA GTGCCACCCA GTAAAATGGA CGAACAAGAG     480
CTTATTAATG AGGGCTATTA TGCGATTTTT GGGGCTGCCG GGGCAAGGAC TGAAGTACCA     540
GGCTGTAGCT TGTGCATGGG CAATCAAGCG AGGGTTAGGG ATAATGCGGT CGTTTTTTCT     600
ACTTCCACAC GGAATTTTGA TAATCGTATG GGTAGAGGGG CTAAAGTGTA TTTGGGCAGT     660
GCGGAGCTTG GGGCGGCGTG CGCTTTACTA GGGAGGATCC CCACTAAAGA AGAATACATG     720
AATTTAGTGA GTGAAAAGCT AGAGAGCCAA AAAGACAAGA TCTATCGCTA CATGAACTTT     780
AACTTAATGG AGAATTTCAG GCTC                                            804
```

(2) INFORMATION FOR SEQ ID NO:998:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

his Sheet Has Been Replaced T



(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998

```
AAAATGCCAT ACGCCTTAAG AAAAAGATTT TTCAAACGCC TTTTATTGTT TTTTTTAATT      60
GTTTGTATGA TAAATTTGCA TGCCAAAAGC TATCTGTTTT CTCCTTTGCC CCCAGCGCAC     120
CAGCAAATCA TTAAGACAGA GCCTTGCTCT TTGGAGTGCT TGAAAGACTT GATGCTGCAA     180
AATCAAATCT TTTCTTTTGT ATCCCAATAC GATGATAACA ACCAAGATGA GAGCCTTAAA     240
ACTTATTACA AGGACATCTT AAACAAACTC AACCCCGTAT TCATCGCTTC TCAAACTCCA     300
GCTAAAGAAA GCTATGAGCC TAAGATTGAA TTAGCGATTT TACTGCCTAA AAAGGTGGTG     360
GGCCGTTATG CGATTTTAGT GATGAACACC CTTTTAGCGT ATTTGAACAC CAGAAACAAC     420
GATTTCAATA TCCAAGTCTT TGACAGCGAT GAAGAAAGCC CTGAAAAATT AGAAGAAACC     480
TATAAAGAAA TTGAAAAAGA AAAATTCCCT TTTATCATCG CTTTATTGAC TAAAGAGGGC     540
GTGGAAAATT TGCTCCAAAA TACGACTATC AATACCCCTA CTTATGTGCC TACGGTGAAT     600
AAAACGCAAT TAGAAAATCA TACCGAGCTT TCTTTAAGCG AGCGCTTGTA TTTTGGGGGG     660
ATTGATTATA AAGAGCAATT AGGCATGCTC GCAACTTTCA TTAGCCCTAA TTCGCCCGTG     720
ATTGAATACG ATGATGATGG CCTGATAGGT GAACGCTTGA GGCAAATCAC GGAGTCTTTA     780
AACGTTGAAG TCAAACACCA AGAAAACATT TCTTACAAAC AAGCGACCAG TTTTTCTAAA     840
AATTTTAGAA AACATGATGC GTTTTTTAAA AATTCTACCT TAATTTTGAA CACCCCTACC     900
ACTAAAAGCG GTCTGATCCT TTCTCAAATA GGGCTTTTAG AGTATAAGCC TCTTAAAATC     960
CTTTCCACAC AAATCAATTT CAACCCCTCT TTACTCTTGC TCACCCAGCC TAAAGACAGG    1020
AAAAATTTAT TCATTGTCAA TGCCTTGCAA AACAGCGATG AAACGCTGAT AGAATACGCT    1080
TCCTTATTAG AGAGCGATTT AAGGCATGAT TGGGTGAATT ATTCCAGCGC GATAGGGCTA    1140
GAGATGTTTT TAAACACGCT AGATCCGCAT TTTAAAAAGT CTTTTCAAGA GAGTTTGGAA    1200
GACAATCAAG TCCGTTACCA CAATCAAATT TATCAGGCTT TAGGGTATTC TTTTGAGCCG    1260
ATAAAAAACG AAAGCGAAAC AAAAAAAGAA                                     1290
```

(2) INFORMATION FOR SEQ ID NO:999:

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

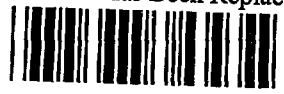
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999

```
TATTTAGATA ATTATTTGAA TACTTTTATT TTTAATGGGT TTTTAAGAAA GATAGACTAT
TATGCGAGTG GGAAATTAAA AAGGATTGGT GCGGTGTTAA AATTTCAAAA ATTACCCTTA
TTGTTTGTTT CCATTCTTTA TAATCAAAGC CCTTTATTGG CTTTTGATTA TAAGTTTAGT
GGGGTAGCGG AATCTGTTTC TAAAGTGGGG TTTAACCATT CCAAACTCAA TTCCAAAGAA
GGGATTTTCC CTACAGCCAC CTTTGTAACC GCCACGATCA AGCTTCAAGT GGATTCCAAT
```

```
CTGCTCCCTA AAAACATTGA AAAACACAGC TTAAAAATAG GCGTTGGGGG GATTTTAGGA     360
GCGCTCGCTT ACGATTCCAC CAAAACGCTC ATAGACCAAG CCACGCATCA AATCTATGGC     420
TCAGAACTTT TTTACCTCAT AGGGCGTTGG TGGGGGTTTT TAGGCAACGC TCCTTGGAAA     480
GACTCCCTCA TAGAATCTGA CGCTCACACC CGTAATTATG TGCTGTATAA TTCCTATCTG     540
TTTTATTCTT ATGGCGATAA ATTCCACCTA AAATTAGGGC GTTATCTCTC TAACATGGAT     600
TTTATGAGTT CCTACACACA GGGTTTTGAA CTGGATTATA AAATCAATTC TAAAATAGCG     660
TTAAAATGGT TTAGCTCTTT TGGGAGGGCG TTGGCTTTTG GGCAATGGAT ACGGGATTGG     720
TATGCCCCTA TTGTAACTGA AGATGGCAGA AAAGAAGTTT ATGATGGCAT CCATGCCGCG     780
CAACTCTATT TTTCTAGCAA GCATGTTCAA GTCATGCCTT TTGCTTATTT TTCGCCTAAG     840
ATTTACGGAG CGCCCGGTGT TAAAATCCAT ATTGATAGCA ACCCGAAATT CAAAGGCTTA     900
GGGTTAAGGG CTCAAACCAC TATTAATGTG ATTTTCCCTG TTTATGCTAA AGATTTATAC     960
GATGTGTATT GGCGTAACTC TAAGATTGGC GAGTGGGGCG CATCGCTTTT GATCCACCAA    1020
CGCTTTGACT ACAACGAATT TAACTTTGGC TTTGGTTATT ACCAAAATTT TGGCAACGCT    1080
AACGCAAGGA TTGGCTGGTA TGGTAACCCC ATCCCTTTTA ATTATAGAAA TAACAGCGTT    1140
TATGGTGGGG TCTTCAGTAA CGCTATTACC GCAGACGCCG TTTCTGGGTA TGTCTTTGGT    1200
GGGGGGGTGT ATAGAGGGTT TTTATGGGGT ATTTTAGGCA GATACACTTA TGCCACTAGA    1260
GCGAGCGAAA GATCCATCAA CTTGAACTTG GGCTATAAAT GGGGTTCTTT TGCTAGAGTT    1320
GATGTGAATT TAGAATACTA TGTGGTCAGC ATGCACAACG GCTATAGATT AGACTATCTC    1380
ACCGGCCCTT TCAACAAAGC CTTTAAGGCT GACGCACAAG ATAGGAGTAA CCTTATGGTT    1440
AGCATGAAAT TCTTTTTT                                                  1458
```

(2) INFORMATION FOR SEQ ID NO:1000:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 762 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

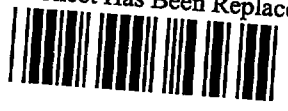
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000

```
GTTTACGCGG GGTTGGCTAT CGCTATAGGC ATGCTCATTG ACTCATCTGT GGTAGTGGTG      60
GAAAACGCTT TTGAAAAATT GAGCGCTAAC ACTAAAACCA CTAAACTCCA TGCAATCTAT     120
CGTTCATGCA AAGAAATCGC CGTTTCAGTG GTGAGCGGGG TGGTGATCAT TATTGTGTTT     180
TTTGTGCCGA TTCTAACCTT ACAGGGGTTA GAGGGCAAGA TGTTTAGGCC TTTAGCGCAA     240
AGCATTGTGT ATGCGCTTTT AGGCACTTTA GTTCTATCCA TCACTATCAT TCCTGTAGTG     300
AGCTCTCTTG TCTTAAAAGC CACGCCCCAT AGCGAAACCT TTTTAACGAG GTTTTTAAAC     360
AGAATCTACG CCCCTTTATT GGAATTTTTT GTGCATAACC CTAAAAAAGT GATTTTAGGA     420
GCGTTTGTTT TTTTAATCGC AAGCCTTTCT TTATTCCCTT TTGTGGGGAA GAATTTCATG     480
CCTGCTTTAG ATGAGGGCGA TGTGGTTTTG AGCGTGGAAA CCACCCCCTC TATTTCCTTA     540
GATCAATCTA AAGATCTCAT GTTAAACATT GAAAGCGCGA TTAAAAAGCA TGTCAAAGAA     600
GTTAAAAGCA TTGTCGCGCG CACAGGGAGC GATGAATTGG GGCTGGATTT AGGGGGTTTG     660
AATCAAACCG ATACTTTTAT TTCTTTCATC CCTAAAAAAG AATGGAGCGT TAAAACCAAA     720
GATGAATTGG TTAGAAAAAA TCATGGATTC TTTAAAAGAC TT                        762
```

(2) INFORMATION FOR SEQ ID NO:1001:

(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:1001

```
TGGTTGTTTC TAACATGCTA TGGTAGTGTG ATAAAGAAAG GCTATATAAG AGGAGATCTT      60
ATGCGTATAG TTAGAAATTT ATTTCTTGTA TCGTTTGTGG CGTATAGTAG TGCGTTCGCA     120
GCGGATTTAG AAACCGGAAC CAAAAACGAC AAAAAGAGCG GTAAAAAATT TTACAAACTC     180
CATAAAAACC ATGGCTCAGA AACCGAGACT AAAAACGATA AAAAGCTTTA TGATTTCACT     240
AAAAATAGCG GATTAGAAGG CGTGGATTTA GAAAAAAGCC CTAACCTTAA AAGCCATAAA     300
AAAAGCGATA AAAAGTTTTA TAAACAACTC GCTAAAAACA ATATCGCTGA AGGGGTGAGC     360
ATGCCGATTG TGAATTTCAA TAAAGCCCTA TCTTTTGGGC CTTATTTTGA AAGGACTAAA     420
AGCAAAAAAA CCCAATACAT GGACGGCGGG TTGATGATGC ACATCCGTTT T               471
```

(2) INFORMATION FOR SEQ ID NO:1002:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 675 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002

```
CCGAAAATTG CACCGCTTGC CATGGCATTA AATCCCAAAA CATTCCAGCC CCTATGGATA      60
GCCTTAGTGC GAGCAACTCT TTTGGGGTGG GGCCACCGGA ATTTAAGCCA TGTGGCGGGG     120
GTTTTGAACG CGAGTTTCTT AGCCCACTTC ATCAAAGACC CGGTGAAAAC GGCGAAATTG     180
AGCCATAAGT TCAACGATGA AAGGCCCTAT CCTATGCCGG CGTTTTCTCA ATTTAGCGAT     240
CAAGATTTGA GCGATATTGT GGCGTATCTC ACTTCTATTT TGCCTAAAAA TTTGAGCGAT     300
AAGGAAGTGT TCGCGCAAAG TTGTCAAAGG TGCCATAGCC TGGATTATGC TAAAGATAAG     360
GCCTTTAGCG ATCCTAAAGA TTTAGCCAAT TATTTAGGCT CTCATGCGCC TGATTTGTCC     420
ATGATGATTA GGGCTAAGGG CGAACATGGC TTGAATGTTT TCATCAACGA TCCGCAAAAG     480
CTTTTGCCTG GCACAGCCAT GCCTAGAGTG GGATTGAATG AAAAAGCTCA AAAACAAGTC     540
ATTTCTTATT TGGAAAAAGC GGGCGATAGG AAAAAGCATG AAAGGAATAC TTTAGGGATT     600
AAGATCATGA TTTTCTTTGC GGTGCTGTCG TTCTTGGCTT ACGACTGGAA AAGAAAAGTT     660
TGGAGCGAAG TGCAT                                                      675
```

(2) INFORMATION FOR SEQ ID NO:1003:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1143

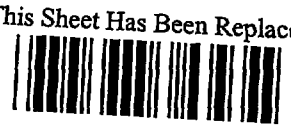
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003

```
ACTTGGCGGT ATCAACTAGG CTCATTAAAA GGCAAAATCC AAATGATTAA AAGCGTAGAG      60
ATTGAAAATT ACAAAAATTT TGAGCACCTT AAAATGGAAA ATTTTAAACT CATCAACTTT     120
TTTACCGGTC AAAACGATGC GGGTAAAACC AATCTTTTAG AAGCTCTTTA TACCAACACA     180
GGCCTTTGTG ATCCTACTGC CAATCAAGTC AGTCTTCCTC CTGAACATGC CGTGAATATT     240
AGTGAATTCA GAAAAATCAA ACTCGATGCC GACAACCTAA AAACCTTTTT TTATCAAGGA     300
AACACCGCTA ATCCCATTAG TATCCGCACT GAATTTGAAC ATGCTACTAT CCCTCTTACT     360
ATCCAATACC CCACACAAAC CAGTTACAGC AAAGACATCA ATTTGAATAG CGATGATGCT     420
CATATGACAA ACCTTATAAA CACAACAATA ACGAAGCCAC AGCTCCAATT TTCCTACAAT     480
CCATCCCTTT CCCCCATGAC AATGACTTAT GAATTTGAAA GGCAAAACCT AGGTTTAATC     540
CATTCTAATT TAGATAAAAT CGCTCAAACC TATAAAGAAA ATGCGATGTT TATTCCTATA     600
GAATTATCTA TTGTTAATTC TCTTAAAGCA TTGGAAAATT TACAATTAGC AAGCAAAGAA     660
AAAGAATTGA TTGAAATCCT ACAATGTTTC AACCCTAATA TTTTAAATGC TAATACAATA     720
AGAAAGTCTG TCTATATCCA AATCAAAGAT GAAAACACAC CGCTAGAAGA AAGTCCCAAA     780
AGGCTTTTAA ATTTGTTTGG TTGGGGTTTT ATCAAATTCT TTATTATGGT GAGCATTCTT     840
ATAGACAATC GTGTCAAGTA TCTTTTTATT GATGAAATAG AAAGCGGTTT GCACCATACA     900
AAAATGCAAG AGTTTTTAAA AGCTCTGTTT AAGTTAGCTC AAAAATTACA GATTCAAATT     960
TTTGCCACCA CGCACAATAA GGAATTTTTA TTAAACGCCA TCAACACGAT ATCCGATAAT    1020
GAAACGGGAG TTTTTAAAGA CATAGCCTTG TTTGAGCTTG AAAAAGAAAG CGCTTCTGGC    1080
TTTATCAGAC ACAGCTATTC TATGCTAGAA AAAGCGCTTT ATAGGGGTAT GGAGGTTAGA    1140
GGC                                                                  1143
```

(2) INFORMATION FOR SEQ ID NO:1004:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 852 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1004

```
ACCCATTGTT TATTCCTTGG TGGTAGTATC AAAATTTTGT TAATCCTTAA AGAGGGCATT      60
GATTTAAACC ATGGTTATTA CCAATTAGGA AAATACACCA TTAAAGACGA CTTTATCCCC     120
AGTAAAAAGG CCGTTGTGGA AGACGTTTTG ATCCAATCTA GCAATGTGGG CATGATAAAA     180
ATCAGTAAAA GCCTCAACCC AGAGGATTTC TATAACGGGC TTTTAGGCTA TGGATTTTCT     240
CAAAAAACCG GCATTGATTT ATCCTTAGAA GCCACAGGAA AGATCCCTCC TTTGTCCGCT     300
TTCAAGCGTG AAGTGTTAAA GGGGAGCGTC TCTTATGGCT ATGGGTTGAA TGCGACTTTT     360
TTGCAGCTTT TAAGGGCTTA TGCGGTGTTT TCTAATGAAG GCAAATTGAC TACCCCCTAT     420
TTAGTGCAAC GAGAAACCGC CCCTAATGGC GATATTTACA TCCCTAGCCC CAAACCCACC     480
TTTCAAGTCA TTAGCCCCAA AAGCGCTAGA AAAATGAAAG AAACCTTAAT TAAGGTGGTG     540
CGTTATGGCA CAGGCAAAAA CGCTCAATTT GAAGGGCTAT ACATAGGGGG CAAAACAGGC     600
ACGGCTAGGG TTGCTAAAAA CGGAAGCTAT AGCGCGGAGT CCTATAACAG CTCTTTTTTT     660
GGGTTCGCTG AAGATGAAAG GCAGGTTTTT ACTATCGGCG TGGTTATCTT AGGCTCGCAT     720
GGCAAGGAAG AGTATTACGC TAGCAAGATT GCAGCCCCCA TTTTTAAAGA AATCACCGAA     780
ATTTTAGTGC GTTACAATTA CCTATCGCCC TCTATTGCGA TTCAAAACGC TTTGGAAAAA     840
AACCGCTTAA AA                                                        852
```

(2) INFORMATION FOR SEQ ID NO:1005:

(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:1005

```
GATAAAAAAA TACTTTTAAT TATTCAAGGA AAATTTATGG AATTTCATCA AGTTTATGAC      60
CCATTAGGCC ATATTTGGCT GAGCGCTTTA GTCGCACTTT CGCCTATTGC GCTCTTTTTT     120
ATCTCTCTTA TTGTCTTTAA ACTTAAAGGG TATAGCGCTG GGTTTTTAAG CTTAGCGCTT     180
TCAATCCTTA TTGCGTTATT TGTGTATAAA ATGCCTGTTC AAATGGTGAG CGCGAGTTTT     240
TTCTATGGCT TTCTTTATGG CTTGTGGCCG ATCGCATGGA TTGTGATCGC TGCGATTTTT     300
CTTTACAACC TTTCAGTGAA GTCCGGGTAT TTTGAAATCT TAAAAGAAAG CGTTCAGTCC     360
ATCACTTTAG ATCACCGCAT TTTAGTGATT TTGATTGGCT TTTGTTTGGC TCATTTT        417
```

(2) INFORMATION FOR SEQ ID NO:1006:

(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

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006

```
CCTAAACCTA AAGGGGTTTG CCCTAAAAAT CTAATGAGTA AAAGAGCGAT CCGTTTCCCT      60
AACAAGCTTT TTTCATACCC TAAACCCAAA ATAAAAGCGA CAAACACAAG CCACACCGTT     120
TTATTCGCAT ACCCGCTCAA ACCCCACGAA ATGGCCTTAT TAGCGCTCGC TACCTCACTG     180
CTCGCTCCAA TTTTTAACGC TATACACAGC ACTAACGCGC TCAACGCTAT CAAACCTGAT     240
GGCACCGGCT CTAAAATTAA CCCTATAATC ATGCCCATGA AAATACAAAA A               291
```

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1596 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007

```
AGAAACGATT TTAAAGGTGT TAGAAAAATG GCATTAAGGG TATTATTATT CTTTTGTTTT      60
TTGTTTTTGC AAGCAGAAGA TAAGAGCCAA GAATTATCAT CTATACAAAA ACAAATGGCT     120
TTGGTGGATA AAAAACTCGC CAAAGACGAT AACGTGTGGT TGAAAAAATT TGAAAACTAT     180
AAAATTTACA ACCAAATTTA TACTGAAAAA GAGAGCGTGA GGCAGGAATT AAGGCGCTTA     240
AAAAACAAAA AAAGCAAGGA TTTATTAAAG ATTAGCACCT TAGAGCATAC CTTAAAGGCT     300
TTAGAGTCCC AGCAAAAAAT GTTTGAAAGC TATGGGGTCA ATCCTTTTAA GGACTTGATA     360
GAGCGCCCCA ATATCCCCAA TATCCCTAAT ATCGCTAACC CTATTGCGAT CATTGATGGC     420
ATTTCTTTCA TCAAGAGCAT GCGTTTAAAG CATGAAAATC TTAAAAATAA CCAGACTTCT     480
TTAGGAGAAG TTTTAAAGCT TTTAGATCAA AAACACCAGC TTTTAAATCA GTGGCACGCT     540
TTGGATAAAA GCGCGAAATT AAGCGATGAG ATTTATCAAA CTCAAGCCAA ACGCTTAGAA     600
TTGCAAGGGG CTCAAAACAT TCTAAAAACC ACGATCGGGA TTTTCCAAAA AGACAGCGAT     660
GAAGCTATAA GCATTGTCAA ATCTCAAGTT AAAAACCAGC TTTTTAAATT GGTTTATGTG     720
TTTTTAGCGG CCCTTTTGAG CGTGGTGTTT GCGTGGATTT TAAAAATCAT TTCCAGTAAA     780
TACATTGAAA ATAATGAGCG CGTCTATACC GTGAATAAAG CCATTAACTT CGTGAATGTG     840
AGCGTGATCG TTTTAATCTT TCTTTTTTCT TATTTAGAAA ACGTTACTTA CTTGGTAACG     900
GTTTTAGGCT TTGCGAGCGC GGGCTTAGCG ATTGCGATGA AGGATTTATT CATGAGCTTG     960
CTCGGGTGGT TTATCATTTT GATTGGGGGG AGCGTGCATG TGGGCGATAG GGTGCGTATC    1020
GCTAAGGGGA CGGATATTTT TATTGGCGAT GTGTTGGATA TTTCTATGTT GCACATTACG    1080
ATTTTAGAAG ACGTAACCTT TACCACTTAC ACGAATAACA GGAGAGCGGG CCGAATTATC    1140
TTTGTGCCTA ACAATTACAT TTTCACCACC ATGTTCGCTA ATTACAGCCA TTTTGGGATG    1200
AAAACGGTTT GGGATGGCGT GGATTTTTGC GTTACATTTG ATTCTGATTT TAAAAAAGCG    1260
TCTAAAATTG CGCTCAATAT CGCTACGGAA TTGTCTAAAG AATACACGGA TATTACCTAT    1320
AAACAGCTCA ATAAAATGCG CGACCGGTAT TCTTTAAGGA GTTTGAGCGT CAAGCCTCGA    1380
TGCTTTTTGA TGCCTGAAAA TAACGGGATA AAAATCTCGG TGTGGTATCA AACCAATTCG    1440
TATGCCACCA TGTCTTTAAG GAGCAAGATT GTGGCTGAAA TTGTTGAAGC CTTTTTGAAA    1500
```

GAAGAAAATA TCCATATCGC TTATACGACC AGCAAGCTGC TTAAAGTGGA TGCTGATGCT 1560
CTAGGCGATG GTTTTGGGAA TAAAAGGGAA CAAAAA 1596

(2) INFORMATION FOR SEQ ID NO:1008:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1041 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008

CGGAGTGAAA GAATGCAAGA AATCTTAATC CCTTTAAAAG AAAAAAGCTA TAAAGTGTTT 60
TTGGGGGAAC TGCCTGAAAT AAAATTGAAA CAAAAAGCGC TCATCATTAG CGATAGCATC 120
GTGGCCGGGT TGCATTTGCC CTATTTGTTA GAGCGCTTGA ACGCCTTAGA AGTCAGAGTG 180
TGCGTGATAG AGTCCGGGGA AAAATACAAA AATTTTCATT CATTAGAGCG GATTTTAAAC 240
AACGCCTTTG AAATGCAATT AAACCGCCAT TCTTTAATGA TAGCCCTTGG TGGGGGAGTG 300
ATAAGCGATA TGGTGGGGTT TGCGAGCAGT ATTTATTTCA GGGGGATTGA TTTTATTAAT 360
ATCCCTACGA CTTTACTCGC TCAAGTGGAT GCGAGCGTGG GGGGGAAAAC AGGGATCAAC 420
ACGCCTTATG GCAAGAACCT AATCGGATCG TTCCACCAGC CTAAAGCGGT TTATATGGAT 480
TTAGCTTTTT TAAAAACCCT TGAAAAAAGG GAATTTCAAG CGGGGGTTGC TGAAATCATT 540
AAAATGGCGG TGTGTTTTGA TAAAAACTTG GTAGAAAGAT TAGAAACAAA GGATTTAAAA 600
GATTGTTTAG AAGAAGTAAT CTTTCAAAGC GTCAATATCA AAGCTCAAGT CGTTGTTCAA 660
GATGAAAAAG AGCGAAACAT CAGGGCTGGG TTGAACTATG GGCATACCTT TGGCATGCTG 720
ATAGAAAACG AGACCAATTA CGAGCGATTT TTGCATGGCG AAGCGATCGC TATTGGCATG 780
CGCATGGCTA ATGATTTAGC CCTTTCTTTA GGCATGCTCA CTTTAAAAGA ATACGAACGC 840
ATAGAAAATT TATTGAAAAA ATTTGATCTG ATATTCAATT ACCAAATCAC TGATATTCAA 900
AAATTTTACG AACGCTTGTT TTTAGACAAA AAAAGCGAGA ACCAAACCCT AAAATTCATT 960
TTGCCTAAAG GTGTTGGAGC GTTTGAGATT GCCTCTCATA TCCCTAAAGA AACGATTTTA 1020
AAGGTGTTAG AAAAATGGCA T 1041

(2) INFORMATION FOR SEQ ID NO:1009:

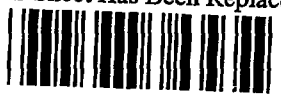
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 588 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

his Sheet Has Been Replaced Th



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009

```
AAATCAAAGA GTATGAAATT AAGGAGAGGG AAAATCATGC CGTTTTCTAA ATTTTTAGAA      60
AACCTCACCG CTCCCTTTAA ACGCATCAAA AACCGCTCGC TTGTTTTGGC GTTAGGGTTT     120
TTGATCCTTA CTTTTTGCTT GTTGCTTTTT TTAATCTTAA GCGATGTTTC TAGGCTCATA     180
TCCAGTAAGG ATTTTCTTTA TGTGATCCAG TCTCACCCTA AACAAACTCT AATTGAAGAT     240
GAAAATTATT TTTATGCTAA CAAGGGTCTT TATAAAACCA ACAAAGAAGC CTTTTTAAGG     300
GTTTATAAAA TCCCAGAGAG CATGCCCATA GAAAAACGAG AAAGTTTAAG CAAGGTTTCT     360
AAAATCTTTT TAGCGTTGCT TTTTTTCATT TCTAGCATGC TTTTTGGGAT CTTTTGGCGT     420
TTGCCCAAAC GATTGGACAC TAAAATGAGT TTAGAGAGCG CGCACAAAAA CGAATTAGAA     480
AATGCATTCC AACGATACGA TGCGCTAGGG GTGCGTTTTG AAGACATTGC AGGGGTGAAT     540
GAAGTCAAAG AAGAATTACT AGAAGTGATA GATTATTTAA AAAAACCC                  588
```

(2) INFORMATION FOR SEQ ID NO:1010:

(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:1010

```
ATGAAACCAT TGCATTTTTC ACACCTGGAC AGAGAGCAAT CAGGCGATGT GGGTTTTATC      60
ATTAAAAACC TTATTTTTTT AGGGGTTTTT TCCTTATTGG GTTGGTTGAA TACCGAGTAT     120
TTTCTATGGC CTAGCATGCT GGAATTAAAA AAAATCCTTT TAGAAGAAAA TCGTAAAAAA     180
AGCGTTTTAG AATACGCGCA AAGGCATTTT GAAACAGCCC TAGCAAACTA CCGCAATCAA     240
AAAGAAACCA GCGAATCTTT GTTAAAGATT TTTAATGATG AAGAGTCCAG GCGGATTTTA     300
GAAAAGATCT TAAAAAAATG TTTTGACGCC TATAAAATCA AACCCTTGCT CTCTCAAAAC     360
CCCTCCCAAA AAACCCAATT TTTTATCATG GCTAGAGCGA GCGAATTGGA AAAAACTTAT     420
CTTTTTTTCA CCTTAATCAA CAAGTATTTA CCGAGCGCTC AAAGCCAATT GCCCTTAAAG     480
ATTTCTAAAG ATAGCGACGG GTTGTTGGTG CAATTTGGCG TGAGTATTGA TCTCCAA        537
```

(2) INFORMATION FOR SEQ ID NO:1011:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1356 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

his Sheet Has Been Replaced TI



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011

```
TTTAAAAGGT ATTTTATAAC GATGAAAATT TTTGGGACTG ATGGCGTGAG GGGTAAAGCA      60
GGGGTGAAAC TCACCCCCAT GTTTGTGATG CGTTTAGGCA TTGCTGCCGG ATTGTATTTT     120
AAAAAACATT CTCAAACGAA TAAAATTCTA ATCGGTAAAG ACACCAGAAA GAGCGGCTAT     180
ATGGTAGAAA ACGCTTTAGT GAGCGCTCTC ACTTCCATAG GCTATAATGT GATCCAAATA     240
GGGCCTATGC CTACCCCTGC GATCGCTTTT TTAACCGAAG ACATGCGCTG TGATGCGGGC     300
ATTATGATAA GCGCGAGCCA CAACCCTTTT GAAGACAATG GCATCAAGTT TTTCAATTCC     360
TATGGTTATA AACTCAAAGA AGAAGAAGAA AGAGCGATTG AAGAAATCTT TCATGATGAA     420
GAATTACTGC ATTCTAGCTA TAAAGTGGGC GAGAGCGTCG GTAGCGCTAA AAGGATAGAC     480
GATGTGATAG GGCGCTATAT CGCGCATTTG AAGCACTCTT TCCCCAAACA TTTGAATTTA     540
CAAAAATTAA GGATCGTGCT AGATACGGCT AATGGCGCGG CTTATAAGGT GGCTCCGGTC     600
GTTTTTAGCG AGCTTGGGGC TGATGTTTTA GTGATCAATG ATGAGCCTAA TGGGTGTAAC     660
ATTAATGAGC AATGCGGGGC TTTACACCCT AACCAATTGA GCCAGGAAGT GAAAAAATAC     720
CGTGCGGATA TAGGCTTTGC TTTTGATGGC GATGCCGATA GGCTAGTGGT GGCGGATAAT     780
TTAGGGAATA TCGTGCATGG GGATAAGCTT TTAGGGGTGT TAGGGGTTTA TCAAAAATCT     840
AAAAACGCCC TTTCTTCTCA AGCGGTTGTC GCTACGAGCA TGAGCAATTT AGCCCTTAAA     900
GAATACCTGA AATCCCAAGA TTTAGAATTG AAGCATTGCG CGATTGGGGA TAAGTTTGTG     960
AGCGAATGCA TGCGATTGAA TAAAGCCAAT TTTGGGGGCG AGCAAAGCGG GCATATCATT    1020
TTTAGCGATT ACGCTAAAAC GGGCGATGGT TTGGTGTGCG CTTTGCAAGT GAGCGCGTTA    1080
GTGTTAGAAA GCAAGCTTGT AAGCTCTATT GCGTTAAACC CCTTTGAACT ATACCCCCAA    1140
AGCCTAGTGA ATTTGAATAT CCAAAAAAAG CCCCCTTTAG AAAGCCTGAA AGGTTATAGC    1200
GCTCTTTTAA AAGAATTAGA CCAACTAGAG ATCCGCCATT TGATCCGTTA TAGCGGCACT    1260
GAAAACAAAT TACGAATCCT TTTAGAAGCT AAAGACGAAA AACTTTTAGA ATCCAAAATG    1320
CAAGAATTAA AAGAATTTTT TGAAGGGCAG TTGTGC                              1356
```

(2) INFORMATION FOR SEQ ID NO:1012:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

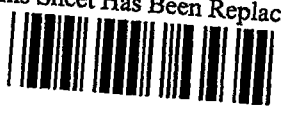
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced T



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012

```
AATCATCAGC GAATACGAAG CCGCCAACAA TTTAGAAAGC CGTTTGATCC CTTTAGAAGA      60
GCAAGCGAGT TAAAAGTGCG ATCTTGCAAA CAGATTTTTG ATAAGGGTTT AAAGCCCTAT     120
TATAAACATT CTGTTTGCTT AAAGCCTTTT TTTAGGTTTT GTTTTCTCAA AATTCATGCT     180
TATCAACAGC GTTATAGAGC GTTTGCTCTA ACGCTCTTTT CTTGTAAGTT TTTTAACGCT     240
TGTAAGATTT TTATTCCCAT AATTGATTTT AAAATCGTTT TTATCCCTAT TCTAAAACAC     300
CAAGCCAAGC TAAAAAGAGT CTCTAATGCC TAT                                  333
```

(2) INFORMATION FOR SEQ ID NO:1013:

(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:1013

```
AAGCGCATGA AAGAATCTTT TTACATAGAG GGAATGACTT GCACGGCGTG TTCTAGCGGG      60
ATTGAACGCT CTTTAGGACG TAAAAGTTTT GTGAAAAAAA TAGAAGTGAG CCTTTTAAAT     120
AAGAGCGCTA ACATTGAATT TAACGAAAAT GAAACCAATT TAGACGAAAT TTTTAAACTC     180
ATTGAAAAAC TGGGTTATAG CCCTAAAAAA ACTCTAGCAG AAGAAAAAAA AGAATTTTTT     240
AGCCCTAATG TTAAATTAGC GTTGGCGGTT ATTTTCACGC TTTTTGTGGT GTATCTTTCT     300
ATGGGGGCGA TGCTTAGCCC TAGCCTTTTA CCTGAAAGCT TGCTTACGAT TAACCATCAT     360
AGTAATTTTT TAAACGCTTG CTTACAGCTT ATAGGCGCGC TCATTGTCAT GCATTTGGGG     420
AGGGATTTTT ACATTCAAGG GTTTAAAGCC TTATGGCACA GACAACCCAA CATGAGCAGC     480
CTTATCGCCA TAGGCACAAG TGCTGCCTTA ATTTCAGCCT GTGGCAATTG TATTTGGTTT     540
ATACCAATCA TTATACCGAT CAGTGGTCTT ATGGGCATTA TTATTTTGAA AGCGTGTGCG     600
```

(2) INFORMATION FOR SEQ ID NO:1014:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 723 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

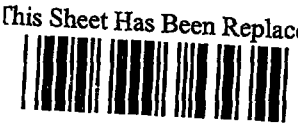
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014

```
AAAGAGTCTC TAATGCCTAT TAACCCTCTC TATCTTTTCC CCAATCTTTT TACCGCTAGC      60
AGTATTTTTT TAGGCATGAT GAGTATTTTT TACGCTTCCA GTTACCAATT TGTCATGGCG     120
TGTTGGTTAG TGGTGGCGAG TCTTATTTTA GATGGGCTTG ATGGGCGTGT CGCAAGGCTT     180
ACCAACACCA CTAGCAAGTT TGGTATTGAA TTTGACTCTT TAGCTGATGT GGTCGCTTTT     240
GGAGTCGCCC CAAGCCTTAT TACTTACTTT TATGTGGGGT ATAACTTTGG GCGTATAGGC     300
ATGGCGGTGA GCGCGTTGTT TGTGATTTTT GGAGCGATAC GATTAGCGCG ATTCAATATC     360
AGCACCAACA CAAGCGATCC CTATTCTTTC ATCGGTATCC CCATTCCTGC GGCGGCGGTA     420
```

```
TTGGTGGTGC TTTGCGTGTT ATTAGATAAT AAATACCATT TCTTAGAAGG CAATACCGAA     480
AAGTTATTTT TAGGCTTTAT TGTCTTATTA GGGGTGCTTA TGGTGAGCAA TATCCGCTAC     540
CCTAATTTTA AAAAAGTCAA GTGGAATCTC AAGCTTTTCA TCTTAGTGTT GATCTTTTTA     600
TCGTTAGTGT TTGTGCGCCC TTTAGAGGCT TTGAGCGTGT TTATGGGGTT GTATTTGATC     660
TATGGCATCA TTCGGTGGAT CTTTTTAATG GTAAAAATTA CTTTTAATAA AAATAAAAGC     720
GCA                                                                  723
```

(2) INFORMATION FOR SEQ ID NO:1015:

(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:1015

```
TATTTGCCCG CAAGCGAAAA CGCCCCCTTG CCCTCTAGTG TTTTTAGTTC AATCGTGGCT      60
TTGAGCTTGA AAATAGACAG CCTGTTTTCT CTTTTTAGCG TGGGTAAAAT CCCTAGCGGA     120
TCTAAAGATC CCTTTGCGTT AAGGCGTTTG AGTTTTGGGC TATTGAAAAT CATCGCGCAT     180
TACGGGTTAG AATTTGATTT GAAAGCGGAT TTAAAAAACC TCTTTGAAAA AGTGGGCGTT     240
TATCAAAGCT TTGATTTAGA GGTTTTAGAA AAGTTTTTAC TGGAGCGCTT TCATAATTTA     300
ATAGATTGTA ACCTCTCTAT TATAAGAAGT GTGTTAAACA CCAACGAGCG AGACATTGTT     360
AAAATCATTC AAAAAGTCAA AGCCTTAAAA CGCTTTTTAG ACAATCCTAA GAACGCTCAA     420
AAAAAAGAGT TGCTTTTTAG CGCTTTCAAA CGATTAGCTA ATATCAATAA AGACAGAAAC     480
CCTAACGAAT CAAGCGGGTT TTCTACGAGT CTTTTCAAAG AATTACAAGA GCATGCCCTT     540
TTTGAAGCGT TCAACGCGAT CAAAACAAGC ACTTTTGAGA GTTTGGATAG CAAAATAGAG     600
GCTTATTTTG GTTTGCATGC GCCTTTAGAA GAATATTTTA AAAGCGTGCT AGTCATGGAT     660
AAAGATATAG AAATCCAAAA AATCGTAAA AATTTCTTGT GGGGCGTGTA TCAAAGTTTC     720
TTAGAGATTG GGGATATTAA AGAAATTGCG ATT                                  753
```

(2) INFORMATION FOR SEQ ID NO:1016:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1782 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature

(B) LOCATION 1...1782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016

```
GTGGTCTTTA AAATTTTAAG TTTATGGTTA GGGGTGTTTT GTTTCCTTAG GGCTACGCAT      60
TTATACTTAG GCGAAGAACC CAAATATAAA GACAATTTCA CGCATTTTGA ATACGCTAAC     120
CCTAACGCTA GAAAAGGCGG TGTTTTGAGA AATGACGCTA TAGGGACTTT TGATAGCCTT     180
AACCCTTTTG CGCTTAAAGG CACTAAAGCC GAAGGCTTGG ATCTCATTTA TGACACTTTA     240
ATGGTGCAAA GCTTAGACGA ACCTTTTGCA GAATACCCCT TAATCGCTAA AGACGCCGAA     300
GTGGCTAAGG ATAACAGCTA TGTGATTTTT ACCCTAGATA AAAGAGCGAG ATTCAGCAAT     360
AACGCTCCCA TTTTAGCGAG CGATGTGAAG TTTAGCTTTG ATACGATAAT GAAATTAGGA     420
TCGCCCCTTT ATAGGCAGTA TTACCAAGAT GTTAAAAAGG CGGTTATCTT AGACAAGCAC     480
CATGTTAAAT TCATTTTCAA AACCACTGAA AATAAAGAAT TGCCCCTCAT TTTAGGGCAG     540
TTGCAGATCT TTTCCAAAAA AGCGTTTCAA AAGGATTATT TTGAAAAAAA CCCTTTACTC     600
ATTCCTGTTT CTAGTGGCCC TTATGTGATC GCTTCTTTTG ATGTGGGCAA GAAAATCACC     660
TACCAAAGAA ACCCTAACTA TTGGGCGAAA AATTTGCCTA GCAGAAAGGG GCAATTCAAT     720
TTTGATCAAA TCAAATTTGA GTATTACAAA GATGAAACCG TCGCCTTACA GGCTTTTTTA     780
AGCGGGGCGT ATGATTGGCG CCTTGAAAGC ACGGCTAAGG TTTGGGCTAG GGGCTATGTG     840
GGGAAAGCTA TGGATAATAA AAAAATCACT AAATACCTCA TAGCCCACAA AATGCCAAGC     900
GGCATGCAAG GGTTTTTCTT CAACACGCGC CGAGAAATTT TCAAGGATAA AAGGGTGCGT     960
GAAGCCTTAT TTTATGCGTT TGATTTTGAA TGGGCGAATA AAAATTTGTT TTTTTCGCAA    1020
TACAAGCGCA CCACTAGTTT TTTCAGTAAC TCTATCTATG CGTCCCCTCC TCTCCCAAGC    1080
CCTGAAGAAA AAGCCCTGCT AGCCCCTTAT GAAAAGAGTT TGGATGAAAG GGTTTTTAAA    1140
GAGCCTTATA TCGTGCCTAG AACCGATGGG CCTGATGTTT TAGGCTATAA TTTGAGGGAA    1200
AATTTAAAAT ACGCCCAAAA GCTTTTAGAG AGCGCGGGCT TTTCCTACAA AAACATGCGT    1260
TTGGTGGATA AGAATAACAA GCCTTTCAGT TTCACTTTGC TTTTAAACAG CCCGGCATTT    1320
GAAAGACTGG CCCTAGCTTT TGCTAAAAAC TTAAGGGTGT TAGGGATTGA AATGAAAATC    1380
CAAAGAGTGG ATTTAAGCCA GTATGTCAAT CGGATCAAAA GCTATGATTT TGACATGATT    1440
GTAGGAGTGA TTGGCCAATC GTCTTTCCCA GGTAATGAGC AGCGCTTTTA TTTTGGCTCT    1500
TTGAGCGCGA AAGCCAAAGG CACAAGGAAT TATGCGCGAA TCTCTAGTAA AGCGGTAGAT    1560
GATTTGATTG AAAGAATCAT TCACGCTAAA GATTATAAGG AGCAATTGGC CGCCATTCAA    1620
GCGATGGATA GGGTGTTGTT GCGGGGGTTT TACGCGATAC CGCATTTTTA TTTGCCTAAT    1680
TACAGGATCG CAGCGTATAA TTACATTGGC ATGCCTGAAA TCAGCCCTAG CTATGGATTT    1740
TCGCCGTATT TATGGTGGAT AAAAAAAGAA AGGGGTCCTA AA                        1782
```

(2) INFORMATION FOR SEQ ID NO:1017:

(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:1017

```
TCTGTGATTG GTGTCTATAT CATTTCTTTA AAAGAAAGTC AAAGGCGTTT GGATACTGAA      60
AAACTCGTTT TAGAATCCAA TGAAAAATTT AAAGGCCGTT GCGTTTTCCA AATCTTTGAC     120
GCCATTAGCC CCAAACATCA AGATTTTGAA AAATTACTTC AAGAGCTTTA TAACGCTCAA     180
AGTTTATTGC AATCTGATTG GTATCATTCT TATGTTGGCG CTGGTTTGAC TTTGCCTGAA     240
TTGGGGTGTT ATTTAAGCCA TTATCTTTTA TGGAAAGAAT GCGTCAAATT AGATCAACCG     300
GTCGTTATTT TAGAAGATGA TGTAACGCTA GAGTCTCATT TCATGCAAGC CTTAGAAGAT     360
```

This Sheet Has Been Replaced

TGTTTGAAAA GCCCTTTTGA TTTTGTGAGA CTCTATGGGT GTTATTGGTA TTACCACGAG 420
ACAAAATTCC ATGTTTTGCC CAAAGAATTT GTATTTCCTC CCTTTGATCA TTCTTTTAAG 480
AATAACCCTA TTTTAGAAAA ATTTAAAAAA TTTTTTGATG TTTCTAGATT TTTAAATCTT 540
TCTACCCATA AAGTCATCCA CCTATATTCT CAAAAAAATA CAAAAAAGCT ATTACGCAAC 600
GCA 603

(2) INFORMATION FOR SEQ ID NO:1018:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1620 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018

TTTAGTGAGC GGGACTTTGA GCTTTTTAGG CAAAAAACAA ACCCCTATGA AAGATGTTCT 60
TGTGGATTTG GATTCTTGTC AGACGCTTCA AAAAGATCCC TTAATCCAAC CTTAATGATG 120
AATAATAATA ATACCCTACC CAAACCCCTA GAAGAAAGCC TAGATTTAAA AGAGTTTATC 180
GCTCTTTTTA AAACCTTTTT CGCAAAAGAA AGAGGTTCTA TTGCTTTAGA AAACGATCTC 240
AAACAGGCTT TCACTTATTT AAATGAAGTG GATGCGATCG GTTTGCCTGC CCCCAAAAGC 300
GTGAAAGAAA GCGATCTTAT TGTTGTCAAA CTCACCAAAT TAGGGACGCT CCATTTAGAT 360
GAAATCTATG AGATTGTCAA ACGATTGCGC TACATTGTCG TTTTACAAAA CGCCTTTAAA 420
CCTTTCACGC ATTTAAAATT TCATGAACGC CTTAACGCCA TTATTTTACC CCCTTTTTTT 480
AATGATTTGA TCCTTTTATT GGATGATGAA GGGCAAATCA AACAAGGGGC GAACGCTACC 540
CTAGACGCTT TGAATGAAAG CTTGAACCGC CTTAAAAAAG AGAGCACTAA AATCATTCAC 600
CATTACGCCC ACTCTAAAGA GCTTGCCCCT TATTTAGTGG ATACGCAAAG CCACCTTAAG 660
CATGGTTATG AATGCCTTTT ATTAAAAAGC GGGTTTTCTA GCGCGATCAA AGGCGTTGTG 720
CTAGAAAGGA GTGCTAATGG TTATTTCTAT CTTTTGCCTG AAAGCGCGCA AAAAATCGCC 780
CAAAAAATCG CGCAAATTGG TAATGAAATA GATTGCTGTA TCGTTGAAAT GTGCCAAACT 840
CTAAGCCGTA GCTTGCAAAA ACACCTTTTA TTTTTAAAAT TCCTTTTTAA AGAATTTGAT 900
TTTTTAGACA GCTTGCAAGC ACGGCTTAAT TTCGCTAAAG CCTACAATTT AGAATTTGTC 960
ATGCCAAGCT TTACGCAAAA AAAAATGATT TTAGAAAACT TTTCGCACCC CATTTTAAAA 1020
GAGCCAAAGC CCTTAAATTT GAAGTTTGAA AAATCCATGC TCGCTGTTAC CGGCGTGAAT 1080
GCGGGCGGGA AAACCATGCT CTTAAAATCG CTTTTAAGCG CAGCTTTTTT GAGCAAGCAT 1140
CTCATTCCTA TGAAAATCAA CGCCCATCAT TCTACTATCC CCTATTTTAG AGAAATCCAC 1200
GCCATTATTA ATGACCCCCA AAACAGCGCG AACAATATCT CTACTTTTGC AGGCAGAATG 1260
AAGCAATTTA GCGCTCTTTT ATCCAAAGAA AACATGCTCT TAGGCGTTGA TGAAATTGAG 1320
CTAGGGACTG ACGCTGATGA AGCGAGCAGT TTGTATAAAA CCCTGTTAGA AAAATTGCTT 1380
AAGCAAAACA ACCAAATCGT TATCACCACG CACCACAAAC GCCTGAGCGT GTTAATGGCA 1440
GAAAACAAGG AAGTGGAATT ACTGGCCGCT CTTTATGACG AGGAAAAAGA ACGGCCCACT 1500
TACACTTTTT TAAAAGGGGT TATTGGCAAA AGCTATGCGT TTGAAACCGC TTTGCGCTAT 1560
GGCGTGCCGC CTTTTTTGAT TGAAAAGCGA AAGCCTTCTA TGGCGAAGAT AAGGAAAAAT 1620

(2) INFORMATION FOR SEQ ID NO:1019:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019

```
AAGCTTACCG AGAAAATTAT GCTTGAAACC CCAAAAGTTT TACTCAAAAA CCTGCAAGAT      60
TGCAAGATCC ATTTCATCGG TATAGGGGGG ATTGGCATTT CAGGCTTAGC CAAATACCTT     120
AAAGCGCAAG GGGCTAAGAT CAGCGGATCT GATATTGCCA TAAGCCCTAG CGTTAAGTAT     180
TTGAAAGCTT TAGGCGTAGA AATTAATATC CCGCATGATC CAAAAGCGAT CAACCATCAA     240
GATGTCATCA TCCATTCAGC CATTATCAAA GAAGACAATA CCGAAATACA AAGGGCTAAG     300
GAATTAGAAA TCCCTATTTT GTCTCGTAAA GACGCTTTGT ATTCTATCCT TAAAGACAAG     360
CGCGTTTTTA GCGTGTGTGG GGCTCATGGA AAGAGCAGTA TCACGGCCAT GTTGAGCGCG     420
ATTTGCCCCG CTTTTGGAGC GATTATTGGG GCGCATTCTA AAGAGTTTGA TTCCAATGTG     480
CGAGAGAGCG CGGATATGAG TTTGGTTTTT GAAGCCGATG AAAGCGATTC AAGTTTTTTA     540
TTTTCCAACC CTTTTTGCGC GATTGTGCCT AACACGGAGC CAGAACATTT GGAGCATTAT     600
GACCACGATT TAGAACGCTT TTTCTTCGCT TATAAATATT TTTTAGACCA TGCTCAAAAA     660
AGAGTGATCT ATAAAGAAGA TCCTTTTTTA AAAAACTATT CTAAAGACGC CATTGTTTTA     720
GAAAAAAAAG ACATTTATAA TATCCAATAC ATTTTAAAAG ACGGAGAGCC TTACACTTCG     780
TTTGAATTGA AAAATTTGGG GGCTTTTTTG GTGTGGGGGT TAGGCGAACA TAACGCCACG     840
AATGCGAGTT TGGCGATTTT AAGCGCTTTA GATGAATTAA ATTTAGAAGA AATTAGAAAT     900
AATTTATTGA ATTTTAAAGG CATTAAAAAA CGCTTTGATA TTTTGCAAAA AAACGATCTC     960
ATTCTCATTG ATGATTACGC CCACCACCCT ACTGAAATTG GCACCACTTT AAAAAGCGCT    1020
AGGATTTATG CCAATTTATT GAATACGCAA GAAAAAATTA TAGTGATCTG GCAAGCGCAC    1080
AAATACTCTC GCTTAATGGA CAATTTAGAA GAATTTAAAA AATGTTTTTT AGAGCATTGC    1140
GACAGGTTGA TCATTTTACC CGTTTATAGC GCGAGTGAAG TTAAAAGAGA CATTGATTTG    1200
AAAGCCCATT TTAAGCATTA TAACCCCACC TTTATAGACA GGGTGCGTAA AAAGGGGGAT    1260
TTTTTAGAGC TGTTAGTCAA TGATAATGTG GTAGAAACGA TTGAAAAAGG CTTTGTGATA    1320
GGCTTTGGAG CGGGGGATAT TACCTATCAG TTGAGAGGCG AAATG                    1365
```

(2) INFORMATION FOR SEQ ID NO:1020:

(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:1020

GCGGTAACCG CCATTTTAGG GTGGGACGAA GAGGGCAAGC TCAAGTTTGG GAAAATCAGG 60
CACAAATATT TAGAAACGAG CAACGTGAAT GCCGGGAACG CCCTAACCAA TCTCATTTTA 120
ATGCAAAGAG GCTATTCTAT GAACGCTAGA GCCTTTGGCG CGGGCGATGA CATGATCAAA 180
GAAGCCATTA GCTTGAAAAA A 201

(2) INFORMATION FOR SEQ ID NO:1021:

This Sheet Has Been Replaced

(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:1021

AAGCTACATC GTGGATCCCA AAAACAAAAC CCTATCAATG ATCCTACTTG GGAAATTGTC 60
GGCTTTGATT CAGCCACGCA CAAAATGAAA TCCGCCCCCA TGACTTTGGA TTTTAAGGGC 120
AATAAACTCA CCTATTCTTT GGATAAGAGC GAAAACATGA TTCTAACCAA ATTGTTCTAC 180
CAAGACTCTA AACTCTTAAA AACGAGTCAA GAACGCAAGC CTAGGGGCAT TTTTAGAGAC 240
ATGCGCATTG AAGAAAATGG CGTGATTTCT CTAGCCTTTA GTAACGGGGT GGTAGAGCCG 300
GTCGCTCGCA TCGGTATTTT AGCTTTCACT AACGATCAAG GCTTAAGGAA AATCGGCGGT 360
AACCTCTATG AAATGCAAGA AGGCACCATT AATGGCGAAA ACAGACCCCT AAGCGGTAAC 420
CGCCATTTTA GGGTGGGACG AAGAGGGCAA GCTCAAGTTT GGGAAAATCA GGCACAAATA 480
TTTAGAAACG AGCAACGTGA ATGCCGGGAA CGCCCTAACC AATCTCATTT TAATGCAAAG 540
AGGCTATTCT ATGAACGC 558

(2) INFORMATION FOR SEQ ID NO:1022:

(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:1022

TGGATGTTTG TAGTTAAAAT GGTGTTAGGG TTTTTGATCC TTTTAAGCCC TTTGTGCGCT 60

ACTGGATTGG ATATTTCACA AACAGACATT ATAGAGCGTT CTTTAAATTT CCTCTTGTTT 120
GTGGGGATTT TGTGGTATTT TTTGGCTAAA AGATTGCGTT CATTTTTGCA TTCCAAAAGC 180
CTTGAAATCT CCAAACGCTT AGAAGAGATT CAAGCCCAAC TTAAAGTGAG TAAAGAACAT 240
AAGAAAAAAC TCCTTAAAGA ATTAGAGCAA GCCAAAGAAA AAGCTGAATT GATTATTTCT 300
GATGCGAATA AAGAAGCCTA CACGATCACG CAAAAATACG AATTACAAAC CAAAATGGAT 360
GTGGAAAATT TGATCAAAAA TTCTAAGGCG TTGATGGATT TAGAAGTTAA AAAGATCAAA 420
AGAGAGTTGG TTGAAAGCGT TTTTAAAGAT CTAAGAGAGA GTAAAAAAGT GTCTTTCAAT 480
GCGCAAGATT GCGTGAATAT TTTGAAACAA AGGCTT 516

(2) INFORMATION FOR SEQ ID NO:1023:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 744 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023

ATGCAAAAAA GTATATTCAA AATAACTCTG TTGTTGGTTT TCCTCTTTTT AAGGAATGCT 60
GTTGGTTTAG ACGATAAAAA AGCAGCTCCT AAAAGCGTTC AAAATACCCC TAAAAATTTA 120
CCCCCTATCC AGTTAAGGCT CGATCAAGCC TATGAAGACC TTATCAAAAT GTTAGACAAT 180
ATGGGAAAAA GCACGCAGTA TGAGTTCCCT AAAATTAAAG AAATCCTAGA ACAAAGCGAA 240
GAGGAATGGC TAGGAGTCGC CCATGAAGAA TGTGTGGCGT TAGTCATGTT AATAAGCCCT 300
AAGGCTTCTA TTGAAAACAG CCCGATTTAT AAGAATTGCT ATGAAGCTTA TGTGAAACAA 360
AGAATCCATG ATTTATATGA TTTTTATATA GAGGGCAAAA AAGTGAAAAG AAAAATCAAG 420
AAAGCCCATG AGCATGAAAT GGCCCTCAAC AAATCCCAAC CCTTAAAAAA GGAACCGCCT 480
AAAAGCGAGA ATAAAAAGGG CTTAACAAAA CCTAGCTTGA AAGACGCAAA GATCCCTAAA 540
GGGTATTACT TGCAAATTGG GGCTTTTTTA AATTCGCCCA GTAAGGATTT TTTGCAAACG 600
CTCAAAACTT TCCCTCACCA AATGGAGGAA AAAGACTCCC TCACGCATTA TTTGATTGGC 660
CCTTATAAAA CCAAAGAAGA AGCCCTAAAA CAGCTTGAAA ATGCGGCTAA AAGCTTTAAA 720
AATAAGCCTG CGTTGGTAGA GAAG 744

(2) INFORMATION FOR SEQ ID NO:1024:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 681 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

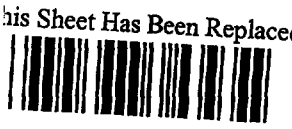
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

his Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024

```
AGTGGATGCT ATTTTGAATC CAACTCTGAT GTGTATGTGG TTATCATTGG CTTGGCCGAT      60
CAAAAAATTG GCGTGATCGT GGATTATTTG ATCGGTCAAG AAGAAGTGGT CATCAAGTCT     120
TTAGGTTATT ATCTTAAAAA CACTAGAGGC ATTGCTGGCG CTACGGTGAG GGGCGATGGG     180
AAAATCACTC TCATTGTAGA TGTGGGGGCG ATGATGGAAA TGGCAAAGAG CATTAAAGTC     240
AATATCACTA CCTTGATGAA CGAGTCAGAA AACACGAAAA GCAAAAATTC TCCTAGCGAT     300
TATGTTGTCT TGGCGATTGA TGACAGCAGC ACGGACAGAG CGATTATCCG CAAATGTTTA     360
AAACCATTAG GCATCACGCT CTTAGAGGCC ACTAACGGCT TAGAGGGCTT AGAAATGCTC     420
AAAAATGGCG ATAAGATTCC GGACGCTATT TTAGTGGATA TTGAGATGCC TAAAATGGAT     480
GGCTACACTT TCGCCTCTGA AGTGCGTAAA TACAATAAAT TCAAAAACCT GCCCTTGATC     540
GCCGTTACCA GTCGGGTAAC TAAAACGGAC AGAATGCGCG GCGTTGAATC CGGCATGACT     600
GAATACATCA CCAAACCTTA TAGCGGTGAA TATTTAACCA CCGTAGTGAA GCGCAGCATT     660
AAATTAGAAG GAGACCAATC G                                               681
```

(2) INFORMATION FOR SEQ ID NO:1025:

(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:1025

```
ATGACCCTTT CACAAGCCCT AAATAAAGCC AAAAAAGAAT TATCGCCAAA AGGCTTTAGG      60
GGGGGGTTAG AGTCTGAAAT TTTATTAGGC TTTGTCTTGC AAAAAGAAAG GGTTTTTTTG     120
CACACGCATG AGCATTTGGA ATTAAGCCAC GAAGAAGAAA CACGCTTTTT TGAATTGGTA     180
GGAAAGCGTT TGAATGACTG CCCCATAGAG TATTTATTAG GAAGCTGTGA TTTTTATGGG     240
CGCTCTTTTT TCGTGAATGA GCATGTTTTA ATCCCACGGC CTGAAACCGA GATTTTAGTC     300
CAAAAAGCCC TTAATATTAT TTCTCAATAC CATTTAAAAG AAATAGGCGA AATCGGCATA     360
GGGAGCGGAT GCGTGTCCGT GAGTTTGGCT TTAGAAAACC CTAATCTCTC TATTTATGCG     420
AGCGATATTT CACCAAAAGC TTTAGAAGTG GCGTTAAAAA ATATTGAACG CTTTTGTCTA     480
AAAGAGCGTG TTTTTTTAAA ACAAACGCGC CTTTGGGATC ATATGCCAAC GATAGAAATG     540
CTTGTCTCTA ACCCGCCCTA TATCGCTAGA AATTATCCTT TGGAAAAATC CGTTCTCAAA     600
GAACCGCACG AAGCCCTTTT TGGGGGGGTT AAAGGCGATG AAATCTTAAA AGAAATCGTT     660
TTTTTAGCCG CTAAATTAAA AATCCCTTTT TTGGTTTGTG AAATGGGGTA TGACCAGTTA     720
AAGAGCTTGA AAGAATGCTT GGAGTTTTGC GGTTATGATG CAGAGTTTTA CAAGGATTTG     780
AGCGGCTTTG ATAGAGGGTT TGTGGGCGTT TTAAAAAGTT TTTTAAGA                  828
```

(2) INFORMATION FOR SEQ ID NO:1026:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 564 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

This Sheet Has Been Replaced Th



(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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:1026

```
AAAGCCGTGT TGTTCAACCC ACTACCAACA AAAAGGTCCG TCATGCCCCA TTCTTTAAAA      60
AAGCGTTTTT TAATCGTTTA TACCCTTTCT ACCTTGCTTT TAGTGGGGGT TTTGTTAGCG     120
TTGTTTTTCT TTTATGCGAA AAATAACCTT TTGGAAAACA CCCAAATACG CATGCAATAC     180
ACCGCTGATG CGATCGCTAA AAGCCTTTTA GAATTAAATA ATGCCTCTTC TTTAGAGCCT     240
TTAAAAATCT TAGAAGAACG ATTCAAAAAC ACCCCCTTTG TTTTGTTGGA CGCAGACAAC     300
AGAGTCAAGT TTTCTAATAT CGGGGTGTTT GTGGCCTCTT TTAAAAATGA CGCCTTAATC     360
AAAACCCCTT ATTTTGCGCT TAAAAAACAG GGCTTTTACC TCACAGACAG CGCCCCAACT     420
AACCGCTTAG GGGTTTCTAA AATCATTATT GCAGAAGAAG AAATTCAAAA AATCTTTATC     480
CCCCTTTATA AAATGATAGG CTATGTGTTT TTGGGCGCGA GTTTGTTTGT CGCGCTAATA     540
GCCATGTGGC TTTATAAAAT CCCA                                            564
```

(2) INFORMATION FOR SEQ ID NO:1027:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

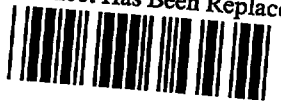
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027

```
AATATGCTTG ATATATGGAT AGATATGATA ATCTGTATTT TTTATTTGCT CTTTTTTACG      60
ACTCCTTACA TTGTAGGCGA TATTTTGCAA TTGAAATTTA TCCGTCAAAA ACTCTGCGAG     120
AAGCCTGTTT TACTCCCACA AAAGGATTAT GAAGAAGCGG GAAATTATGC TATTAGGAAA     180
ATGCAATTAT CCATTATTTC TCAAATTTTA GATGGGGTGA TCTTTGCTGG TTGGGTCTTT     240
TTTGGTTTGA CGCATTTAGA AGATCTCACG CATTATTTAA ACCTTCCTGA AACGCTAGGT     300
TACTTGGTGT TTGCCTTGTT GTTTTTAGCG ATTCAAAGCG TTTTAGCTTT ACCCATTAGC     360
TACTATACTA CCATGCATTT GGATAAGGAA TTTGGCTTTT CTAAGGTGAG TTTATCGTTG     420
TTTTTTAAGG ATTTTTTCAA AGGATTATTG CTCACTTTAG GCGTGGGGTT GTTGTTGATT     480
TACACTCTCA TAATGATCAT TGAACATGTG GAGCATTGGG AGATCAGCTC GTTTTTTGTC     540
GTGTTTGTTT TCATGATTTT GGCTAATCTT TTTTACCCTA AAATCGCCCA GCTTTTCAAC     600
CAATTCACCC CCTTGAATAA TAGGGATTTA GAAAGTCAAA TTGAGAGCAT GATGGATAAG     660
GTGGGTTTTA AATCTCAAGG CATCTTTGTG ATGGACGCTA GCAAGAGGGA TGGGCGTTTG     720
AACGCGTATT TTGGAGGCTT GGGTAAAAAC AAGCGGGTGG TGTTGTTTGA CACTTTGATC     780
```

```
TCTAAAGTTG GGACAGAAGG GCTTTTAGCC ATTTTAGGGC ATGAGTTAGG GCATTTTAAA     840
AATAAGGATT TGTTGAAAAA TTTAGGGATT ATGGGAGGCT TGCTCGCTCT TGTTTTTGCT     900
TTGATCGCTC ATTTGCCGCC GTTGGTTTTT GAAGGCTTTA ATGTCTCGCA AACGCCAGCG     960
AGTTTGATCA CGATTCTACT CTTGTTTTTG CCGGTGTTTT CCTTTTACGC CATGCCTTTG    1020
ATTGGGTTTT TTAGCCGCAA GAACGAATAC AATGCGGACA AGTTTGGGGC GAGTTTAAGC    1080
TCTAAAGAGA CTTTAGCCAA AGCGTTAGTG TCCATTGTGA ATGAAAATAA AGCGTTCCCC    1140
TATTCGCACC CTTTTTATGT TTTCTTGCAT TTCACGCACC CGCCGCTATT AGAACGCCTA    1200
AAAGCTTTGG ATTATGAAAT TGAA                                           1224
```

(2) INFORMATION FOR SEQ ID NO:1028:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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:1028

```
ATTAGAAGGA GACCAATCGT GAGCAATCAA TTAAAAGATT TATTTGAAAG ACAAAAAGAA      60
GCTAATGCAA GCTCTAAACA AGAAGACAAT GAAGAAATTT TGCAATTCAT TGGCTTTATT     120
ATTGGCGATG AAGAATACGC CATTCCCATT TTGAATATTT TAGAGATCGT CAAACCCATT     180
GGCTACACGC GAGTCCCTGA AACCCCAAAC TATGTGCTTG GCGTGTTCAA TTTAAGGGGC     240
AATGTCTTCC CTTTGATCAG TTTGCGTTTA AAGTTTGGCT TGAAAGCCGA AAAACAAAAC     300
AAAGACACTC GTTATTTGGT GGTACGCCAT AACGATCGAT CGCTGGGTTT TTCATCGCTT     360
TCTGGACTGA TGCCATCCGA ATCAGCATCC ACTATTGACC CGTCGCAGAA ACTGTGCGCG     420
ATAACAATAA TT                                                        432
```

(2) INFORMATION FOR SEQ ID NO:1029:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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:1029

This Sheet Has Been Replaced



```
TCGTTCTCTA TCAATAGTTT TAAAAAGGCA AAGGGAATGA AATCTACAAG AATTGGTTCT     60
AAAATTGTCA TGATGGTGTG TGCGGTTGTT ATTGTCATTA GCGCTGTTAT GGGCGTTATT    120
ATCAGCTACA AGGTTGAAAG CGTGTTGCAA AGCCAAGCCA CAGAATTGCT GCAAAAAAAA    180
GCTCAGTTAG TCAGTTTTAA AATTCAAGGC ATTATGAAGC GCATTTTTAT GGGCGCTAAC    240
ACCCTTGAAA GGTTTTTAAG CGATGAAAAT GGCGCTATTA ATGACACCCT AAAAAGACGC    300
ATGCTCTCTG AGTTTTTGTT AGCAAACCCT CATGTGTTAT TGGTTAGCGC GATTTATACG    360
AATAATAATG AACGAATGAT CACTGCAATG AACATGGATT CAAAAATCGC CTACCCTAAT    420
ACCGCACTCA ATGAAAACAT GACCAACCAA ATCCATTCGC TCAAAAGTAT AACCCGTTCA    480
GATCCCTATT ATAAAGAGGT TAATGGCGAT AAAATCTATG GCATGGACAT TACCCTCCCC    540
CTAATGGGCA AGAATCAAAA TGTTATAGGC GCGCTGAATT TCTTTTTAAA CATTGACGCT    600
TTTTATACTG ATGTGGTAGG CAAGAAAAAG AGCAACACCT TTTTAATGGG GAAAGACGGC    660
AGGATTTTAA TCAACCCTAA TCGTGAGATT CAAGATAAGA TTTTAAGCGC TATCAATCCG    720
GATAAAAGAG TCGCTAAAGC TGTGGAGTAT TACAATCAAA ACGAAGCGGG CACTTTGAGC    780
TACCATTCAT TGAGCGGGAA TACAGAAACC TTTTTAGCCA TACAGCCCTT TGATTTTTTT    840
GAAGAAAAAG GGAATAACGG CCAATCATTG GCGTTGGGCA ATTGGGAAAT ATGTCAA       897
```

(2) INFORMATION FOR SEQ ID NO:1030:

(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:1030

```
GGGGTATTTT ACAATAGCTC TCTCCCACAG CCCCCAACTA AAAACCCCCT AACCCGAGAA     60
TACCGCTTTT TAAAGAGATT ATCACTTATT TATGCAAGCT CTTTTATTGT ATTTATTTTA    120
AAAAATGCCC TTAAGCTTTT TTTAATTTTG TTACTCATGC TTAATAAGCC AAAGCCTTTA    180
TTTTTGCTCT TGGTTAAGCC TTTCTTCTAT CTTTTTGATT TGGTGGCTCA TTTGAGCACT    240
CGCATTGATT TGATTGATAA GCATGTAAAG GTTTATCATC ATCAAAAGCA CCACCACAAG    300
CCC                                                                  303
```

(2) INFORMATION FOR SEQ ID NO:1031:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced

(ii) MOLECULE TYPE: DNA (genomic)

(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:1031

```
TTTATCACTG GGATAGAAAT CCACCCGGGC GCTAAGATTG GGAGAGGGCT TTTTATTGAT      60
CATGGCATGG GTGTGGTGAT TGGCGAGACC ACAGAGATTG GAGATGATGT TACCATTTAT     120
CATGGCGTAA CTCTGGGGGG TACGGGCAAG TTTAAGGGCA AACGCCACCC TACTTTAGGC     180
AACCGAGTGG TAGTTGGGGC AGGGGCTAAG GTCTTGGGCG CGATTTGCGT GGGCGATGAT     240
GTGAGGATTG GGGCTAATGC GGTGGTGCTT TCAGATTTAC CCACGGGTTC TACGGCTGTA     300
GGTGCTAAAG CCAAAACCAT CACAAAGGAT CGT                                  333
```

(2) INFORMATION FOR SEQ ID NO:1032:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032

```
AAAGGTTTTT TAGGTGTTAA AAAAGTTATT GTTTTTATTA AAAAAAAGGG TGAGATGGTC      60
GTCAACTCCA AAGTGCAAAC GCTTAAAGTC TTTTCAAAAT TTTTCAGCAA TTTCAAAATC     120
ACTAAACTCA AAGACAACCA CGAAGAAGCC CACAAACTTT TTGGAGAAAA TAGCCGTAAA     180
GCCCATGACA CTGAGATCAT TTACTCCACT TTGCAAGTGG TCCCCAGGTA TTCAATAGAA     240
ACCGTGGGCT TTAGTTTGTT GATTTTAGCG GTCGCTTACA TCTTATTCAA ATACGGCGAA     300
GCTAGAATGG TACTCCCTAC CATTTCTATG TATGCCCTAG CGCTTTATCG CATACTCCCT     360
TCTGTAACTG GAGTGATCAG CTATTATAAT GAAATCGCTT ACAACCAGCT TGCAACCAAT     420
GTTGTTTTTA AAAGCCTTTC TAAGACCATC GTTGAAGAGG ATTTAGTCCC TTTAGACTTT     480
AATGAAAAAA TCACTCTCCA AAACATTTCA TTCGCTTATA AGTCAAAACA CCCGGTTTTA     540
AAAAATTTCA ACCTCACCAT TCAAAAAGGT CAAAAAATCG CTCTCATAGG CCATAGCGGG     600
TGCGGAAAAT CCACGCTGGC GGATATTATT ATGGGGCTTA CCTACCCTAA AAGTGGGGAA     660
ATTTTTATTG ATAACACCCT TTTAACCAGC GAAAACAGGC GCTCATGGCG TAAAAAAATA     720
GGCTATATCC CCCAAAATAT TTACCTTTTT GATGGCACTG TGGGGGATAA TATCGCTTTT     780
GGGAGTGCTA TAGATGAAAA ACGCTTGATT AAGGTGTGCA AAATGGCTCA TATCTATGAT     840
TTTTTATGCG AGCATGAGGG CCTTAAAACC CAAGTGGGCG AAGGGGGCGC TAAGCTTAGC     900
GGCGGTCAAA AACAGCGCAT AGGCATCGCA AGAGCCTTAT ACGATAACCC TGAAATTTTG     960
GTTTTAGATG AAGCCACTTC AGCCCTAGAC AATGAAACCG AGAGTAAAAT CATGGATGAA    1020
ATCTATCAAA TCGCTAAAAA TAAAACCCTA ATCGTTATCG CCCACCGCTT AAGCACGATT    1080
GAACGCTGTG AAGTCATCAT TGACATGAGC CAACACAAAG ACAATCTCGG C              1131
```

(2) INFORMATION FOR SEQ ID NO:1033:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 687 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

This Sheet Has Been Replaced



(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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:1033

```
GCCTATAAAA AGGGGAAAT CATGGCGCTT GAAGTGGTTT TATGGGATTT TGATGGCGTG      60
ATTTTTGACA GCATGCATTT AAAATATGAA GGGTTTAAGG CGTTGTTTCA AAAGCATGGC     120
AACGATAGTA AAGAGGGTTT GAAACAATTT GAAGTTTATC ACTATCAAAG TGGGGGGATT     180
TCAAGGAATG AAAAGATCCA ATATTTTTAT AACGAGATTT TAAAAACCCC TATCGCTCAA     240
GAAGAAATAG ATGCATTAGC CCTAGAGTTT GGCGCTATCA TAGAGCAAAA GCTTTTTGAT     300
AGGGGGCATT TGAATAGCGA AGTGATGGCG TTTATTGATA AGCATTATCA AAATTATATT     360
TTCCATATCG CTTCAGCGGC CTTGCATAGC GAATTGCAAG TGTTGTGCGA GTTTTTAGGG     420
ATTACTAAGT ATTTTAAGAG CGTTGAAGGG AGTCCGCCTG ATAAACCCAA GATTATCGCT     480
AATATCATTC AAAAATACGC CTATGACCCA AGCCGTATGC TAATGATAGG CGATAGCGTC     540
AATGATTATG AAAGCGCTAA GGCTAATAAA GTGGCGTTTT TGGGCTATAA CAGCAAGGTT     600
TTGAAAAATT TAGTGGGGCA AGATGGCTAT CAAGGGAAGT ATTTGGAGAG CTTTAAGGGG     660
TTTGATTTAC AAAACTTCGC AAAAGAG                                         687
```

(2) INFORMATION FOR SEQ ID NO:1034:

(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:1034

```
AATAAAAGCA TGCAGCATTT AGTCTTAATC GGTTTTATGG GGAGCGGTAA AAGCTCTCTA      60
GCACAAGAAT TGGGGCTGGC TTTGAAATTA GAAGTGCTGG ATACGGATAT GATCATTAGC     120
GAGAGGGTGG GCTTGAGCGT GAGAGGGATT TTTGAAGAGC TTGGCGAAGA CAATTTCAGG     180
ATGTTTGAAA AAAATTTGAT TGATGAATTA AAAACGCTCA AAACCCCCCA TATCATTTCT     240
ACCGGTGGGG GCATTGTGAT GCATGAAAAT CTTAAGGGTT TAGGCACAAC TTTTTACCTC     300
AAAATGGATT TTGAGACCTT GATTAAGCGT TTGAATCAAA AAGAAAGGGA AAAACGCCCC     360
CTTTTGAATA ACCTCACTCA AGCCAAAGAG CTTTTTGAAA AACGACAAGC CCTCTATGAA     420
AAAAACGCTT CCTTTATCAT TGATGCAAGG GGTGGTTTAA ATAATTCTTT AAAACAAGTG     480
CTACAATTCA TCGCA                                                     495
```

(2) INFORMATION FOR SEQ ID NO:1035:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 975 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1035

```
ATTTTTTTTA AAGGCCTTGT GATGTTAAGT AGAGACATTG TCCAATATTC CAAGATCCGC     60
ACCGAGTTAT ACGCCTACCT CACTTATTTG TTTTCGCACA ATATCCGCAA CCACCTTCCT    120
GAAATCACTT TGGATTATTT AAACAGGCAA ATCAGTAAGA TGCAAGCTGA AATCAAAATG    180
GCAAAAAGTT TTTTTGTTTT AGACGCTAAG GGCATGCTCA TGCTTAAGCC AAGCCAATTT    240
AAAGAGCAGG GGCATAAGGA AGGGCTATTA GAGCATGATT TAACAGAAGG GATTGAATTA    300
GAATCGCATG TCAGTTTTAG CGATAAGTAT TATTTTTATC AAGCCGTGAA TGAAAAGCGT    360
TGCATTTTAA CCGACCCCTA TCCTTCTAAA AAAGGGAACC ATTTGGTAGT GAGCGCGTCT    420
TACCCGGTGT ATGATCAAAA TAACGATCTA GCGTTTGTGG TGTGCTTGCA AATCCCTTTG    480
AGGGTGGCGA TTGAAATCAG CTCGCCTTCA AAGTATTTTA AAACTTTTAG CGAAGGGAGC    540
ATGGTCATGT ATTTTATGAT TTCTATCATG CTCACTTTAG TGTCGCTGCT TTTATTCGTG    600
AAATGCATTT CTAGCTTTTG GACAGCGATC GTGCATTTTA GCAGTTTTGA CATTAAAGAA    660
GTGTTCCACC CCATTGTGCT TTTAACCCTA GCTTTAGCCA CCTTTGATTT GGTCAAGGCG    720
ATTTTTGAAG AAGAAGTGTT GGGTAAAAAT AGCGGGGACA ACCACCATGC GATCCACCGC    780
ACCATGATCA GGTTTTTAGG CTCTATCATT ATCGCATTAG CCATTGAAGC GTTAATGCTC    840
GTGTTTAAAT TCAGCGTGAG CGAGCCGGAT AAAATCACTT ATGCGGTGTA TTTGGCTATC    900
GGCGTGGCGG TGCTTTTGAT CAGTTTGGCG ATTTATGTTA AATTCGCTTA TAGCGTGTTG    960
CCCAAACGAG AACGC                                                     975
```

(2) INFORMATION FOR SEQ ID NO:1036:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 592 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...592

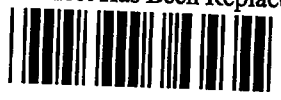
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036

```
GAGAGTTATC AAACGGTATT TACACGCCAG AGGTATTATC AGCGGTTGTT TAGACGAGCT      60
GTTTGTAGGA ACCTGCGCGT CTGTGAGTTC ACAAATCAAA ATAACAAGAG GGGTGATTGT     120
CAACGTCAGC AGTAGCTTTT CTATGGGGCT TACCATGGCG AGTGCTTATG ATCCCATTTC     180
AGGATCGCAA AAACCCATTG TGGGGCAAGC CCTTTTATTG TTAGCGATTT TAATTTTATT     240
GGATTTATCG TTCCACCATC AAATCATTTT ATTTGTGGAT CACAGCTTAA AAGCCGTCCC     300
TTTAGGGCGA TTTGTCTTTG AGCCAGAATT AGCTAAAAAC ATTGTCAAAG CCTTTTCACA     360
CTTGTTTGTC ATAGGGTTTT CTATGGCGTT CCCTATTTTA TGCTTGGTGT TATTGAGCGA     420
TATTATTTTT GGCATGATCA TGAAAACCCA CCCTCAATTC AACCTGCTCG CTATCGGGTT     480
TCCGGTTAAA ATTGCGATCG GGTTTGTGGG CATTATTTTA ATCGCTTCGG CTATCATGGG     540
GCGTTTTAAA GAAGAAATCA GCCTGGCCTT TAGCGTTATT AGTAAAATCT TT              592
```

(2) INFORMATION FOR SEQ ID NO:1037:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1332

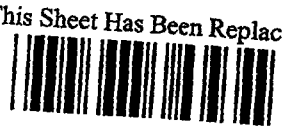
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037

```
GGGGTTTTGC GTTTCTCTAT CTTTTTTAAA GTTGTCGCTT TGTTTATGAT AACGCTCTTT      60
AGTTTTGGAG CGTTCGCTTA CTATTTCGTG TCTTCTCAAA TCAGTCACGA AAACTATCAA     120
AACGAAATGC GCCATTACCA GTTTGTTACC ACTATCAATG AAATTTTAAA TAACTACTCT     180
GATTATAGAG CCATAGAAGA TTACCTCTAT AAAATTGGCT TTAGAGAAAC CACAATAGAA     240
AATTTAGAAA AGGTTTTAGC CAAAAGACGC CACCAGTTGC ACCACAGAAA TATTTGGTAT     300
GCTGAAGTGT TTAAATTCAG CGATATGGTT TTTATCCTTT TAAAAAAGGA TGAGCATTTT     360
GTGCTTTATA AAGATTTGCA TTCGGTTTCT TATAGGAATT ATTTCTTAGC CATTACGGTG     420
GGTTTATTAT TGATTTTATT CCTCTTTTTA TTTGTTTTGC AGAGTTTATT GCCTTTAAGA     480
GAGTTAAGAT CTCAAGTGAA ACGCTTCGCT CAAGGGGATA AAAGCGTGAG TTGTAAAAGC     540
AAGCAAAAAG ATGAAATAGG GGATTTGGCT AACGAATTTG ACAATTGCAT CCAAAAAATC     600
AATGCGATGA ATGAATCTCG GGTTTTATTT TTGCGCTCTA TCATGCATGA ATTACGCACC     660
CCTATCACTA AGGGCAAGAT ACTAAGCTCT ATGCTCAAAG AAGAGCTGTC TTGCAAACGC     720
TTTTCATCTA TATTTGATCA CTTGAACATG TTGATTGAGC AATTTGCCCG CATTGAGCAG     780
CTCGCTTCCA AAAATTATGG GAGCAATAAA GAAAAATTTT TAATGAGCGA TTTGATAGAT     840
AAGATTGAAA AAATGCTTTT AATTGATGAA GATAAAAAAA GCCCTATCCA TGTATCCTCT     900
TCAAATTACA TCATTGAAGC GGATTTTGAA TTGTTTGCTA TAGCGTTAAA AAACATGATA     960
GACAATGCGA TCAAATACAG CGATGACAAA CAGGTGTTTT TGGATTTCAT AGGGAATAAT    1020
TTAGTGGTGT CCAATAAAAG CAAACCTTTA AAAGAAGATT TTGAAAAGTA TTTGCAACCC    1080
TACTTTAAAT CTTCTAACCC CAGCCAAGCC CATGGGTTTG GGTTAGGCAT GTATATCATT    1140
AAAAACGCTT TAGAGGCTAT GGGATTGAAT TTGAGCTATC ATTATAGCAA TGGAAGAATC    1200
TGTTTCACTA TCCATGATTG CGTTTTTAAT AGTTTTTACG ATTTAGAAGC GGATAATGAA    1260
GAGCTACCCC CCCCCCGAAA ATTTGAGAGA GGTGAAGGGA ATGAAGGGAA CAGAAAAAGC    1320
CAATTGTGGG GT                                                        1332
```

(2) INFORMATION FOR SEQ ID NO:1038:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 990 base pairs
(B) TYPE: nucleic acid

This Sheet Has Been Replaced



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

(ii) MOLECULE TYPE: DNA (genomic)

(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:1038

```
AGAAAAACAA AAAGAGAGAA CATGTTCAAA CGATTGAGAA GATTACGAAG CAGCGAAAAT      60
TTAAGAGCGA TGGTGAGAGA AACACGTTTA AATATTAATG ATTTCATCGC TCCCTTATTT     120
GTCATAGAAA GCGATAGCGG TATTAAAAAC GAAATCAGCT CCATGCCTGG CGTGTATCAA     180
ATGAGTATAG AGCCTCTTTT AAAAGAATGC GAAGAATTAG TGGGTTTAGG CATAAAAGCC     240
GTTTTATTGT TTGGCATTCC TAAACATAAG GACGCTACAG GAAGCCATGC GTTAAATAAG     300
GATCACATTG TCGCAAAAGC TACGAGAGAA ATTAAAAAAC GATTTAAGGA TTTGATCGTT     360
ATAGCGGATT TGTGTTTTTG CGAATACACC GACCATGGGC ATTGCGGGAT TTTAGAAAAC     420
GCTTCTGTGT CTAACGATAA AACGCTAAAG ATTTTAAATC TTCAAGGGCT TATTTTGGCT     480
GAAAGCGGTG TGGATATTCT AGCTCCAAGC AACATGATGG ATGGCAATGT TTTAAGCTTG     540
AGAAAAGCAC TGGATAAGGC CGGGTATTTT CACACGCCCA TCATGAGTTA TTCCACTAAA     600
TTTGCGAGCA GTTATTACGG GCCTTTTAGA GATGTAGCCA ATTCTCCGCC GAGTTTTGGC     660
GATCGCAAAA GCTATCAAAT GGATTACGCT AACCAAAAAG AAGCGCTTTT AGAAAGCTTG     720
GAAGATGAAA AACAGGGTGC GGATATTTTA ATGGTGAAGC CGGCTTTAGC GTATCTGGAT     780
ATTGTTAAAG AAATCAGAGA TCACACTTTG CTCCCTTTAG CGCTCTATAA TGTGAGTGGG     840
GAATACGCCA TGCTCAAACT CGCTCAAAAA CACAACCTGA TCAACTATGA AAGCGTTTTA     900
TTAGAAACGA TGACTTGTTT TAAAAGAGCG GGAGCGGATA TGATTATTAG CTATCATGCT     960
AAAGAAGTGG CTAACTTATT ACAAAGGAAT                                      990
```

(2) INFORMATION FOR SEQ ID NO:1039:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1086 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039

```
AGCGCAGGGC GCATTTTGGC AGAGGATATT ATTTGCGTTC ACGCTTTGCC TAAATTCAAT      60
CAAAGCGCTA TGGACGGCTA TGGGTTTAAA ATGCAAGACT TGGGCCAAAA AACTCAAGTT     120
ATCCAACACA TCTTTGCCGG GGATGATGTG AGCGCTTTAG AAGTCAAAGA AAATGAATGC     180
GTTAAAATCA TGACTGGAGC GATGGTGCCA AAGGGAATAG AAACGATCGT TCCCATAGAA     240
TGCATGCTAG AGAGTCATAA AGATTTCGCC CTAGCTCCTA AAGATTTTAA AATTCACGCT     300
```

AATATCCGTC AAAAGGGCGA GAACGCTTCT TTAAACAGCG TTTTAGTCCC TAAAAATACC 360
CGTTTGAATT ATGGCCATAT CGCGCTCATT GCCTCTCAAG GGTTCAAAGA AATCAAAGCG 420
TTTAGAAAAT TAAAAATCGC TCTCTTTAGT AGCGGCGATG AATTAGTGCC TTTAGGGCAA 480
AACGCCCTAG AGTGCCAGGT TTATGATGTT AATTCAGTGG GTGTTTTTAA CATGCTTAAA 540
AACTACAACA CGCATTTTCT AGGGGTTTTA AAAGATGATA AAAATTTACA GCTTAAAATA 600
CTTGAATTGC AAGGCTATGA TGTCATCCTT TCAAGTGCGG GGGTGAGCGT AGGGGATAAA 660
GACTTTTTTA AAGACGCTTT GAAAGAAAGA AACGCCCTTT TTTATTACGA AAAAGTCAAT 720
CTCAAACCTG GAAAGCCGGT AACTTTAGCC CAACTCAATC AAAGCATTAT TATAGGCTTA 780
CCGGGTAATC CTTTAAGTTG CTTACTGGTT TTACGAGTTT TGATTCTACC CTTATTGGAG 840
CGCTTATCCT TAAATAAAGA TTTTAAATTA AAACCCTTTA AGGCTCAAAT CAATGCCCCT 900
TTAAAGCTTA ATAACAAACG GACGCATTTA ATCTTAGGCA ACTATTCAAA CCACCAATTC 960
ATTCCTTACA ACAACCGCTA TGAATCAGGA GCGATTCAAG CCCTTGCGCA AGTGGATTCT 1020
ATCGCTTTAA TTGATGAAGG AGTGGGATTG GTTCAGGGCG AAATTGAAAT TTTAAGGTTT 1080
GAAAAT 1086

(2) INFORMATION FOR SEQ ID NO:1040:

(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:1040

GGGAATTACG GCCTAGAGAT TAGATTTAAG GAAATGGCAG TGTTAAAAAA GATGATAGGT 60
TTGGTGGCGG TTTTAAGCGT TTTATTAGCC AGAGACAACC CTTTTGAGCC TGAAATCAAT 120
TCCAAGAATT TGCAAGGGGG CTTTAGCGGG ATCTATGATG ACTACCTCAA AGAAATCCAT 180
GTGGATTTGC CCACGAGCGC TAGGATCTTA AAAAAAATCA CGCTCACTTA CCAAGATATT 240
GATGGCTCTA TCCATTCTAA AGTCGTGGGT ATTGATAAAA GCATTGATTG GCACTACCCC 300
TTAAAACTTT CCCAACACAC CCTTAATCAA GACGCCTTTG AAAAACGCTA CCAGATCCAA 360
GATTTTGATT TTTTAATGGC AAACAACACG ATGATTTTGC GTTCCCCTTA TAAAATTTTG 420
CGCTCTTTTG TGTTAGTCAA TCCTTATAGA ATCGTGTTAG ACACGCAAAA AGGCCCTTTG 480
GATATTTATC AAAACATGGA TTTAAACCAG AAGTTTTTTT CTCACATTAA AGTCGGCACG 540
CACAAAGATT ATTACCGCAT CACGCTCATT TTAGACGGGA AATACCGCTA TCTTTTGGAA 600
GAAAAAAACG GGGCGTATGA ATTAAAACTG AAA 633

(2) INFORMATION FOR SEQ ID NO:1041:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1056 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041

```
AAAGCAGTGG CTACGCCTCA CCACACCCCC TTATGGCTCA GCGTGTATGA AAGCTTTAAA      60
GAAGCCCTAG ACTTTAAGGA AGTCATTCTA GTTGTTAGCG AATTGGATTA TGTTTATATT     120
CAACGCCATT ACCCCAAAAT CAAGCTTGTA AAAGGCGGGG CATCAAGGCA AGAATCCGTG     180
CGTAACGCTT TGAAAGTAAT TGATAGCACT TACACGATCA CCAGCGATGT GGCTAGGGGT     240
TTAGCGAATA TGGAAGCGCT TAAAAGCTTG TTTTTAACCC TCCAACAAAC GAGCCATTAT     300
TGCATCGCCC CTTACTTGCC TTGCTATGAC ACAGCGATCT ATTATAACGA GGCTTTAGAT     360
AGAGAAGCGA TCAAACTCAT TCAAACCCCG CAATTAAGCC ACACCAAAAC GCTCCAATCA     420
GCCCTAAACC AAGGGGGTTT TAAAGATGAA AGCAGCGCGA TTTTACAAGC TTTCCCTAAC     480
TCTGTGAGCT ATATTGAAGG CAGTAAGGAT TTGCACAAAC TCACCACAAG CGGCGATTTA     540
AAGTTTTTTA CGCCTTTTTT TAACCCAGCA AAGGACACTT TTATAGGCAT GGGTTTTGAT     600
ACGCATGCGT TCATTAAAGA TAAGCCTATG GTTTTAGGGG GGGTTGTTTT GGATTGCGAG     660
TTTGGGTTAA AGGCTCATAG CGATGGCGAT GCTTTATTGC ATGCGGTTAT TGATGCGATT     720
TTAGGAGCGA TTAAAGGGGG GGATATTGGC GAATGGTTCC CTGATAATGA CCCCAAATAC     780
AAAAACGCCT CTTCTAAAGA GCTTTTAAAA ATCGTGTTGG ATTTTTCTCA AAGCATTGGG     840
TTTGAATTGC TTGAAATGGG AGCGACCATC TTTAGCGAAA TCCCTAAAAT CACTCCTTAC     900
AAACCGGCGA TTTTAGAGAA TTTGAGCCAA CTTTTGGGTT TAGAAAAATC TCAAATCAGC     960
TTGAAAGTCA CTACAATGGA AAAAATGGGG TTCATTGGCA AACAAGAAGG GCTGTTAGTC    1020
CAAGCGCATG TGAGCATGCG TTATAAACAA AAACTT                              1056
```

(2) INFORMATION FOR SEQ ID NO:1042:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 615 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042

```
TGCTTGGGGA TGTGTTTTAT TCTAAAGCCT TTTTTGAGTT GTCTAAAATG GGCGAATCCA      60
TCGCTCAAGC CCCTCTCTAA TGCGGTTTTA AGGCTCTCTA GGGGCGAGAT TGAAGACGTG     120
TTTGTGGGGG AATGTTTTAA TAGCGACAAA CAAAAATACT GGCGTATTTT AGAAGACAAG     180
ACCGCCCATT TCATAGAAGC GAGCTTAAAA AGCATGGCGA TTCTTTTAAA TAAAGACGCC     240
AAAATGTATG CGGATTTTGG GTTGCATTTT GGCATGGCGT TTCAAATCAT TGATGATTTG     300
TTAGACATCA CTCAAGACGC CAACACTCTA GGTAAGCCCA ATTTTAGCGA TTTTAAAGAG     360
GGCAAGACCA CTCTACCCTA CTTGCTTTTA TATGAAAAAT TGAATCAGCA TGAACAAGGG     420
CTTTTAATTT CCTATTTCAA ACAAGATAGT CATGAAATCA TAGAATGGAC TAAGGAAAAA     480
TTCAAGCAAC ATGGTATCAT AGAAGAAACC CTTAAAATCG CTCAAGTTTA TTCTAAAAAG     540
GCCCTTGAAG CCATTAAAGG GGAAAACAAT TTGATTTTAG AAAAACTAGC GCAAGATGTC     600
ATTTATAGGA CTTTT                                                     615
```

(2) INFORMATION FOR SEQ ID NO:1043:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043

```
AAGAAGGTAA AGATGAATAT CAAAATTTTA AAAATATTAG TTGGAGGGTT ATTTTTTTTG      60
AGCTTGAACG CCCATTTATG GGGGAAACAA GACAATAGCT TTTTAGGGAT TGGTGAAAGA     120
GCCTATAAAA GCGGGAATTA TTCTAAAGCG GCGTCTTATT TTAAAAAAGC ATGCAACGAT     180
GGGGTGAGTG AAGGCTGCAC GCAATTAGGA ATCATTTATG AAAACGGGCA AGGCACTAGA     240
ATAGATTATA AAAAAGCCCT AGAATATTAT AAAACCGCAT GCCAGGCTGA TGATAGGGAA     300
GGGTGTTTTG GCTTAGGGGG GCTTTATGAT GAGGGTTTAG GCACGGCTCA AAATTATCAA     360
GAAGCCATTG ACGCTTACGC AAGGCATGCG TTT                                  393
```

(2) INFORMATION FOR SEQ ID NO:1044:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 717 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044

```
TCCAGCAAAA CAGCATTCAG GGCAAAGCAA ATCATCACCG CAACCGATAT TAGCGCTCAA      60
AAACGCCAAG AGCGGCTCGC TTCTATGGGG AAAATTTCAG CGCATTTAGC CCATGAAATC     120
AGAAACCCCG TAGGCTCTAT CTCTCTTTTA GCTTCGGTGT TATTAAAGCA TGCGAACGAA     180
AAAACTAAAC CCATTGTTGT AGAATTGCAA AAAGCTTTAT GGCGCGTAGA AAGGATCATT     240
AAAGCCACCT TGCTTTTTTC TAAAGGCATT CAAGCCAACC GCACCAAGCA AAGTTTGAAA     300
ACGCTAGAGA GCGATCTCAA AGAAGCCCTA AACTGCTACA CTTACTCTAA AGACATTGAT     360
TTTCTTTTTA ATTTTAGCGA TGAAGAAGGG TTTTTTGACT TTGATTTAAT GGGGATTGTG     420
TTACAAAATT TCTTGTATAA CGCCATTGAT GCGATTGAAG CCTTAGAAGA GAGCGAACAA     480
GGTCAGGTCA AAATTGAAGC GTTCATTCAA AATGAATTTA TTGTCTTCAC CATTATTGAT     540
```

```
AATGGCAAGG AAGTGGAAAA TAAAAGCGCT TTATTTGAGC CTTTTGAAAC CACTAAATTA     600
AAGGGGAATG GCTTAGGGTT AGCCCTGTCT TTGCAAGTCG TTAAAGCCCA TGAAGGGAGC     660
ATTGCGCTAT TAGAAAATCA AGAAAAAACC TTTGAAATTA AGATTCTTAA CGCTTCT        717
```

(2) INFORMATION FOR SEQ ID NO:1045:

(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:1045

```
AAGCCTAAAA CAATTTTAAA AAAAGGACTT TTGATGAAAA CATTTGAAAT TTTAAAACAT      60
TTGCAAGCGG ATGCGATCGT GTTATTTATG AAAGTGCATA ACTTCCATTG GAATGTGAAA     120
GGCACCGATT TTTTCAATGT GCATAAAGCC ACTGAAGAAA TTTATGAAGG GTTTGCGGAC     180
ATGTTTGATG ATCTCGCTGA AAGGATCGTT CAATTAGGAC ACCACCCCCT AGTCACTTTA     240
TCCGAAGCGA TCAAACTCAC TCGTGTTAAA GAAGAAACTA AAACGAGCTT CCACTCTAAA     300
GACATCTTTA AAGAAATTCT AGAGGACTAC AAACACCTAG AAAAAGAATT TAAAGAGCTC     360
TCTAACACCG CCGAAAAAGA AGGCGATAAA GTTACCGTAA CTTATGCGGA CGATCAATTA     420
GCCAAGTTGC AAAAATCCAT TTGGATGCTA GAAGCCCATT TAGCT                     465
```

(2) INFORMATION FOR SEQ ID NO:1046:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046

```
GGAATTTGCA TGCAAGAAAA ACGACTTAAA GCCATTCAAA ACAAAATCGC TTCTTGGATC      60
AAGGAAATTG AAAGCGGCTT TATAGATGCA TTGTTTTCTA AGATTGGCCC TTCAAAGATG     120
CTGCGCTCCA AACTCATGCT CGCTTTGTTA GACGAAAAAA CAGACGCTAT TTTATTAGAT     180
AAAGCGCTCA ATTTGTGTGC GATTGTGGAA ATGATACAGA CCGCTTCTTT ATTGCATGAT     240
```

GATGTGATTG ACAAGGCGAC CATGCGCCGA AAGCTCCCTA GCATTAACGC TCTTTTTGGG 300
AATTTTAACG CCGTGATGCT TGGGGATGTG TTTTATTCTA AAGCCTTTTT TGAGTTGTCT 360
AAAATGGGCG AATCCATCGC TCAAGCCCCT CTC 393

(2) INFORMATION FOR SEQ ID NO:1047:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1731 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047

TGCATGCTAT TTTCAAAACT TTTTGCCCCA ACGCTCAAAG AACCCCCAAA AGACGCCGTG 60
TTAAAAAGCC CTAAGCACCC CGGGAACGGG GGACACCCCC TTCAAATAGG CAGTGGGATT 120
TATAATTTCC TACCCTTAGC TAAAAAAGTG CTAGACAAAA TAGAAAACGT CACGCACAAA 180
CGCATGCAAG AGCATGGGGC GCAAAATATT TTAATGAGTT TTGTGGTTTT GGCGAGTTTG 240
TGGGAAAAAT CAGGCCGTTT GGATAAATAC GGCAAGGAAT TATTGGTTTT TAAAGACCGA 300
AAAGACAATG ATTTTGTTTT AAGTCCCACT TTAGAAGAAA ATATCACCGA AATTGCCGCT 360
AATTTCATCA AAAGCTACAA GCAATTACCC GTGCATCTCT ATCAAATCCA CACGAAATTC 420
CGTGATGAAA TCCGCCCAAG ATTCGGGTTG GTGAGAGCGA GGGAATTTAT CATGAAAGAT 480
GGTTATAGCT TTCATGAAGA CGCTGAAAGC TTGGATAAGG AAATTTTAAA CACGCAAAGC 540
GCTTATAAAG AGATTTTAAG CGATTTGGGT TTGGATTTTC GCATTGTGGA AGCGGATAGC 600
GGGGCGATTG GGGGGAGTAA AAGCAGGGAA TTTGTCGTTT TAACAGAATG CGGGGAAGAC 660
ACGATCGTGG TGTGTCAAAA TTGCGATTAT GCCGCCAATA TTGAAATCGC TAAACGCTCT 720
AAAAGAACTG AGCCTTTAAT GTCCCCAAGC GCATTAGCGA AATTCCCCAC CCCTAATACC 780
ACCAGCGCTC CAAGCGTGGC GGAGTTTTTT AAAACAGAGC CTTATTTTGT CTTAAAAGCG 840
CTTGTTAACA AAGTGATCCA TAAAGATAAA GAAACCCTAG CGTGCTTTTT TGTTAGGGGC 900
GATGACAATT TAGAAGAGAC TAAAGCCCTA AACACTTTGA ATCTTTTGGG GGCGAACGCT 960
TTAGAATTAA GAGAGGCCAA TGAAGAAGAT TTAAATAAAG CAGGGTTAAT AGCGGGCTTT 1020
ATAGGGCCTT ATGGCTTGAA AAAGCATGTT TGTTATATTA TTTTTGATGA AGATTTAAAA 1080
GAGGGCGATT GCTTGATCGT TGGGGCTAAT GAAAAGGATT TTCATGCGGT GGGCGTGGAT 1140
TTAAAAGGGT TTGAAAACCT TGTTTATGCG GATATTGTCC AGGTTAAAGA GAGCGATTGT 1200
TGCCCTAATT GTCAAGGAGC GTTGAAATAC CATAAGAGTT TGGAAGTGGG GCATATTTTC 1260
AAACTCGGGC AAAGCTATGC TAAAAGCTTG AAGGCTAGTT TCTTGGATAA GAATGGCAAA 1320
GAGCGGTTTT TTGAAATGGG GTGCTATGGG ATAGGCATTA GCCGGTTGCT CAGCGTGATT 1380
TTAGAGCAAA AAAGCGATGA TCTAGGCTGT GTGTGGACGA AAAATACCGC TCCTTTTGAT 1440
GTGGTGATCG TGGTTTCTAA CCTGAAAGAT GAAGCGCAAA AAAAACTCGC TTTTGAAGTG 1500
TATGAAAGAC TGCTCCAAAA GGGCGTTGAT GCGCTGTTAG ATGACAGAGA CGCTCGTTTT 1560
GGGGCGAAGA TGAGGGATTT TGAATTGATT GGGGAACGAT TAGCCTTGAT TGTTGGGAAG 1620
CAAACTTTAG AGAGTAAGGA ATTTGAATGC ATCAAACGCG CTAATTTAGA AAAGCAAACG 1680
ATCAAAGACA TAGAATTAGA AGAAAAAATT TTAGAAATGT TAGCGAGCGA A 1731

(2) INFORMATION FOR SEQ ID NO:1048:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 552 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1048

```
ATTCGTGAGC CACAGGTTGC AATAATGACT GCAATGATGC GTTATTTTCA CATCTATGCG      60
ACCACTTTTT TCTTCCCTTT GGCGCTTCTT TTTGCGGTTA GTGGGCTTTC ATTGCTCTTT     120
AAAGCGCGCC AAGACACTGG CGCTAAGATC AAAGAATGGG TTTTAGAAAA ATCCTTAAAA     180
AAAGAAGAAC GATTGGACTT TTTAAAAGGC TTTATAAAAG AAAACCATAT CGCTATGCCT     240
AAAAAGATAG AGCCTAGAGA GTATAGGGGA GCGTTAGTCA TTGGCACGCC TTTGTATGAA     300
ATCAACCTTG AAACTAAAGG CACTCAAACG AAAATCAAGA CCATTGAAAG GGGCTTTTTA     360
GGCGCGCTCA TCATGCTGCA TAAGGCTAAG GTGGGCATCG TGTTTCAGGC GCTTTTAGGG     420
ATTTTTTGCG TGTTTTTATT GTTGTTTTAC TTGAGCGCGT TTTTAATGGT GGCTTTTAAA     480
GACACTAAAC GCATGTTTAT AAGCGTTTTA ATAGGGAGCG TGGTGTTCTT TGGAGCGATC     540
TATTGGTCTT TG                                                         552
```

(2) INFORMATION FOR SEQ ID NO:1049:

(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:1049

```
CTAATAAAAA GCAAATCAAA AAAGTGGCTT TTGGTAGGGG AAGGGGCGAA TAGTGAAATC      60
TTTGAAGCTT CCATGCAATC GCTTTTAAAA ACGGATGGCG TTTATTCTAA CCACAAACCT     120
ATTTATCAAG AGTTTTACGA ACTCAATTCG CATAACGGGT TGTATTATCA GCCTAATGTC     180
TTTTTTGCTT ATGAATCTTG CGCGTTAGGG TTTAGAAAAG GGGGGTTAAT TTTGGATAAT     240
TTTTCTAAAT TCGTGAGCCA CAGGTTGCAA                                      270
```

(2) INFORMATION FOR SEQ ID NO:1050:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 849 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

This Sheet Has Been Replaced



(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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:1050

```
ATGCTAGAGA GCGTGAACGT TAAAATTTCT GCAGACGATA TTAAATCTAA AAATGTCGCT      60
GCCGTGATGA TTACAGCCTC CTTGCCCCCC TTTGCAAGAC AGGGCGATAA AATTGATATT     120
CACATTTCTT CTATTGGCGA TGCGAAATCC ATTCAAGGAG GGACTTTAGT GATGACCCCT     180
TTAAATGCGG TAGATGGGAA TATTTACGCC CTCGCTCAAG GGGCTATCAT TTCGGGTAAT     240
TCTAGTAACT TGCTCTCAGC CAATATCATC AACGGGGCGA CTATTGAAAG GGAAGTTTCG     300
TATGATTTGT TCCATAAAAA CGCCATGACT TTAAGCCTGA AAAACCCCAA TTTTAAAAAC     360
GCTATCCAAG TGCAAAACAC TTTAAATAAG GTATTTGGTA ATAAAGTAGC CATAGCGCTA     420
GATCCCAAAA CCATTCAAAT CACCCGCCCA GAGCGTCTTT CTATGGTGGA GTTTTTAGCT     480
TTAGTGCAAG AAATCCCCAT TTACTACCGC GCGAAAAATA AGATCATTGT AGATGAAAAA     540
TCAGGCACGA TCGTTTCAGG AGTGGATATA ATCGTGCATC CTATAGTGGT TACAAGCCAA     600
GACATCACGC TTAAAATCAC TAAAGAGCCT TTAAATGATT CTAAAAACAT GCAGGATTTA     660
GACAATAACA TGTCCTTAGA CACCGCTCAC AACACGCTGA GTTCTAACGG GAAAAACATC     720
ACCATTGCCG GGGTGGTAAA AGCCTTACAA AAAATTGGCG TGAGCGCTAA GGGGATGGTT     780
TCAATCTTGC AAGCCCTAAA AAAAAGCGGC GCGATTAGCG CGAAATGGAG ATACTATGAT     840
AAACAACAA                                                             849
```

(2) INFORMATION FOR SEQ ID NO:1051:

(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:1051

```
ACGGGACATG GCAGGTTAGG GTGGATATTA AATCCAAAGA AGGCCAAGTT TATCGCACTA      60
AAACAAGCCT GGATTTATGA GCGCATGCTA TCTTTTATAA GCGCGTTTGA TAAAAGGGGC     120
GTTTCAATAC GCCTTCTAAC AGCCTTGTTA CTGCTTTTTA GTTTGGGTTT GGCTAAAGAT     180
TTAGAAATCC AAACTTTTGT GGCTAAATAC CTTTCTAAAA ATCAAAAAAT ACAAGCCCTA     240
CAGGAGCAAA TTGACGCTTT AGATTCTCAA GAAAAAGTCG TTAGCAAATG GGATAACCCT     300
ATTTTGTATT TAGGCTATAA CAACGCTAAC GTGAGCGATT TTTTCAGGCT GGATAGCACC     360
TTAATGCAAA ACATGAGCTT GGGTTTGTCT CAAAAAGTGG ATTTAAATGG TAAAAAACTC     420
ACGCAGTCTA AAATGATCAA TTTAGAAAAA CAAAAAAAAA TATTAGAGCT TAAAAAAACC     480
```

AAGCAGCAAT TGGTGATTAA TTTAATGATA AACGGCATTG AAAACTATAA AAACCAACAA 540
GAAATAGAGC TTTTAAACAC AGCGATTAAA AATTTAGAAA ACACCCTCTA TCAAGCCAAC 600
CATTCCAGTT CGCCCGATTT AATAGCGATC GCCAAGTTAG AAATTTTAAA ATCGCAATTA 660
GAAATC 666

(2) INFORMATION FOR SEQ ID NO:1052:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1041 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052

ATTGTTTTTC ATCAAGGGAG TTTGAGCGTG AGCGGTTTGT TTAAAATGCG TATTCTGAGT 60
TTTAAAAAGA ATAAGCGGGC GGTGTTTTCA CTCTATCTTT TTATCGCTTT GTTAGCGCTT 120
TCTCTTTTAG CCCCCTTGTG GGTCAATGAT CGCCCTTTAT TCATCTATAA AGACAATAAA 180
GCGTATTTCC CTATGTTTAA AAACTATGCG GAAGTGGAGT TTGGAGGCGA TTTTTTCACC 240
CCTACGGACT ATAACGATCC TTATGTGCAA AACACGCTTT TAAAAGACGC TTTCATCATC 300
CATGCGCTCA TCCCTTATAG CTACGATACG ATCATTATGG ATTTAGACTC GCCTGCCCCC 360
ACCCCCCCAA GCTTCAAACA CCTTTTAGGC ACAGACGATC AAGCCAGAGA CGTGTTAGCC 420
AGGCTGGTTT ATGGCTATCG GGTTTCGTTA GTGTTTGGGA TTTTACTCAC CCTTTTTAGC 480
GTTCTTATTG GCGTGAGTTT GGGGGCGTTT CAGGGGTATT ATGGAGGGCT AGTGGATTTA 540
GTGGGGCAAA GGTTGAGCGA AATTTGGAGC GCGATCCCCA TGCTTTTTTT ACTCATTGTG 600
ATTTCTAGCG CGTTCAATTC TAATTTTTGG ATCATCTTGT TTTTAGTCTT GCTCTTTAGC 660
TGGATGGGGC TTTCTCAAGT CGTGCGCACG GAGTTTTTAA AAGCAAGGAA TATGGACTAC 720
ACCAAAGCCG CTAGAGCGCT TGGGGTGAAT GATTTAAAAA TCATTTTCTA CCATGTTTTA 780
CCCAACGCTT TAGTGGCAAC GATCACTTAC ATTCCTTTTT TAATGGCGGC TAGTATTTCC 840
ACTTTAGTGT CTTTGGATTT CTTAGGTTTT GGCATGCCTA TAGGGAGCGC GAGCTTGGGC 900
GAATTGGTCA ATCAAGGCAA GGATAACCTC ACCACGCCTC ATTTAGCGGT TGTAGCCTTT 960
GTAGCCATTA GCTTGTTGCT TTCTGTTTTG GTGTTCATTG GCGAAGGGGT GCGCGATGCT 1020
TTCAACGCTA ACATGCTCAA A 1041

(2) INFORMATION FOR SEQ ID NO:1053:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1557 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053

```
AGGGGTTACA TGCTAGAAAT CAAGAATTTA AACTGCGTTT TAAACTCTCA TTTTTCGCTC      60
CAAAACATCA ATATTTCTTT AAGTTATAGT GAAAGGGTGG CGATCGTGGG CGAAAGCGGG     120
AGCGGGAAAA GCTCTATCGC TAATCTCGTC ATGCGATTAA ACCCTAGATT CAAGCCCCAT     180
AATGGCGAAA TCCTGTTTGA AACAACCAAT CTTTTAAAGG AAAGCGAAGC GTTCATGCAG     240
CATTTAAGGG GGAATATTAT CGCTTACATC GCCCAAGACC CCCTATCCAG CCTAAACCCC     300
TTGCATAAAA TCGGCAAGCA AATGAGTGAA GCCTATTTTT TACACCATAA AAACGCTTCT     360
CAAGTGCTCC TTAAAGAACA AGTTTTAAAC GCCATGAAAC AAGTCCAATT GGATGAAAAA     420
TTTTTGGATC GTTACCCTTA TGAGCTCAGC GGTGGGCAAC GCCAAAGGGT GTGTATCGCT     480
ATGGGCATTA TTAACGCGCC AAAACTGCTC ATTTGCGATG AGCCTACCAC CGCGCTAGAT     540
GCGCAAATCC AAAACCAGAT TTTAGACTTG CTCAAGCAAT TGAGCGTGGA AAAAAACATC     600
GCCCTTTTAT TCATTAGCCA TGATTTAAAG GCGGTTAAAC GATTGGCTGA TAGGGTTTAT     660
GTGTTAAAAA AAGGCGAGAT AGTAGAAACC AATTTGACTA AAGAGCTTTT TAATGACCCC     720
AAGCACGAAT ATTCAAAACT CTTGATTCAG GCTTCAAACT TGCCCGCTAA AAATTTAAAA     780
GCGCTAGATG AGACGCTTTT AGAGGTGAAA GATTTTAGCG TTTATTACTT GCAAAAACGC     840
TTCTTTAGGC CTTCTTTAAA AAAACCCCTT ATCGCATCGG TGGATTTTTC CCTCAAAGCT     900
AAAGAAAACA TCGGCATCAT TGGCGAAAGC GGGAGCGGGA AAAGCTCTCT AGCGTTAGGG     960
CTTTTAAAAC TCGCTTTAAA CAGCGGGGAA GAAAAGATTT TAGGCCAAAG CGTGGGGCTT    1020
TTAAATTCTA AGGCGTTCAA ACCCTACCGC AAGATTTTGC AAATGGTGTT TCAAGACCCC    1080
TACGCATCAT TAAACCCTCG CTTAAGCATT CAAAGCATTT TAATAGAAGC TTTGCGCTTT    1140
GCTTACCCTA AAGCTTCACA ACAAGAATGG CACCATTTAG CTGAACTTTG CTTAGAAGAA    1200
GTGTGTTTAA ACCCTGAATT GCTTAACTTT TACGCTTATG AGCTCAGCGG AGGGGAGCGC    1260
CAAAGAGTGG CGATCGCTAG AGCGATTGCC TTAAAACCTA GAATCATTCT TTTAGATGAG    1320
CCAACCTCTG CTTTAGACAA AAGCATTCAA AAAAGCGTGT TGGAATTATT GTTGAATTTA    1380
CAAGAAAAGC AGGATTTGAG CTATTTGTTT ATCAGCCATG ATTTAGATGT GATCAAAGCT    1440
TTTTGCGATA GGGTGTTAGT GGTGAGTGAG GGGAAAATCG TGGAAACAGG CGCTATTGAA    1500
GAGGTGTTTG ACAACCCCAA ACACGCTTAT ACCAAGCGTT TGTTGGAATC CAGGCTT       1557
```

(2) INFORMATION FOR SEQ ID NO:1054:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 549 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054

```
GGGGGACTTA TGAATACTAT TATAAGATAT GCGAGTTTAT GGGGCTTGTG TATTACTCTA
ACTCTAGCGC AAACCCCCTC TAAAACCCCT GATGAAATCA AGCAAATCCT TAACAATTAT
AGCCATAAGA ATTTAAAGCT CATTGATCCG CCGACAAGTT CTTTAGAAGC GACACCGGGT
TTTTTACCCT CGCCTAAAGA AACAGCGACC ACGATCAATC AAGAGATCGC TAAATACCAT
GAAAAAAGCG ATAAAGCCGC TTTGGGGCTT TATGAATTGC TAAAGGGGGC TACCACCAAT
CTCAGTTTGC AAGCGCAAGA ACTCAGTGTC AAGCAAGCGA TGAAGAACCA CACCATCGCC
AAAGCGATGT TTTTGCCTAC TTTGAACGCG AGTTATAATT TTAAAAATGA AGCTAGGGAT
```

```
ACTCCAGAAT ATAAGCATTA TAACACCCAA CAACTCCAAG CTCAAGTCAC ATTGAATGTG     480
TTTAATGGCT TTAGCAATGT GAATAATGTC AAAGAAAAGT CTGCGACTAC CGATCCACTG     540
TGGCTAATT                                                             549
```

(2) INFORMATION FOR SEQ ID NO:1055:

(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:1055

```
GTGAAATTCA GCGTTTTAAC CCTTTTCCCG CAACTCATCT TGCCTTATTT TGAAGATTCT      60
ATTTTAAAAA GAGCGTTAGA AAAAAACCTT TTTGAATTGG AAGTGTTAAA CCTTAGAGAT     120
TTTAGCGCTA ACAAATATCA AAAAGCGGAT CACACGCTCA TTGGTGGGGG TGCGGGGCAA     180
ATTTTAGACC CTGAGATGAT AGAAAACGCA CTCCACTCTG TTAAAAACCC TAAACACACG     240
ATTTTTTTAA GCGCGGTGGG CAAGCCTTTC AAGCAAATAG ACGCGATGCG TTTGGCTCAA     300
AAAAAGCATG TCGTTTTGGT GTGCGGGCGT TATGAGGGCT TTGATGAACG CTCTATTGAA     360
TTGGGTGCTG ATGAGGTTTT TTGTATAGGC GATTTTATTT TAACAGGGGG CGAGCTTGGG     420
GCGTTGTGCT TGATAGATAG TATCGCTCGC CACATTCAAG GGGTTTTGGG TAACGCCCAA     480
TCTTTAGAAA ATGAGAGTTT TGAAAATAAT TATTTGGAGA CCCCTAATTT CGCTAACGCT     540
GTTTTTAAAT CCAAAGAAAT CAATAAAATC CCTGCACCTT TAGAATATTC TAAAGGAAAT     600
CATGCTAAAA TCAAGCAACT AAAGCTTGAT TTGTCAAAAT TAAGGACAAA ATTTTACCGC     660
CTTGATTTAT TCAAACAGCA CAAATCA                                         687
```

(2) INFORMATION FOR SEQ ID NO:1056:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1098 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056

This Sheet Has Been Replaced



```
AGGGAGCAGT GGTTTCACTT TCGCTCAACG CCCCCCACCG TGGTTTTAAT GGCAGGTTTG      60
CAAGGGAGCG GGAAGACAAC CACCACCGCT AAACTCGCCC ACTATCTCAA AACCAAAAAT     120
AAAAAAGTGC TTTTATGCGC ATGCGATTTG CAACGCTTAG CAGCGGTGGA GCAATTAAAG     180
GTTTTGGGCG AACAGGTGGG CGTGGAAGTT TTTCATGAAG AAAATAAAAG CGTGAAAGAA     240
ATCGCCAACA ACGCTTTAAA AAGGGCTAAA GAAGCGCAAT TTGACGTGTT AATCGTGGAT     300
AGCGCGGGGC GTTTAGCGAT TGATAAAGAG CTTATGCAAG AATTAAAGGA AGTTAAAGAA     360
GTCTTAAATC CCCATGAAGT GCTGTATGTC GCAGACGCGT TGAGCGGGCA AGATGGGGTC     420
AAAAGTGCGA ACACCTTTAA TGAAGAAATA GGCGTGAGCG GGGTGGTGTT AAGCAAATTT     480
GATAGCGATT CTAAAGGGGG TATCGCCTTA GGCATCACTT ATCAATTGGG CTTACCCTTG     540
CGTTTTATTG GGAGTGGGGA AAAAATCCCT GATTTAGACG TGTTTATGCC TGAAAGGATT     600
GTGGGGCGTT TGATGGGGGC TGGAGATATT ATCTCGCTCG CTGAAAAAAC CGCCAGCGTT     660
TTAAACCCTA ATGAAGCCAA AGATTTAAGC AAAAAGCTCA AAAAAGGGCA ATTCACTTTC     720
AACGATTTTT TAAACCAAAT TGAAAAAGTG AAAAAATTAG GCTCTATGAG TTCTCTGATC     780
TCTATGATTC CAGGTTTAGG GAATATGGCA AGCGCGCTAA AAGACACGGA TTTAGAAAGT     840
TCTTTAGAAG TGAAAAAAAT CAAGGCCATG GTTAATTCCA TGACGAAAAA AGAGCGAGAA     900
AACCCCGAGA TTTTAAACGG CAGCCGAAGA AAAAGGATCG CTTTAGGGAG CGGCTTAGAA     960
GTGTCTGAAA TCAATCGCAT CATCAAACGC TTTGATCAGG CGAGCAAAAT GGCGAAACGA    1020
CTCACGAATA AAAAGGGTAT TAGCGATTTG ATGAATCTAA TGAGTCAGGC TAAAAATCAA    1080
ACGCCCCCTA AAATGCGC                                                  1098
```

(2) INFORMATION FOR SEQ ID NO:1057:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 810 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1057

```
AGGAAAGCGA TGAACACCCA CCTCAAACAA TTGATTGAAA TTTCGCACTT GGATAAAGAA      60
ATTGACTCTT TAGAGCCGTT GATCAGAGAA AAACGGAAAG ACTTGGATAA AGCCTTGAAT     120
GATAAAGAAG CTAAAAATAA AGCGATTTTG AATTTGGAAG AAGAAAAATT AGCCCTAAAA     180
TTACAGGTTT CTAAAAACGA GCAAACCCTA CAAGACACGA ACGCTAAAAT CGCCAGTATC     240
CAAAAGAAAA TGAGCGAGAT CAAATCCGAA AGGGAGTTGC GCTCTTTAAA CATTGAAGAA     300
GATATTGCTA AAGAGCGATC CAATCAAGCC AACAGAGAAA TTGAAAACCT GCAAAATGAA     360
ATCAAGCACA AAAGCGAAAA ACAAGAAGTT TTGAAAAAGG AAATGCTAGA GCTTGAAAAA     420
TTAGCGTTGG AATTGGAAAA TTTAGTGGAA AACGAAGTCA AAAACATCAA AGAAACCCAA     480
CAGATCATCT TTAAAAAGAA AGAAGAACTC GTGGAAAAAA CCGAGCCTAA AATCTATAGC     540
TTTTATGAAA GGATTAGGAG GTGGGCGAAA AACACGAGCA TCGTAACGAT CAAAAAACAG     600
GCTTGTGGGG GTTGTTTTAT TCGGTTGAAC GATAAGATTT ATGCCGAAGT GCTAACGAGT     660
GGGGACATGA TCACTTGTCC GTATTGCGGG CGTATTTTAT ACGCTGAGAG TACGCATGAA     720
AGTAACGCTC AACCTCCAAA AGAAAGCCAA CCAAAAGAAA GCCAAGAAGA AAGCCAAGAA     780
GAAAGCCAAG AAGAAAGCCA AGAATCCGTT                                      810
```

(2) INFORMATION FOR SEQ ID NO:1058:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1701 base pairs
(B) TYPE: nucleic acid

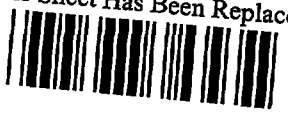
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058

```
ATGAACGAAA TTGACAAATC CGTTGATATC GGATTCTTAC GGATTCTGGA TGTTATTAAA      60
AAAGTTAAAA CCCCAAAGGG TGGTATTGAG GTTTTAAGGA CTTTAATTGA TTTCACGCCC     120
AAAATTGAAA ACGCCCTAAA TTTAGCGACC AAAAGCCATA AGGGGCAATA CAGAAAGAGC     180
GGTGAGCCTT ATATTGTCCA TCCTATTTGC GTGGCGAGCG TGGTGGCGTT TTGTGGGGGC     240
GATGAGGCGA TGGTGTGCGC CGCGCTTTTG CATGATGTGG TAGAAGACAC GCCTTGTGAG     300
ATTGAAACGA TTGAGCGAGA ATTTGGGCAA GATGTGGCTA ATTTAGTGGA TGCGCTCACC     360
AAAATCACTG AAATCAGGAA AGAAGAGTTA GGCGTGAGTT CTCAAGATCC CAGAATGGTG     420
GTTTCAGCCC TCACTTTTAG AAAGATCCTT ATTAGCGCGA TACAAGATCC AAGAGCCTTA     480
GTGGTAAAGA TTAGCGACAG GTTGCACAAC ATGCTCACCT TAGACGCCTT GCCTCATGAC     540
AAGCAGGTGC GTATTTCTAA AGAAACTCTA GCGGTGTATG CCCCCATAGC GAGTCGATTG     600
GGCATGTCTT CAATCAAAAA CGAATTAGAA GACAAGAGCT TTTATTATAT TTATCCAGAA     660
GAGTATAAAA ATATTAAGGA GTATTTGCAC AAAAACAAAC AGTCTTTACT CTTAAAACTC     720
AACGCTTTTG CGAGCAAGTT AGAAAAAAAG CTTTTTGACA GCGGGTTTAG CCATTCGGAT     780
TTTAAACTCG TTACAAGGGT GAAACGCCCT TATTCTATTT ATCTTAAGAT GCAACGAAAA     840
GGGGCGGTTA ATATTGATGA AATTTTGGAC TTGTTAGCCA TTAGGATTTT ATTGAAAAAC     900
CCGATTGATT GCTACAAGGT TTTAGGGATT ATTCATTTGA ATTTCAAACC CATTGTTTCT     960
CGTTTTAAAG ATTACATCGC TTTGCCCAAA GAAAATGGCT ATAAGACAAT ACACACGACG    1020
ATTTTTGATG AATCTTCTGT TTATGAAGTG CAGATCCGCA CTTTTGATAT GCACATGGGG    1080
GCGGAGTATG GTAATTCAGC CCATTGGAAG TATAAAGCCG GGGGCGTGGA TCATGAAGAA    1140
CATCATGAGG GCATGCGGTG GTTGCAAAAT TTTAAATACC ATGACAGCGA TTTGAAAAAC    1200
GACCCTAAGG AATTTTACGA ACTCGCTAAG AACGATTTGT ATCGTGAAGA TATTGTCGTT    1260
TTTTCGCCCC ATGGGGACAC TTACACTTTA CCGGTGGGCG CGATCGCTTT AGATTTCGCT    1320
TACATGGTGC ATAGTGATTT GGGCGATAAA GCCACGGACG CTTATATCAA TAGTAAAAAA    1380
GCCTTACTCA ATCAAGAATT AAGGAGTGGG GATGTGGTTA AAATCATTAA AGGCGATAAA    1440
GTAATACCTC GTTTCATTTG GATGGATCAG CTTAAAACTT CTAAGGCTAA AAACCATTTG    1500
CGCATCCAAA GAAGAAACCG CTTGAAAGAA ATTGACACTA AGAGCATGAT CAATATCTTA    1560
TCGACTTTTT TTGGGCGCTC TGTTTTTGAA GATGCGGATT TGAAAGATTA TAAAAACTTT    1620
GAAGAAAAAT TAACAGATTG TGGGGTGGAG ACCACCTTAA CAGAAGCGAT GAAAAGCTTT    1680
GAAAATTTGG GCCAAACTCA C                                              1701
```

(2) INFORMATION FOR SEQ ID NO:1059:

(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:1059

```
GTTACAATCA AAAGCTTTAT TAATGGATTA AGAAGGGATC ATGCAGGCAA AGATAAAAAA      60
CAAGCGGGTT TTGGTGAAAT TTTCTGGGGA AGCGTTAGCT GGGGACAACC AGTTTGGATT     120
GACATTCATG TGTTAGATCA CATCGCTAAA GAGATCAGAA GTTTAGTGGA AAACGATATT     180
GAAGTGGGTA TTGTGATTGG TGGAGGCAAT ATCATTAGGG GGGTTAGCGC GGCTCAAGGG     240
GGGATCATTA GGCGCACCAG TGGGGATTAT ATGGGCATGT TAGCCACCGT GATTAATGCG     300
GTAGCCATGC AAGAAGCTTT AGAGCATATC GGTTTAGACA CAAGAGTGCA GAGTGCCATT     360
GAAATCAAAG AGATTTGTGA AAGTTATATT TATAGGAAAG CGATCAGGCA TTTAGAAAAG     420
GGTAGGGTGG TGATTTTTGG CGCTGGCACA GGAAACCCGT TTTTCACCAC CGATACGGCC     480
GCTACTTTAA GAGCGATTGA AATTGGATCG GATCTAATCA TTAAAGCGAC TAAAGTGGAT     540
GGCATCTATG ACAAAGACCC TAACAAATTC AAAGACGCTA AAAATTGGAC ACTT           594
```

(2) INFORMATION FOR SEQ ID NO:1060:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1017 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1060

```
ATGAATGCAT TGAAGCGTGC GTGTTTAAGA TTGATGGGCG AAACCAATAC CGATGATTTA      60
AGCCCAGCGA GCGACGCTTT CACACGGAGC GATATTCCTT TACACGCCAA AGCCATGCTA     120
AAAAACCGGA TTGAAAATTA CGAACAACGC ATTGAAGCCA TTAAAACTAA AGGCGTTCCT     180
GTAGCGTATG TGGGCGATGT GGTTGGCACA GGAAGCTCTA GAAAAAGCGC GACTAACTCT     240
ATCATGTGGC ATTTTGGTAA GGACATTCCT TTTGTGCCTA ATAAAAGGAG TGGAGGCATT     300
GTGATTGGGG GGGTGATCGC TCCGATTTTC TTTGCGACTT GTGAAGATAG CGGGGCGTTA     360
CCCATTGTGG CTGATGTTAA GGATTTGAAA GAGGGCGATA TCATTAAAAT CTACCCTTAT     420
AAAGGCGAAA TCACGCTGAA CGATAAGGTG GTTAGCACCT TTAAGCTAGA GCCTGAAACT     480
TTATTAGATG AAGTCAGGGC TTCTGGGCGT ATCCCCTTAA TCATTGGTAG GGGTTTGACC     540
AATAAAGCGC GTAAATTTTT AGGGCTAGGC GAATCGGAAG CGTTCAAAAA ACCATCCGCT     600
CCTAAAAGCG ACGCTAAAGG CTACACTTTA GCCCAAAAAA TTGTAGGCCA TGCTTGTGGG     660
GTAAAAGGGA TCTTACCTGG TGCTTATTGT GAGCCAAAGG TTACCACCGT GGGCAGTCAA     720
GACACCACAG GGGCGATGAC CAGAGATGAG GTTAAAGAAT TAGCGAGTTT GAAATTTGAT     780
GCGCCTTTTG TGTTGCAGAG TTTTTGCCAT ACCGCTGCTT ACCCAAAACC TAGTGATGTG     840
AGTTTGCATG CAACCTTGCC TGGCTTTATC ACTCAAAGAG GGGGCGTGGC GTTGCATCCG     900
GGCGATGGCG TGATCCATAC ATGGCTTAAT CGCATGGGAT TGCCTGACAC TTTAGGCACA     960
GGGGGGGATA GCCACACCCG TTTCCCTTTA GGCATCAGTT TCCGGCAGGG AGCGGGC       1017
```

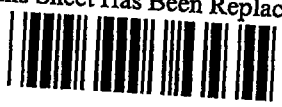
(2) INFORMATION FOR SEQ ID NO:1061:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 462 base pairs

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

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(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:1061

```
ACATTTACTA TAAAGAGATT TGTTTTGATG AAAATTAAAA TCCAAAAAAT CCACCCAAAC     60
GCCCTTATCC CTAAATACCA AACCGAAGGC TCTTCAGGCT TTGATTTGCA CGCTGTAGAA    120
GAAGTAGTGA TCAAACCTCA TAGCGTGGGA TTGGTAAGGA TTGGGATTTG TTTGTCTTTA    180
GAAGTGGGGT ATGAACTGCA GGTACGCACC CGTAGCGGCT TGGCTTTGAA TCATCAGGTG    240
ATGGTGTTAA ATTCCCCTGG CACGGTGGAT AATGATTATA GGGGCGAAAT TAAGGTCATT    300
TTAGCGAATT TGAGCGATAA AGATTTTAAA GTTCAAGTAG GGGATAGGAT CGCTCAAGGG    360
GTGGTTCAAA AAACTTATAA AGCCGAATTT ATAGAATGCG AACAATTAGA TGAAACTTCA    420
AGGGGTAGCG GGGGGTTTGG CAGCACAGGA GTGAGTAAGG CA                       462
```

(2) INFORMATION FOR SEQ ID NO:1062:

(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:1062

```
AGAAAGAAAC CATTCAAGGA ACGCATTGAT TTGATGAATA AACCATTTTT AATCTTACTC     60
ATAGCCCTAA TTGCCTTTAG CGGCTGTAAC ATGAGAAAAT ACTTCAAACC CGCTAAACAC    120
CAAATTAAAG GCGAAGCGTA TTTCCCTAAC CATTTGCAAG AAAGCATCGT TTCGTCTAAT    180
CGTTATGGAG CCATTTTGAA AAATGGAGCG GTTATAGGCG ATAAAGGTTT AACGCAGCTA    240
AGAATTGGTA AGAATTTCAA TTATGAAAGC AGTTTTTTAA ATGAGAGTCA AGGGTTTTTC    300
ATCCTTGCAC AAGATTGTTT GAACAAGATT GATAAAAAAA CAAGCAAAAG CAGGGCGGCT    360
AAGACTGAAG AAACGGAATT GAAATTAAAG GGCGTTGAAG CGGAAGTCCA AGATAAAGTC    420
TGTCATCAAG TGGAATTGAT TAGCAATAAC CCTAACGCCA GCCAACAATC TATCGTTATT    480
CCTTTGGAGA CTTTTGCCTT GGCGCGAGCG TTAAAGGGAA TCTTT                    525
```

(2) INFORMATION FOR SEQ ID NO:1063:

(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:1063

```
GGCATGAGCA TTAAGGAAAA TTTAGAGCAA GTTAGAAACG AATTTAAAAG CGATGAAAAG     60
CTTTTAGAAG GAGCGTTTAG ATTAGAAAAG TTTTTCAAAC GCTACAAGTG GGTGTTGTTG    120
TTTATCGTGG TGGCTTTTAT CGCTTATTTA GGGGATACAA AATTACAAGA TTATAAGCAT    180
GAGCAAACGA GAGAGCGGAT CACTCAAATT TATAATGAAG TGCTAGAGAG TCCTAATAAT    240
ATAGCCTTGC AAAAAAGATT GAAAGAAGTC GCCCCAGAGT TGTATGACTT GTATCAGTTC    300
GCCAGAGCGA GTGAGAGGAA CGATGCAAAC GAGTTTAAAA GGCTTTCGCA ATCTTCTAAT    360
GAAATCGTTA AAGCGTTCGC CAAATATTCT TACGCATCGC TCTCTAGAGA TAAAAACCTG    420
CTTGAAAAAA GCCCCATTCT TAAAGAAATG AGCGCTTTAC AAGAAGTGAA CTTGTTGTAT    480
GAAGAAAATT CTAAAGACGC AATCAAAAAA GCGCATCAAA GTTTATCAAC TATCCCTCTA    540
AGTTCTTCAC TCTATGCTAT AATCTCTGTT TTAAAACATT ATGGAATGTT AGAAGATATT    600
CAGCAAAACC CTTCCAAACC AACCAATCTA AAGAAAGAAA CCATTCAAGG AACGCAT       657
```

(2) INFORMATION FOR SEQ ID NO:1064:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064

```
AAGCGCTATA AAAGGCTAGA GCAAGAAATA AAAAAAAGGG ATAAAATGAT AGTGGGTTTG     60
ATAGGGGTTG TGGAAAAAAT CTCTGCTTTA GAAGCGCATA TAGAAGTGCA AGGGGTTGTT    120
TATGGGGTGC AAGTTTCTAT GCGAACGGCT GCTTTGCTCC AAACGGGCCA AAAAGCGCGT    180
TTGAAAATCT TACAAGTGAT TAAAGAAGAT GCGCATCTTT TATACGGGTT TTTAGAAGAG    240
AGCGAAAAAA TTCTCTTTGA AAGGCTTTTG AAAATCAATG GGGTAGGGGG GCGTATCGCT    300
TTAGCCATTC TTTCAAGCTT TTCGCCGAAT GAATTTGAAA ACATTATCGC TACTAAAGAA    360
GTCAAAAGAC TCCAGCAAGT CCCAGGCATA GGGAAAAAGC TCGCCGATAA GATCATGGTG    420
GATTTGATTG GCTTTTTTCAT TCAAGATGAA AACAGACCCG CGCGCAATGA AGTCTTTTTA    480
```

GCCCTAGAGA GTTTGGGCTT TAAAAGCGCT GAAATCAATC CAGTTTTAAA AACCCTAAAA 540
CCCCATCTCA GCATAGAGGC AGCGATTAAA GAAGCCTTAC AGCAACTGCG CTCT 594

(2) INFORMATION FOR SEQ ID NO:1065:

(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:1065

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
CTCAAACAAG CCGAAGAAGC GAATAAAACC CCAGATAAAC CCGATAAAGT TTGGCGCATT 300
CAAGCAGGAA AAGGCTTTAA TGAATTTCCT 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 TTCACAAGCT ATAAGGATAG CGCTGATCGC 600
ACCACGAGAG TGAATTTCAA CGCTAAAAAT ATTTCAATTG ATAATTTTGT AGAAATCAAT 660
AATCGTGTGG GTTCTGGAGC CGGGAGAAAA GCCAGCTCTA CGGTTTTGAC TTTGCAAGCT 720
TCAGAAGGGA TCACTAGCAG 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
GCCCCTCCAG AAGGTGGCTA CAAGGATAAA CCTAATAGTA CCACTTCTCA AAGTGGCACT 1080
AAAAACGACA AGAAAGAGAT CAGTCAAAAT AACAATAGCA ACACAGAGGT CATTAACCCA 1140
CCCAATAACA CGCAAAAAAC AGAAACTGAA CCCACCAAGT CATTGATGGG CCTTTTGCTG 1200
AAGGCAAAGA CTCGGTTGTC A 1221

(2) INFORMATION FOR SEQ ID NO:1066:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

This Sheet Has Been Replaced



(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066

```
GTAATAAATA CAACTAGTAT GCTAAAAAAA ATATTTTTAA CCAACAGCTT AGGGATTTTA      60
TGCTCTAGGA TTTTTGGCTT TTTACGGGAT TTAATGATGG CCAATATCCT AGGGGCTGGG     120
GTGTATAGCG ATATTTTCTT TGTGGCTTTC AAATTGCCTA ATCTATTCAG GCGTATTTTT     180
GCGGAGGGCT CTTTTTCTCA AAGCTTTTTA CCGAGCTTCA TACGGAGTTC CATTAAGGGG     240
GGTTTTGCGA GTTTGGTGGG GCTTATTTTT TGTGGCGTTT TATTCATGTG GTGCTTATTA     300
GTAGCGCTCA ATCCCTTATG GCTAACCAAA CTCCTAGCTT ACGGCTTTGA TGAAGAAACG     360
CTCAAACTAT GCACCCCTAT TGTAGCGATC AATTTTTGGT ATCTTTTATT GGTGTTTATC     420
ACCACTTTTT TAGGCGCGCT TTTACAATAC AAACACAGCT TTTTTGCCAG CGCTTATAGC     480
GCAAGCTTAC TCAATTTATG CATGATTTTA GCCCTTTTGA TTTCTAAAGA AAAAACGCAT     540
TTAGAAGCGT TGTATTATTT GAGCTATGGC GTGCTTTTAG GGGGCGTGGC TCAAATCTTA     600
TTACACTTTT ATCCTTTAGT AAAATTAGGC TTATGGGATT TATTATTTAA AGGGTTGTTG     660
GGTTTTAAGA CTAAAAATAC AAACAAAAAA GAATATCGTT TGAATAGGGC TAAAAAGGAT     720
CTAAAAGCGT TTTTCAAGCA ATTCTTCCCC AGCGTCTTAG GCAATTCTAG CGCTCAGATC     780
GCTTCTTTTT TAGACACCAC AATCGCTTCT TTTCTGGCGA GCGGGAGCGT GTCTTATTTG     840
TATTACGCCA ATAGAGTCTT CCAGCTCCCT TTAGCCTTAT TCGCTATCGC TATCTCCACA     900
GCTCTTTTCC CTAGCATTGC GATCGCGCTT AAAAACAACC AGCAGGATTT AATCTTACAA     960
CGCTTGCAAA AGGCGTGGTT TTTTTTGGTG GGGGTTTTGC TTCTTTGCAG CATTGGGGGG    1020
ATAATGTTAA GCAAAGAAAT CACCGAACTT TTATTTGAAA GGGGGCAATT TAGCCCTAAA    1080
GACACCCTAA TCACTTCGCA AGTCTTTTCG CTCTATCTTT TAGGCTTGCT CCCTTTTGGG    1140
CTAACCAAAC TCTTTTCTTT ATGGCTTTAT GCGAAATTAG AGCAAAAAAA AGCGGCTAAA    1200
ATCTCTTTAA TTTCGCTTTT TTTAGGTTTA GCGGCTTCTT TGAGTTTAAT GCCTTTGTTA    1260
GGGGTTTTGG GTTTGCGT                                                  1278
```

(2) INFORMATION FOR SEQ ID NO:1067:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067

```
TTTCGCTTAC CAAGTCCCCT TACCTCAATT TTAATGCGCC TAGATTACGC CCTATTCAAC      60
CAGCATTTAG CAAATAGCAG AGAAAAAGCT AAAGCGTTGG TTTTAAAAAA ACAGGTTTTA     120
GTCAATAAAA TGGTGGTTTC TAAACCCTCT TTTATCGTTA AAGAGGGCGA TCAAATTGAA     180
CTCATCGCTC CCAATCTATT CGTTAGCAGG GCTGGGGAAA AATTAGGGGC TTTTTTAGAA     240
GATCATTTTA TAGATTTTAA AGAAAAGGTT GTTTTAGATG TGGGAGCGAG TAAGGGAGGC     300
TTTAGTCAAG TGGCTCTTTT AAAAGGGGCT AAAAAGGTGC TTTGCGTGGA TGTGGGGAAA     360
ATGCAATTAG ATGAAAGTTT GAAAAACGAC CAACGCATAG AATGTTACGA AGAATGCGAT     420
ATTAGAGGGT TTAAAACGCC AGAAAAAATT GATTTAGCAC TTTGTGATGT GAGCTTTATT     480
TCTTTATATT GTATTTTAGA AGCGATTTTG CCTTTAAGCG GTGAATTTTT AACGCTTTTC     540
TCCGCAAT TTGAAGTGGG CAGAACAATA AAACGCAATA AAAAGGGGGT GGTGATGGAT     600
```

AAAGAAGCCA TTTTGAACGC TTTAGAAAAC TTTAAAAACC ATTTAAAAAC AAAGGATTTT 660
CAAATCTTAA CGATCCAAGA AAGCTTAGTG AAAGGGAAAA ACGGGAATGT TGAATTTTTT 720
ATCCATTTCA AGCGAGCC 738

(2) INFORMATION FOR SEQ ID NO:1068:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2547 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068

AGACATGTGC AACCGATGAA ATCTAAAAAA CTTTATTTAG CTTTAATCAT AGGGGTTTTA 60
TTAGCGTTTT TAACCCTATC TTCATGGCTA GGTAATAGCG GTTTAGTGGG GCGTTTTGGG 120
GTGTGGTTTG CCGCAATCAA TAAAAAATAT TTTGGGTATC TTTCATTGAT TAATTTACCC 180
TATTTGGCGT GGGTTTTATT CCTTTTATAC AGGGCTAAAA ACCCTTTTAC AGAAATCGTT 240
TTAGAAAAAA CTTTAGGGCA TCTATTAGGC ATTTTATCTT TACTCTTTTT GCAATCTAGC 300
CTGTTGAATC AAGGGGAAAT CGGCAACAGC GCGCGTTTGT TTTTACACCC TTTTATAGGG 360
GACTTTGGGC TTTATGTGCT GATAATGCTT ATGGTAGTTA TCTCTTATTT AATTTTATTC 420
AAACTGCCCC CTAAAAGCGT TTTTTACCCT TATATGAACA AAACACAAAG CCTTTTAAAA 480
GAGATTTACA AACAATGCTT GCAGGCCTTT AGCCCTAATT TTAGCCTGAA AAAAGAGGGT 540
TTTGAAAACA CCCCATCAGA TTCTCAAAAA AAAGAAACCA ACAACGACAA AGAAAAAGAA 600
AACCTCAAAG AAAACCCTAT TGATGAAAAC CACAACACCC CTAACGAAGA ATCGTTTTTA 660
GCGATCCCTA CCCCCTATAA CACGACCTTA AATAATTCAG AGCCGCAAGA AGGCTTAGTC 720
CAAATTTCCC CACACCCCCC TACCCATTAC ACCATTTACC CTAAAAGAAA CCGATTTGAT 780
GATTTGACTA ACCCCACTTT AAAAGAACCT AAGCAAGAAA CCAAAGAAAG AGAACCCACG 840
CTAAAAAAAG AAACGCCCAC CACACTCAAA CCTATCATGC CCATATCCGC ATCCAACACA 900
GAAAATCATG ACAAAACAGA AAACCACAAA ACCCCTAACC ACCCCATAAA AGAAGATGAT 960
TTACAAGAAA GCCCACAAGA AAACCCACAA AAAGAAAATA TAGAAGAAAA TATAGAAGAA 1020
AAAGAAACGC AAAACGCTCC AAGCTTTAGC CCACTAACCC TCACCAGCGC TAAAAAACCC 1080
GTTATGGTTA AAGAATTGAG CGAAAATAAA GAGATATTAG ACGGGTTGGA TTATGGCGAA 1140
GTGCAAAAAC CCAAAGATTA TGAGCTTCCC ACAACGCAAT TATTGAATGC GGTTTGCTTG 1200
AAAGAAACTT CTTTAGACGA AAACGAGATT GACCAAAAAA TCCAGGATTT ATTGAGCAAG 1260
CTGCGCACCT TTAAAATTGA TGGCGATATT ATACGCACTT ATTCAGGCCC TATTGTAACC 1320
ACCTTTGAAT TCCGCCCAGC CCCTAGCGTT AAGGTGAGCC GTATTTTAGG CTTGAGCGAT 1380
GATTTAGCGA TGACTTTATG CGCTGAATCC ATCCGCATTC AAGCCCCTAT CAAAGGTAAA 1440
GATGTCGTTG GTATTGAAAT CCCTAACAGC CAAAGCCAAA TTATTTATTT AAGAGAAATT 1500
TTAGAAAGCG AATTGTTTCA AAAATCCAGC TCGCCTCTAA CCCTAGCTTT AGGCAAAGAC 1560
ATTGTGGGTA ACCCTTTCAT CACGGATTTA AAAAAGCTCC CCCACTTGCT CATCGCCGGC 1620
ACGACAGGGA GCGGTAAGAG CGTGGGCGTG AATGCGATGA TTTTATCCTT ACTTTATAAA 1680
AACCCCCCTG ATCAACTCAA ATTAGTGATG ATCGATCCCA AAATGGTGGA ATTTAGCATT 1740
TATGCGGACA TCCCTCATTT ACTCACGCCC ATTATCACTG ACCCTAAAAA AGCTATCGGG 1800
GCTTTGCAAA GCGTGGCTAA AGAAATGGAG CGCCGATACT CTTTAATGAG CGAATACAAG 1860
GTTAAAACCA TTGATTCTTA TAATGAACAA GCCCAAAGTA ACGGCGTTGA AGCGTTCCCC 1920
TATTTGATTG TGGTGATTGA TGAATTAGCG GATTTGATGA TGACAGGGGG CAAAGAAGCG 1980
GAGTTTCCTA TCGCTAGAAT CGCTCAAATG GGGCGAGCGA GCGGCTTGCA CCTCATTGTG 2040
GCGACCCAAC GCCCGAGCGT GGATGTCGTA ACCGGCTTGA TTAAAACCAA CTTGCCTTCA 2100
AGGGTGAGTT TTAGGGTAGG CACTAAGATT GATTCTAAAG TGATTTTAGA CACCGATGGG 2160
GCGCAAAGCT TACTAGGAAG GGGCGATATG CTCTTTACCC CCCCAGGAAC AAACGGGTTA 2220

```
GTGCGCTTGC ATGCCCCCTT TGCCACTGAA GATGAAATCA AAAAAATCGT GGATTTTATT    2280
AAAGCCCAAA AAGAGGTGGA ATACGATAAA GATTTCTTGC TAGAAGAATC GCGCATGCCT    2340
TTAGACACCC CTAACTATCA AGGCGATGAC ATTCTAGAAA GGGCTAAAGC GGTGATTTTA    2400
GAAAAAAAGA TCACTTCTAC GAGCTTTTTA CAACGCCAAT TAAAAATCGG CTACAACCAA    2460
GCCGCCACCA TTACTGACGA ATTAGAAGCT CAAGGCTTTC TATCCCCAAG AAACGCCAAA    2520
GGCAACAGAG AGATTTTGCA AAATTTT                                        2547
```

(2) INFORMATION FOR SEQ ID NO:1069:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

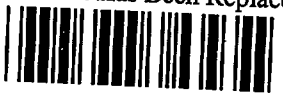
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069

```
AATTACCTAA AAATTTCATG TTCAAGGATA GCCATGAACC CCCAGATTCA ACCCGCCACT      60
AAAAAACCCT TAAAATCCCT TTTAGCCGCT AGTTCAGGCA ATTTAGTGGA ATGGTATGAT     120
TTTTACGCTT ATGCGTTCCT TGCTCCTTAT TTCGCTAAGG AATTTACCCA CACCAATGAC     180
CCTACTCTAG CGCTCATCTC AGCTTTTTTA GTTTTTATGC TAGGGTTTTT CATGCGCCCT     240
TTGGGGAGTT TGTTTTTTGG TAAATTGGGG GATAAAAAGG GGCGTAAAAC TTCCATGGTG     300
TATTCCATTA TCCTTATGGC GCTAGGCTCT TTCATGCTCG CATTGCTCCC CACTAAAGAA     360
ATCGTAGGGG AATGGGCGTT CTTGTTTTTA TTGTTAGCCA GGCTTTTACA GGGCTTTAGC     420
GTGGGAGGAG AATATGGCGT GGTCGCCACT TATCTCTCTG AATTAGGCAA GAATGGTAAA     480
AAAGGTTTTT ATGGCTCTTT CCAATATGTA ACTTTAGTGG GAGGGCAACT CTTAGCTATT     540
TTTTCGCTCT TTATCGTTGA AAACGTTTAC ACGCATGAGC AAATCAGCGC GTTTGCTTGG     600
CGTTATTTAT TCGCTTTAGA GGGTATATTA GCCCTACTCT CGCTCTTTTT GAGAAATATC     660
ATGGAAGAAA CTATGGATAA TGAAGCGACT CCTCAAAAAA AGACTAATGT AAATAATACA     720
AAAGAAACCC ATATCAAAGA AACCCAAAGA GGCAGTTTAA AGGAATTGCT CAACCATAAA     780
AAAGCCTTAA TGATAGTCTT TGGGCTAACT ATGGGAGGGA GTTTGTGCTT TTACACTTTT     840
ACGGTGTATT TAAAAATCTT TTTAACCAAC AGCTCATCGT TTAGCCCTAA AGAAAGCAGT     900
TTTATCATGC TTTTAGCGCT CTCTTATTTC ATCTTCTTAC AACCCTTATG CGGGATGCTT     960
GCGGATAAAA TCAAACGCAC CCAAATGCTG ATGGTTTTTG CGATCACAGG GCTTATTGTA    1020
ACGCCTATTG TCTTTTATGG TATCAAGCAT GCCACTAGCG TGTATGAAGC CCTATTTTAT    1080
GAAATACTCG CATTGAGCAG CATGAGTTTT TACACTTGCA TTGCTGGGGT TATTAAGGCG    1140
GAATTATTCC CTGAACATGT GCGAGCGCTT GGCGTGGGTT TAGCCTATGC GATCGCCAAT    1200
GCGCTTTTTG GAGGGAGCGC GAGTTATATA GCGTTAGAGT TCAAACAGCA TGGTTTTGAA    1260
GAGGGGTTTG TGGGCTATGT CATGTTGAGT ATTGTTATCT TTATGGTTAT GGTTATCATA    1320
TTCCCTAAAA AAACCTATTT GGAG                                           1344
```

(2) INFORMATION FOR SEQ ID NO:1070:

(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:1070

```
AAATGGAAAA ATTTGATGCA ATTGAGTAAC GCTGATTTAG AACGATTAAA AAGCATGGCG      60
AACACGCTTC GCTTTTTGTG TGCGGACATG ATAGATAAGG CTAATAGCGG GCATCCAGGC     120
GTGTGTTTAG GGCTAGCTGA TGTGATGGTG GTTTTAAGCT TGCACCTCAA CCTAAACCCC     180
ACCAACCCTA AATGGCTCAA TAGGGACAGG TTGGTTTTTA GCGGAGGGCA TGCGAGCGCG     240
TTAGTGTATA GTTTGTTGCA TTTGTGGGGC TTTGATTTGA GTTTAGACGA TTTAAAGCGT     300
TTCAGGCAAT TACACTCTAA AACCCCAGGA CACCCTGAAT TACACCACAC CGAAGGCATT     360
GAAATCACCA CAGCGCCTTT AGGGCAAGGT TTTGCTAACG CTGTAGGCTT TAGCATGGCG     420
AGCCAATACG CTCAAACCCT TTTAGATAAA GAGGCGATTT CTCATAAAGT CTATTGCTTG     480
TGTGGGGATG GGGATTTGCA AGAAGGCATT AGTTATGAGA GCACTTCTTT AGCCGGGCAC     540
CTTCGCCTTG ATAATCTCAT TGTGATTTAT GACAGCAACC AGATCAGCAT TGAAGGCGCT     600
ATTAATATTA GTTTTAGCGA ACAGGTTAAA ACACGCTTTT TAGCGCAAAA TTGGGAAGTG     660
CTAGAATGCG ATGGGCATGA CTATCAAGCG ATTCATAACG CTTTAGAAGA AGCCAAAAAA     720
TCCCATAAAC CCACGCTTTT AATCGCTCAT ACGATCATTG GTAAGGGGGC TATTGGCTTA     780
GAGGGGAGTG AAAAAACGCA TGGCTCGCCT TTAAGTAAAG AAGTGTTGAA ACAATCCAAA     840
GAAAACGCTC AAATCAATCC TAACGAAAGC TTTATAATTA GCCCAAAAAA CAAAATGCAT     900
TTTGAAGAAG TGAAAGTTAG GGGTATTAGT TTAGAAGCCT TATGGGAAAA GTCCTTAAGC     960
CCTAAAACAA AAGAAAAGAT CCATGCGTTA AAGAATTTTG ATTTTAACGC CATTAATTAC    1020
CCCGCCTTTA AAAAAGGCGA ATCTCTAGCC ACGAGAGTGA GTAACGGCAT GATTTTAAAC    1080
GCTATCGCTA AAGAATGCGA GGGCTTTTTA GGAGGGAGTG CGGATTTAGC CCCATCCAAT    1140
AACACGCATT TGAAACACTC TGGCGATTTC CCTTTAGGGC AAAACCTGCA TTTTGGGATC    1200
AGGGAGCATG CCATGGGGGC TATCACTAAC GCTTTAGCGG CGTATGGCTT GTTTGTGCCT    1260
TTTTGCGCGA CCTTTTTTGT GTTTAGCGAT TATTTAATGC CTAGCATTCG TTTGAGCGCT    1320
TTAATGAAAT TAAAAGCCCT TTTTATCTTC ACGCATGACA GCATTGGGGT GGGCGAAGAC    1380
GGGGCGACGC ACCAGCCCAT AGAGCAATTG AGCCATTTAC GAGCCTTGCC GCATTTCTAT    1440
GCTTTCAGGC CTAGCGATGC TTTTGAAAAT AAGGCTTGCA TGCAAGTGGC ATTAAGTTTG    1500
AACGCCCCTA GCGCTCTTAT TTTATCGCGC CAGAATTTGT CCGTGCTTGA TGAGGTTTCT    1560
AAAGAGCAGG TTCTAAAAGG GGCGTATGTT AAACACCACT CTAAAGATCC CATTATCACG    1620
CTTGTTGCGA GCGGGAGCGA AGTCTCTTTA GCTTTAGAGA GCGCTAAGAT TTTAGAGCGA    1680
GAAAATATTC CCACTCAAGT AGTGAGCGCG CCATGCTTTG ACTTGTTGGT AGAGCAAGAT    1740
GAAAGCTATT TTAAAGAACT CTTTAAGGGT AAAGTCTTAG TGATTGAAGC GAGCCGCGCG    1800
ATAGAGTGGT ATCGTTTTGC GGATAAAATC ATTGGCATGG ATTCTTTTGG GAGCTCAGCA    1860
AAGGGCGATA AACTCTTTGA AAAATTTGGC TTTAGCGTTG AAAACATTAC CGCTCAAGCG    1920
AAAAGGTTAC TCAACGCA                                                  1938
```

(2) INFORMATION FOR SEQ ID NO:1071:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

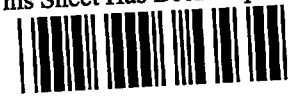
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071

```
AAGGATTATT GCATGCAAAA TGGGTATTAT GCGGCCACAG GGGCAATGGC TACACAATTT      60
AACCGCTTGG ATTTAACCTC TAACAATTTA GCCAACCTAA ACACCAACGG CTTTAAAAGA     120
GACGATGCGA TTACAGGCGA TTTTTTAAGG CTTTACCAAG AATACCGAGA GCAACTGCCC     180
TTAGAAGATC AAACCAAAGC GAGCGCGAAG TATCTCAACC GCAACCTCAA TCGTGTGCCT     240
ATTCTATCAG AAATCTATAC GGATAGGAGT CTTGGCGCGT TTGAAGGGAC GAATAACCCC     300
CTAGATTTTG CCCTAACAAG CCCTAACCTC TATTTTGCGA TACAGACTAA TGAGGGCGTC     360
GCTTATACCA AAGACGGGCA TTTCAGCGTT GATAAAGACG GCTTTTTGGT AACCCTTAAT     420
GGTTTTAAGG TGCTTTCACG CTCCGGTTTG AACGAAAAAG GAGGGATCAT GCTCATGCCT     480
AACGCTGAAA TTGAAGTGGA TCAAAATGGT GGAATCACTT TTAGGGATAA TGAAGCCCAA     540
ATTCAAGCGG GCGCGTTGGC TTTAGTGAGT TTTAGCGAAC CTAAAAATCT TAAAAAAATA     600
GGGCAAAACC TTTATACCTA TCAGGGCGAA GGCGTTCATC AAGTCTCTGA CTCTGGTGCG     660
TTAAGGCAAT CCATGCTAGA AAAAAGCAAT GTCAATGCGG TGCGTGAGAT GAGCACTTTG     720
ATTGAAATCA ACCGCTTTTT GGACATGTAT TCTAAAGTGC TAAAAACCCA TCAAGATGAC     780
ATGAACGCTG AAGCGATTAA CAAACTCGCT ACAAAAGCT                            819
```

(2) INFORMATION FOR SEQ ID NO:1072:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1776 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072

```
GGAATGATAG CGCTGAATTT CAACCTCTTA GATAAAGAAA CAAACACGCC CTTATTTGAA      60
AAAAGCCCGC TAGATTCAAG CTTAGAGCTA TATAAAAATA GCGAAATTCA CATGCTCTAT     120
CCTTATTTGT ATTATTTTGG CTTGGGTAAT GGGGTGTTTT ATCGCTTGCT TTTAGGCAAT     180
GAAAATTTAA AACGCTTGGT GGTCATTGAG CCTGAAATAG AGGTGATTTT CATTGTGCTG     240
AATCTTTTGG ATTTTTCCAC TGAGATTTTA GAAAATCGTT TGATTTTATT GCATGCAAGT     300
TTTTGCAATT ACAACATGAT TGCTTCATTA TTTGATATGG ATAAAAAGTC TCGTTTATAC     360
GCAAGAATGT ATGATTTAAA ACTTTTTAAC GCTTATTATG AACGATACTC TCATCAAATG     420
ATAGAAATCA ACCAGCATTT CACGCGCGCT TTAGAGCATG GCGCTATTAG CGTAGGCAAT     480
GACGCTAAAG ACGCACTCAT AGGCATCAAA CAGCATGTCG CTAATTTGCC TGAAGTCATC     540
AAAAGCCCTA GTTTAGTGGA TTTTGTGAAC GCTTTAAAAA ACAGAGACAC CGCTATTATC     600
GTTTCAACCG GGCCTAGTTT AAATAAGCAA CTCCCCCTTT TAAAAGAAAT CGCTCCTTAC     660
GCAACGCTTT TTTGCATAGA CGCTTCTTTC CCTATTCTAG CCAGAGCCGG TATCAAGCCT     720
GATATTGTGC TGTCTTTAGA AAGGGTGGAT TTAACGGCGA AATTCTATGA AGAAACCCCC     780
TTAGATTTTC AAGAAGGCGT TATTTTTGCT CTGACTTCCA TTGTGCATAA ACGATTGATT     840
CAAGCGATTC AAAAAGGGGT TAAGCAATTC AGTTTCCGCC CCTTTGGCTA TACCAACCTT     900
TTTGATTTGC ACCAGTATGG TTATGTGGGC ATAGGCATGA GCGCAGCGAA CATGGCGTAT     960
GAATTAGTGG TGCATTCTCG TTTCAAAAGG TGCGTGTTTA TCGGGCAAGA TTTGAGCTTT    1020
TCACAAAGCG GTAACAGCCA CGCTAGTGGG GCGATTTATG GCGATAGAGA GATCAAGCCT    1080
AAAAAGGATA AAGACAAGAT TTTTATAGAA AAATACGGGG GTAATGGGAA AGTAGAAACC    1140
```

```
ACTTTAGTGT GGAAACTTTT CTTAGAATTT TTTGAAAAAG ATATTTTTAA CACGCCCTAT    1200
AAATTAGAAG TCATTAACGC TACTGAGGGG GGGGCTAGGA TTAAAGGGAC TAAAGAAATG    1260
CCCTTTAAAG AAGTGTGCGA AAAAATAGAC AAATCCAAGC CAAAGCCTCC TATCAATCTT    1320
ATTTATCCCA CCCAATCAGA ACAGGCTAAA AATTTAAAGA TCGCCAAGAA AAAATGCGAA    1380
GAGATCATCA AATACGCCAA TGAGAAAAAA ACGCAAGTTG AAGAAGCGTT TTTAAAGGTG    1440
GCAGAGTTTT TAGAAAAAGT GGAAAAGCTT CATGAAAAAA ACAAATTAGA AGAGTTGGAT    1500
TTTGAAGAAT TAGAAAATTT GAGCGCTGAA ATTGATAACG TTAAAGAGCT TTTTGATGAC    1560
AAACGATTCA ATTCGTATTT TATGGATGCG ATACAATCTT ACATTTTCCA CCAGGAATTG    1620
CATATCGCTG AAATCGTGTG TAAAAAAACG AGTAATGAAG ACGGATTAAG GGCTAAGCAA    1680
TTAGAATACA TTTACGCGCA CAAATACTGG CTTTTTAGTT TAGCGGGTGG GATGGATTGC    1740
GTGATAGAAG CGATCAAAAT GGCTTTGAAA GAATGG                               1776
```

(2) INFORMATION FOR SEQ ID NO:1073:

(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:1073

```
GTGCATTTTA CGTGTATCTT TCTAACCCTA TTAAAATGGA TTTTGCCAGC CAAAAACAAG      60
CAGGCGTGCA AAAAGCCACC AACCAGATCC ATTCAAGGTC TGCAAAACAT CCAGCAAAAT     120
ATCCCCCCTC AAGTATTAAC CCCTCAAATC CAAGCGGGTA TACAAGGGGT GATGCAAGGT     180
TTTGGGGCTT TGAGCAGCAC TTTAGAAGCC CCCTTATTGT TTTCTAAGCA AAATGTGGTG     240
ATTGGGGGCT TTGAGCATTA TTTATCCCCT TTATATGGGT GGGGCAAGAT TCACGATGGT     300
GCGCATTGCC GAATTGAATG CAAAAAGACG CCAATGAAGT GTATCGCT                  348
```

(2) INFORMATION FOR SEQ ID NO:1074:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1074

```
CGCATGAATT TTTTTAAAAT CCTTTTAATG GAGTTAAGAG CCATTGTTTC TCATAAGGGC      60
GTTTTATTGA TCCTTATAGG CGCTCCTTTA ATCTATGGCT TGTTATACCC TTTGCCTTAT     120
TTGAAAGACA TCGTAACGCA GCAAAAAATC GCCCTTGTAG ATGAAGACAA TTCCTTCCTT     180
TCTAGGCAAT TAGCCTTCAT GGTGCAAAGC TCCAACGAGT TAGAAATCGC TTTCTTTAGC     240
CCCTCTATGC TGGAAGCCAA AAAGCTTTTA AAAGAAGAAA AAATTTATGG GATCTTACAC     300
ATTCCCTCTC ATTTTGAAGC CAATATTTAT AAACAAGTGC CTGTAACGAT AGATTTTTAT     360
GCGAACGCCA ATTACTTTTT GATTTATGGT GCGTTAGCGA ATGCGGTGGT GGGGAGCATC     420
AACGCCTTAA ACGATGAAAT CAGGTTCAAA CGCAACGCCC AAATAGAAGA AGCTGAATTA     480
GGGACAGACG GGATTAAGAT TAAGCCTATC GCTTTGTATA ACCCTAGTGA GGGGTATTTG     540
AATTACGCGC TCTCTAGCGT GTTTATTTTC ATCTTACACC AGGTGATGCT CATTGCAAGC     600
AGCATGTTTA CTAGCTCCAG GCGTTTGGAA TTGGCCCTTT TAGACAAGAA ACAAATCGCT     660
TTAAGGCTGT GCGCAAGACT CTTGGTGTTC ATGGGGGCGT TTAGCGTTTT TGTTTTATGG     720
TATTTTGGGG CGCTGTTTTC TTTTTATGGG ATCGAACGGC ATGGAAGCGC TTTAATGGTG     780
TTTTTGAACA GCTTGATTTT CATGCTTGCG GCCTTGAGTT TGGGGTCGTT TTTAGGGGCA     840
TGGATCAAAA ATGAAGCCCA CACCACTCAA ATCGTTTTGA TTTCTTCTTT GCCCTTGATT     900
TTTATGATGG GTTTTGTGTG GCCTTTTGAA TCCTTGCCCT CTTATTTGCA AGTCTTCGTT     960
CAAATAGTGC CTGCTTATCA TGGGATCAGT TTGCTCGGGC GATTGAATCA TATGCATGCG    1020
GAATTTATAG ATGTTTATAT CCATTTTTAC GCGCTTATTG CGATTTTTAT CGTGAGTTTT    1080
ATAGGGTGCG TGTTCAAACT CAGCTCTTTA AAGAAAGCTT GTGAAAACGC T             1131
```

(2) INFORMATION FOR SEQ ID NO:1075:

(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:1075

```
ACCTTAAAAG GGATTGTTTT GTTCAGATTG ATAAGCGCAT GGGTTTTACA AGACAAGTTC      60
TTGTTTGTCG TGTGTTTTAT ATTGCCTTTT TGTTTAGGGG TTTTAGGCAC GCAAATCTTT     120
AAACAAGAGA CCCCAAGACA GCTCCCTATC GTGGTGGTGG ATTTGGATAA GACCACTACA     180
AGCCATCAAG TGGCGTTTGA ATTAGGCGCA ACGAGTGCGG TTGAAATCAA ATACCAAGTG     240
ACTAGCCTTT CAGAAGCTAA ACGCTTT                                         267
```

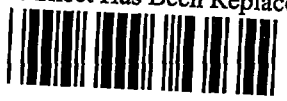
(2) INFORMATION FOR SEQ ID NO:1076:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

This Sheet Has Been Replaced



(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076

```
AGCATGAAAA AAACAACCCT CTTTGTATTG GGCTTATTAT TCAATAGCTC TTTAAGCGCT      60
GTTGATGGGA TTTCTCAAAC CGAGCCTTCT TCTTTGAATT TGGCTGAAGA TAGCCTGCCT     120
TTGAACCATT CTAACGCCCA AAAACTCTCT TTAAAAAACG CATGGAATAG GGTGTTGTCT     180
AATCATGAAG GCTTGCATGC GCAGAATACG CCATTAAGCG AGCGAGTAAA A              231
```

(2) INFORMATION FOR SEQ ID NO:1077:

(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:1077

```
GTAAGGAGAC AAACTATGAA AAAGGTTATT GTGGCTTTAG GCGTTTTGGC GTTCGCAAAT      60
GTTTTAATGG CAACCGATGT TAAGGCTCTT GTAAAAGGTT GTGCCGCTTG CCATGGGGTT     120
AAGTTTGAAA AGAAAGCTTT AGGTAAAAGC AAAATCGTTA ACATGATGAG CGAAAAAGAG     180
ATTGAAGAGG ATCTTATGGC TTTTAAAAGC GGTGCCAACA AGAATCCTGT CATGACCGCG     240
CAAGCTAAAA AATTAAGCGA TGAAGACATC AAAGCTTTAG CCATATACAT CCCCACTCTC     300
AAA                                                                  303
```

(2) INFORMATION FOR SEQ ID NO:1078:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078

```
AGACCTATGC TACATAAAAA ATATCGTCCT AATGTTGCGG CCATTATCAT GTCGCCAGAC      60
TACCCTAACA CATGCGAAGT TTTTATCGCT GAGCGCATAG ACATTGAAGG GGCGTGGCAG     120
TTCCCCCAAG GAGGCATTGA TGAGGGAGAG ACCCCTTTAG AAGCACTCTA TAGAGAATTA     180
CTAGAAGAAA TTGGCACGAA TGAAATAGAG ATTTTGGCGC AATACCCTAG ATGGATCGCC     240
TATGATTTCC CAAGCAACAT GGAGCATAAA TTCTATTCGT TTGACGGGCA AAAGCAGCGT     300
TATTTTTTAG TGCGCCTAAA GCATGTTAAC AACATTGATT TGAACAAACA CACGCCAGAA     360
TTTAGATCCT ATCAATTCAT CCAGCTTAAG GATTTGCTTA AAAAAATCGT TCCCTTCAAA     420
CGCCAAGTGT ACCGCCAAGT CATCGCTTAT TTTAGAAAAG AGGGGTATTT GGGGTGT        477
```

(2) INFORMATION FOR SEQ ID NO:1079:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079

```
TGCATGAATC TTGTCTTTTT GTGGGCCGCT CTAGGAGGGG CTATAGGGAG CTCGTTAAGG      60
TATTTTGTGG GCAAAATGAT GCCCAGTAAA TTTTTAATGT TTGAAAGTTT CCCTTTAGGG     120
ACTTTTAGCG TGAATCTCAT AGGGTGTTTT ATCATCGGCT TTATGGGGCA TTTGGCCGCT     180
AAAAAAGTTT TTGGTGATGA TTTTGGGATT TTCTTTGTAA CCGGAGTTTT AGGGGGTTTT     240
ACGACCTTTT CTTCTTATGG GTTAGACACT TTAAAACTCT TGCAAAAATC CCAATACCTT     300
GAAGCCATTT CTTATGTCTT AGGCACTAAC CTTTTAGGGC TTATTGGGGT AGCTATCGGT     360
TGGTTTTTGG CTAAGAATTT TGTAGGCGTT AAT                                  393
```

(2) INFORMATION FOR SEQ ID NO:1080:

This Sheet Has Been Replaced

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080

```
TATTTATCAA TCGTGGTGGA AGATCAGAAA GGCATTTTCC CTATCGCAGC GTCAAAAAGA      60
AAAAGCCAAA GCTCTGTGAT CATTGAAGAC GTGTGCTTCA GCAAAGAGGA TTTTGTAGAA     120
GGGGCAAAAG CGATTGAGGG GCTTTTAAAA AAACATGGCT TTAAGGATAA TGGCATTATT     180
TTTGGGCATG CGTTAAGCGG GAATTTGCAC TTTGTCGTTA CGCCGATTCT AGAAAATGAA     240
GCTGAAAGAA AAGCGTTTGA AAATTTAGTT TCTGAGATGT TTTTAATGGT GAGCAAAAGC     300
TCTGGCTCTA TTAAAGCCGA ACATGGCACA GGCAGGATGG TAGCCCCTTT TGTGGAAATG     360
GAGTGGGGAG AAAAAGCTTA TAAGATCCAC AAACAAATCA AGGAATTGTT TGATCCTAAT     420
GGCCTTTTAA ACCCTGATGT GATCATCACA AACGATAAAG AAATCCACAC TAAAAATTTA     480
AAGAGCATTT ACCCTATTGA AGAGCATTTG GACATGTGCA TGGAATGTGG GTTTTGTGAA     540
AGGATCTGCC CCAGTAAAGA TTTATCCTTA ACGCCACGAC AACGCATCGT CATCCACAGA     600
GAGGTAGAGC GTTTGAAAGA AAGGGTAAGT CATGGTCATG ATGAAGATCA GGTTTTACTA     660
GATGAGCTTT TAAAAGAGTC TGAATACTTA GCGCATGCCA CTTGCGCGGT GTGCCATATG     720
TGTTCCACTT TATGCCCTTT AGGGATTGAT ACCGGGAGTA TCGCTTTAAA TCATTATCAA     780
AAAAACCCTA AAGGCGAAAA GATCTGCTTC AAAGATTCT                            819
```

(2) INFORMATION FOR SEQ ID NO:1081:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 723 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...723

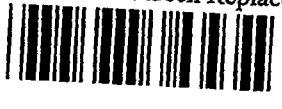
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081

```
CGATTTTTAC AAAAGAGTGC GCAAATTTGG GGAATTAAAA TGCTAGTAGA AATAGAGAAT      60
TTGACTAAAA CTTATGGGAG TTTAAAAGCG CTAGACAATA TCAGTTTGAA ACTACCCAAA     120
CAGCAATTTA TAGGGCTTTT AGGGCCTAAT GGGGCGGGTA AAACCACTCT GTTAAAAATT     180
TTAGCCGGAT TGAATTTGAA CTATCAAGGG GAAGTGAAAA TTTTAAACCA AAAGATTGGT     240
ATAGAGACTA AAAAAAGCGT GGCGTTTTTA AGCGATGGCG ATTTTTTAGA TCCTAAATTA     300
ACGCCTTTAA AAGCGATCGC TTTTTATAAG GATTTTTTTA GCGATTTTGA TGAATCAAAA     360
GCCCTAAATT TGTTAAAACG CTTCAGCGTG CCTTTAAAAA GAGAGTTCAA AGCCCTTTCA     420
AAAGGCATGA GGGAAAAATT GCAGCTGATT TTAACCCTAT CACGAAACGC TTCTTTGTAT     480
CTTTTTGATG AGCCGGTGGC TGGGATTGAC CCTATTGCAA GAGAAGAGAT TTTTGAGTTA     540
ATCGCTAAGG AGTTTAGCCA AAACGCAAGC TTGCTAGTCT CTACGCATTT GGTGGTGGAT     600
GTGGAAAAGT ATTTAGACAG CGCGATTTTT TTAAAAGAAG CTAAAGTGGT GGCTTTTGGG     660
GATGTGGGGG AATTAAAAAA AGGGTATAGC AGTTTGGAGG CAGCGTATAA AGAAAGGTTG     720
AAA                                                                  723
```

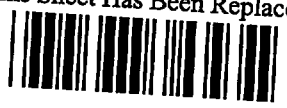
(2) INFORMATION FOR SEQ ID NO:1082:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 864 base pairs
(B) TYPE: nucleic acid

This Sheet Has Been Replaced



This Sheet Has Been Replaced



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

(ii) MOLECULE TYPE: DNA (genomic)

(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:1082

```
AAATCGTGGT TTTTCTATGC CCCTTTTTAT GGTTTGTGGT GTTTAAAAAC CCCTATCATA      60
GGGCATGGCA TGAAGAAAAA AGCAAAAGTC TTTTGGTGTT GTTTTAAAAT GATTCGTTGG     120
TTGTATTTGG CGGTCTTTTT TTTGTTGAGC GTATCAGACG CTAAAGAAAT CGCTATGCAA     180
CGATTTGACA AACAAAACCA TAAGATTTTT GAAATCCTTG CGGATAAAGT GAGCGCCAAA     240
GACAATGTGA TAACCGCCTC AGGGAATGCG ATCCTATTGA ATTATGACGT GTATATTCTA     300
GCGGATAAGG TGCGTTATGA CACCAAGACT AAAGAAGCGT TATTAGAAGG CAATATTAAG     360
GTTTATAGGG GCGAGGGCTT GCTCGTTAAA ACCGATTATG TGAAATTGAG TTTGAACGAA     420
AAATATGAGA TCATTTTCCC CTTTTATGTC CAAGACAGCG TGAGCGGGAT TTGGGTGAGC     480
GCGGATATTG CTAGCGGGAA GGATCAAAAA TATAAGATTA AAAACATGAG CGCTTCAGGG     540
TGCAGCATTG ACAACCCCAT TTGGCATGTC AATGCGACTT CAGGCTCATT TAACATGCAA     600
AAATCGCATT TGTCAATGTG GAATCCTAAG ATTTATGTCG GCGATATTCC TGTATTGTAT     660
TTGCCCTATA TTTTCATGTC CACGAGCAAT AAAAGAACTA CCGGGTTTTT ATACCCTGAG     720
TTTGGCACTT CCCACTTAGA CGGCTTTATT TATTTGCAAC CCTTTTATTT AGCCCCCAAA     780
AACTCATGGG ATATGACCTT TACCCCACAA ATCCGTTACA AAAGGGGTTT TGGCTTGAAT     840
TTTGAAGCGC GCTACATCAA CCCT                                            864
```

(2) INFORMATION FOR SEQ ID NO:1083:

(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:1083

```
ATCGTTAGAA AGAAGTTAAT GTTAGAGATG AGTTTGCAAG CATTAAATAC ACAAGATTCT      60
TCTGTGATGG CTCAATCCTT GCTTGTCCAT GCCTTTTTTG CCGCCTTGCT CGCCCTAGCC     120
TTTATGATCA ATCTTTACAC CCTTTTTTAAA GAAAAGAATT TCATCCAATT GAACCGGAAA     180
ATCTATCTTG TCATGCCAGC GATTTATATT CTTTTAAGCA TCGCTCTTTT GAGTGGGGTT     240
TTTATTTGGG CGATGCAACA ATTTGAATTT TCTTTTAGCG CTGTTGTCAT GCTTTTGGGG     300
TTGTTGTTGA TGCTCATTGC AGAAATCAAA CGCCATAAAA GCGTGAAATT CGCTATCACT     360
AAAAAAGAAA GGATGAAAGC CTATATCAAA AAAGCTAAAA TCCTGTATTT TTTAGAAACG     420
```

ATTCTTATCA TCGTGTTAAT GGGCATT 447

(2) INFORMATION FOR SEQ ID NO:1084:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1084

```
CCAGAAGGAG GGAATGAACT CAATGTGTTT GAGCCGGTTA TCGCTTACAA GCTTTTCCAT     60
TCCTTTGTGA TTTTAGGGTG CGCGATTGAA ACTTTAACGA CTAAATGCGT GGAAGGCATC    120
ACGGCTAATG AAAAGATTTG CCACGATTAT GTTTTTAACA GCATTGGCAT TGTTACCGCG    180
CTCAACCCTC ATATCGGCTA TGAAAAATCC GCTATGATCG CCAAAGAAGC CTTAAAAAGC    240
GATCGCTCTA TCTATGATAT CGCTTTAGAA AAGAAAATCT TAACCAAAGA GCAACTGGAC    300
GATATTTTCA AGCCAGAAAA CATGCTAAGC CCTCACGCTT TCAAAAAGCA TAAAGAC       357
```

(2) INFORMATION FOR SEQ ID NO:1085:

(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:1085

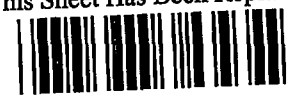
```
AAAAGGCTTA TGGTTTTGTT TCTATCCATT TTTAAAAAAA GCTTTAATGA TTTTTTAAGC     60
GCTAGAATGC TTTTAATCAA TCTTGGCCCT ATCCTTTTGA GTTTGGCGTT TTTTGGAGCT    120
ATCTTTTTATT ACAATGGCGG GAGTATTGTG AATTATTGCC AAACTTTATT ACCGCAATCT    180
TTGAATGATT ACGCTCATTC TCAAGGCTTT TTTGCCGGTG TGTTCGCATG GGTTTTTAAA    240
GCGTTAGTGT ATTTTCTTAT TTTTTGGATC GTAATTCTTT TGAGTTTAGT CATCAATATT    300
TTTGCGTCTA TTTTTTACAC CCCTTTAGTG GTCTCTTATT TGCACCAAAA ATATTATCCC    360
CATGTCGTTT TAGAAGAATT TGGCTCTATC CTTTTTTCTA TTAAATATTT TTTAAAATCG    420
CTCACTTTTA TGCTTTTATT CTTAGCGGTT TTAACGCCCC TTTATTTCAT TCCCTTTATA    480
```

GGGGTCTTTG GGGTCTTTTT TTCTATAGTC CCGCATTTCC TCTTTTTCAA AAACACCATG 540
AGTTTGGATA TAGCCAGCAT GATTTTCAAC CATCAAAGCT ATCAAAATTT ACTCAAACAG 600
CACCGATTGA AGCATTATCG TTTTTCGTTT TTTTGCTATC TTTTTTCCTT GATTCCTTTT 660
TTTAATTTTT TTGCCACCTT GTTGCAAACC CTAATGTTAA CGCAC 705

(2) INFORMATION FOR SEQ ID NO:1086:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1086

GAATGTAAAG GAATGGAATT TATGAAAAAG TTTGTAGCTT TAGGGCTTCT ATCCGCGGTT 60
TTAAGCTCTT CGTTGTTAGC CGAAGGTGAT GGTGTTTATA TAGGGACTAA TTATCAGCTT 120
GGACAAGCCC GTTTGAATAG CAATATTTAT AATACAGGGG ATTGCACAGG GAGTGTTGTA 180
GGTTGCCCCC CAGGTCTTAC CGCTAATAAG CATAATCCAG GAGGCACCAA TATCAATTGG 240
CACTCCAAAT ACGCTAATGG GGCTTTGAAT GGTTTTGGGT TGAATGTGGG TTATAAGAAA 300
TTCTTCCAAT TCAAGTCGCT AGATATGACA AGCAAGTGGT TTGGTTTTAG AGTGTATGGG 360
CTTTTTGATT ACGGGCATGC CGATTTAGGT AAACAAGTTT ATGCACCTAA TAAAATCCAG 420
TTGGATATGG TCTCTTGGGG TGTGGGGAGC GATTTGTTAG CTGATATTAT TGATAAAGAC 480
AACGCTTCTT TTGGTATTTT TGGTGGGGTC GCTATCGGCG GTAACACTTG GAAAAGCTCT 540
GCAGCAAACT ATTGGAAAGA GCAAATCATT GAAGCCAAAG GTCCTGATGT TTGTACCCCT 600
ACTTATTGTA ACCCTAATGC CCCTTATAGC ACCAACACTT CAACCGTCGC TTTTCAAGTG 660
TGGTTGAATT TTGGGGTGAG AGCCAATATC TACAAGCATA ATGGCGTGGA ATTTGGCGTG 720
AGAGTGCCGC TACTCATCAA TAAATTTTTG AGCGCGGGTC CTAACGCTAC TAACCTTTAT 780
TACCATTTGA AACGGGATTA TTCGCTTTAT TTGGGGTATA ACTACACTTT T 831

(2) INFORMATION FOR SEQ ID NO:1087:

(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:1087

```
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 ACGCCCCTGG AAAGGCATTA TCCAAATCGC TTATGACATG     360
TTTAAAGAGC AAAAGGATTT GAGCGATTAC ATGAGCGAAA AAACCTGTTC TTCGTGTAAT     420
GGGCATCGCT TGAAAGCCTC AAGTTTGAGC GTCCAAGTCG CTGGCTTGAA AATGGCGGAT     480
TTTTTAACTA AGCCCATTGA AGAAGTCTAT CATTTTTTTA ATGATCCCAC 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 CCAAATTTGA 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 AACCCCACGA AGCAACCCCG CCACTTACAC GGGAGTGATG    1320
GATGAAATCA GGATTTTATT TGCCGAGCAA AAAGAAGCTA AAATTTTAGG CTATAGCACG    1380
AGCCGTTTCA GCTTTAATGT TAAAGGAGGG CGGTGTGAGA AATGCCAAGG CGATGGGGAT    1440
ATTAAAATAG AAATGCACTT TTTGCCTGAT 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 CCCTTTATAT TTTAGATGAG CCTACCACCG GTTTGCATTT TGAAGATGTG    1800
AATCACCTTT TACAAGTCTT GCATTCTTTG GTGGCGTTAG GCAATTCCAT GCTAGTGATT    1860
GAGCATAATT TAGACATCAT CAAAAACGCT GACTACATTA TAGACATGGG GCCTGATGGG    1920
GGGGATAAGG GCGGGAAAGT CATTGCGAGC GGCACGCCTT TAGAAGTGGC GCAAAATTGC    1980
GAAAAAACCC AAAGCTATAC GGGAAAATTT TTAGCTTTGG AATTGAAA                 2028
```

(2) INFORMATION FOR SEQ ID NO:1088:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1088

```
GCGCGTTTTG TTAAAATCAC AGCGGATTAT TTTTCCCCTA TGGAAAACGT GTTTTACCGC      60
TCCATTACCA TGACGCTTTT ACTCTTGCTT ATCTATCCTT TCAAACCCTA CCGCTTGAAG     120
AGTTACAAAC AAGGCGGTTT TAAAAAGCTC GCCTTTAGGG TCGTTGTGGG GGGCTTAGCC     180
```

```
ATGCTGGCGT TTTTTTATAA TATTGAAAAA ATTTCGCTCG CCACAGCGAA CGCTTTCTCA     240
CAATGCGCGC CTATTTATAC GGTGCTCCTT TCCCCTTTGC TTTTGAAAGA AAAGCTCAAA     300
AGAAGCGCGT TAATTTCCGC ATGCATCGGG CTAGTGGGGG TGGTGTTGAT TTCAGATCCT     360
AGCGTGGAAA ATGTAGGACT AGTTGAAATC ATTATGGGCA TATTGAGCGG GATCTTTGTG     420
TCTTTAGCGT ATATCACTTT AAGGGATTTG AGGGAATATT ACGACAAGCA GGCCGTGATT     480
TTAGCGTTCG CCTTTGGCAT GAGTCTTCTT GGATTAGCGG GCATGTTCAT TGATATTCCT     540
TTTTTATCCA CAGGCGTTCA TATCCCTAGA AAAGAGGATA TTTTATGGAT TTCTTTAATA     600
GGGATTAGCG GGACTTTAGG GCAGTATTTC TTAACCTATG CTTACATGAA CGCTCCTGCT     660
GGGATCATCG CCCCCATTGA ATACACCCGC ATTGTTTGGG GGCTATTGTT TGGGCTGTAT     720
TTAGGCGATA CATTTTTGGA TCTTAAAAGC TCTTTAGGGG TGGCTTTGAT CTTATGTTCA     780
GGCTTGCTCA TTGCCTTGCC CGCTCTTTTA AAAGAATTAA AAAAAATT                   828
```

(2) INFORMATION FOR SEQ ID NO:1089:

(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:1089

```
GTCATGCAAC TAAGCCCCTT ACAAAGCGCG CTGTTATATT TCCGTTACTT TATTTATCCG      60
GAAAAAAAAA CAAGGAGCTT TGATTTAAGC GATTTAATTT TTATTGTCAT GGTTTTTTTA     120
GTCCTAGCTT TGGGGCTGTT GATGAGCGAA GAAATTTCTA TCAGCTACAA TGAAGCGAAA     180
GACTTTTTTT ATAGCGATGC GTGGTTTGTC AAAATCGCTC AAAAAAGCGT AGCCATTTTA     240
GGCCAAAACG ATTTGGCTTT AAGATTGCCT TTTTTGATCG CTCACGTCAT CAACATGTTT     300
TTATTCTACC TCATAGGGCG AAAGATTTTA AAAAAGCCTA AAGACGCTCT TTATGTGGTA     360
TTGACTTACG CTTTATTGCC TGGGGTGAAT CTCTTTGCGA TTTTACTGGC TAAAAGCGTG     420
CTGGTGTTAA GCCTTGGGCT TTTGATTAGC TATTTGTATA TTAAAACCCA AAAAATCCCT     480
TATTTAACCC TTAGCGCTTG CGCGTTTTTA GACGGTGCGT TCATCCCGCT TTTACTAGGG     540
GTTTTTGCCT ACGCTTTAAG AAAACGCTAT TTTAAGAGCG CGATCTTTGC TTTGGTGGTT     600
TTAATTGTGA ATACCGCTCT TTTTAGTGGG GATTTTAATA AAGGCTTGCC TAGCGGGTAT     660
TTTATAGACA CTTGCTTAGA ACTCATGCTT TTGTATTCGC CCTTATTGTT CCTCTACTAC     720
CCTTATACGC TCTATAAAGC CCTTTTGGAT AAAAAGCCAT CGTTACTAGC CTTTATGGCG     780
CGAGCGGCTG GCTTTTCCCT TTGCTTT                                         807
```

(2) INFORMATION FOR SEQ ID NO:1090:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 723 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090

```
AGCCCTTTTA TGGATAGAAA ACTCTTAAGA TTATACCAGC CCTTAAACGC TTATTCTTAC      60
AATAGCGATT CGCTTTTTTT ATACGATTTT TCACGCCCTT TTATCAAAAA TAGCGGCGCG     120
ATTTTAGACA TAGGCTCAGG GTGTGGGGTT CTAGGCTTGC TCTGCGCTAG AGACAACCCG     180
CTAGCGAGCG TTCATTTAGT GGAAAAGGAT AGCAAAATGG CGTTTTGCTC CCAAAAAAAC     240
GCCCTTAAAT TCCCTAACGC TCAAGTGTTT GAGAGCGATT TTTTAGATTT TAACCCTCCG     300
ATTTTGTATG ATGCGATTGT GTGCAACCCT CCTTTTTATG CTTTAGGATC TATTAAATCT     360
CAAATTAAAG GGCATGCGAG GCACCAGAGC GAATTAGACT TCGCTTCTTT GGTGGCTAAA     420
GTGAAAAAAT GCCTGAAACC TAAAGGGTAT TTTATTTTTT GCTATGAAGC CTTGTCGCTT     480
TGCTTGGTCA TAGAGAGCTT AAAAAGCGTT AAACTCACGC TAGAAACTTT AAGGTTTGTC     540
CAAAGTTTCA AAGACAAAAA CGCCCATTTG ATGCTTGGAG CGGCTAGGAA TAATTCCAAA     600
AGCGCTCTAA AAGTTTTGCC CCCTTTAATC ACGCACAATT CCAAAAACCA AAGCGACAAC     660
ACCAAAGAAG TTTTAAACAT CTATCAAATT TGTAACACTT ATTCTATCAA AGCGCCTTTA     720
GAT                                                                  723
```

(2) INFORMATION FOR SEQ ID NO:1091:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

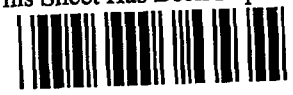
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091

```
TCTCGTTCTT TTAGGGGGCT ATTATATTAT AATAAGATAA ATTTGATTAA TAAGGATACA      60
GGCTTGCAAG AAATTAAATT AGACATTTAT GCCACTTTAG TGTGCATGGT TTTGGTGTTG     120
CTTTTGGGGC GTTATGTGAT TTCTAAAGTC AAGTTTTTAA GAGATTATGA TATTCCAGAG     180
CCTGTTGTGG GTGGGGTTTT AGTCGCTTTT TTTATCATGT TAGCGCGTCA ATTTTATCAT     240
TTTGGCTTGC AGTTTGATTC TTCTTTAAAA GATCCTTTAA TGCTGACTTT CTTCATCACC     300
ATTGGTTTGA GCGCGGATTT CAAATCTTTA CAAAAAGGCG GGAAAATGCT TGCGGTTTTT     360
TTGCTGGCTG TAGCGGGGTT TGTGGTGTGC CAAAATGCAG TGGGGATTTC TATCGCTAGC     420
CTTTTAGGGG TCAATCCTTT AATGGGGCTT TTAGGGGGAT CGATCGCTTT AGTGGGTGGG     480
CATGGCACTA GTGCGGCATG GGCTAATTTT TTCACCCAAC CACCTTATCA TTTTAGCTCT     540
AGCTTGGAAG TGGGCATGGC GTGCGCGACT TTTGGCTTGG TGAGCGGGGG GATTATTGGA     600
GGGCCTGTCG CTAAATATTT GATTTCTAAA TACAAACTAG AACCTAAAGA CACTAAAGAA     660
AAAGACACTT TAGAGGGCGT GGTGTCTAAA GGTTTTGAAA CCCCTAAAGA GCAGCGCCTA     720
ATCACTGCAT CCAGTTTTGT AGAAACTTTA GCTCTCATTG CAATAGCTTT ATTAGTGGGG     780
ACTTTTTTAT CGCATTTGAT GCCTAAAAGT TTCACCTTAC CGACTTTCGT GTGGTGTTTG     840
TTTGTGGGGG TTATCTTAAG GAACGCTTTG TCGTTTTTTA AAATCCATAG CGTGTTTGAC     900
AGAGAGGTTT CAGTTATAGG GAATGTGAGC TTGAGCCTGT TTTTAGCTTA CGCTTTAATG     960
AGCGTGAATT TATTGGAATT GTTAAAACTC GCTGTGCCTT TAGCGGTTAT TTTGAGCGTT    1020
```

```
CAAGTGGCGG TTATGATCCT TTATGTGGTG CTTGTAACCT TTAGGGTATG CGGGAAGGAT    1080
TATGATGCGG CGGTGTTGTG CGCGGGGCAT TGCGGTTTTG GGCTTGGAGC GACCCCAACG    1140
GCTATGGTGA ATATGCAAAC CATCACCAAC CACTATGGGC CATCGCATGT GGCGTTTATC    1200
GTCGTGCCTT TAGTGGGAGC GTTTTTTGTT GATATTATTA ACGCTTTAGC GATTAAAGGC    1260
TTTTTGCTTT TGCCTTTTTT CCCTAGT                                        1287
```

(2) INFORMATION FOR SEQ ID NO:1092:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092

```
AAATTCGTTT TGCGTTCAAT TTCAAGGATA AAGATGCTTT CAGTGTATGA AAAAGGGAAT     60
GCCCTAGACA AAAGGGTGCT TGAAGAATGG CTTTTAAGCG AAGACATTTT AATGGAAAAC    120
GCCGCTATGG CTTTAGAAAG GGCGGTTTTA CAAAACGCTT CTTTGGGCGC TAAGGTCATT    180
ATTCTTTGTG GGAGTGGGGA TAATGGAGGT GATGGCTATA CTCTAGCCAG GCGTTTAGTG    240
GGGCGTTTTA AAACGCTGGT CTTTGAAATG AAATTAGCAA AAAGCCCCAT GTGCCAATTG    300
CAAAAAGAAA GGGCTAAAAA AGTAGGGGTA GTCATCAAAG CATGGGAAGA AAAGAATGAA    360
GATTTAGAAT GCGATGTGTT AGTAGATTGC GTGGTAGGGA GCGCTTTTAA GGGCGGATTA    420
GAGCCGTTTT TAGATTTTGA AAGCCTTTCT CAAAAAGCAC GCTTTAAAAT CGCTTGCGAC    480
ATTCCTAGCG GGATAGATTC TAAAGGCAGG GTGGATAAGA GGCGTTTAAG GCGGATACGA    540
CTATCAGCAT GGGCGCTATC AAGTCATGCT TAC                                 573
```

(2) INFORMATION FOR SEQ ID NO:1093:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

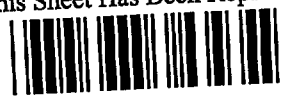
(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093

This Sheet Has Been Replaced



```
AATGCCCACA ACTTGAAAGA TAAAACCTTT CAGGGGGGGT TTGAACTTCT TACGACCCCC      60
AAAGAATACT CATGGTGTGG GGTTGTTTTA AGCCTTTTGT TGGCGATTAA CCTTTATTTA     120
GAATACTTGA ATCACCAAAA GCTTGATTTT TCAAAACCTA CAAGCTTGAA CGCTCAAATC     180
TTATTACAAT ACCCTAAAAC GAAAGATCAA AAAACCTATT TTGTCTTAAA ACTCCAATCT     240
AAGGGCATGA TCTTTTACAC CACCATTAAA GAGCCTTTAA AAAACCTCCA ATACCGCTAT     300
GCGCAATTTT TTGGCAAGAT CAAGCCTTGT TCGTTCTTAG AGTCTCTAAA ATCATGCTTT     360
TTTCAAACCT ATTCTTTTTC TTTAACGCGA AAACAAGATT TCAAATCGCA TTTGCGCCAT     420
TTCATTGACA GCGCCCATTC CAACGCCTTA GTGGGTAATT TGTATCGAGC GTTATTCATA     480
GGGGATAGCT TGAATAAAGA CTTAAGAGAC AGGGCTAACG CGCTAGGGAT CAACCACTTA     540
CTGGCCATTA GCGGGTTTCA TTTAGGGATT TTGAGCGCGA GCGTGTATTT TCTTTTCTCT     600
CTTTTTTATA CCCCCTTACA AAAACGCTAT TTCCCTTACA GGAACGCTTT TTATGATATA     660
GGGGTTTTGG TGTGGGTTTT TTTGCTGGGG TATTTATTGC TATTAGATTT TTTACCCTCT     720
TTTTTCAGGG CGTTTTTAAT GGGCTTATTA GGGTTTTTGG CATGCTTTTT TGGGGTAAGG     780
ATTTTGAGTT TTAAACTTTT GGTTTTAGCG TGCTGTATCG CCATAGCGTT ACTCCCTAAA     840
TTGCTTTTTA GCGTGGGGTT TTTGCTTTCT GTTTGTGGGG TGTGGTATAT CTTTTTGTTT     900
TTAAAACACA CTCAAATTTT TTTTAAAGAT TCTTCTTTTT TCAAGCGATC GTTTCAAGCG     960
ATCGCTTTAA GCGTGTTAGT GTTTTTGAAC ATGCTCATTG TTGCGCATGC CTTTTTCCCT    1020
ATGTTTTCGC CCTACCAGCT CTTTAGCATT CCTTTAGGCT TGATTTTTAC TGTGTTTTTC    1080
CCTTTGAGCT TGTTCTTGCA TGCGGTGGGT TTAGGGTCTT TATTGGATAA TATTCTAAGC    1140
ATGCCTTTAA CCATCCCCAC GATTTCGGTT TCTTCGCCTT TATGGCTTTT GGGGGCGCAT    1200
TTGTTTTTAA CGATTTTAAG CGTGCGTTTT TTTAAGGTTT ATTTAAGCAT GAATGTTTTG    1260
AGCATGGGCT TTTTCTTGTA TTGTTGCTAT CAATATATTA TAATGCCTAG TTTAATTGTG    1320
GGT                                                                  1323
```

(2) INFORMATION FOR SEQ ID NO:1094:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094

```
GAGGCGTTTA AGGCGGATAC GACTATCAGC ATGGGCGCTA TCAAGTCATG CTTACTAAGC      60
GATAAGGCTA AAGACTATAT AGGGGAATTG AAAGTGGGGC ATTTAGGGGT TTTTAATCAA     120
ATTTATGAGA TCCCAACAGA CACTTTTTTA CTAGAAAAAA GCGATTTGAA ACTGCCCTTA     180
AGGGATAGAA AAAACGCTCA CAAAGGCGAT TACGGGCATG CGCATGTGCT TTTGGGCAAG     240
CATAGTGGGG CGGGGTTGTT GAGCGCTTTA AGCGCGTTAA GTTTTGGATC TGGGGTGGTG     300
AGTATCCAAG CGTTAGAGTG CGAGATAACT TCTAATAACA AGCCTTTAGA ATTGGTTTTT     360
TGTGAAAATT TCCCTAAAAA GCTCAGCGCG TTCGCTCTTG GCATGGGGTT AGAAAATATT     420
CCAAAGGATT TTAAGAAGTG GCTTGAATTA GCCCCATGCG TTTTAGATGC GGGCGTTTTT     480
TATCATAAAG AAGTGTTACA AGCCTTAGAA AAAGAAGTGA TCTTAACCCC TCACCCTAAA     540
GAGTTTTTAT CGTTATTGAA ATCAGTGGGG ATCAATATAA GCATGCTAGA ATTACTAGAC     600
AATAAACTAG AAATCGCAAG GGATTTTTCT CAAAAATACC CCAAGGTGGT TTTGCTTTTA     660
AAGGGGGCTA ATACCCTAAT CGCTCATCAA GGGCGGGTTT TTATCAACAA TTTAGGGAGC     720
GTGGCTTTAG CCAAAGCAGG CAGTGGCGAT GTGTTAGCGG GGCTGATTGT AAGCCTACTT     780
TCTCAAAACT ACACGCCTTT AGACGCCGCC ATTAACGCAA GTTTGGCGCA CGCCCTAGCG     840
GGTTTAGAAT TTAAGAATCA TTACGCTTTA ACGCCCCTAG ATTTGATAGA AAAGATCAAA     900
CGACTA                                                               906
```

(2) INFORMATION FOR SEQ ID NO:1095:

(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:1095

```
CTCGCTTTAG CGTCAAAAGC GACCGGGTTT CCCATTGCAA AAGTGGCTAC CATGCTTGCG      60
GTGGGTTTTA GCTTAGATGA AATTAAAAAC GATATTACCA ACACCCCAGC GAGCTTTGAG     120
CCTAGTTTGG ATTATATCGT GGTGAAAATC CCTCGCTTTG CGTTTGAAAA ATTTGCCGGT     180
GTTTCTAGCA CTTTAGGGAC TTCCATGAAA AGCATTGGAG AAGTGATGGC GATAGGGGGG     240
AATTTCTTAG AAGCCTTACA AAAAGCGTTA TGCTCTTTGG AAAACAATTG GCTAGGGTTT     300
GAATCGTTAA GCAAAGATTT AGAGGCGATA AAAAAGGAAA TCCGCCGGCC CAATCCCAAA     360
CGCTTGCTCT ATATTGCTGA TGCGTTCAGG TTGGGCGTTT CTGTGGATGA AGTGTTTGAA     420
TTATGCCAGA TTGACAGGTG GTTTTTATCT CAAATTCAAA AACTAGTCAA AGCAGAAGAG     480
GGCATCAATT CTAGCGTTTT AACGGACGCC AAAAAATTGA GAGGGCTTAA AAATTTAGGC     540
TTTAGCGATG CCAGGATTGC CACTAAAATC AAAGAAAATG AAAATTTAGA GGTCAGCCCT     600
TTTGAAGTGG AATTAGCTAG ATCTAATTTA CAAATCGCGC CCCATTTTGA AGAAGTGGAC     660
ACTTGCGCGG CGGAGTTTTT ATCGCTCACG CCTTATTTGT ATTCCACCTA TGCCCCTAAC     720
CCTTTGCCCC CTATTGGAAA CAAACAAGAA AAACAAGAAA AGAAAATCCT AATCATAGGC     780
TCTGGGCCTA ACCGCATCGG TCAAGGCATT GAATTTGATT ATTGTTGCGT GCATGCGAGC     840
TTTGCTTTAA AAGATTTGAA CATTAAAAGC GTCATGCTCA ATTGCAATCC AGAAACCGTA     900
AGCACGGATT ATGATACTAG TGATACGCTC TATTTTGAAC CCATACATTT TGAATGTGTG     960
AAGAGTATCA TTCAAAGGGA GCGAGTGGAT GGCATTATCG TGCATTTTGG GGGACAAACC    1020
CCTTTAAAAC TCGCTAAAGA TTTAGCCAAA ATGCAAGCCC CCATTATTGG CACGCCTTTT    1080
AAGGTGATTG ATATTGCAGA AGACAGAGAA AAATTTCCCT CTTTT                    1125
```

(2) INFORMATION FOR SEQ ID NO:1096:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096

```
CGTCCAGTCA TTAGCGCCAA AGAAGGGAGC GATCCAAGCT CTCTAGCTTA CAACACCATA      60
GAAAGCGCGA TCGCTAAAAA TATAGATGAA GTTTTTATAG ACACCGCCGG GAGGTTGCAC     120
AACCAGACCA ACCTCAAAAA CGAGCTTTCT AAAATCGCGC ACACCTGCTC TAAAGTTTTA     180
AAAGACGCCC CCTTTTACAA ATTCCTTATT TTAGACGGCA CGCAAGGGAG TTCTGGGCTA     240
ACGCAAGCGA AGATTTTCCA TGAGACTTTG GCGCTAGATG GCGTGATTAT GACTAAGCTT     300
GATGGCACTT CTAAGGGCGG AGCGATTTTA AGCGTGCTGT ATGAGTTGAA ATTACCCATT     360
CTTTATTTAG GAATGGGCGA AAAAGAAGAC GATTTGATCG CTTTTGATGA AGAACGCTTT     420
ATAGAAGATT TGGTTGATGC GGTGTTTGTG GAACAA                               456
```

(2) INFORMATION FOR SEQ ID NO:1097:

(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:1097

```
AATTTAAGGA TTATAACCAT TAAAACGATT TTTAGAGATT TTTGTAAAGA ACGCTTGAAA      60
AGGGCTAAAT CAAAAAATAA AGTCAGGGAT AAATTGGCTT GCAAGCTTTT GTTTTGGAAA     120
CTCAAAGATT ATCAAAATAT TTTATTGTAT AGCCCATTAG GGCATGAGCT TGACATTAGG     180
CCTTTGATTT TGAAGTTAAG ACAAAAAAAT AAGCGCGTGT GGTTGCCTAA AAGCATCAAA     240
AAAGGCGCTC ATTTTTCTAA AGAGGGTTTT ACTATCGCGC CCTTTAGGTT GCCATTAAGG     300
CGTTTGGGGT GGTTTGATGA GCCGAGTTTG TCGCGCTATT ATAAGCGGGA ATTGGATTGT     360
ATTGTCGTGC CGATTTTAGG AATGGATACA AGCTTTAGGC GCGTGGGTTT TGGGCTAGGC     420
ATGTATGATA GGAGTTTACC CCAATTATTC AAAAAGCAAC TAAAACGCCC CTTAGTCATA     480
TTTGTAAGTA GGGAGTTAGC GCTGGCTAAT GGTATTCTTA CAGACGCCTA TGACATTGAA     540
GCAAATCTTT ACATGAATGC TCGTATCGTT ATGAAGAATA ATAAAAGGAA ACATTATGAG     600
CAGCGGGTTA ATTTACATTT CATTAGAAGT CTTGGTAGCG TGTTTGATCA CCGCTCTAAT     660
CATGTATTAT GTGATGAAAA AGATCTATTA CGC                                  693
```

(2) INFORMATION FOR SEQ ID NO:1098:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 600 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

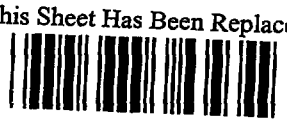
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

This Sheet Has Been Replaced



(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098

```
AGAATAATAA AAGGAAACAT TATGAGCAGC GGGTTAATTT ACATTTCATT AGAAGTCTTG      60
GTAGCGTGTT TGATCACCGC TCTAATCATG TATTATGTGA TGAAAAAGAT CTATTACGCT     120
AGAGGGCAAG CCATTTTAAA AGGCGCTTCA GCCAAAGCTA AATTAATGGA ATTTCAAGCG     180
AAATCTTTCG TGGAAGCTGA AGAAATGCGC ATGAAAAGCC AAGAATGCAA GTTGCAACAG     240
CAATATGAAA ATAAGAATTT GCAACTCCAA ACCCATTTTG ATAAAAAAGA AGCGCATTTG     300
AAGCATTTAG AAGCGCAGCA CAAAGAATTT GTAAGAGATG AAAAACGCTA TTTGGAAAAG     360
GAAAAAAAAG AGCTTGAAAA AGAACGCCAA ATTTTAGAAC AAGAGAGGGA AAATTTTAAA     420
AAACAGCGCG CCATTTGTAA AGAAGCTCAA GCCAAAGCGC TAGATGCGAT GCTCAATTAC     480
ATGGCTTATA CCAAAGATGA AATTAAAAGC ATGATCTTAG AGCAATTAGA ACAGGAACTA     540
GAAGCGCAAA AGAGCGCCTT GATCAGGCGT TATGAAGAAG AAGCCTTTAT TATGTGTTTA     600
```

(2) INFORMATION FOR SEQ ID NO:1099:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1050 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099

```
ATAAGGTCAT CAAATGACAC CCAAACCACC CAAACACCAT GGCACTCAAA CACCAGACGG      60
CCAAAACCCA CCCCTAAACC CATTAAAAAA GAGGCTAAAA AGGCTAAAGA GAAAACAACT     120
AAGCATGCGC ATTCAAAGCA TGCGCACTCT CCATTGAACG AAAGGAGCGC TAAAAAAGAA     180
ATTCCTAAAA AAGAAATCCC TAAAAAAGAA ATCCCTAAAA AAGAAATCCC TAAAAAAGAA     240
ATCCCTAAAA AAGAAATCCC TAAAAAAGAA ATCCCTAAAA AAGAAATCCC TAAAAAAGAA     300
GCAGAAAATG AGAGTAAGAA CCAAATCTTT ATAGCAGAAA AAAATGATAC TTGGATCAAA     360
ACCAAGCGCA AAAAACACAA AAAGATCGTT TTGGACGCTG GGCATGGGGG GAAAGATTGC     420
GGGGCGATGA GCGCGAATTT GGTGTGTGAA AAGGACATTG TTTTAGAAGT GGTGAAGTTT     480
TTGCATAAAG AGCTTAAAAA AAGAGGCTAT AGCGTTTTAT TGACAAGGGA TAAGGACATT     540
TACATTGATT TAGTGGCCCG AACGGAATTA GCCAATAAAA AAGGGGCGGA TTTATTCATC     600
TCAGTGCATG CCAATTCCAT CCCTAAACGC TCCACCTCTA ACGCCCATGG CATAGAGACT     660
TATTTTTTAT CCACCGCAAG GAGTGAAAGG GCTAGGAAAG TGGCTGAGCA AGAAAATAAA     720
GACGATGTGA ATTTAATGGA CTATTTTTCT AAAAGTTTGT TTTTAAATTC ATTGAACACG     780
CAGCGATTGA TCGTCTCCAA CAAATTAGCG ATTGACGTGC AATACGGCAT GCTCCAAAGT     840
GTCCGCAAAA ATTACCCTGA TGTGGTGGAT GGGGGTGTTA GGGAGGGGCC TTTTTGGGTG     900
TTAGCCGGGG CTTTAATGCC TTCAATTTTA ATAGAAATTG GTTATAATTC CCATGCGATA     960
GAATCTAAAC GCATCCAAAG CAAACCGTAT CAAAAAATCT TGGCTAAGGG CATTGCTGAT    1020
GGCATTGATA GTTTCTTCAG CAAGAATGAT                                      1050
```

(2) INFORMATION FOR SEQ ID NO:1100:

(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:1100

```
AGAGTATCTA TGAATGTCAA AAAAAAGGGA AAGCCACAAA GTGGAAAGAT TGATAGGGTG      60
GATTGTTTGG AGAAACTTGG GAAAGAAAAC ACTACTTTTT TAAGCAGTAT AGCTATGGGG     120
AGCATTGGTC AATTAGCGAT CCCCATTCCT GGAGTTGGAG TGCTCATTGG GGGCTTTGTG     180
GGTGGGGTGA TGAGTAAAAC TTTTTATGAT GTCTCGCTAA CGATTTTCAA AGAGGCTAAA     240
TTAGCGCGTC AAAGGCGTAT TGAGATTGAA AAAGAATGCC GTGAGAGTAT CAGACAGTTA     300
GAGATGTATC AAAATCAATT TAATGAAGTG TTTGAGCGGT ATTTTCATGG GACTATAAAA     360
TTCTTTAATG AAAGTTTTGA TGAGCTGGAG AGGGCGCTTT GTGCGGGCGA TGCGGATTTG     420
GCTATAGCAG TCAATAACAA GATCCAAGAG GGGATGGGTC AAGAGTTGCT GTTTGACAAT     480
AAGCAAGAGT GCTGGGAATT TATCACTAGC CGTAAAGAGG GTTGGAATTT CGTCACTAGC     540
CGTGGAAAAA CAGAAATT                                                  558
```

(2) INFORMATION FOR SEQ ID NO:1101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1086 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101

```
AAGAGGGATC AAATGGCCGA AGAAGAAAAG ACCGAACTCC CTAGCGCGAA AAAAATCCAA      60
AAAGCCAGAG AAGAAGGCAA TGTGCCTAAA AGCATGGAAG TGGTGGGGTT TTTAGGGTTA     120
TTGGCTGGGC TAATGAGTAT TTTTGTTTTT TTTATATGGT GGGTGGATGG CTTTAGCGAG     180
ATGTATCGCC ATGTGTTGAA AGATTTCTCC CTAGATTTTA GCAAAGAAAG CGTTCAAGAG     240
CTGTTTAACC AGCTGGCTAA AGACACTTTT TTATTGCTTT TGCCTGTTTT AATCATTTTA     300
ATGGTGGTGG CGTTTTTGTC TAATGTCTTG CAATTTGGCT GGCTCTTTGC CCCTAAAGTC     360
ATTGAGCCTA AATTTTCTAA AATCAACCCT ATCAATGGCG TCAAAAACCT TTTTTCTTTA     420
AAAAAGATCC TTGATGGGAG TTTGATCACT TTAAAAGTTT TTTTAGCTTT TTTTCTGGGG     480
TTTTTCATCT TTTCCTTATT TTTAGGGGAA TTAAACCATG CGGCTCTTTT GAATTTGCAA     540
```

This Sheet Has Been Replaced



```
GGCCAGTTGT TGTGGTTTAA AAGCAAGGCG TTATGGCTCA TTTCTTCGCT TTTATTTTTA     600
TTTTTTGTCT TGGCTTTTGT GGATTTAATC ATCAAACGCC GCCAATACAC TAACTCTTTA     660
AAAATGACTA AACAAGAAGT TAAGGACGAA TACAAACAGC AAGAAGGAAA CCCAGAAATC     720
AAAGCCAAAA TCCGCCAGAT GATGGTAAAA AACGCCACGA ATAAAATGAT GCAAGAAATC     780
CCCAAATCCA ATGTCGTGGT GACTAACCCT ACCCATTATG CCGTCGCTCT CAAATTTGAT     840
GAAGAACACC CTGTGCCTGT GGTAGTGGCT AAAGGCACGG ATTATTTAGC CATTAGGATT     900
AAGGGTATCG CCAGAGAGCA TGACATAGAA ATTATAGAAA ATAAAACGCT CGCTAGAGAG     960
CTTTATAGAG ACGTGAAATT GAACGCCACC ATACCAGAAG AATTGTTTGA AGCGGTAGCG    1020
ATTGTCTTCG CTCAAGTGGC TAAATTAGAG CAAGAACGCC AAAAACAAAA GATCATTAAA    1080
CCTCTT                                                               1086
```

(2) INFORMATION FOR SEQ ID NO:1102:

(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:1102

```
GAAAATACTA TGCAAGATTT ACAACATTTC AAAAATGATA TTACGCTCAT TCTGTCTAAA      60
GACAGATTAG ATACTTATGA CAGCCTAGAG CAATACAAAG AAAATTTAAA ACTCATTTCT     120
TTCATCACGC CTAAAATCTC TAACTTAGAG ATTTATTTAC GCAACGCTTT AGACTATTGC     180
TTAACCCAAA TTAAGGGGAG CGAATGGGTG TTTAATGAAA ATTCTTTAAC AGATTTAATT     240
AACGAACAAA AAGAAAAGAA AAAAGAAATC ACGCATTCTT TAATCTTATC TAAAATGTCT     300
TTAGGGGCAG TGGTTAGGCT TATTTTTTGT TATAAGTTAG AGGGGGTAAT ATTAGATTTG     360
AGAGCGTATC GTTTGAGAGC TTATTATCAC GAAAATAAAG ATACCTTGCT TATTAAAGGC     420
AAAAAACGCC TTCTTTACAA TTATATTAAA GCCCATATTG CTTTAAACTT GCTATGGACA     480
ATTAGAAATC GCACGTATCA TTGGGAAAAT TTACTCAAAA TCCAACCGAA CAACCGCCCA     540
CAA                                                                  543
```

(2) INFORMATION FOR SEQ ID NO:1103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 567 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

This Sheet Has Been Replaced



(A) NAME/KEY: misc_feature
(B) LOCATION 1...567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103

GCTAATGGAT GCGAAAAAAG GATTTTCATG CTGCTTTGCG CGGGAAGGAA TGAGACTTTA 60
AAAAAAGCGG TGCCTATTGG TGTGGGCTTG ATAGAGAGCG CGATCAATTT AACGAGAATG 120
TGCCTTAAAA ACCCTGATAC AGAAAGCCTT ATTTTTATAG GGAGCGCGGG GAGTTATAGC 180
CCAGAAACGG AGATTTTGAG CGTGTTTGAA AGCATTGAAG GCTATCAAAT TGAAGAGAGT 240
TTTAGCCATT TAAACAGCTA CACGCCTTTG GATAATTTCA TTCACATAGA AACTAAAGAG 300
CAGGCTCTTT TTGAAAGGGT GCGTGTGAAT AGCAGTAACT ACATCCACAC CAGCGAAATG 360
TTTGCTAAAA AAATGGTTCA AAAGGGCGTT TTATTAGAAA ACATGGAGTT TTTTAGCGTC 420
TTAAGCGTGG CTAAAATTTT TTCTTTAAAG GCTAAAGGGA TTTTTTGCGT GAGCAATCAT 480
GTAGGGCTTA ACGCGCATAA GGAATTTAAA GAAAACCACG CCAAAGTCAA ACAGATTCTA 540
GAAAACATCA TTGATAGTTT GATAGTT 567

(2) INFORMATION FOR SEQ ID NO:1104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1018 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104

TTTTAATGAG TTTTATAAGC TTGCAATCGC CTCTTGGCAA GAACCCTTAA GAGTGAGTAT 60
AGAATTTGTG GATTTGCCTA AAAAAATCAT CCGTTTTCCG GCCCATGATT TGAAAGTGGG 120
GGAGTTTGGT TTTGTGGTTA CTCAACTTTC AGATTATGAA ATCGTTAATT CTGAAGTGGT 180
CATTATTGCT GTTGAAAATG GCGTCGCAAC GGCTAAATTC AAAGCGTTTG AGTCGATGAA 240
ACAAAGCCAT TTACCCACTC CAAGAATGGT CGCTAAAAAA GGGGATTTAG TCTATTTCAG 300
GCAATTTAAC AACCAAGCGT TTTTGATCGC TCCTAATGAT GAACTCTATG AGCAAATCAG 360
AGCGACTAAC ACCGATATTA ATTTCATTAG CTCTGATTTG TTGGTTACTT TTTTGAATGG 420
GTTTGACCCA AAAATCGCTA ATTTAAGGAA AGCGTGCAAT GTTTATAGCG TGGGGGTGAT 480
TTATATTGTA ACCACCAACA CGCTCAATAT TTTAAGTTGT GAGAGTTTTG AAATTTTAGA 540
AAAAAGAGAG CTGGATACAA GCGGCGTTAC TAAAACTTCC ACGCCGTTTT TTTCTAGGGT 600
TGAGGGCATT GATGCAGGCA CGCTAGGGAA ACTTTTTTCA GGCAGTCAAT CTAAAAATTA 660
CTTCGCTTAC TATGACGCTT TAGTGAAAAA AGAAAAACGA AAAGAAGTAA GGATTGAAAA 720
GAAAGAAGAA AGGATTGATG CTAGAGAAAA TAAACGAGAA ATCAAGCAAG AAGCCATTAA 780
AGAGCCTAAA AAAGCCAATC AAGGCACAGA AAACGCTCCC ACTTTAGAAG AGAAAAACTA 840
CCAAAAAGCA GAGCGAAAAT TTGACGCTAA AGAAGAAAGG CGTCGTTCAA GAGATGAAAG 900
GAAAAAAACT AAAGCCACCA AAAAGGCTAT GGAATTTGAA CAAAGAGCGA GAGAACATCA 960
AGAAAGAGAT GAAAAAGAGC TTGAAGAAAG AAGAAAAGCT TTAGAAATGA ATAAGAAG 1018

(2) INFORMATION FOR SEQ ID NO:1105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 852 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

This Sheet Has Been Replaced



(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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:1105

```
GGAGAAACAA CAATGAAACT GAGAGCAAGT GTTTTAATCG GTGTGGCAAT TCTGTGCTTA      60
ATTTTAAGTG CGTGCAGTAA CTATGCGAAA AAAGTGGTGA AACAAAAGAA CCATGTTTAT     120
ACGCCTGTGT ATAATGAACT GATAGAGAAG TATAGTGAGA TCCCCTTAAA TGACAAACTC     180
AAAGACACAC CATTCATGGT GCAAGTGAAG TTGCCAAATT ACAAGGACTA TTTGTTGGAT     240
AATAAACAAG TTGTACTAAC TTTCAAACTT GTTCACCATT CTAAAAAGAT TACGCTCATA     300
GGCGATGCCA ATAAGATCCT CCAATACAAG AATTACTTCC AAGCTAACGG GGCAAGATCT     360
GACATTGATT TTTACTTGCA ACCCACTTTG AATCAAAAGG GTGTGGTGAT GATAGCGAGT     420
AACTACAATG ATAATCCCAA CAACAAAGAA AAACCACAGA CCTTTGATGT GTTGCAAGGA     480
AGTCAGCCAA TGCTAGGAGC TAACACAAAA AACTTGCATG GCTATGATGT GAGTGGAGCA     540
AACAACAAGC AAGTGATCAA TGAAGTGGCA AGAGAAAAAG CTCAGCTAGA AAAAATCAAT     600
CAGTATTACA AGACTCTCTT GCAAGACAAG GAACAAGAAT ATACCACTAG GAAAAATAAC     660
CAACGAGAAA TTTTAGAAAC ATTGAGTAAT CGTGCAGGTT ATCAAATGAG GCAGAATGTG     720
ATTAGTTCTG AGATTTTTAA GAATGGCAAC TTGAACATGC AAGCCAAAGA AGAAGAAGTT     780
AGGGAGAAGC TACAAGAAGA AAGAGAGAAT GAATACTTGC GCAATCAAAT CAGAAGTTTG     840
CTCAGTGGTA AG                                                        852
```

(2) INFORMATION FOR SEQ ID NO:1106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 723 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

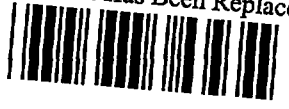
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106

```
AGTTATTGTC AAATGAAAAC ACTCGTGAAA AATACCATAT ATTCTTTTTT GCTATTGTCT      60
GTTTTGATGG CAGAAGATAT AACAAGCGGC TTAAAGCAAC TGGATAACAC CTACCAAGAG     120
ACCAACCAAC AAGTGCTCAA AAACCTAGAT GAGATTTTTT CAACCACTAG CCCTAGCGCT     180
AATAATAAAA TAGGTCAAGA AGATGCTCTA AACATCAAAA AAGCGGCCAT TGCTTTGAGA     240
GGAGATTTAG CGTTATTGAA AGCCAATTTT GAAGCGAATG AGTTATTTTT CATCTCAGAA     300
GATGTGATTT TTAAGACTTA TATGTCTAGC CCTGAACTTT TATTAACCTA TATGAAAATC     360
AATCCCTTAG ACCAAAAGAC TGCTGAGCAA CAATGCGGAA TATCCGATAA AGTTTTAGTT     420
CTTTATTGTG AGGGGAAGCT GAAAATCGAG CAAGAAAAAC AAAATATAAG AGAGCGTTTA     480
```

GAAACTTCTC TAAAGGCATA TCAGAGCAAC ATTGGAGGTA CAGCTTCCTT AATCACTGCT 540
TCACAGACGC TTGTAGAAAG CCTAAAAAAT AAAAATTTCA TCAAAGGAAT CAAAAAGCTT 600
ATGTTAGCTC ACAACAAGGT CTTTTTAAAT TATTTAGAGG AGTTGGACGC ATTAGAAAGA 660
TCCCTAGAAC AAAGTAAGCG ACAATACCTA CAAGAAAGGC AATCAAGTAA GATCATTGTT 720
AAA 723

(2) INFORMATION FOR SEQ ID NO:1107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1617 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1617

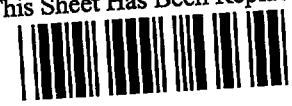
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107

ATAAATAAGA ACATGTTTAA TATTAAAAGG ACTTTTTTAA TAACGATCAT AAGTTTTTTT 60
CTCATTGTTC CTAATTGGTT GAAAGCTATT GATTTGCCCA TTGTTTCAAA TCTCAAAATT 120
TACCAAACAG TTTATTGCAT GCTGATACCG AGTTATGTTT TAACCAACAA AAGTTTTGCA 180
GATATTTTGA CAGGCTATAC ATCTATTGGT GCATCAGGGA GTGGAAAGAG TTCAGGGCAG 240
GGTGTGATCG AAGCGCTTAG CACACCATTA GCCACAAGTT TAGCCGCTAG CAATCTGGTG 300
AAATATTTGA ATACTTTAGG TCCTTTATGG GGATCGGCGT GGGCAAGTGT TGCTACAGCT 360
ATACAAGGTT TTGCTCTAAC GCCATCAAGT GGCTGTAATT TTGGTTGGAA CGCATTGATA 420
AATAAAAACA TAGATGTATC CATGGATAGC GTACTAGACA ATTTGAGCAA CAAGATTCAG 480
AATTTTACCA AAGGCGGTGT TGAGGACAAT GTGAAAGGCA ATATTCTTTT ACAAATAATT 540
GGCTCAATAA CCGCTCAAGC TTCTACGAAT ATTACAGCTG ATGGTTTAAT TTGGCTGATT 600
GGTAAAGAAT TCACTGCAAA TAAACTGCAA AACAACACTA TAGCCATGCT TGCTTTTGCC 660
GCATTAGAAT CTGTTGTCAA AGGAGCGGAC GCTGCTGTTC TTCCTGCATA TGGTGTAGTC 720
AATCTGCCTG ATATTATCAT AGGGCAAGGG TCATATCTTG ATTTTGTTTC TTACCTAATT 780
TATATTGTTT TTGGGATTTT TGTTTTTATT TCTTTTATGA AATTGAGAGA TATTTCAAAC 840
GGCATTCAGA TTAACATAGG TTTTGAATAC ATGCGATTTG TTGGGGGGAC ATTATTCAAA 900
ATGGCGATGG TCTCTTTTAT CGCCTATGCA GGTTTTGGTT ATCTTTATAA AATCTCTTAT 960
TCTATTTATT TTGGTTTAGC AGGTGCTTTT GGGCTGAATC AAGTTCTTTT TTGGGCTTTA 1020
GATTTAGTGC TGAATTACAC TGTTAATTCA ATTTTACCTG CGGTAAGAGC TGTTTTTTCT 1080
AATGTTGGCA ACAACGCTCC TAGTTTGTTA CAAGGCTTGC AAGTGGCAGG TATTTCTTTA 1140
TTCGCTATTT TTATGCAAGT AACTATCATT ATGAGAATAA GCACTGTTGT TGTGAAACCT 1200
TTGATAGCGG GGGCTTTTAG CGGTATTGTT TTCCCTATTG CAGTATGTTT GATCGTGCTA 1260
GATTGGTTCA AAGATTCTAT GAAAAACATA TTGATATGGT TTATTAATAA TCTGTTTATC 1320
TTGGTTCTAG CTATTCCTAT TTTGCTCTTT GGTGTTTTGG CATTATTGGC ATTCAATTTG 1380
ACCATAACGC CCTCTGTTGC TATACAAAAC ATCAATCAAG GGGGATTGGG TATCGATTCA 1440
ACTATTGCGA GTTTGATCAC TCTATTTATT TTAAAAGGTT TCATAGAGAC GATTATTGAG 1500
AGCGTCAATG CGATCGTTAA CACCATTTTC AGCTCTGTCT CTATGGATGG TAGCAGAATG 1560
GATAGAGAAA GAGATGCCTT AATGGTGGGA AGAGTTGGTG GATCTATGTT TAAAGGA 1617

(2) INFORMATION FOR SEQ ID NO:1108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 768 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

This Sheet Has Been Replaced



(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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:1108

```
CTCCATAGAA TTATCTCCTG CGATAGCGCT TGGAGGACTA ATCTTGTTGT GCGGACCAAT      60
AAAGCCTTGT ATCAATTCAT TTTGAGGATA GCCCAAAAAG ACAATTTTGC TTCAGCGTAT     120
CTAACAGTCA AATTAGAATA CCCACAAAGA CACGAAGTCT CTAGCGTTAT TGAAGAGGAA     180
TTAAAAAAGA GAGAAGAAGC AAAGAGGCAG AGAGAATTGA TCAAGCAAGA AAATCTCAAC     240
ACCACAGCCT ACATCAATAG AGTAATGATG GCGAGCAATG AACAGATTAT CAACAAAGAA     300
AAAATAAGAG AAGAAAAACA AAAAATTATA CTAGATCAAG CAAAGGCGCT AGAGACCCAA     360
TATGTGCATA ATGCGTTAAA AAGAAACCCT GTGCCTAGAA ACTACAATTA CTACCAAGCG     420
CCTGAAAAAC GCTCTAAACA TATTATGCCC TCTGAAATTT TTGATGATGG CACATTCACT     480
TATTTTGGTT TCAAAAACAT CACTCTCCAA CCTGCTATTT TTGTGGTTCA ACCTGATGGG     540
AAATTGAGCA TGACTGATGC CGCCATTGAT CCTAACATGA CTAATTCAGG ATTGAGATGG     600
TATAGAGTTA ATGAAATTGC AGAGAAGTTT AAGCTCATTA AAGACAAAGC CCTTGTAACA     660
GTGATCAATA AAGGCTATGG GAAAAATCCA TTGACAAAAA ATTACAATAT CAAAAACTAT     720
GGTGAATTGG AGCGTGTGAT TAAAAAGCTC CCTCTTGTCA GAGATAAA                  768
```

(2) INFORMATION FOR SEQ ID NO:1109:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109

```
ACTAGTTCTT TCAAAACCAA AATGAAACGA CCGATCAGCA AATTGAAACA AAACTTTTTA      60
CAATTCAAAC ATTCTTTCAA CAAACATTTA GATAAGTACA GCCTTTATTA TAGGCTGTTC     120
AATATCAGCT CTATCGTTAT AGGTTTTTTA ATAGCGCTTT TTTCTTATGG GGCAGGGGTG     180
ATTTTAGTTT ATCCAATATT ATTCTTGTTT GCTCTTATAA TAAAACCTAG CTTTTTTTAT     240
TACACTACTT ATCTTTTGCT ACTCGTTTCT CTCAGCATAA TAAGCAAATA CTATCTCCTA     300
AGCCACGCAA ATTTCACAAT GAAGCTAATC ATGCTTATGA CTCAATGGCA AAATTGGTTC     360
TTA                                                                  363
```

(2) INFORMATION FOR SEQ ID NO:1110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110

```
GTATGCTATT GTGAAATGCT TCCTACTAAA ACACGCATTA GAGATCCGAA CAAGCAAGAA      60
CTTACACAAC CAAAAATAAA AGGATTGAGT ATGGGAAAAA TTTTAGCTTC TTTGTTGGGT     120
GGCGGAACAA ATCTTTTTAC AGGTTTATCC AGTGATTTGT TTTCTATGAT ATTAAATTTT     180
TTGTTCTTCC TGATGTTAAT GATGGGACTT AATGAAGCAT TAGGGAAAAA ATTTAACTTG     240
CCTATGGACA ATATCAAGAA TTTTATGGCA GAAGTGCTGA AGAATGGATT CGATAGTATC     300
AAAAACATGG GATCTGCTTT GGTTGGTAAT GGTTTTGGTA GCAGCAAATC AGACAAAACC     360
ACTAATAAAA TGAGTGTCCC ACAAGTAAGA CTC                                  393
```

(2) INFORMATION FOR SEQ ID NO:1111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 891 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

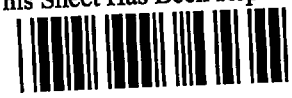
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111

```
GAGGAATTGT TGATGGGGCA GGCATTTTTT AAAAAAATTG TTGGCTGTTT CTGTCTTGGT      60
TATTTATTTT TATCTAGCGC AATAGAAGCA GTAGCACTTG ACATTAAGAA TTTTAATCGT     120
GGTAGGGTGA AAGTGGTGAA TAAGAAGATT GCTTATTTGG GAGATGAAAA ACCTATTACG     180
ATTTGGACTT CATTAGACAA TGTTACCGTG ATCCAACTTG AAAAAGATGA AACTATTTCT     240
TACATCACAA CAGGTTTCAA TAAAGGTTGG AGTATTGTGC CTAATTCTAA TCATATATTC     300
ATTCAACCTA AATCGGTAAA AAGTAATCTC ATGTTTGAAA AAGAAGCAGT GAATTTTGCC     360
CTAATGACAA GAGATTACCA AGAATTTTTA AAGACAAAAA AACTTATCGT AGATGCGCCT     420
GACCCTAAAG AATTAGAAGA ACAAAAAAAA GCTCTAGAAA AAGAAAAAGA AGCTAAAGAA     480
CAGGCGCAAA AGGCACAAAA AGATAAAAGA GAAAAAAGAA AGGAGGAGCG TGCAAAAAAT     540
AGAGCCAATT TAGAAAATCT CACTAACGCT ATGAGTAACC CACAAAATTT GAGCAATAAC     600
AAAAATCTTA GCGAATTGAT CAAGCAACAG AGAGAAAATG AATTAGACCA AATGGAACGA     660
```

CTAGAGGACA TGCAAGAGCA GGCTCAAGCT AACGCACTCA AACAAATTGA AGAGCTCAAC 720
AAGAAACAAG CTGAAGAGGC AGTTAGGCAA AGAGCCAAGG ATAAAATCAG TATTAAGACA 780
GATAAATCTC AAAAAAGCCC CGAGGATAAC TCCATAGAAT TATCTCCTGC GATAGCGCTT 840
GGAGGACTAA TCTTGTTGTG CGGACCAATA AAGCCTTGTA TCAATTCATT T 891

(2) INFORMATION FOR SEQ ID NO:1112:

(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:1112

AGCTGTCGCA TGTTAGGGAA AAAAAACGAA GAAGTCTTGA TTGATGAAAA TTTGGTTGGG 60
GGTGTGATAG CCCTTGATAG ATTGGCAAAA CTCAATAAGG CCAATAGGAC TTTCAAAAGG 120
GCTTTTTATC TCTCTATGGT GCTCAATGTC GCCGCTGTAA CGAGTATTGT GATGATGATG 180
CCTTTGAAGA AAACAGATAT ATTTGTTTAT GGCATTGATC GATACACAGG AGAATTTAAA 240
ATCGTCAAAC GCTCCGATGC TAGGCAAATC GTCAATTCTG AAGCCGTTGT GGATAGTGCA 300
ACTTCAAAAT TTGTCTCATT GCTGTTTGGT TATAGCAAAA ATTCTTTGAG GGATCGCAAG 360
GATCAACTAA TGCAGTATTG CGATGTGAGT TTCCAAACCC AAGCAATGAG AATGTTCAAT 420
GAAAATATCA GACAATTCGT AGATAAAGTC CGAGCAGAAG CTATCATTAG CTCCAACATA 480
CAAAGAGAAA AAGTCAAAAA TAGTCCCTTA ACGAGATTAA CATTTTTCAT TACCATCAAA 540
ATCACGCCTG ATACAATGGA AAATTATGAA TATATCACTA AAAAACAAGT AACTATTTAT 600
TATGATTTTG CTAGAGGTAA CTCTTCTCAA GAAAATCTTA TCATCAACCC TTTTGGCTTC 660
AAAGTGTTTG ACATTCAAAT CACGGATTTA CAAAACGAAC AGACAGTAAG CGAAATTTTG 720
AGAAAGATTA AAGAAGTGGA ATCAAAAAAT AAGGCATTAA ATAAA 765

(2) INFORMATION FOR SEQ ID NO:1113:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113

```
AAGCGCCTAA TTCAAAGAGA TGAGACAATC GCAACTCAGA GAGAGAATGG TATAATATCA      60
AAACAATTTC TCAATTTAAT TCTTGAAAGG AGTTTCATGA ACGATACAAC AGAGCACCAT     120
GGATCCAATC CGCTAAACGC CCCACCACCT AGCAACTCAC AGAGCAACGA TCTCTTAAAT     180
TTGCTAGACT CGTTATATCC TAAAGGGAGT TTAGGGGAAC AAAGATTTCA CGAAGCTTTA     240
AAGAATCAAG AAGAGTTGAA AAATATCCTA ATAGAAATAG AAAAGCTACC GCAAGAAAAA     300
AGGTATGAAC TTCTGATGCA GATAGGACAA GCCAAACAGA GAATAATGGA AGCATACGCT     360
CATTCATTCT TAGGATATAT AGGGGGACTA GAGCATCTGT TAGGATTGTG TATGGGTGGG     420
ATATTTGTTT TGTTTGCAAT CTATTTTGTA TTTTTAAGAA CTAGCAAAAA CACAGAGCTA     480
GTGGAAAGTC TAAAAACAAA ATTAAAACTT CAGTATTTTT ACTATGCCTT TGGTGTGGGT     540
GCGGTTTTGT TTTTTGGATT AGAAACAATT AGATCGATTT ATGAACTATA TATCTTAGGA     600
ATTGGTAGCA CTAACGACAA GGTGCTCTTT GTTTTGAAAA ACATTTGCTT CATAGGTATG     660
GGCTATTTGA TTTATAAAGT TATTAAAGTT ATTGGTATAA AAAATTTTAT CAATGGTCTT     720
TTCGCTTCAA AGAAACAAGG CGGTGCAGAA                                      750
```

(2) INFORMATION FOR SEQ ID NO:1114:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114

```
GGTTACAAAA ACTATAAGAT GCTTGCAAAA ATCGTTTTTA GCTCATTGGT TGCGTTTGGA      60
GTTTTGTCGG CTAATGTGGA GCAGTTTGGT TCATTTTTCA ACGAGATAAA AAAAGAACAA     120
GAAGAAGTGG CCGCAAAAGA AGACGCTCTT AAAGCTCGCA AGAAGCTCTT AAACAATACG     180
CATGATTTCT TAGAAGACTT GGTTTTTAGA AAACAAAAAA TCAAAGAGCT TGTGGATTAC     240
AGAGCTAAAG TTCTTTTAGA TTTAGAAAAC AAGTACAAAA AAGAAAAAGA GGCTCTAGAG     300
AAAGAGACAA GAGGTAAAAT CCTTACTGCT AAGTCAAAGG CTTATGGTGA TCTAGAGCAA     360
GCCTTAAAAG ATAACCCTCT TTATAAGAAA CTTCTTCCTA ACCCTTATGC TTATGTTTTA     420
AACCAAGAAA CATTCACGCA AGAAGATAAG GAGCGTTTGA GTTATTACTA CCCCCAAGTG     480
AAAACGAGCA GTATTTTTAA AAAAACTACC GCTACCACTA AAGATAAGGC TCAGGCTTTG     540
CTTCAAATGG GTGTGTTTTC TTTAGATGAA GAGCAAAACA AAAAAGCGAG CCGATTAGCT     600
TTATCTTACA AGCAAGCGAT TGAAGAATAT TCCAATAACA TTTCTAATTT ATTGAGCAGA     660
AAAGAATTGG ATAATATAGA TTATTACTTG CAGCTTGAAA GAAACAAATT TGACTCCAAA     720
GCAAAAGATA TTGCTCAAAA AGCCACCAAC ACGCTTATTT TTAACTCGGA ACGCTTGGCG     780
TTTAGCATGG CGATTGATAA GATCAATGAG AAATACTTAA GGGGCTATGA AGCTTTTTCT     840
AACTTGTTGA AAAATGTCAA AGATGATGTG GAGTTGAATA CTTTGACTAA AAACTTCACC     900
AATCAAAAAT TGAGTTTCGC ACAAAAACAA AAATTGTGTT TGTTGGTTTT AGACAGCTTC     960
AATTTTGATA CCCAATCCAA AAAATCTATA TTAAAAAAGA CTAATGAATA CAATATCTTC    1020
GTAGATAGCG ATCCTATGAT GAGCGACAAA ACAACTATGC AAAAAGAACA CTACAAGATA    1080
TTTAATTTCT TCAAAACAGT GGTTTCTGCA TACCGGAACA ATGTTGCCAA GAATAACCCC    1140
TTTGAA                                                               1146
```

(2) INFORMATION FOR SEQ ID NO:1115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115

```
AAATTTAGTG AAGTATATTT TATAATGAAA ACTAAGGCAG GCTTTGTAGC TCTTATAGGC      60
AAACCAAACG CTGGAAAAAG CACTCTTTTA AACACTTTAT TAAACGCTCA TTTAGCCCTT     120
GTTTCGCATA AGGCTAATGC GACTAGAAAA TTGATGAAAT GCATCGTGCC TTTTAAAGAC     180
AAAGAAGGGT ATGAGAGCCA AATCATTTTT TTAGACACTC CAGGGCTCCA TCATCAAGAA     240
AAATTACTCA ACCAGTGCAT GCTCTCACAG GCTTTAAAAG CGATGGGCGA TGCTGAATTG     300
CGCGTTTTTT TGGCTTCTGT GCATGATGAT TTGAAAGGGT ATGAAGAGTT TTTGAGTTTG     360
TGCCAAAAAC CCCATATCTT GGCTTTGAGT AAGATTGACA CAGCCACGCA TAAGCAGGTT     420
TTACAAAAAT TACAAGAGTA TCAAAAATAT TCATCGCAAT TTTTAGCTCT AGTGCCTTTG     480
AGTGCGAAAA AATCTCAAAA TTTAAACGCG CTTTTAGAAT GCATCAGTAA GCATTTAAGC     540
CCTAGCGCAT GGCTTTTTGA AAAGGATTTG ATGAGCGATG AAAAAATGCG CGATATTTAT     600
AAGGAAATCA TTAGGGAGAG TTTGTTTGAT TTTTTGAGCG ATGAAATCCC TTATGAAAGC     660
GATGTGATGA TTGATAAATT TATAGAAGAA GAACGCATAG ACAAGGTGTA TGCGCGCATT     720
ATCGTAGAAA AAGAAAGCCA AAAAAAAATC GTGATAGGTA AAAACGGGGT GAATATCAAA     780
CGCATCGGGA CTAACGCGCG ATTGAAAATG CAAGAAGTGG GCGAAAAAAA GGTTTTTTTA     840
AACTTGCAAG TGATCGCTCA AAAATCATGG AGTAAGGAAG AAAAAAGCTT GCAAAAACTA     900
GGCTATATCT ATCAAAGGAA TAGGGAT                                         927
```

(2) INFORMATION FOR SEQ ID NO:1116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116

```
TTTCTGTCTC TAAGTCTCAT AGAAAGGGAC TTGAAAACTA TGGCAAAGAT ATTAAAACCT      60
AATTTAGATA GAGATGAGTT AAACACACTT TATAAGGCAA ATCTTGCTTA TGCTAAAAAC     120
ACGCATGAGC ATTATTTCAA ATTTAAAAAA GATGTAGACT ACAAACTCTT TAATCCTAGC     180
ATTATGCATG AGCAATGTTC TATAAGCTTT GTAGGCGGAC AAGGAGCTAA AAGATTATTA     240
```

```
TACATACTCT ACAAGCTCGC ATTTAATGCT AAGTCTAATA AGATTGCCCT AGATAGACAT     300
TACGCCAAAA TGTTTTTGCA AGTTGTAGCA AGAACTCTAA TAAAGAATGT CAATATATTA     360
GAAGAGCAAG GTTTTATTGA AGTCATTAAA GGAAAACAAA GATACTTGTA TGTGTATCTT     420
AAAGATTACA GAGAATTAGA ATGCTTAGTG AAGAGCAAGA TGGCTAAGTA TGTGATGTAT     480
TTAAGACAAT TCTTTGATTA TTTGGATAGA AAAAGGCGTT ATGGCTTTGA TTTTACGCTT     540
AAAAACCTAG CCTTTGCTAA GACCAAAGAA AGCTTACCCA GACATTTAAA CGATAAAGAC     600
TTAAAGAGTT TTTTAAAAAC ACTCTTAGAC TATAAGCCAG CTACAAGCTT TGAAAAACGC     660
AATAAGTGTA TTCTACTTAT TGTAATACTT GGGGGACTTA GAAAATGCGA AGTGTTAAAC     720
ATAGAATTAA AACACATTCA AGTAGAAGAG CAAAACTACT CTATTTTAAT TCAAGGTAAA     780
GGTAGAAAAG AGAGAAAAGC TTATATTAAA AAGAGTTTGT TAGAACCAAG CTTGAATGCT     840
TGGATTAGTG ATGATTACAG ACTAAAATAT TTCAATGGAG CATATCTCTT TAAAAAGGAT     900
AAGCAAAAAT CACAAAATTC TTTAACGCTT TATAATTTTA TCCCCTTAAT CTTTAAATTA     960
GCCCAAATCA AACATTACAA ACAATATGGC ACAGGCTTAC ATCTATTTAG GCATAGTTTT    1020
GCAACACTCA TTTATCAAGA AACCCAAGAC TTAGTTTTAA CTTCAAGGGC GTTAGGGCAT    1080
AGCTCCTTAC TCTCTACTAA GATTTATATT CATACCACAC AAGAGCATAA CAAGAAAGTG    1140
GCTCTTGTGT TTGATAGTTT GATAGAGAAC AAGAAG                              1176
```

(2) INFORMATION FOR SEQ ID NO:1117:

(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:1117

```
AAAAGAAAGG AACATTGCAT GAAAAATTTA AGGCATTTTA GAAAGCTTAT CGCCTTTTTA      60
GGTTTTTCAC CTCTTTTATT ACAAGCGGAT ATGACTACCT TTTTTAATTC CATTGAACAA     120
CAGCTCACTA GCCCTACGGC TAAAGGCATT TTAATGGTTA TTTTTTTAGG ACTTGCTATT     180
TTTATATGGA AAAACTTAGA TAGATGGAAA GAAATTTTAA TGACCGTGCT TGCTTTAAAA     240
GAAGTCCCCA TGCAATTAGT TGCTATTTCA GTTTCTAATC TCAAAGAAAT CAGCTCCAAA     300
GAAAAATTTC TTTGGCTCAA TGCTAAGAGT TTTTTACTCT CAGGATTTGT GCCTTTTATT     360
ATGATACCTT GGCTAGATAT ATTGAACTCT TTTGTGCTTT ATGTGTGCTT TCTCTTAATT     420
TTTAGCATAG CGGAGTTCTT TGATGAAGAT ATAAGTGACA TTTTAATCGC TCATTCCAAA     480
ATTAAAACCA AAGCTAATTC ATTTTACGCT                                      510
```

(2) INFORMATION FOR SEQ ID NO:1118:

(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

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118

```
AAGTCTCGCA ACTTTAGCTA TAATCAAACA GAAAAAATTT GGGAAAACCA CTTTAACTTA      60
TTTTCAGTAG GAATAGGCAT GGCAGAAGAA CAAGAAAATA CCGCGCAACA ACCCCAAAAA     120
AAAAGCAAAG CCCTTTTATT TGTCATTATT GGAAGCGTGC TAGTGATGCT TTTATTGGTG     180
GGGGTGATTA TCATGCTGCT TATGGGGAAT AAGGAAGAAT CTAAAGAAAA CGCTTCTAAA     240
AACACCCAAG AAGTCCAAGC TAATCCTATG GCGAACAAGA ATCAAGAAGC CAAAGAAGGC     300
TCTAATATCC AGCAATATTT GGTGCTTGGG CCTTTGTATG CGATTGATGC GCCTTTTGCG     360
GTGAATTTGG TCTCTCAAAA TGGCAGACGC TACCTTAAGG CTTCTATTTC GCTAGAATTG     420
AGCAATGAAA AGCTTTTGAA TGAAGTCAAG GTTAAAGACA CGGCGATTAA GGACACGATT     480
ATAGAAATTC TATCGTCTAA AAGCGTGGAA GAAGTGGTTA CTAACAAAGG CAAAAACAAG     540
CTTAAAGATG AAATTAAGAG CCATTTGAAT TCGTTTTTGA TTGATGGCTT TATTAAAAAT     600
GTCTTTTTCA CTGATTTCAT TATCCAA                                         627
```

(2) INFORMATION FOR SEQ ID NO:1119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 549 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...549

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119

```
GGAAGCATGA TGACGGAAAT GGAATTAAAG CTCATTAAAA TAGACACAAG CCATTATTTT      60
GAAAAAAAAC CAGGCTTGGG GGAGAGAATG GATTATGCGG GTCGTTGTTA TTATAATAAA     120
TTCCAAAGAG TGAATGCCAT GCTCACAAGC TCGCTCATTC AAAAGCATTT GAAAAGGGAG     180
ATAGAAATCG CGCACAACCT CATTTTGCGT AACGATAAGG TGGAAAACAT CGTGTTTGAT     240
TATAATGGGA GGAATCCGGA GCGTTTTTAT CATAAGGCGC AGTTATTGCT TCGTGAGGAA     300
GGTTTTATGA ATTTTACCGC TTATAACACG AAGACGCCAG GGCATTTGCA TTTGTATGTG     360
CATAAGGGGC ATACGGAATT AGGCGAGGGT GAAAGGCTGA TTAAAACTTT ATCCATGAAA     420
TTAGCGCAAG GGTTGCCTAA AGAATGGAGG GTTTTCCCTA GCAATGAATG GCCTAAGGAA     480
TTTAATATTT TAGCTTTACC TTATGAAGTG TTTGCAAAAG AGCGCGGGAG CTCTTGGGCG     540
AAGCATTTA                                                            549
```

(2) INFORMATION FOR SEQ ID NO:1120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120

```
CCATTTTTGA AAGGATTTTT GATGTCAGAA AAAGAAAGAC TGAATGAAGT GATCTTAGAA     60
GAAGAGAATA ATGGGAGTGG TACTAAAAAG GTGTTTTTGA TCGTGGCCAT AGCCATTATC    120
ATTTTGGCGG TGCTTTTAAT GGTGTTTTGG AAAAGCACCA GAGTCGCTCC TAAAGAGACT    180
TTTTTACAAA CCGATAGTGG CATGCAAAAA ATAGGCAACA CTAAAGATGA GAAAAAAGAC    240
GATGAGTTTG AAAGCTTGAA TATGGATTCT CCCAAACAAG AAGACAAGTT AGACAAAGTG    300
GTGGATAATA TTAAAAAACA AGAGAGTGAA AATTCTATGC CCATTCAAAC CGATCAAGCT    360
CAAATGGAGA TGAAAACAAC AGAAGAAAAA CAAGAATCTC AAAAAGAATT AAAAGCTGTT    420
GAGCCTATTC CCATGAGCAC TCAAAAAGAA TCTCAGGCTG TGGCTAAAAA AGAAACCCCC    480
CATAAAAAGC CTAAAGTAGC GCCAAAAGAT AAAGAAGCGC ATAAAGATAA AGCTAAGCAT    540
GCAGCTAAAG AGCCAAAAGT CAAAAAAGAA GCTCGTAAAG AAGTTTCTAA GAAAGCTAAT    600
TCTAAAACCA ATCTTACTAA AGGGCATTAT TTGCAAGTGG GGGTTTTTGC GCACACGCCC    660
AACAAAGCCT TTTTACAAGA GTTTAATCAA TTCCCCCATA AAATTGAAGA TAGGGGGGCT    720
ACTAAACGCT ACCTCATAGG CCCTTATAAG AGCAAGCAAG AAGCCTTAAT GCATGCCGAT    780
GAAGTCAGCA AGAAGATGAC TAAACCGGTT GTCATAGAAG TGCGG                    825
```

(2) INFORMATION FOR SEQ ID NO:1121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 567 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

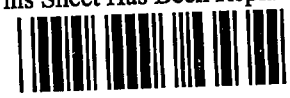
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121

```
TCAAGGCTTC AAAAAGCCAT AATTAAAAGA GTTGAGATGT TGGAAAAACT GATTGAAAGA     60
GTGTTGTTTG CCACTCGTTG GTTGCTAGCC CCTTTATGCA TTGCCATGTC GTTAGTGTTG    120
GTGGTTTTAG GCTATGTGTT CATGAAAGAG TTGTGGCACA TGCTCAGCCA TTTAGACACC    180
ATTAGTGAAA CGGATTTGGT TTTATCAGCC TTAGGTTTAG TGGATTTGTT GTTCATGGCC    240
GGGCTTGTTT TGATGGTGCT GCTCGCCAGT TATGAAAGCT TTGTTTCTAA ATTAGACAAG    300
GTGGATGCTA GCGAAATCAC TTGGCTAAAA CACACAGATT TTAACGCTTT AAAATTAAAG    360
GTTTCCCTCT CCATTGTAGC CATTTCGGCG ATTTTCTTGC TCAAACGCTA CATGAGTTTA    420
GAAGACGTTT TATCCAGTAT TCCTAAAGAC ACGCCCCTAT CGCATAACCC TATTTTTTGG    480
CAAGTGGTGA TCCATTTGGT GTTTGTGTGT TCAGCGCTGT TAACCGCTGT TACCAATAAC    540
ATCGCTTTTT CGCAGAAAGA AAGGCAT                                        567
```

(2) INFORMATION FOR SEQ ID NO:1122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 711 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122

```
GGTTTGAACT ATATTGATTT GGCGTTACTT GTGGTAGTGG TAGCCTTTGG GATTAGGGGG      60
TTTTATCATG GCTTCGTGAG TGAAATAGCA GCGACTTTGG GGATTGTGCT TGGCGTTTAT     120
TTGGCGTCTC GCTATTCTGT GGCTGTTGGG AATTTATTTT CAGAGCATTT GTATGATTTA     180
AGAAATGAAA CCATGACCAA TCTCATTGGT TTTTTACTGG TGTTGGCGTC CATTTGGGTG     240
TTTTTTTTAG CTCTTGGAGT GTTGCTAGGC AAGATGTTAG TCTTTAGCGG TCTAGGCATT     300
ATAGACAAGG CGTTAGGGTT TATTTTTTCA TGTTTGAAGA CTTTTTTAGT GCTTTCTTTC     360
ATCCTTTATG CGCTCTCTAA AATGGATTTA ATGAAAGACG CTAACGCCTA TTTGCAAGAA     420
AAGAGCGCTA TTTTCCCCAC CATGAAAAGC GTCGCTAGTA AGATCATGCG CCTTGATGGC     480
GTCAAACATG TGGAGAAAAA CCTTAAAGAC AACCTTGAAG AAATGAGCGA TGAAGTTAAA     540
AATAAAGGAT CTATTGATAA CGCCAAAGAA TCTTTTAATA AGGCTACGGA TAAGGGCGTA     600
GAAGCTTTAA AAGAAAAGGC TAAAGATTTG CCTAAAAACA TGCTAGAGCC AAAACACAAT     660
AAACCCAACC AAACCCCACC AATCCCAACC CCATCTAATA AAGAACCCCT A               711
```

(2) INFORMATION FOR SEQ ID NO:1123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123

```
AGCTTATGGG TTGAAAACCC TATATTACTA TCACACTCAC AAGTCTATAG CCCCCCAAGA      60
TGCTGGGTTT TTAAAACCCC TAGAAACAGC GCTTTTGCTT TGGGTTTTTT CGTGGGGGCG     120
TTATTGTTTT ACTGGTGCGC TTTAAGGCTT TCGCATTCGG ATTTCACTTA TTTATTGCCC     180
```

```
TTAATCATTG TTTTAGTAGC GTTAGTTTAT GGGGTTTTAT TTTATTTGTT GCTCTATTTT    240
GAAAACCCCT ACTTCAGGCT TTTGAGTTTT TTAGGCTCTA GTTTTATCCA CCCTTTTGGA    300
TTTGATTGGT TAGTCCCGGA TAGCTTTTTT TCTTATAGCG TGTTTAGGGT GGATAAATTA    360
TCTTTAGGGC TTATTTTTTT AGCTTGCATT TTTTTGAGCG CTCAAAATCT TAAAAAATAC    420
AGAATGATAG GGGTTTTATT GCTGCTTGGC GCGTTGGATT TTCATTTTTT TAAAATAAGC    480
GATTTAAAAG AGGTTGGAAA TATTGAATTA GTCTCTACAA GAACGCCCCA AGATTTGAAA    540
TTTGACTCAA ATTACCTTAA TAATATTGAA AACAACATTC TTAAAGAAAT CAAACTCGCT    600
CAAAGCAAGC AAAAAACCTT GATTGTTTTT CCAGAGACCG CTTACCCTAT CGCTTTAGAA    660
AACTCCCCTT TTAAAACCCA ACTAGAAGAT TTAAGCGCCA AGATCGCCAT TTTAATAGGG    720
ACATTGCGCG CTCAAGGCTA TAGCCTTTAT AACAGCTCGT TTTTATTTTC TAAAAAAAGC    780
GTTCAAATCG CTGATAAAGT GATCTTAGCC CCCTTTGGCG AGATAATGCC TTTACCGGAG    840
TTTCTTCAAA AACCCCTTGA AAAGCTCTTT TTTGGCGAGA GCGCTTATTT ATACCGCAAC    900
GCTCCCCATT TCAGCGATTT TACATTAGAC GATTTCACTT TTCGCCCCTT GATTTGCTAT    960
GAAGGCACTT CCAAACCCGC TTATTCAAGC AGCCCTTCAA AAGTTTTTAT CCTAATGAGC   1020
AATAACGCAT GGTTTAGCCC AAGCATTGAA CCCACCTTAC AAAGAACGCT TTTAAAATAC   1080
TACGCAAGGC GTTATGATAA AATCATCTTG CACAGCGCGA ACTTTTCAAC TTCTTACATT   1140
TTAAGCCCTA GCTTATTGGG CGATATTCTT TTTAGGAAAC GATCA                   1185
```

(2) INFORMATION FOR SEQ ID NO:1124:

(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:1124

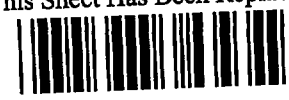
```
GAAACGATCA TGATTAAAGC GATTGATATT TCTCATGCTT TTGAAAAACC TCTTTATAAT     60
GGCGTGAATT TGCGCATTAA ACCCAAAGAA AGCCTGGCGA TTTTAGGCGT GAGCGGGAGC    120
GGTAAAAGCA CGCTTTTAAG CCATTTGGCC ACCATGCTAA AACCGGATAG CGGAACAGTC    180
AGTTTGTTAG AACACCAAGA TATTTATGCC CTAAATTCCA AAAAGCTTTT GGAATTGCGG    240
CGCTTAAAAG TGGGCATCGT TTTTCAATCG CATTACCTTT TTAAGGGTTT TAGCGCTTTA    300
GAAAACTTGC AAGTCGCTTC AATCCTAGCC AAGCAAGAAA TAAATCATTC CCTTTTAGAA    360
CAATTAGGCA TAGCCCACAC CCTAAAACAA GGCGTGGGCG AATTGAGCGG CGGCCAGCAA    420
CAACGCTTAA GCATCGCCAG AGTGCTTTCT AAAAAACCCC AAATCATTAT CGCTGATGAA    480
CCCACCGGGA ATTTAGACAC CACTAGCGCT AATCAAGTCA TCAGCATGCT GCAAAATTAC    540
ATTACAGAAA ACGAAGGGGC GTTAGTCTTA GCCACGCATG ATGAGCATTT AGCCTTCACT    600
TGCTCTCAAG TCTATCGCCT AGAAAAAGAA TCTTTGATTA AGGAAAAA                 648
```

(2) INFORMATION FOR SEQ ID NO:1125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(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:1125

```
TCGCTCGCCC CTAAATTAAA AGCGTTTTTT AAGGTAGCGT TATCCTGTAA GGCGGTGATA      60
AAAATCACAG GCGTAGAGAT TAAAAAATCG TTTTTGATGC GCTTGAATAA TTCCAAGCTA     120
TTCATTTCAG GCACTTGCAC GTCTAAAAGC AAGAGGTTAA AGCGCTCAAC AGAGAGCCTT     180
TCA                                                                   183
```

(2) INFORMATION FOR SEQ ID NO:1126:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126

```
TTTGCGTTGC ATAAAAAAGT TCTGTTGGCT TTAACTGCCA GCTTGATTTG CCAAGAGTCT      60
TTGTTCGCTA AGGATAAAGA CTACACTTTG GGCAAGGTTT CTACTGCCGG TAAAAAGGAT     120
AGATCTGACT ATTCTGGGCA GGTCAATTTG GGTTATAGCG GGATTACCGC GCCTAAGAGT     180
TGGCAAGATG AAGAAGTGAA AAAATACACA GGAAGCCGCA CGGTGATCTC TAACAAAGCG     240
CTCACCCAAC AAGCTAACCA AAGCATTGAA GAAGCTTTAC AGAATGTCCC CGGTCTGCAA     300
ATTAGGAATG CCACAGGTGT GGGGGCTATG CCTACTATCC AAATCCGTGG CTTTGGAGCG     360
GGGGGTTCAG GGCATAGCGA TGCGACGCTC ATGTTAGTTA ATGGTATTCC TGTTTATATC     420
GCCCCTTACG CTCACATTGA GCTAGACATT TTCCCTGTTA CCTTTCAAGC CATTGATCGC     480
ATTGATGTGA TCAAAGGTGG AGGCAGCGTG CAATATGGGC CTAACACTTA TGGGGGTATT     540
GTCAATATCA TCACTAAACC TATCCCTAAT CAATGGGAAA ACCAAGCGGC TGAAAGGATC     600
ACTTATTGGG CTAAGGCTAG AAACGCTGGG TTTGCCGCTC CCCCTGATAA AACCGGCGAT     660
CCTTCTTTCA TCAAGTCTTT AGGCAACAAC CTCCTCTATA ACACTTATGT GAGGAGCGGA     720
GGGATGATCA ATAAGCATGT GGGTATCCAA GCGCAAGCTA ACTGGGTTAG AGGCCAAGGC     780
TTTAGGGACA ATAGCCCCTC TAGTATTTCA AACTATTGGC TGGATGGGGT CTATGACATC     840
AATGAAAGCA ATGGGATTAA AGCCTATTAC CAATACTACG ATTTTGCTAT CGCCCAACCC     900
```

(2) INFORMATION FOR SEQ ID NO:1127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127

```
GTGTCAATAC TAGTTATAAT AGAACCTTAC ACTTTTTACA AAAGGGAGGA GAGTGTCATG      60
TTGGGGAGCG TCAAAAAAGC GGTTTTTAGG GTTTTGTGTT TGGGGGCGTT GTGTTTATGC     120
GGGGGGTTAA TGGCAGAGCA AGATCCTAAA GAGCTTATAT TTTCAGGTAT AACTATTTAC     180
ACGGATAAAA ATTTCACTAG AGCTAAGAAA TATTTTGAAA AAGCTTGCAA ATCAAACGAT     240
GCTGATGGCT GTGCAATCTT AAGAGAGGTT TATTCTAGTG GTAAAGCCAT AGCGAGAGAA     300
AACGCAAGAG AGAGCATTGA AAAAGCTCTT GAACACACCG CTACTGCTAA AGTTTGTAAA     360
TTAAACGATG CTGAAAAATG CAAGGACTTA GCAGAGTTTT ATTTTAATGT AAACGATCTT     420
AAAAATGCTT TAGAATATTA CTCTAAATCT TGTAAGTTAA ATAATGTTGA AGGGTGTATG     480
CTGTCAGCAA CTTTTTATAA CGATATGATA AAGGGTTTGA AAAAAGATAA AAAAGATCTA     540
GAATATTATT CTAAAGCTTG CGAGTTAAAT AACGGTGGAG GGTGTTCTAA ATTAGGAGGG     600
GATTATTTTT TTGGTGAAGG CGTAACAAAA GATTTCAAAA AAGCTTTTGA ATATTCTGCC     660
AAAGCTTGTG AGTTGAACGA TGCTAAAGGG TGTTACGCTC TAGCAGCGTT TTATAATGAG     720
GGTAAAGGCG TGGCAAAGGA TGAAAAGCAA ACGACAGAAA ACCTTGAAAA GAGTTGCAAG     780
CTAGGATTAA AAGAAGCATG CGATATTCTC AAAGAACAAA AACAA                      825
```

(2) INFORMATION FOR SEQ ID NO:1128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 417 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

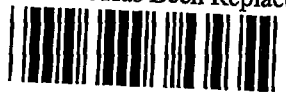
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128

```
ACCCGCAAAT CATCAGCATC CATGTCAGAA AATGAAAAAC ACCCCCATAG GGTGTTGCAA      60
CTCATTAAAA GTTCAGGCAT CACGCCAGGC ATTGTCCTAA ACCCCCACAC GCATGAAGAA     120
AGTATTAAAT ACTTGCTAGA AAGCGTGGGG CTAGTGCTTT TAATGAGCGT GAATCCGGGC     180
TTTGGCGGGC AGAAGTTTTT AGATCTAGTG CTAGAAAAGT GCTTGAAAGT TAAAGAACTG     240
ATCAAACGCT ACAACCCTAG CTGTCTTTTA GAAGTGGATG GGGGCGTGAA TGATAAAAAT     300
ATCTTTGAAC TCCAACAAGC GGGCGTGGAT GTGGTGGTTT CAGGGAGTTA TATTTTTGAA     360
TCCAAAGATC GTAAGCTGGC TATTGAAGGC TTACAGAATG TCAGACAACC TCTTGCA        417
```

(2) INFORMATION FOR SEQ ID NO:1129:

(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:1129

```
AAACTTTTAA GAGTTTTACA TAAGATGATT AAAAAAGCGG CTAAAACCCC TTTTTTTAAA      60
ATTTTGTTTC AAGCTTTAAG CTACAATATA CGCATGAAAG ATTTAAACAA GACTATCGGC     120
GTGTTTGTGC GGCCCACTCA TCATCAAAAC GCTCTTTTTA AAGAGCTAGA GCAGGCTAAA     180
GAATGGGTTT TAACGCTTTT AGAAGATGAG GGGTTTGAAA GCTTTATGAT TGATAGCCTT     240
GATGGGGCAA AAGATGCACA ATTGATAAAA AAAGCTTACG CGTTTTTGTG TTTAGGAGGC     300
GATGGCACGA TTTTAGGGGC TTTAAGAATG ACGCATGCTC ACAATAAGCC ATGCTTTGGG     360
GTGAGGATTG GGAATTTAGG GTTTTTGAGC GCGGTTGAAT TGAACGGGTT GAAAGATTTC     420
TTACAAGATC TCAAGCAAAA CAGGATCAAA TTAGAAGAGC ATTTGGCTTT GGAGGGCCGT     480
ATTGGAAACA CTTCTTTTTA TGCGATCAAT GAAATCGTGA TCGCTAAAAA AAAAGCTTTA     540
GGGGTTTTAG ACATCAAAGC GTGCGCGGGC CATACGCCCT TTAACACTTA TAAAGGCGAT     600
GGGCTTATCA TTGCCACGCC CCTAGGCTCA ACCGCTTATA ATTTGAGCGC TCATGGGCCC     660
ATTGTGCATG CTTTAAGCCA AAGCTATATT TTAACGCCCT TGTGCGATTT TTCTTTAACG     720
CAACGCCCTT TAGTGTTAGG GGCGGAATTT TGCTTGAGTT TTTGCGCTCA TGAAGACGCT     780
CTTGTGGTTA TTGATGGGCA AGCCACCTAC GATTTAAAAG CCAACCAACC CCTATACATT     840
CAAAAAAGCC CCACGACCAC CAAGCTCTTA CAAAAAAATT CAAGGGATTA TTTTAAAGTG     900
CTTAAAGAAA AGCTGTTATG GGGGGAAAGC CCTAACAAAA AAAGA                     945
```

(2) INFORMATION FOR SEQ ID NO:1130:

(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:1130

```
CGCTACAATA CCCCCATGCA AAAAAAGATT TTTTTACTAG AAGACGATTA CCTTTTAAGC      60
```

This Sheet Has Been Replaced



```
GAGAGTATCA AGGAGTTCTT GGAGCATTTA GGCTATGAAG TGTTTTGCGC TTTTAACGGG     120
AAAGAGGCTC ATGAAAGGCT CTCTGTTGAG CGCTTTAACC TCTTGCTTTT AGACGTGCAA     180
GTGCCTGAAA TGAATAGCTT GGAATTATTC AAGCGCATCA AAAACGATTT TTTAATCTCT     240
ACGCCTGTGA TTTTTATCAC CGCCTTACAG GATAACGCTA CCTTAAAAAA CGCTTTTAAT     300
TTAGGGGCGA GCGATTATTT GAAAAAGCCT TTTGATTTGG ACGAATTGGA AGCGCGCATT     360
AAAAGGTTTT TCAATGATGA TCCGATAGAA ATCATGCCTA ACATTTTTTA CCACCAACAC     420
GCTTTGAACG TTAAAGGGAA AAAGGAAATC TTAGCGCCCA AAACCGCCCA ACTTTTAGAA     480
TATTTTTTAG AGCATAAAGG GCAAATCATC AGCTCTCAAG CGTTAGAAAA CAACTTATGG     540
GAGCAAGCGA TTGATGATTC CACCTTACGC ACTTACATTA AAGTGTTGCG CAAGCTTTTG     600
GGTAAAAATT GCATAGAAAC GCATAAGGGG GTGGGCTATC GCTTTAACCC ACTA           654
```

(2) INFORMATION FOR SEQ ID NO:1131:

(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:1131

```
TGTGGCGCTA ATCGCTCAAA AGGGCGTGGA GGTTTTAGTT CAAAATGCGC GGGCGCGAAT      60
AGCGGTTATA GTAACGAAGC GTATGAAAGC GTGGGGGCTA AAATCGTGGA TTCTAAAACG     120
GCGTGGGGGC AGGATTTGGT GGTCAAATGC AAAGAGCCTT TAGAGCATGA ATACCCTTTG     180
CTCAAAGAAA AAGCGACTCT GTTTAGTTAT TTGGATTTAG CGTATCAAAA AAGCTTGTGT     240
GAAATGTTTA TTAATAAAAA AATCACTTCT ATTTGCACTG AAACCATTGC CGGGCCTAAA     300
AACGACTACC CTATTTTAGC GCCTATGAGC GTGGTGGCTG GGAGGTTGGC TGCGCATTTA     360
GTCCAGCATT ATTTACTGGC TTTAGAGCAT GTTAAAGGGT TTATGGGTAA GGGGGTCATG     420
CTAGGGGGTT TGTCGGGTGC GCAAAGGGCT AAAATCGTCG TAATTGGAGG CGGTGTGGTT     480
GGCATGGAGA GCGCGAAAGT CTTAAGCCAA ATGGGGGCTA AAGTAACGAT TTTAGAATTA     540
GACTACGCTA AATTACAAAA CCACCCTTAT TATCATTTGT ATGATTTAGA AGTCTTAAGC     600
GTGAATGAAG CCAATATCAT TCAAGCCTTA AACGGGGCGG TGGGGCTAGT GGGAGCGGTG     660
CTGGTTACAG CGAGCCAAAC CCCTAAAGTG ATCTTAAGAA GGCATTTAAA ATACATGCAG     720
ACACAAGGGG TAGTCATTGA TGTGGCTTGC AGTTTAGGGG GGTGCATAAG AGCCATACGC     780
CAAGCAAGCC ATTCTAACCC GGTGTATGTG GAAGAAAGTT TGTTGCATTA TGGCGTGCCG     840
AACATGCCAG GGATTGTCGC TAAAACGAGC TCTACGGCTT ATAGCCATGC GAGTGTGCCG     900
TATTTGTTGT ATTATTTAGA GCATGGCTTG AAGGGTTTTT TAACAGCCAA CACTAAAATC     960
GTGGCGAACA CGCTTGGAGG CTTGAGCGCT TATAACGGCT ATATCACCCA AGAAGGCATC    1020
GCTAAAGCGT TCAATCTGGC GTTCAAATCG CCTTTAGAAA TTTTAAAGGA GCTT          1074
```

(2) INFORMATION FOR SEQ ID NO:1132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(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:1132

```
AAGGGTAAAA GGGTAAAAAA CATGCGAGAT TTCAATAACA TTCAAATCAC ACGCTTAAAA      60
GTGCGTCAAA ATGCCGTTTT TGAAAAACTG GATCTGGAGT TTAAAGATGG CTTGAGCGCG     120
ATTAGTGGGG CTAGTGGGGT GGGGAAAAGC GTCCTTATTG CGAGCCTTTT AGGGGCGTTT     180
GGGCTTAAAG AGAGCAACGC TTCAAACATT GAAGTGGAAT TGATCGCGCC TTTTTTAGAC     240
ACGGAAGAAT ACGGCATTTT TAGAGAAGAT GAGCATGAAC CCTTAGTTAT TAGCGTGATT     300
AAAAAAGAAA AAACACGCTA TTTTTTAAAC CAAACAAGCC TATCTAAAAA CACGCTCAAA     360
GCGTTATTAA AGGGGCTTAT TAAACGCTTA TCTAACGACA GATTCAGCCA GAATGAACTC     420
AACGATATTT TAATGCTCTC CTTATTAGAT GGCTATATCC AAAATAAAAA TAGGCGTTTA     480
GCCCCCTTT                                                            489
```

(2) INFORMATION FOR SEQ ID NO:1133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 891 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...891

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133

```
TCAAATCATA AAAGGGTTTT TATGGATTAC AAACGTTTTA AAGGCAAGCA TGCGAACATC      60
GTTATAGAAA TCATCAGTCT TTTAGAAAAA GGGGTTAAAA AAGCCCAAGA GATTTTAGAA     120
AAGCCGGACG CTGGGAGTTA CACTCAGTTA GAAAACAGCA GCGGGGATAC GCCTATTAAA     180
GCGGATTTAG CCCTAGATAA GTTTTTAGAG GAAACTTTTT TGAGTTTAGA GAATGTGAAA     240
AGCGTTTTTA GCGAAGAAAA AGAAACGCCT GTTACTAAAG AAAACGGCTC TTATTTGATC     300
GCTTATGACC CCCTAGATGG GAGTTCAGTG ATGGAGGCGA ATTTCTTAGT AGGCACGATT     360
ATAGGGGTTT ATGAAAAGGA TTATAAGGCG CAAAATTTAG TTGCAAGCCT TTATGTGGTT     420
TTTGGGCATA AAATAGAATT GGTGGTGGCT TTAGAAGAAG TTTATCGTTA CGCTTTTTAT     480
CAAAACAAGT TTCATTTTAT AGAAACCATC GTTTTAGAAA ATAAGGGTAA AATCATCGCT     540
AGCGGAGGCA ATCAAAAGGA TTTTTCTTTG GGCTTAAAAA AGGCTTTAGA AGGGTTTTTT     600
GCAGAAAATT ACCGCTTGCG ATACTCAGGA TCTATGGTGG CTGATGTCCA TCATGTGTTG     660
GTTAAAAAGG GCGGAATGTT TTCCTACCCG CAAAAGAAAT TGCGAAAGCT TTTTGAAGTC     720
TTTCCTTTAG CCTTGATGGT TGAAAAAGCT AAAGGGGAAG CGTTTTATTT TGATAAGGGG     780
GTTAAAAAGC GTTTGCTAGA TCAAAGCGTA GAAAGCTACC ATGAAAAAAG CGAATGCTAT     840
TTAGCCAGCC CGCATGAAGC TCAGATTTTA GAAAAACATT TAAAGGGAGA A               891
```

(2) INFORMATION FOR SEQ ID NO:1134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 789 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134

```
ACTTTTTTAA TTATTTTTTG GGTATTCTTT TTAAGAATTA AGCATTATGT TAAGGAATTA      60
TCCATGAAAA AATTTTTTTC TCAATCTTTG TTAGCTCTTA TTATCTCTAT GAATGCGGTA     120
TCTGGCATGG ATGGTAATGG CGTTTTTTTA GGGGCGGGTT ATTTGCAAGG ACAGGCGCAA     180
ATGCATGCGG ATATTAATTC TCAAAAACAA GCCACCAACG CTACGATCAA AGGCTTTGAC     240
GCGCTCTTGG GGTATCAATT TTTCTTTGAA AAACACTTTG GCTTACGCCT TTATGGGTTT     300
TTTGACTACG CTCATGCCAA TTCTATTAAG CTTAAAAACC CTAACTATAA TAGCGAAGCG     360
GCGCAAGTGG CTAGTCAAAT TCTTGGGAAA CAAGAAATCA ATCGTTTAAC AAACATTGCC     420
GATCCCAGAA CTTTTGAGCC GAACATGCTC ACTTATGGGG GGGCTATGGA CGTGATGGTT     480
AATGTCATCA ATAACGGCAT CATGAGTTTG GGGGCTTTTG GCGGGATACA ATTGGCCGGC     540
AATTCATGGC TTATGGCGAC ACCGAGCTTT GAGGGCATTT TAGTGGAACA AGCCCTTGTG     600
AGCAAGAAAG CCACTTCTTT CCAATTTTTA TTCAATGTGG GGGCTCGCTT AAGGATCTTA     660
AAACATTCTA GCATTGAAGC GGGCGTGAAA TTCCCCATGC TAAAGAAAAA CCCCTACATC     720
ACTGCAAAAA ATTTGGATAT AGGGTTTAGG CGCGTGTATT CGTGGTATGT GAATTACGTG     780
TTCACTTTC                                                            789
```

(2) INFORMATION FOR SEQ ID NO:1135:

(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:1135

```
TGGATTGACG CTAAAAATAA AGAAGAAGCC ATCATTCAAG GCTACACTAT CATTGATCCA      60
AGCACCGTTA TTGCGACGCA CACCAGCGAA TTAGTGAAAA AATACGCTGA AGATTTTATC     120
ACCAAAGATG AAGTGAAATC CCTTTTAGAG CGCTTGGCTA AAGACTATCC TACGATTGTA     180
GAAGAGAGTA AAAAAATCCC CACCGGTGCG ATCCGCTCAG TCTTGCAAGC CTTGTTGCAT     240
```

This Sheet Has Been Replaced



```
GAAAAAATCC CCATTAAGGA CATGCTCACT ATTTTGGAAA CGATTACTGA TATTGCTCCA     300
TTGGTTCAAA ACGATGTGAA TATCTTAACC GAACAAGTGA GGGCGAGGCT TTCTAGGGTG     360
ATCACCAACG CTTTTAAATC TGAAGACGGG CGTTTGAAAT TTTTAACCTT TTCTACCGAT     420
AGCGAACAAT TTTTGCTCAA TAAATTGCGA GAAAATGGCA CCTCTAAGAG CTTATTACTC     480
AATGTGGGCG AATTGCAAAA ACTCATTGAA GGGGTTTCTG AAGAGGCTAT GAAAGTCTTG     540
CAAAAAGGGA TCGCTCCGGT GATTTTGATT GTAGAGCCTA ATTTAAGAAA AGCCCTTTCT     600
AATCAAATGG AGCAGGCTAG GATTGATGTG GTCGTGCTAA GCCATGCGGA ATTAGATCCT     660
AACTCTAATT TTGAAGCCTT AGGCACGATC CACATTAACT TT                        702
```

(2) INFORMATION FOR SEQ ID NO:1136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 885 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136

```
AAAAAAAAGA CCCTAAACAT TTCACAATTA GGAAAAACCA TGCATGTTGC TTGTCTTTTG      60
GCTTTAGGGG ATAACCTCAT CACGCTTAGC CTTTTAAAAG AAATCGCTTC CAAACAGCAA     120
CAGTCCCTTA AAATCCTAGG CACTCATTTG ACTTTAAAAA TCGCCAAGCT TTTAGAATGC     180
GAAAAACATT TTGAAATCAT TCCTGTTTTT GAAAATATCC CTGCTTTTTA TGACCTTAAA     240
AAACAAGGCG TTTTTTGGGC GATGAAGGAT TTTTTATGGT TATTAAAAGC AATTAAAAAA     300
CATCAAATCA AACGTTTGAT TTTAGAAAAA CAAGATTTTA GAAGTTTTCT TTTATCCCAA     360
TTTGTTTCCA TAACCACTCC AAATAAAGAA ATTAAAAACG TTTATCAAAA CCGCCAGGAG     420
TTGTTTTCTC AAATTTATGG GCATGTTTTT GATAACCCTC CATATCCCAT GAGTTTAAAA     480
AACCCCAAAA AGATTTTGAT CAACCCTTTC ACAAGAGAAA ATGATAGGAA TATTTCTTTA     540
GAGCATTTAA AAATCGTTTT AAAACTCTTA AAACCCTTTT GTGTTACGCT TTTAGATTTT     600
GAAGAACGAT ACGCTTTTTT AAAAGACAGA GTCGCTCATT ATCGCGCTAA AACCAGTTTA     660
GAAGAAGTTA AAAACCTGAT TTTAGAAAGC GATTTGTATA TAGGGGGGGA TTCGTTTTTG     720
ATCCATTTGG CTTACTATTT AAAGAAAAAT TATTTTATCT TTTTTTATAG GGATAATGAC     780
GATTTCATGC CGCCTAATAG TGGGAATGAG AATTTCCTAA AAGCCCATAA AAGCCATTTC     840
ATAGAACAGG ATTTAGCCAA AAAATTCCGC CATTTGGGGC TATTA                      885
```

(2) INFORMATION FOR SEQ ID NO:1137:

(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:

This Sheet Has Been Replaced



(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137

```
AACACACAGC GCCAAACACT CCCCCTAGTC AAGTCCCGCC CACACCCCCT AGTCAAAATT     60
TACCTAAAAC AAATGTGTGG AATGGGGTTT ATTGGCTTCA AAACAAAACT TACTCAAACA    120
AAGGCATTTA TTATATTGAT CCCAATCTTT CAGGACAGAG CGGTCAAAGC GGCAACACGC    180
TCAGCACCTA TACAGCTAAT TTGT                                           204
```

(2) INFORMATION FOR SEQ ID NO:1138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...4239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138

```
ACGCTAATAT CAATTTTCAG CGCAAGCCAG GCTGATTTTG GAGGCAACAC GACTATTGAT     60
ACAGCAAGCT TTAATTTTGA CAGCGCAAGT TCATTGAATT TTAATAACCT TACGGCTAAT    120
GGGGCGTTAA ATTTTAATGG TTATGCGCCC TCTTTAACTA AGGCTTTAAT GAATGTCAGC    180
GGGCAGTTTG TTTTAGGGAA TAATGGGGAT ATTAATTTAT CTGACATCAA TATCTTTGAC    240
AACATCACAA AATCTGTAAC TTACAACATC TTAAACGCTC AAAAAGGGAT TACTGGCATT    300
AGTGGGGCTA ATGGCTATGA AAAAATCCTT TTTTATGGCA TGAAAATCCA AAACGCTACC    360
TATAGCGATA ATAACAACAT CCAAACTTGG TCGTTTATAA ACCCTCTCAA TTCTTCTCAA    420
ATCATTCAAG AGAGCATTAA AAATGGGGAT CTAACCATAG AAGTTTTAAA TAACCCTAAC    480
TCGGCTTCCA ACACTATTTT TAATATCGCT CCTGAGCTTT ATAATTACCA AGATTCTAAG    540
CAAAATCCTA CCGGCTATAG CTATGATTAT AGCGACAATC AAGCAGGCAC TTATTACTTG    600
ACAAGCAACA TTAAAGGTCT TTTCACCCCT AAAGGCTCTC AAACGCCTCA AACCCCAGGC    660
ACTTATAGCC CATTTAACCA GCCTTTGAAT AGTTTGAATA TCTACAATAA GGGTTTTTCT    720
AGCGAGAATT TAAAAACGCT TTTAGGGATC CTTTCTCAAA ATTCCGCCAC CTTAAAAGAA    780
ATGATTGAAT CCAACCAACT AGACAATATC ACTAACATTA ATGAAGTGTT GCAACTCTTA    840
GATAAGATTA AAATCACCCA AGCGCAAAAG CAAGCGCTCC TAGAAACGAT CAACCATTTG    900
ACTGACAACA TCAATCAAAC CTTTAATAAC GGGAATCTCG TTATAGGCGC TACCCAAGAT    960
AATGTTACAA ACTCTACTAG CTCTATATGG TTTGGGGGCA ATGGCTATAG CAGCCCTTGC   1020
GCGCTAGATA GCGCCACTTG TTCTTCTTTT AGAAACACTT ACTTGGGGCA ATTATTAGGC   1080
TCAACTTCCC CTTATTTAGG CTACATTAAC GCTGATTTTA AAGCTAAAAG CATTTATATT   1140
ACCGGGACAA TTGGAAGTAG TAACGCTTTT GAAAGCGGAG GGAGCGCGGA TGTAACCTTT   1200
CAAAGCGCTA ATAACTTAGT GTTGAATAAA GCTAACATAG AAGCTCAAGC CACAGACAAT   1260
ATCTTTAATC TTTTGGGTCA AGAAGGGATT GATAAAATCT TTAATCAGGG GAATTTAGCG   1320
AATGTTCTTA GTCAAATGGC TATGGAAAAA ATCAAGCAAG CCGGCGGTTT AGGGAACTTT   1380
ATAGAAAACG CTCTAAGCCC TTTGAGTAAG GAATTACCCG CTAGCTTGCA AGATGAAACC   1440
TTAGGCCAAC TTATAGGTCA AAATAACTTA GATGATTTAT TGAATAATAG TGGAGTCATG   1500
AATGAAATCC AAAACATTAT CAGTCAAAAA CTAAGCATTT TTGGCAATTT TGTTACCCCA   1560
TCCATCATAG AAAACTACCT TGCTAAGCAG TCTTTAAAAA GCATGCTAGA CGATAAAGGG   1620
CTTTTGAATT TTATCGGTGG GTATATAGAC GCTTCTGAAT TAAGCTCTAT TTTAGGCGTG   1680
```

```
ATTTTAAAGG ATATTACTAA CCCCCCTACA AGCCTGCAAA AAGACATTGG TGTGGTAGCG    1740
AACGACTTGT TGAACGAGTT TTTAGGACAA GATGTTGTCA AAAAGCTAGA AAGTCAAGGC    1800
TTGGTGAGTA ATATCATCAA TAATGTTATT TCTCAAGGCG GGTTGAGCGG CGTTTATAAT    1860
CAAGGTTTAG GGAGCGTGTT GCCGCCCTCT TTACAAAACG CGCTCAAAGA AAACGATTTA    1920
GGCACTCTTT TATCGCCTAG AGGCTTGCAT GATTTTTGGC AAAAAGGGTA TTTTAACTTT    1980
TTAAGCAATG GCTATGTTTT TGTCAATAAC AGCTCTTTTA GTAACGCTAC TGGGGGTAGT    2040
TTGAATTTTG TCGCCAACAA GTCTATTATC TTTAATGGCG ATAATACGAT TGACTTTAGC    2100
AAGTATCAAG GCGCATTGAT TTTTGCTTCT AATGGTGTTT CTAATATCAA TATCACCACC    2160
CTAAACGCCA CTAATGGCTT AAGCCTTAAT GCGGGTTTGA ATAATGTGAG CGTTCAAAAA    2220
GGAGAAATTT GTATCAATTT AGCCAATTGC CCTACAACCA AAAACAGCTC TCCTGCAAAC    2280
TCTAGCGTAA CCCCCACTAA TGAGTCTTTA AGCGTGCACG CTAATAATTT CACTTTCTTA    2340
GGCACAATCA TCTCTAATGG GGCTATTGAT TTGTCTCAAG TAACAAATAA TAGCGTTATA    2400
GGCACGCTCA ATCTCAATGA AAATGCGACC TTGCAAGCTA ATAATTTAAC GATCACCAAC    2460
GCTTTTAACA ACGCCTCTAA CTCTACGGCT AATATTGATG GTAATTTCAC CTTAAACCAA    2520
CAAGCGACTT TAAGCACTAA CGCTAGTGGT TTGAATGTCA TGGGGAATTT TAATAGCTAT    2580
GGCGATTTGG TGTTTAACCT CAGTCATTCA GTTAGTCATG CTATTATCAA TACTCAAGGC    2640
ACAGCGACGA TCATGGCCAA TAATAACCCT TTGATCCAAT TCAACGCTTC TTCACCAGAA    2700
GTGGGTACTT ACACGCTGAT TGATAGCGCT AAAGCCATTT ATTACGGGTA TAACAACCAA    2760
ATCACAGGAG GCAGTAGCCT GGATAATTAC CTTAAGCTTT ATGCGCTCAT TGATATTAAT    2820
GGCAAGCACA TGGTGATGAC TGACAACGGC TTAACCTATA ACGGGCAAGC CGTGAGCGTT    2880
AAAGATGGCG GTTTAGTTGT AGGCTTTAAG GACTCTCAAA ATCAATACAT TTACACTTCC    2940
ATTCTTTATA ATAAAGTGAA AATCGCTGTT TCTAATGATC CTATCAATAA CCCACAAGCC    3000
CCCACTTTAA AACAATATAT CGCTCAAATT CAGGGCGTTC AAAGCGTGGA TAGCATCGAT    3060
CAAGCTGGGG GAAATCAAGC GATTAATTGG CTCAATAAAA TCTTTGAAAC TAAAGGAAGC    3120
CCTTTATTCG CTCCCTATTA TCTAGAGAGC CACTCCACAA AAGATTTAAC CACGATCGCT    3180
GGAGATATTG CTAACACTTT AGAAGTCATC GCTAACCCTA ATTTTAAAAA TGACGCCACT    3240
AATATTTTAC AGATCAACAC CTACACGCAG CAAATGAGTC GTTTAGCCAA GCTCTCTGAC    3300
ACTTCAACTT TCGCCCGTTC TGATTTCTTA GAACGCTTAG AAGCCCTTAA AAACAAGCGA    3360
TTCGCTGATG CGATCCCTAA CGCTATGGAT GTGATTTTAA AATACTCTCA AAGGAATAGA    3420
GTTAAAAATA ATGTGTGGGC GACAGGAGTT GGAGGGGCTA GTTTCATTAG TGGAGGTACT    3480
GGAACTTTAT ATGGTATCAA TGTAGGGTAT GATAGGTTTA TTAAGGGCGT GATTGTGGGA    3540
GGTTATGCCG CTTATGGGTA TAGCGGGTTC CATGCAAACA TCACTCAATC AGGCTCTAGC    3600
AATGTCAATG TGGGCGTTTA TAGCCGAGCG TTTATCAAAA GAAGCGAGCT AACCATGAGC    3660
TTGAATGAGA CTTGGGGATA CAATAAAACT TTCATCAACT CCTATGACCC CCTACTCTCA    3720
ATCATCAATC AGTCTTACAG ATACGACACT TGGACGACTG ACGCTAAAAT CAATTATGGC    3780
TATGATTTCA TGTTTAAAGA TAAAAGCGTT ATTTTTAAAC CCCAAGTAGG CTTAAGCTAT    3840
TATTACATTG GTTTGTCTGG TTTAAGGGGC ATTATGGATG ATCCTATTTA CAACCAATTC    3900
AGAGCCAATG CTGACCCTAA TAAAAAATCC GTTCTAACGA TCAATTTTGC CCTAGAAAGT    3960
CGGCATTATT TCAATAAAAA CTCTTATTAT TTTGTGATTG CGGATGTGGG CAGAGACTTA    4020
TTCATTAATT CTATGGGGGA TAAAATGGTG CGTTTCATCG GTAATAACAC CCTAAGCTAT    4080
AGAGATGGTG GCAGATACAA CACTTTTGCT AGCATTATCA CAGGCGGGGA GATAAGATTG    4140
TTCAAAACCT TTTATGTGAA TGCGGGCATA GGGGCTAGGT TTGGGCTTGA TTATAAAGAT    4200
ATTAATATTA CCGGAAATAT TGGTATGCGC TATGCTTTT                           4239
```

(2) INFORMATION FOR SEQ ID NO:1139:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139

```
AGGGATAACA TGGAGCTTAT TTTAGGCTCT CAATCCAGCG CTAGGGCGAA TCTTTTAAAA      60
GAGCATGGGA TTAAGTTTGA ACAAAAAGCG CTCTATTTTG ATGAAGAAAG CCTAAAAACC     120
ACAGACCCTA GGGAGTTTGT CTATTTGGCG TGCAAGGGGA AATTAGAAAA AGCTAAAGAG     180
TTACTTGCGA ATAATTGCGC TATCGTGGTG GCTGATAGCG TGGTGAGCGT GGGTAATCGC     240
ATGCAACGAA AAGCTAAAAA CAAGCGAGAA GCCCTTGAAT TTTTAAAACG CCAAAATGGC     300
AATGAAATAG AGGTTTTAAC TTGCTCTGCA TTGATTTCTC CTGTGTTGGA ATGGCTGGAT     360
CTATCGGTTT TTAGAGCGCG TTTAAAGGCG TTTGATTGCA GCGAAATAGA AAAATATTTA     420
GAGAGCGGTT TATGGCAAGG AAGTGCGGGC TGTGTGCGTT TAGAGGACTT TCATAAGCCT     480
TATATTAAAA GCTCAAGCAA GAATTTAAGC GTGGGGTTGG GGCTGAATGT GGAAGGCTTG     540
TTAGGGGCAC TAAAATTAGG GGTTAAACTT TCATTATTA                             579
```

(2) INFORMATION FOR SEQ ID NO:1140:

(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:1140

```
AGAATGGCTC TTTTTGGTTC AAAGAGTAAG ATGTTAGAAA CTTATGCACT TAAAAGTGGG      60
GCTGTTTTTA TCTCTGATGC GCATTTTTTG CCCAAAAGCC CTCATTTAAT CCATACGCTT     120
AAAGAACTTT TAAGCGCCAA ACCCCCGCAA GTCTTTTTCA TGGGCGATAT TTTCCATGTT     180
CTTGTGGGCT ATTTACCCCT AGATAAAGAG CAGCAAAAAA TCATTGATTT AATCCATGCG     240
TTGAGCGAAA TTTCACAAGT CTTTTACTTT GAAGGCAACC ATGATTTTTC CATGCGTTTT     300
GTATTCAATT CCAAAGTAAT GGTTTTTGAG CGCCAAAACC AACCCGCATT ATTCCAGTAT     360
GATAACAAAC GCTTTTTGCT AGCCCATGGG GATTTATTCA TCACTAAAGC GTATGAATTT     420
TACATCACGC AGCTCACTTC CACTTGGGCT AGATTTTTTT TAACTTTTTT AAATTTATTA     480
AGTTTTAAAA CCTTATACCC TTTT                                            504
```

(2) INFORMATION FOR SEQ ID NO:1141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 960 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

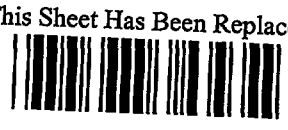
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141

```
AATGATGATG AGAATAAAGT AATTGAATTA AAAACAAGGA ATAACATGCG CATCGTATTT      60
ATGGGAACGC CTAGTTTTGC TGAAGTGATC TTAAGGGCGT TGGTTGAAAA TGAAGATAAA     120
AAGATAGAAG TGGTGGGGCT ATTCACTCAA AGGGACAAAC CTTTTGGGCG CAAAAAAGAA     180
TTGAAAGCCC CAGAGACTAA AACATACATT TTAGAAAATC ATTTAAATAT TCCCATTTTC     240
CAGCCGCAAA GTTTGAAAGA GCCTGAAGTT CAAATCTTAA AAGGTTTGAA GCCTGATTTT     300
ATCGTGGTGG TGGCTTATGG TAAGATTTTG CCTAAAGAGG TTTTAACCAT CGCTCCTTGC     360
ATTAATTTGC ATGCGTCGTT ATTGCCCAAA TACAGGGGGG CTTCGCCCAT TCATGAGATG     420
ATACTCAATG ACGATAGGAT TTATGGCATA AGCACCATGC TTATGGATTT GGAATTGGAT     480
AGCGGGGATA TTTTAGAAAG CGCTTCTTTT TTAAGAGAAG ATTATTTGGA TTTAGACGCT     540
TTAAGTTTAA AATTAGCGCG CATGGGGGCG ACTCTGCTTC TTTCAACGCT CAAAAATTTT     600
CATTCCATCA CAAGAAAGCC TCAAGATCAC ATGCAGGCTA GTTTTTGTAA AAAAATCGCC     660
AAGGCCGATG GGTTAGTGGG TTTTAAAGAC GCTAAAAACT TGTTTTTAAA ATCGCTTGCG     720
TTTAAATCTT GGCCAGAAAT CTTTTTAGAA AATAGCCTTA AACTTTTAGA AGTGGAGTTA     780
GTGGAGAATG AAAAGAGCCA CAAGGAAGGC GAGATTTTAG CAATTGATGA AAGAGGCGTT     840
CTTGTAGGTT GTTTGAAAGG CAGCGTGCGT ATAGCAAGGT TGCAAGCGGT GGGTAAAAAG     900
CCTTTGAAAG CGAAGGATTA TTTGAATGGC AGGCGTTTGA AAGTGGGCGG TATTCTAACA     960
```

(2) INFORMATION FOR SEQ ID NO:1142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

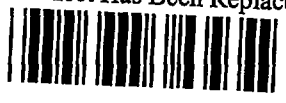
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142

```
AAAAGCACAA GGAAAACAAT AATGGAAGCG CAATTACGAT TTACGGGTGT TGGAGGGCAA      60
GGCGTGTTGT TAGCGGGAGA GATTTTAGCT GAGGCTAAGA TCGTGAGCGG GGGCTATGGC     120
ACTAAGACTT CCACCTACAC TTCGCAAGTG CGTGGAGGTC CCACTAAAGT GGATATTTTC     180
TTAGATAAAG ATGAAATTAT TTTCCCTTAT GCTAAAGAGG GCGAGATTGA TTTCATGCTT     240
TCAGTCGCTC AAATCAGCTA CAACCAGTTT AAAAGCGACA TTAAAAAAGG CGGTATCGTT     300
GTCATTGATC CCAATCTAGT AACCCCCACT AAAGAAGATG AGGAAAAATA CCAGCTTTAT     360
AAAATCCCTA TCATTAGTAT CGCTAAAGAT GAAGTGGGTA ACATTATCAC GCAATCTGTG     420
GTGGCGTTAG CCATTACCGT GGAGCTGACT AAATGCGTGG AAGAAAATAT CGTTCTAGAT     480
ACCATGCTTA AAAAAGTTCC CTGCAAAAGT CGC                                  513
```

(2) INFORMATION FOR SEQ ID NO:1143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1284 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1284

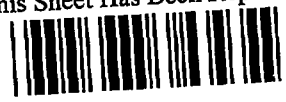
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143

GCATGTTTAA AACAAGAAAA TATTACTAAT ACGCAGATAT TGCATATCGG TGATAATTCT 60
TGGGCAGATG ACGCTATGCC TAAAAGTTTA GGCATAGCAA CGCTATTTAG AAAAAGCGTG 120
TTGAAACAAT TAGAAGAAGT TTTTCCTAAA TACAAAACAT TTAATCCAAC CAGTGTTGCG 180
CAAAGTTTTA TTTTAGGATC TTTATGCGTT TTTTATAAAA ATTATATTCA AAAACATGAA 240
AAATTTGATT ATTGGTTTCT TTTAGGAGCG ATGCAGGCAG GAATTGCAGC CGTTGCTTAT 300
TGCCAGTTTA TCTATAAGGA GATTCACAAA AGAAATATTG ATACTTTAGT GTTTGTTGCG 360
CGAGATGGTT ATTTATTGCA AAAAATTTTT AATATTTTAT ATCCAAATTC ATATAAAACT 420
ACTTATGTCT ATGCTCCCAG AATTTTAAAA AAAGCGGTAT TTTTAGAAGT CGTAGAGGGC 480
GAGAGTTTGG AAATTTTGCG TATTTTAGAA GGCGAAGAAG AAGTTAAAAA GAAGCAAATC 540
ACCACCAACC AACAGGCGTA TGTATATCTC TATAGCAATT TTGAACATTG CCGCCATTTA 600
GCGTTAAAAT GTTTAGATAA TTACAGAAAA TACTTGTTTT CATCAAATTT AGAAGGAAAT 660
ATCGCTATTG TAGATACGAT TACTTTAGGC TATTCTTCGC AAGGGTTAAT CCAAAAAGCT 720
TTAAATAAAG AAGTTTTTGG GTGCTATGTG GATCTCCTAA GAATTTTAAA TTATGATTGC 780
GTGAGTTTCT TACCTTTTTC ACACCCTAAA CCCGTTTATT TTCATAATTG GGATTTTATG 840
GAGTTTTTGC TAACAAGCCC TGAATACCCT ATTTTAAATG TAGAAAATGG CGTTCCAATC 900
TATCAAAAAG ACGTTTCATC TTGTGAAAAA CACCGCTCTA AAGCTTATGA AAAAATAGTA 960
GAAGGGGCTG TTGGATATGC TTCATATTTT AAAGAAAGTC AAATTTCTTT AGACATTCAT 1020
GATGTGATAG AATGGGTGAA TTTCTTCATT GACAATCCTA GTATTCAAGA TCAAGAGCAA 1080
TTCAGACAAA TTTATTTTCT TCCAGACGCG ACGCATAAAA ACGCTCTGCC CTTGTTTTGC 1140
AACGATGTTT CTTTGTTGTC TTGTATTTTA AAGCCTTCAC AAAGTTATAG CGTATTAAAA 1200
AGGAGTCTTA GGACAAACAA GCAAGAGAGG TTGTTTAAAA TATTGTCTCT AATTAAAAAA 1260
ATCTATGGGA AGTTAAAAAA GAAA 1284

(2) INFORMATION FOR SEQ ID NO:1144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1144

GGGTTATTAG CTTGTTTGCT GGTCTTACTC AATCTAAAGA TTACGCCGAA TTTGATGTGG 60

```
CCTTTAGATA TTATTGTGGT TGTGGCATGG GTGTTATGGG GGGTTAATAT GTTTGGGAGC     120
ATGAGCGTTA GAAGAGAGAA TACTATTTAT GTGTCTTTGT GGTATTACAT CGCTACTTAT     180
GTGGGTATAG CGGTGATGTA TATCTTCAAT AACCTTTCTA TCCCCACCTA TTTTGTCGCT     240
GATATGGGGA GCGTTTGGCA TTCTATTTCT ATGTATTCAG GCAGTAATGA TGCGCTCATT     300
CAATGGTGGT GGGGGCATAA TGCGGTCGCT TTTGTCTTTA CGAGTGGGGT GATTGGCACG     360
ATTTATTATT TCTTGCCTAA AGAGAGCGGC CAGCCTATCT TTTCTTACAA ACTCACTTTG     420
TTTTCTTTTT GGAGTTTGAT GTTTGTTTAT ATTTGGGCGG GCGGGCACCA TTTGATCTAT     480
TCCACCGTGC CTGATTGGGT ACAAACCCTT TCTAGCGTGT TTTCAGTGGT GTTGATCTTG     540
CCTTCGTGGG GGACAGCGAT TAACATGCTT TTAACGATGA GAGGCCAATG GCACCAGCTC     600
AAAGAAAGCC CTTTGATCAA GTTTTTAGTT TTAGCCTCAA CTTTCTACAT GCTTTCCACG     660
CTAGAAGGCT CCATTCAAGC CATTAAAAGC GTGAACGCCT TAGCCCACTT CACCGATTGG     720
ATTATAGGGC ATGTGCATGA CGGCGTGCTT GGGTGGGTAG GCTTCACTTT GATTGCGAGC     780
ATGTATCACA TGACCCCTAG GCTTTTCAAA AGAGAGATCT ATTCAGGAAG ACTTGTGGAT     840
TTCCAATTTT GGATCATGAC TTTAGGGATT GTGCTTTACT TTTCGTCCAT GTGGATTGCA     900
GGGATCACGC AAGGGATGAT GTGGAGGGAT GTGGATCAAT ACGGGAATCT CACTTACCAA     960
TTCATTGACA CGGTTAAGGC GCTAATCCCT TATTACAATA TTAGAGGCGT TGGGGGTCTT    1020
ATGTATTTTA TTGGATTTAT TATTTTTGCT TACAATATCT TTATGACAAT CACGGCAGGC    1080
AAAAAATTAG AGCGTGAGCC CAATTACGCC ACGCCTATGG CCAGA                    1125
```

(2) INFORMATION FOR SEQ ID NO:1145:

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

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1145

```
GGTTTTGATG ACGATATGGA AATTAGAAAC ATCAAAGAGT TTGAAAAAGC TTCCAAAAAA      60
CTCCAAAAAG ACACTTTAAA GATCGCTCTC GCTCTTTTGT TCCTCATTGG CGCCGCTTTG     120
CTCGCTCTCA TTTTTGGGCA GGCTAATTCT AAGGGATTGT TGCTCATCTT TGCGGCCGTG     180
ATTGGGGGGT ATATGGCGAT GAATATTGGC GCGAACGATG TGTCTAATAA TGTCGGCCCG     240
TCCGTAGGCT CTAAAGCCAT TAGCATGGGT GGGGCGATTT TGATCGCTGC GGTTTGTGAA     300
ATGCTAGGAG CGATCATTGC TGGGGGGGAA GTGGTTTCTA CGATTAAGGG CCGTATCGTT     360
TCGCCTGAAT TTATTAACGA TGCGCATGTT TTCATTAATG TCATGTTGGC TAGCCTTTTG     420
AGTGGGGCGT TATGGTTGCA TGTAGCCACT TTAATAGGCG CTCCCGTTTC CACTTCGCAC     480
TCCGTAGTGG GAGGGATTAT GGGGGCTGGA ATGGCAGCAG CTGGAATGTC TGCTATCAAT     540
TGGCATTTTT TATCCGGCAT TGTGGCTAGT TGGGTAATCT CGCCTTTAAT GGGGGCTTTG     600
ATAGCCATGT TTTTTTTAAT GCTCATTAAA AAGACTATCG CTTATAAAGA AGATAAAAAG     660
AGCGCGGCTT TAAAGGTCGT GCCTTATTTG GTGGCGTTGA TGAGCTTAGC CTTTAGCTGG     720
TATTTGATCG TGAAGGTTTT AAAACGCCTC TATGCGGTGG GTTTTGAAAT CCAGCTCGCT     780
TGCGGTTGTG TCCTTGCGCT TTTGATTTTT ATCCTTTTTA AAAGATTTGT GTTAAAAAAA     840
GCCCCGCAAT TAGAAAATAG CCACGAAAGC GTCAATGAGC TTTTTAATGT CCCTTTGATT     900
TTT                                                                  903
```

(2) INFORMATION FOR SEQ ID NO:1146:

(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:1146

```
AGAATGAAGC TTAAAAAAAC CCTGACTTAT CAACACCACG CCTATTCTTT TTTAAGCGAT      60
AACACGAATG AAGTTTTAGA AAACCCTAAA GAAATCCTTT TTGTCAAAAC GCCTTTAAAC     120
GAAAAATACG CCCCTTTAAT CGCAGAAAAA AACCTGGCTA TTTTGGATTT TAACGAGCTT     180
AAAAACTACT TTGATTTTAA GATTAAGATT GTAGGGATTA CAGGCACTAA TGGTAAAACG     240
ACCACAGCGA GCTTGATGTA TTCCTTGCTC TTAGATTTGA ATAAAAAGAC CGCTCTTTTA     300
GGCACAAGAG GGTTTTTTAT CGACGACAAA CACATCAAAG AAAAGGGCTT GACCACGCCC     360
ACTCTTTTAG AGCTTTATAG CGATTTGGAA GAAGCGATTC GTTTAAAATG CGAATACTTC     420
ATTATGGAGG TGAGCTCCCA TGCGATTGTC CAAAAACGCA TCGCTGGGCT TGATTTCGCT     480
CTTAAAATTC TCACCAATAT CACAAGCGAT CATTTAGATT TCCATCAAAA TATAGAAAAT     540
TACAGGGACG CTAAAAACAG CTTTTTTAAA GATGAGGGCT TAAAAGTCAT CAACAGAGAT     600
GAAACAAACG CCCTTTTTAA CCCCATTAAC GCGCGCACTT ACGCACTGGA TAAAAAAGCG     660
CATTTGAATG TTCAAGCCTT TTCGCTCAAC CCTTCCATTA GCGCGTCTTT ATGCTACCAA     720
CACGATTTAA GAGATCCCAA TCTTAAAGAA ACCGCCCTGA TCCATTCCCC CCTTTTAGGG     780
CGTTACAACC TTTATAATAT TTTAGCGGGC GTTTTAGGGG TTAAATTGCT CACTCAATTG     840
CCTTTAGAAA CGATCGCACC GTTATTGGAA AACTTTTATG GGGTTAAGGG GCGTTTGGAA     900
ATTGTACATT CTAAACCTTT AGTGGTCGTG GATTTTGCCC ACACAACAGA CGGCATGCAA     960
CAAGTTTTTG AAAGCTTTAA AAATCAAAAG ATCACCGCTC TTTTTGGGGC AGGGGGCGAT    1020
AGGGATAAAA CCAAGCGCCC TAAAATGGGA GCGATAGCGA GTTGTTACGC GCATCAAATC    1080
ATCTTAACTT CAGACAATCC TAGAAGCGAA AACGAAGAAG ACATCATTAA GGATATTTTA    1140
AAAGGCATCA ATAATTCTTC TAAAGTCATT GTAGAAAAAG ACCGAAAAAA GGCCATTTTA    1200
AACGCTTTAG AAAATTTAAA AGACGATGAG GTGTTGTTGA TTTTAGGCAA GGGCGATGAA    1260
AACATTCAAA TCTTTAAAGA CAAAACGATT TTTTTT                              1296
```

(2) INFORMATION FOR SEQ ID NO:1147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 981 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147

AGATTATTAT CTCAATTTAA AACAAGGATA AACATGCAAG AATTCAGTTT GTGGTGCGAT 60
TTTATAGAAA GGGATTTTTT AGAAAACGAT TTTTTAAAGC TCATCAATAA GGGGGCTATT 120
TGCGGGGCGA CGAGTAACCC TAGTTTGTTT TGCGAAGCGA TCACAAAAAG CGCGTTTTAT 180
CAAGATGAAA TCGCTAAACT CAAAGGCAAA AAAGCTAAAG AAATTTATGA AACTCTGGCA 240
CTAAAGGATA TTTTACAAGC CTCTAGCGCG TTAATGCCTT TGTATGAAAA AGACCCTAAC 300
AACGGCTACA TCAGCCTAGA AATTGACCCC TTTTTAGAAG ACGATGCGAT TAAAAGCATT 360
GATGAAGCCA AGCGGTTATT CAAAACATTA AACCGCCCCA ATGTGATGAT TAAAGTCCCG 420
GCGAGTGAAA GCGCTTTTGA AGTCATTAGC GCTCTGGCTC AAGCCTCTAT CCCCATTAAT 480
GTAACTTTAG TCTTTTCGCC TAAAATTGCC GGTGAAATCG CTCAAATCTT AGCCAAAGAA 540
GCACGAAAAA GAGCGGTCAT TAGCGTGTTT GTCTCACGAT TTGACAAAGA AATAGACCCA 600
CTAGTGCCAC AAAATTTGCA AGCTCAAAGT GGGATCATGA ACGCTACCGA GTGTTATTAT 660
CAAATCAACC AGCATGCTAA TAAGCTAATA AGCACCCTTT TTGCATCCAC CGGCGTTAAA 720
TCTAATTCTT TAGCTAAAGA TTACTACATT AAAGCGCTGT GTTTTAAAAA CTCTATCAAC 780
ACAGCCCCCC TAGACGCCCT AAACGCTTAT TTGCTTGACC CAAACACCGA GTGTCAAACC 840
CCTTTAAAAA TCACAGAAAT TGAAGCGTTC AAAAAAGAAT TAAAAACGCA CAATATTGAT 900
TTAGAAAACA CCGCCCAAAA ACTCCTTAAA GAAGGCTTGA TAGCGTTCAA ACAATCCTTT 960
GAAAAGCTTT TAAGCAGTTT T 981

(2) INFORMATION FOR SEQ ID NO:1148:

(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

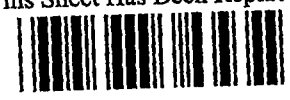
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148

GGGTTTAAAG TGCGTTTGTT TAGATTTGTG GGGTGGTATT ATTTCAAATA CTTTTTAATC 60
GTGCTTTTAG CTTTGGAATT GTTTTTTGTA GGCATTGACA GCCTGAAATA CGCCGATAAA 120
ATGCCTGATT CTGCGAACAT GATCATTTTA TTTTTCACCT ATGATATTTT ATTCGCTCTC 180
AATTACACCT TGCCCATTTC CTTGCTTTTA GCGATGGTTT TATTTTATAT CACCTTCATT 240
AAATCCAACC AATACACCGC CCTGCTCTCT ATTGGATTTT CCAAATGCCA GATTTTAAGC 300
CCTATTTTTT TGATTAGCCT GTTTTTCACG GCTGTTTATG TGGGGTTGAA CGCGACTCCT 360
TTTGTGTATA TGGAAGAAAA AACGCAAAAT TTAATTTATA AAGACAATTC TTTGAGCGTT 420
TCAGAGCATT TGTTAGTGAA ATACAACGAT GATTACGTGT ATTTTGATAA GATTAATCCC 480
TTATTGCAAA AAGCCCAAAA TATCAAGGTT TTTCGCCTAA AAGATAAAAC TTTAGAATCT 540
TATGCTGAAG CTAAAGAAGC TTTTTTTGAA GACAAATATT GGATTTTACA TGACACTACT 600
ATCTATGAGA TGCCCTTGAG TTTTGAACTG GGCGCGAACG CTTTAAACAC CACGCATTTA 660
GAAACCTTTA AAACGCTCAA AAATTTCCGC CCTAAAGTTT TAGACACCAT TTATCAAAAC 720
AAGCCTGCGG TTTCTATCAC AGACGCTCTT TTATCCTTGC ATGCTTTAGT GCGCCAAAAC 780
GCGGACACGA AAAAAGTGCG CTCGTTTTTG TATGTGTTTG CGATTTTGCC CTTTTTTGTG 840
CCGTTTTTAA GCGTTTTAAT CGCTTATTTT TCGCCCAGTC TCGCCCGCTA TGAAAACCTG 900
GCTCTTTTAG GGCTAAAGTT TATCATTATC ACGCTCGTTG TTTGGGGGCT ATTCTTTGCT 960
TTAGGGAAGT TCAGCATTTC AGGGATACTC ATTCCTGAAA TAGGCGTTCT ATCGCCCTTT 1020
TTCGTATTTC TAGCTCTCAG TCTTTGGTAT TTTAAAAAAC TTAATAAGAG ATTG 1074

(2) INFORMATION FOR SEQ ID NO:1149:

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149

```
AAGAGAAGAG TGGTGAAATT CTATACTTAT AGTGGGGAAA CGGCCGCTGA AGCTTTAAAG     60
ATCGCTCAAA GCCACCATGG GGTGGATACG CTGGTGTTTA AAACCCAAGA AATCCGTAAA    120
AAAACGCTCA CTTCTTCTGG GCTTTATGAA ATCGTTGTGG CGGTTGAAGA AGAAGAAAAC    180
AAAAAAGCCC CCCTCATTCC AGAGAGTTTG TATGATGAAG AATTGAATGA AGAAGACGTG    240
GTCATGCAGC TTTCAAGCAC CGTAGAAGAA ATGCGCAAAC TCGCCGGGGT TTCATCTAAC    300
CAGCGCAACT ATACTTTTTC AAAAAATAAG ACTCTTTTAG AAAAAGACGC TCCATTAGAG    360
GATACGCCTT TAGAGGCTAA TAAGCAAGAC GCCTTGTTGC AAGCCTTAAA AGATGAAGCC    420
AACCATAAAA AAGAAAGAGA AAAAAGAGAA GTCAAACAAG AAGAAGAAAT TAAAGATATT    480
AATGCGCAAC TAAGTAAAAT CAGAGACAGC TTAAAACTCA TTCAAAACAT GTTTTGGGAT    540
GAGAAAAACC CTAATTCTGT CAATATCCCT CAAGAATTTG CCGAAATTTA CAAACTAGCC    600
AAACAAAGCG GCATGAAATC CAGTCATTTA GATGAAATCA TGCAATTAAG CCTGGAATTG    660
ATGCCTTTAC GCATGCGGGA AAATTCCGTA ACGATCAAGC GCTATTTTAG AGAAGTGTTG    720
CGTAAAATAA TCCTGTGTCG CCCTGAAGAT TTGAATTTGA GGCAAAAACG CATTTTAATG    780
CTTGTAGGGC CAACAGGCGT GGGGAAAACG ACGACTTTGG CTAAATTAGC CGCACGCTAT    840
TCTAGAATGC TGGCTAAAAA ATACAAGGTG GGCATTATCA CTTTAGACAA TTATCGCATT    900
GGGGCTTTGG AGCAATTGAG TTGGTATGCT AATAAAATGA AAATGAGTAT AGAAGCGGTG    960
ATTGACGCTA AGGATTTTGC TAAAGAAATT GAAGCTTTGG AATACTGCGA TTTTATTTTA   1020
GTGGATACGA CAGGGCATTC GCAATACGAT AAGGAAAAAA TTGCCGGTTT GAAAGAGTTT   1080
ATAGATGGGG GTTATAATAT TGATGTATCC TTAGTGCTTT CGGTTACCAC TAAGTATGAA   1140
GACATGAAAG ATATTTATGA TTCTTTTGGG GTGTTAGGGA TTGACACTTT AATCTTTACG   1200
AAATTAGATG AGAGTAGGGG GTTAGGGAAT TTGTTTTCTT TAGTGCATGA AAGCCAAAAG   1260
CCTATCAGTT ATCTTTCTGT CGGCCAAGAA GTGCCTATGG ATTTGAAAGT GGCTACTAAT   1320
GAGTATTTAG TGGATTGCAT GCTAGATGGC TTTAGTAACC CTAATAAGGA ACAAGCA      1377
```

(2) INFORMATION FOR SEQ ID NO:1150:

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

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169

```
AATAAAATCC TAGCCAGTGA GCTAGAATTT AAATTTTTAA TCAAAGGAGT CATCATGGCA      60
CACCATGAAG AACAACACGG CGGGCACCAC CACCATCACC ACCACACACA CCACCACCAT     120
TATCATGGCG GCGAACACCA CCATCACCAC CACAGCTCTC ATCATGAAGA AGGTTGTTGC     180
AGCACTAGCG ATAGTCATCA TCAAGAAGAA GGTTGTTGCC ACGGGCATCA CGAG           234
```

(2) INFORMATION FOR SEQ ID NO:1170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1035 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170

```
GGGGTTTTGA TTAGAACCCC CAAGCATTTA ACCAAGCAAG AGAGCGTGAA TTTAGGGGCT      60
TACTACACGC CCCCTTATTT AGTGGATTGC GCTTACAAGC TTTTAAAAAA GCATGTTGGT     120
ATTGAAAACT ACACGCTTTT AGACACCGCA TGTGGTAATA AAGAGTTTTT AAAGCTCCAC     180
CACCCTAAAA AAATAGGAGC GGATATTGAC CCTAAGTGTG ATGCTTTAAT AATAAACGCT     240
CTAGCCAATC CTAAAAGAGA AAATTATGGC ATTAGCCAAG ATGAACCTTT AATCATCGTG     300
GGCAATCCCC CCTATAACGA TAGAACTTCC TTTATCAAAC AAGATATTAA AAATAAAGAT     360
TTCATTTTTG AGATAGACAA CGATTTGAAA TCCCGAGATT TAGGGATAAG TTTTTTAAAA     420
TCTTTTGCAA TTTTAAAGCC GGCGTTTATT TGCGTGCTAC ACCCTTTATC TTATCTCATC     480
AAAGAAGCTA ATTTTAAGCA ATTAAAGCTA TTTAAGGATC ATTACAGGCT TTTAGACGCT     540
TTTGTTGTTT CTTCTAAATC TTTCACTAAA AGTAACGAAT TTCCTATTGT GATAGCTTTA     600
TATGAGCGAG GGCGAATGGA CTATGCAGGT ATTAGGCGTT TTGTTTTTCC AACTGATTGC     660
GATACGACGC TATGCTTAAA CGATTTTGAC TACATAGCCA ATTATGTGGA TAAATACCCT     720
AACGCTAAAA AGGTTGGGGC ATGCGTGGGC TATTTTTTTC CTATGCGAGA CATTAACGCT     780
CTCAAACGCA ACAAAACTTT TTTAAACGCG CCAAGCGAAA ATGCGGTGCG AATCAGTCAA     840
GATAAATTGA TTTATTACCA ATATATCCAT TATTTTAAGG AAATTGCTCC TAAAATCCCT     900
TATTATTTTG GTAATTTGGA TATTATCATT GATCATTTTG CTTTTTTAGA AATTAAAGAC     960
GCTTTTTTAA AAGATAAAAG AGCGCGTTTA GAATATTTTA AAAAATTGTT TCAAGGACAC    1020
```

CCTTGTGAGT TTGAT 1035

(2) INFORMATION FOR SEQ ID NO:1171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 786 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171

AATATTTTAA AAAATTGTTT CAAGGACACC CTTGTGAGTT TGATTAAAGT TAGTGGTGAT 60
AAAAAAGTGA TTGAGGTTTC TATTCCTTTA ACTTCCATTT CAGGCAAAGC GCGTGTGAAA 120
ATCAGACATG CCTTTAGCGA TTATGGTATT TCAACAGCGA CTAGAAAAAT CCCTTTTAGT 180
TTAAAGCATT ATGTAGAGTG GCAGATCGGT TATGATGTCC CCATTAAAGA TAAAGAAAAA 240
TTTGAACTCA CTACTTTAAA AGATGAAAAA TATCATTTTT TAGGGGCTAA TAATAAAGTA 300
AAAACTCTTT ATGAATTGAG CGAAATGATT TATTACGCTA AGCGATTGGG TTTAATCAGT 360
TTAGAAAATT TAGAAAATAC TTTAAAATTT TTAGAAAAAC AAAAACAATT TATAGAAGAT 420
AATTTTATGA TTACAAGAGA AAGATTTAGA TCGCATCAAT TTGGTGGCAT GGATTTTGAA 480
CTCTTACGCA TTTCTTATCC TTTGCTCATT CATTCTTTTG ATGATAATGA GTTGAGCGAA 540
ATAGTTATTA AGGAACAACA ATATGGCTCT AAAACCCAAG CCATGCTGTA TTTTTGCTTT 600
TCTATTTTGG AGTTAAAAAC CGCTACCCCC TTATTAAACA GAACCGCTAT GCCCAAAGAA 660
CATGCCCTTT TGATTATCCA TGAAACCAAC GCTCTTGTGT TTTTAGAAAT GCTTAAAATT 720
TTTGGACTTT TAAGCCAAGT GCACCATAAC GATGTGTTAA AGATTTTAGA AAAAATACTT 780
CAAAAT 786

(2) INFORMATION FOR SEQ ID NO:1172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172

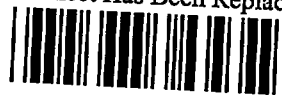
This Sheet Has Been Replaced

```
TTGAAGGCAT TAAACGACTG CATGGTATTT TTTCATAAGA AAATTATTTT AAATTTTATC      60
TATTCTTTAA TGGTTGCTTT TTTATTCCAT TTATCCTATG GGGTTCTTTT AAAAGCCGAT     120
GGAATGGCTA AAAAGCAAAC TCTTTTAGTG GGTGAAAGGC TTGTGTGGGA TAAGCTCACG     180
CTGTTAGGGT TTTTAGAAAA AAACCATATC CCCCAAAAAC TCTACTACAA TTTGAGCTCT     240
CAAGATAAAG AATTGAGTGC TGAAATCCAA AGCAATGTTA CCTACTACAC TTTAAGAGAT     300
GCAAATAACA CGCTCATTCA AGCCCTTATC CCTATTAGCC AGGATTTGCA AATCCATATT     360
TACAAAAAAG GAGAGGATTA TTTTTTAGAC TTTATCCCCA TTGTTTTCAC TCGTAAAGAA     420
AGAACCCTCC TTCTTTCCTT ACAAACTTCG CCCTATCAAG ATATTGTCAA AGCCACCAAT     480
GACCCCCTTT TAGCCAACCA ATTGATGAAC GCGTATAAAA AAAGCGTGCC TTTTAAACGC     540
CTAGTGAAAA ACGATAAAAT CGCTATCGTT TATACAAGGG ATTATCGTGT GGGGCAAGCG     600
TTTGGCCAGC CGACCATCAA AATGGCGATG GTTAGCTCTC GTTTGCACCA ATACTATCTT     660
TTTTCCCATT CAAACGGGCG TTATTACGAT TCAAAAGCGC AAGAAGTGGC AGGGTTTTTA     720
CTAGAAACCC CGGTGAAATA CACCCGCATT TCTTCGCCTT TTTCGTATGG GAGGTTCCAT     780
CCTGTTTTAA AAGTTAAACG GCCTCATTAC GGCGTGGATT ATGCGGCTAA ACATGGCAGT     840
TTGATCCATT CTGCTTCAGA CGGCCGTGTG GGTTTTATAG GGGTTAAGGC GGGTTATGGG     900
AAGGTGGTTG AAATCCATTT GAATGAATTG CGCTTGGTGT ATGCTCACAT GAGCGCGTTC     960
GCTAACGGAT TAAAAAAAGG CTCGTTCGTT AAAAAAGGGC AAATCATAGG AAGAGTGGGA    1020
AGCACGGGTT TAAGCACCGG GCCGCATTTG CATTTTGGCG TGTATAAAAA CTCCCGCCCC    1080
ATTAATCCTT TAGGCTATAT CCGCACCGCT AAAAGCAAGC TGCATGGCAA ACAAAGAGAG    1140
GTTTTTTTAG AAAAAGCTCA GTATTCTAAG CAAAAATTAG AAGAACTTTT TAAAACCCAT    1200
TCTTTTGAAA AAAATTCATT TTATCTTTTA GAGGGTTTT                           1239
```

(2) INFORMATION FOR SEQ ID NO:1173:

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

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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

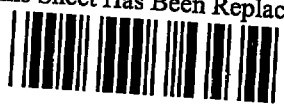
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173

```
GGATGCTTGA TGAAAAGCAT TTTGCTCTTT ATGATTTTTG TAGTTTGTCA GTTAGAAGGC      60
AAAAAATTTT CACAAGATAA TTTTAAGGTG GATTATAACT ACTATTTGCG CAAACAGGAT     120
TTGCACATCA TTAAAACGCA AAACGATTTG TCCAATGCCT GGTATCTCCC TCCACAAAAA     180
GCCCCCAAAG AACATTCTTG GGTGGATTTT GCTAAAAAAT ATTTAAACAT GATGGATTAT     240
CTAGGCACTT ATTTTTTGCC TTTTTATCAT AGTTTCACCC CCATTTTTCA ATGGTACCAC     300
CCTAATATCA ACCCCTACCA ACGCAATGAG TTTAAGTTCC AAATCAGTTT TAGAGTGCCT     360
GTATTTAGGC ATATTCTTTG GACTAAAGGC ACGCTTTATC TGGCTTATAC CCAAACTAAC     420
TGGTTTCAAA TTTATAATGA CCCTCAATCC GCCCCCATGC GAATGATCAA TTTCATGCCT     480
GAACTCATCT ATGTTTATCC TATTAATTTT AAACCTTTTG GGGGTAAAAT AGGGAATTTT     540
TCTGAAATTT GGATAGGTTG GCAGCACATT TCTAATGGTG TGGGGGGTGC GCAATGTTAC     600
CAGCCTTTTA ATAAAGAAGG TAATCCTGAA AACCAGTTTC CAGGACAACC TGTAATCGTT     660
AAAGATTATA ACGGGCAAAA AGATGTGCGC TGGGGGGGGT GTCGTTCGGT GAGCGCGGGC     720
AACGCCCTGT GTTTCGTTTG GTGTGGGAAA AGGGAGGCC                           759
```

(2) INFORMATION FOR SEQ ID NO:1174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 272 base pairs

This Sheet Has Been Replaced



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

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174

```
ATGTGAAATT AAAGGGCATG GATAAAGAAG AAAATGAAGA AAATAAAATT AACCAAGCGA      60
ATGATAGCTA CGGCCAAAAA AGCCCTTTCC AAAAGCTATG GATATTGTTT GGTGGGGCGT     120
TTTTTAATTT TCTTTTTGCG GTTTTAGTGT ATTTTTTTCT GGCATTGAGC GGGGAAAAAG     180
TCTTACTGCC CGTCATTGGC GGTTTAGAAA AAAACGCGCT AGAAGCCGGG CTGTTAAAGG     240
GGGATAGAAT CCTTCTATCA ACCATCAAAA AA                                    272
```

(2) INFORMATION FOR SEQ ID NO:1175:

(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:1175

```
AGAATTGAGT GGGGTAATAG GCATTGTGGG GCGTTAAGCC ATGCCAATAG CGTGAGCATG      60
CTTTTGTTGT TTGGGGCGTT TTTATCTATC AATCTAGGGA TTTTAAATTT ATTACCCATT     120
CCAGCCTTAG ATGGGGCGCA AATGCTAGGG GTCGTTTTTA AAAATATTTT TCATATCGCT     180
TTGCCAACGC CCATACAAAA TGCGTTGTGG CTAGTGGGGG TGGGGTTTTT GGTTTTTGTC     240
ATGTTTTTAG GGCTTTTTAA TGACATTACT CGTTTGCTA                             279
```

(2) INFORMATION FOR SEQ ID NO:1176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176

```
AATTTAGGCG GAGCGGCCAA TGTGGCTAAT AACCTTACCT CTTTAAAAGC TAAAGTCTTT      60
TTATGTGGGG TAGTGGGAGA TGATTTAAAA GGCAAGCATT TCATTAGCAC TTTAAATTCT     120
ATAAGGATTG ACACTTCAGG TGTTTTAATA GATAAAACCC GTTGCACCAC GCTTAAAACG     180
CGCATCATCG CGCAAAACCA GCAAATCGTG CGCGTGGATA AGGAAATCAA AGACCCCTTA     240
AACGCTGATT TAAGAAAGAA TCTTTTAGAT TTTATCGCAG AAAAAATTCA AGAAATAGAT     300
GGCGTGATCC TTTCAGATTA CAATAAGGGT GTGTTGGATT TTGAACTCAC TCAAACCATC     360
ATCACGCTAG CTAATAAGCA TCATAAGCTC ATTTTATGCG ACCCTAAAGG AAAGGATTAT     420
AGCAAATATT CCCATGCGAG TTTGATCACG CCTAATCGCG CTGAATTAGA GCAAGCGCTC     480
CATTTGAAAT TAGACAGCCA TGCGAATTTA TCAAAAGCGC TCCAAATTTT ACAAGAAACT     540
TATCATATCG CTATGCCTTT AGTAACCTTG AGCGAACAAG GCATCGCTTT TTTAGAAAAA     600
GGCGAGTTAG TCAATTGCCC CACTATCGCT AAAGAAGTTT ATGATGTAAC GGGGGCAGGC     660
GATACGGTGA TAGCGTCTTT AACGCTCTCT TTATTGGAAT CAAAAAGCTT GAAAGAAGCT     720
TGCGAGTTTG CTAATGCGGC TGCGGCGGTG GTGGTGGGTA AAATGGGGAG CGCGTTAGCG     780
AGTTTAGAAG AAATCGCTTT GATTTTGAAC CAAACGCACC CTAAAATCCT CCCTTTAGAA     840
AAGCTGTTAG AAACTTTAGA ACGCAACCAG CAAAAAATCG TTTTCACCAA TGGCTGTTTT     900
GATATTCTCC ATAAAGGGCA TGCGAGCTAT TTGCAAAAGG CTAAAGCTTT AGGGGATATT     960
CTTGTTGTGG GGTTAAATAG CGATAATTCC ATTAAAAGGC TTAAGGGGGA TAAACGCCCC    1020
ATAGTGAGCG AAAAAGACAG GGCGTTTCTT TTAGCGAGCT TGTCTTGCGT GGATTATGTT    1080
GTGGTGTTTG GAGAAGACAC GCCCATAAAA TTGATTCAAG CCCTAAAGCC TGATATTTTA    1140
GTCAAGGGAG CGGACTACCT CAATAAAGAA GTCATAGGGA GCGAGTTGGC TAAAGAAACC    1200
CGTTTGATAG AATTTGAAGA AGGTTATTCC ACAAGCGCTA TCATAGAAAA AATTAAAAGG    1260
ACACATAATG AT                                                        1272
```

(2) INFORMATION FOR SEQ ID NO:1177:

(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:1177

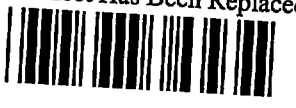
```
GGATCGCTTA TGGTGAATGT GTTTTTCAAG CAGCAAAAAT TCGTCATTAA AAAACGCTTT      60
AATGACTTTA ATGGTTTTGA TATAGAAGAA AATGAAGTGT TGTGGTTTGA ATTAATCAAC     120
CCTACGCCCA ATGAATTAGC CACTCTAAGC CAAGAATACG CTATCCACTA CAACACGGAT     180
CATTCCCAAC GAGTCTCATC AGTTACCAAA TACTGGGAAG ACAGCTCCAG CGTTACGATC     240
```

```
AACGCTTTTT TCACCAACCA GGATGAAAAT GAGACTTTCC ACATGGAAAT GGCGACCTTT     300
ATTTTGTCTA ATAACATTCT TTTCACGATT TATTACGGGA CTTTAGAAAT CTTTGATTCT     360
ATCCAAAAAA AGGTTTTGGC TAGCCCTAAA AAATTTGAAG ACGGGTTTGA TATTCTAACT     420
AAAATCTTTG AAGTGTATTT TGAAAAAGGG GTGGAATGTT TGGAATGGAT CAACAAACAA     480
ACGAGCCTGT TGCGCAAAAA CATCATTTTC AAAGAAACTT CTACGCATGA TGATATTTTA     540
GTGCGCTTGT CCAATTTGCA AGAATTTAAT GTGGCTTTAA GGGATTCCTT TTTTGACAAA     600
CGGCGCATTA TCACCGCTTT ATTAAGGAGC AATAAAGTGG ATAGCGATAC TAAAAATAAT     660
TTAAATATCA TTTTAACCGA TTTTAGCTCT TTGGTGGAGT CTACAACGGT CAATCTCAAC     720
TCGCTTGATA ACATTCAAAA CCTGTTCGCT TCTCAAGTCA ATGTGGAGCA AAATAAAATC     780
ATTAAACTCT TCACTGTGGC GACTATGGCG ATGATGCCCC CCACATTGAT TGGCACGATT     840
TATGGCATGA ATTTTAAATT CATGCCGGAG TTAGAATGGC AATACGGGTA TCTTTTTGCG     900
CTGATTGTCA TGGCGATTTC TACGATTTTG CCGGTGATTT ATTTCAAAAA GAAGGGTTGG     960
TTG                                                                  963
```

(2) INFORMATION FOR SEQ ID NO:1178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 732 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178

```
CCTTTCATGG AATTTTTATC CTCACTCTTA GACGCTCTTT CTACACCGCA TGGCATAGTC      60
TCCTTGGCTA CGCTCACGCT TTTAGAGATC GTTCTAGGGA TTGATAATAT CATTTTTATC     120
ACGGTGATGG TTTATAAACT CCCCAAACAC CAGCAAAATA AGGTCATGAT TTTAGGCTTG     180
GGCTTAGCGA TGATCACTCG TATAGGGCTT TTAGGGAGCT TGTTTTTCAT CAGCCATTTG     240
CAAAAGCCTT TATTCGCTAT AGCGGGCATG AGCTTTTCAT GGCGTGATGT GGTGCTGCTT     300
TTAGGGGGGG CGTTTTTGGC TTTTAAGGCG TTAGTGGAAT TAAAAGAGCA GATCTATCCT     360
AAAGAAAAAC GCCAAGAAAA AGCGTTTGGC TTTTTCATCA CTTTAATAGA AATCATGTTT     420
TTAGACATTG TTTTTTCTTT GGACTCCGTG ATCACGGCTA TTGGGATCGC TAAACACTTA     480
GAAGTCATGG CGCTTGCTAT TATTTTATCT GTAATCGTGA TGATGTTTTT TTCCAAAATC     540
GTTGGCGATT TTATTGAAAA GCATTATCGC GTCAAAACTT TAGCCTTTGT GTTTTTGCTC     600
GTTGTGGGCG TGTTTTTGTT TTTAGAAGGC TTGCATTTAC ACATCAATAA AAACTATTTG     660
TATGCGGGTA TTGGTTTTGC CTTGCTCATA GAATGCTTGA ATATTTTCAT AGAAAAGAAA     720
ATGAAAAAAA GT                                                        732
```

(2) INFORMATION FOR SEQ ID NO:1179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 487 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179

```
GTTTATGGCT TTTGGGCTTG TGTTTTGTGC TAGGGATTTA AGTTTGGTTT TGTTTATTTT     60
GCGCAAACAA GGCGTTTCA ATTTAGACAA AACCATTCTT TCCATTAGCG CTATCAATGA    120
AATGAGCATG ATTTTAGGCC TGTTCATGCT CACAGCCGGG AATTTCTTAG GTGGGGTGTG    180
GGCGAATGAA TCTTGGGGGC GCTATTGGGG GTGGGACCCT AAAGAAACTT GGGCGTTGAT    240
TTCTATTTGC GTCTATGCCT TGATCTTGCA TTTGCGTTTT TTAGGCTCTC AAAATTGGCC    300
CTTTATTTTA GCGAGCAGCA GCGTGCTAGG GTTTTATTCG GTTTTAATGA CTTATTTTGG    360
CGTGAATTAC TACCTTTCTG GCTTGCACAG CTATGCCGCA GGTGATCCTT TGCCGATCCC    420
TACTTTTTTA TACTTTTTGG TAGCGATACC TTTCGCTCTC GTATCTTGGC GTATTTCAAA    480
CGCCATT                                                             487
```

(2) INFORMATION FOR SEQ ID NO:1180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1180

```
CGATATTCCG ATCAGACGAA TCTATTAGCC CTAAATGCTG CTATTGAAGC CGCAAGGGCC     60
GGCGAGCATG GTAGAGGCTT TGCGGTGGTG GCTGATGAAG TTAGGAATTT AGCTGGGCGC    120
ACTCAAAAGT CTTTAGCCGA AATCAATTCC ACTATCATGG TGATTGTCCA AGAAATCAAT    180
GATGTGAGTT CGCAAATGAA TCTCAATTCG CAAAAAATGG AGCGCTTGAG CGATATGAGT    240
AAAAGCGTGC AAGAAACTTA CGAAAAAATG AGTTCTAATT TAAGCTCAGT CGTTTTAGAC    300
AGCAATCAAA GCATGGACGA TTACGCTAAA TCCGGACACC AAATTGAAGC TATGGTAAGC    360
GATTTTGCAG AAGTGGAAAA AGTGGCTTCT AAGACTTTGG CTGATTCTTC AGATATTTTA    420
AACATCGCTA CGCATGTGAG TGGAACGACC ATGAATTTAG ACAAACAAGT GAATTTGTTT    480
AAAACT                                                              486
```

(2) INFORMATION FOR SEQ ID NO:1181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(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:1181

```
ATTTGTTTAA AACTTAATCA GGGGGGAGTT TATCAAAAAA GGGTTGGATT GTTAAAGGTT      60
TCTGTGATCA CGGCGTGTTT TAATAGCGAA AAAACCATTG AAGACACCAT TCTTTCCGTG     120
CTTAATCAAA CTTATAAAAA CATTGAATAC ATCATTATAG ATGGGGCTAG CGCGATAGCA     180
CTT                                                                  183
```

(2) INFORMATION FOR SEQ ID NO:1182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1992 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182

```
AATCATATTG TGCGTGGCGT TGATTGTGAT CGTGGCGTGA GCATTTTAGG GGTGTCCTTA      60
AACAGCAGGG TGAAAGAGAT TTTAAAAGAA AGCGCTCTGC ATTCAATGCA AGATAGTTTG     120
CATTTCAAGG TTAAGGAAGT GCAAAGTGTT TTGGAAAACA CTTATACGAG CATGGGCATT     180
GTCAAAGAAA TGCTCCCTGA AGACACCAAA AGAGAAATCA AAATCCAGTT GTTAAAAAAC     240
TTCATTTTAG CCAATTCGCA TGTCGCTGGG GTGAGCATGT TTTTTAAAGA CAGAGAGGAT     300
TTGAGATTGA CGCTTTTACG AGATAACGAT ACGATCAAGT TGATGGAAAA CCCGTCATTA     360
GGGAGTAACC CTTTAGTGCA AAAAGCGATG AAAAATAAAG AAATTTCTAA AAGCTTGCCT     420
TATTACAGGA AAATGCCTAA CGGGGCGGAA GTTTATGGCG TGGATATTCT TTTACCACTA     480
TTCAAGGAAA ACACGCAAGA AGTGGTGGGG GTTCTGATGA TTTTCTTTTC CATTGACAGC     540
TTCAGTAATG AAATCACTAA AAACAGGAGC GATTTATTTT TAATTGGCGT TAAAGGTAAA     600
GTGCTTTTGA GCGCGAATAA AAGCTTGCAA GACAAATCCA TCACCGAAAT TTATAAAAGC     660
GTGCCTAAAG CCACTAATGA AGTGATGGCT ATTTTAGAAA ATGGCTCTAA AGCGACTTTA     720
GAATACTTGG ATCCCTTTAG CCATAAGGAG AATTTTTTAG CCGTTGAAAC CTTTAAAATG     780
CTAGGCAAAA CAGAAAGTAA AGACAATCTT AATTGGATGA TCGCTTTGAT CATTGAAAAA     840
GACAAGGTCT ATGAGCAAGT GGGATCGGTG CGTTTTGTGG TGGTTGCAGC GAGTGCTATC     900
ATGGTGTTAG CCTTAATCAT AGCGATCACT CTTTTAATGC GAGCGATCGT GAGCAATCGT     960
TTGGAAGTCG TTTCTAGCAC CTTGTCTCAT TTCTTTAAAT TATTGAACAA TCAAGCCCAT    1020
TCTAGCGACA TTAAATTGGT TGAAGCGCGA TCTAATGACG AATTAGGGCG CATGCAAACA    1080
GCGATCAATA AAAATATCTT GCAAACCCAA AAAACCATGC AAGAAGACTG GCAAGCCGTC    1140
CAAGACACCA TTAAAGTGGT TTCAGATGTG AAAGCGGGGA ATTTTGCGGT GCGCATCACG    1200
GCTGAACCCG CAAGCCCTGA TTTGAAAGAA TTGAGAGACG CGCTAATGGA TCATGCACTA    1260
TTTGCAAGAA AGCGTGGGAC TCACATGCCA AGCATTTTCA AAATCTTTGA AAGCTATTCT    1320
```

```
GGCTTGGATT TTAGAGGGCG GATCCAAAAC GCTTCGGGTA GGGTGGAATT GGTTACTAAC    1380
GCTTTAGGGC AAGAAATCCA AAAAATGCTA GAAACTTCGT CTAATTTTGC CAAAGATCTA    1440
GCGAACGATA GCGCGAATTT AAAAGAATGC GTGCAAAATT TAGAAAAGGC TTCAAACTCC    1500
CAACACAAAA GCCTGATGGA AACTTCCAAA ACGATAGAAA ATATCACCAC TTCCATTCAA    1560
GGCGTGAGCT CTCAAAGTGA AGCCATGATT GAACAAGGGA AAGACATTAA AAGCATTGTA    1620
GAAATCATTA GAGATATTGC CGATCAAACG AATCTATTAG CCCTAAACGC TGCTATTGAA    1680
GCCGCACGAG CCGGCGAGCA TGGCAGAGGC TTTGCGGTGG TGGCTGATGA GGTGAGGAAG    1740
CTCGCTGAAA GGACGCAAAA ATCCCTCAGT GAGATTGAAG CCAATATTAA TATTCTCGTT    1800
CAAAGCATTT CAGACACGAG CGAAAGCATT AAAAACCAGG TTAAAGAAGT AGAAGAGATC    1860
AACGCTTCTA TTGAAGCCTT AAGATCGGTT ACTGAGGGCA ATCTAAAAAT CGCTAGCGAT    1920
TCTTTAGAAA TCAGTCAAGA AATTGACAAA GTCTCTAACG ATATTTTAGA AGATGTGAAT    1980
AAAAAGCAGT TT                                                        1992
```

(2) INFORMATION FOR SEQ ID NO:1183:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183

```
CGTGGTGAAT GCTATTTTGA AAGAGAAATT GGATTGATGA GGAAAATTTT TTCTTATATT      60
TCTAAGGTTC TATTATTTAT TGGGGTGGTT TATGCAGAGC CTGATTCTAA AGTGGAAGCC     120
TTAGAAGGGA GGAAGCAAGA GTCTTCTTTG GATAAAAAAA TCCGCCAAGA ATTGAAGAGT     180
AAGGAATTGA AGAATAAGGA ATTAAAGAAT AAGGATTTGA AAAATAAAGA AGAAAAGAAA     240
GAAACAAAAG CCAAGAGAAA ACCCAGAGCA GAAGTCCATC ATGGGGACGC CAAAAATCCC     300
ACTCCAAAGA TCACGCCTCC TAAAATCAAA GGGAGTAGTA AGGGCGTTCA AAATCAAGGC     360
GTTCAAAACA ACGCGCCAAA ACCTGAAGAA AAAGATACAA CCCCTCAAGC TACTGAAAAA     420
AATAAGGAAA CAAGCCCTAG CTCTCAATTC AATTCCATTT TTGGTAATCC TAATAACGCT     480
ACCAACAACA CCCTTGAAGA TAAGGTCGTA GGGGGCATTT CATTGCTTGT TAATGGTTCG     540
CCTATCACGC TGTATCAAAT CCAAGAAGAG CAAGAAAAAT CTAAAGTGAG TAAGGCTCAA     600
GCTAGGGATC GTTTGATCGC TGAACGCATT AAAAACCAAG AAATTGAGCG CTTAAAAATC     660
CATGTAGATG ATGACAAGCT AAACCAAGAA ATGGCGATGA TGGCGCAACA ACAAGGCATG     720
GATTTAGACC ATTTCAAACA GATGCTTATG GCTGAGGGGC ATTATAAACT CTATAGAGAT     780
CAACTTAAAG AGCATTTAGA AATGCAAGAA TTGTTGCGTA ATATTTTGCT CACGAATGTG     840
GATACCAGCT CTGAAACCAA AATGCGCGAA TATTACAACA AACACAAGGA GCAATTCAGT     900
ATCCCCACAG AAATAGAAAC CGTGCGCTAC ACTTCCACCA ATCAAGAGGA TTTAGAAAGG     960
GCTATGGCAG ACCCTAATTT GGAAGTCCCA GGGGTGAGTA AGGCCAATGA AAAAATAGAG    1020
ATGAAAACCC TAAACCCTCA AATCGCCCAA GTCTTTATTT CGCATGAGCA AGGCTCTTTC    1080
ACGCCCGTTA TGAATGGGGG TGGGGGGCAG TTCATCACCT TTTATATCAA GGAAAAAAGG    1140
GGTAAAAATG AAGTGAGCTT CAGTCAGGCC AAGCAATTCA TCGCCCAAAA ATTAGTGGAA    1200
GAATCTAAGG ATAAGATTTT AGAAGAGCAT TTTGAAAAAT TGCGCGTTAA GTCTAGGATT    1260
GTGATGATCA GAGAG                                                     1275
```

(2) INFORMATION FOR SEQ ID NO:1184:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1008 base pairs

This Sheet Has Been Replaced



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

(ii) MOLECULE TYPE: DNA (genomic)

(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:1184

```
ATTGTGCAAC ACTTCAATTT CCTCTATAAA GATTCTTTAT TTTCTATCGC TTTATTCACT      60
TTCATTATCG CTCTTGTGAT TTTATTAGAA CAGGCTAGAG CGTATTTCAC CCGAAAGAGA     120
AACAAAAAAT TTTTGCAAAA ATTCGCCCAA AATCAAAACG CCTATGCGAG CAGCGAGAAT     180
TTAGACGAGC TTTTAAAGCA TGCTAAAATT TCCAGTTTGA TGTTTTTAGC TAGGGCGTAT     240
TCTAAAGCGG ATGTGGAAAT GAGCATTGAA ATCTTAAAAG GGCTTTTGAA TCGCCCCTTA     300
AAAGATGAAG AAAAAATCGC TGTTTTAGAT TTATTGGCTA AAAATTATTT TAGCGTGGGG     360
TATTTGCAGA AAACAAAAGA CACCGTGAAA GAAATTTTGC GCTTTTCCCC AAGGAATGTG     420
GAAGCGTTGT TGAAGCTTTT GCATGCGTAT GAATTAGAAA AAGATTATTC AAAGGCTTTA     480
GAAACTTTGG AATGTTTGGA AGAATTAGAG GTGCCTAAAA TTGAAACGAT TAAAAATTAC     540
CTCTATTTAA TGCATTTAAT AGAGAATAAG GAAGATGCGG CTAAAATCTT GCATGTTTCA     600
AAAGCGTCGT TAGATTTGAA AAAAATCGCT CTGAATCACT TAAAATCGCA TGATGAAAAT     660
CTTTTTTGGC AAGAAATTGA TACAACCGAA CGGCTAGAAA ATGTGATCGA TCTTTTATGG     720
GATATGAATA TCCCTGCTTT TATTTTAGAA AAACATGCCC TTTTGCAGGA CATCGCGCGA     780
TCTCAAGGGT TGCTTTTGGA TCACAAACCT TGCCAAATTT TTGAATTAGA GGTTTTACGC     840
GCTCTATTGC ATAGCCCTAT AAAAGCGAGT CTGACTTTTG AATACCGCTG CAAGCATTGC     900
AAACAAATCT TTCCTTTTGA AAGCCATAGG TGTCCTGTGT GTTACCAGTT AGCGTTTATG     960
GATATGGTGC TTAAAATCTC TAAAAAAACG CATGCTATGG GAGTGGAT                  1008
```

(2) INFORMATION FOR SEQ ID NO:1185:

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

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1185

```
ATTAGAGGCG CAAAAACGGG TCAAAACGAC CACTTAAAGG GAAAAATGAT GAAAAACAAA      60
CGCTCTCAAA ATAGCCCTTA TGTAACGCCT GACAACCCTT ATCTAACGCT AGAAAAAGCT     120
TTAGGGTATT CTTTTAAAGA CAAGCGTTTA TTGGAGCAAG CCTTAACGCA TAAATCATGT     180
AAGCTCGCTT TAAACAATGA GCGCTTGGAA TTTTTGGGCG ATGCGGTGTT GGGCTTGGTG     240
```

```
ATAGGGGAGC TGCTATACCA TAAATTCTAT CAATACGATG AGGGCAAACT CTCTAAATTA     300
AGGGCTTCTA TTGTGAGCGC GCATGGTTTC ACTAAATTAG CGAAAGCGAT TGCTTTACAA     360
GATTATTTGC GCGTTTCTTC TTCTGAAGAA ATTTCTAAGG GGAGGGAAAA ACCCTCTATT     420
CTGTCAAGCG CTTTTGAGGC TTTAATGGCT GGGGTGTATT TAGAAGCAGG GTTAGCTAAG     480
GTGCGTAAAA TCATACAAAA TTTACTCAAT CGTGCTTACA AGCGTTTGGA TTTGGAGCAT     540
TTGTTTATGG ATTATAAAAC CGCTTTGCAG GAATTGACCC AAGCGCAGTT TTGCGTGATC     600
CCCACTTACC AATTACTCCA AGAAAAAGGC CCCGATCACC ATAAAGAATT TGAAATGGCT     660
CTATACATTC AAGATAAAAT GTATGCGACC GCTAAAGGCA AGAGTAAAAA AGAAGCCGAA     720
CAGCAATGCG CTTATCAAGC GCTTCAAAAA CTTAAGGAAG TCAAA                     765
```

(2) INFORMATION FOR SEQ ID NO:1186:

(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:1186

```
GCGCATCAAT CATCTCGTGG TGTTAGCATG ATTTTAGCAT GCGATGTGGG GTTAAAACGC      60
ATTGGAATCG CTGCGCTTTT AAACGGCGTT ATCTTGCCTT TGGAAGCGAT TTTACGCCAC     120
AACAGGAATC AAGCCTCTAG GGATTTGAGC GATTTATTGA GAAAAAAAGA CATTCAAGTG     180
CTGGTGGTGG GCAAACCCAA CGAAAGCTAT GCAGATACCC ACGCCCGCAT TGAGCATTTT     240
ATCAAGCTTG TAGATTTTAA GGGCGAAATC GTTTTTATCA ATGAAGATAA TTCTAGCGTA     300
GAAGCTTATG AAAATTTAGA GCATTTGGGT AAGAAAAATA AGCGGATCGC TACCAAAGAT     360
GGCCGGTTAG ACTCTTTGAG CGCTTGTAGG ATTTTAGAGC GCTATTGCCA GCAGGTTTTA     420
AAAAAGGGC                                                             429
```

(2) INFORMATION FOR SEQ ID NO:1187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1731 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1731

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187

```
AAGAATGAAA ATTTTATCAA GGTTTTAATA TTGGATTTAA AGGTATTATT GCAACGGATT      60
GTTGATTTTT TCATCAAGCT CAATAAAAAG CAAAAAATCG CCCTGATCGC AGCGGGGGTT     120
TTGATCACCG CTTTACTCGT GTTTTTATTG CTCTATCCTT TTAAAGAAAA AGACTACGCG     180
CAAGGGGGTT ATGGGGTTTT ATTTGAAAGA TTGGATTCTA GCGATAACGC CTTAATCTTA     240
CAACACCTCC AGCAAAACCA AATCCCTTAT AAAGTCTTAA AAGACGACAC CATTCTTGTC     300
CCTAAAGATA AAGTGTATGA AGAAAGGATC ACTCTGGCTT CTCAAGGGAT CCCTAAAACG     360
AGTAAAGTGG GCTTTGAAAT CTTTGACACT AAAGACTTTG GGGCGACTGA TTTTGATCAA     420
AACATCAAAC TCATTCGCGC CATTGAGGGG GAATTGTCGC GCACGATTGA AAGTTTAAAC     480
CCCATTCTTA AAGCCAATGT GCATATTGCA ATCCCTAAAG ACAGCGTGTT TGTGGCTAAA     540
GAAGTCCCTC CTAGCGCTTC AGTGATGCTC AAGCTTAAGC CTGACATGAA GCTTTCACCC     600
ACTCAAATTT TAGGGATTAA AAATTTAATC GCTGCAGCTG TGCCTAAACT CACGATAGAA     660
AACGTGAAAA TCGTGAATGA AAATGGCGAA TCAATAGGCG AGGGCGATAT ACTAGAAAAC     720
TCCAAAGAAT TAGCCTTAGA GCAATTGCGC TACAAACAAA ATTTTGAAAA CATTTTAGAA     780
AATAAGATCG TCAATATCTT AGCCCCTATT GTGGGGGGTA AAAACAAGGT GGTCGCAAGG     840
GTCAATGCGG AGTTTGATTT CAGCCAAAAG AAAAGCACCA AAGAGACTTT TGATCCCAAT     900
AATGTCGTAA GGAGCGAGCA AAATTTAGAA GAAAAAAAAG AAGGCGCTCC TAAAAAACAA     960
GTTGGCGGTG TGCCGGGAGT TGTGAGCAAT ATTGGGCCTG TGCAAGGATT GAAGGACAAT    1020
AAAGAGCCAG AAAAATACGA AAAGTCTCAA AACACGACCA ATTATGAAGT GGGTAAAACC    1080
ATTATCGAGA TCAAGGGCGA GTTTGGCACC TTAATGCGTT TGAATGCGGC GGTTGTGGTG    1140
GATGGCAAGT ATAAAATCGC GCTCGAAGAC GGGGCAAACG CTTTAGAATA CGAGCCTTTA    1200
AGCGATGAAT CGCTTAAAAA AATCAACGCC CTAGTCAAAC AAGCCATTGG TGATAATCAA    1260
AATAGAGGCG ATGATGTGGC GGTGAGTAAT TTTGAGTTTA ACCCTATGGC GCCTATGATT    1320
GACAACGCCA CTTTGAGCGA AAAAATCATG CATAAAACTC AAAAAATCTT AGGCTCATTT    1380
ACGCCTTTAA TCAAGTATAT TTTGGTGTTT ATAGTGTTAT TCATTTTCTA TAAAAAAGTG    1440
ATCGTGCCTT TCAGCGAACG CATGCTGGAA GTGGTGCCTG ATGAAGATAA GGAAGTGAAA    1500
TCCATGTTTG AAGAAATGGA CGAAGAAGAA GATGAGTTGA ACAAACTCGG CGATTTGAGG    1560
AAAAAAGTAG AAGATCAATT AGGGCTTAAT GCAAGCTTTA GCGAAGAAGA AGTAAGATAT    1620
GAAATTATTT TAGAAAAGAT TAGAGGAACC CTTAAAGAGC GTCCTGATGA AATCGCCACG    1680
CTCTTTAAAC TCTTAATCAA AGATGAAATC TCTTCAGACA GCGCGAAAGG T             1731
```

(2) INFORMATION FOR SEQ ID NO:1188:

(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:1188

```
AAATGGTGCG GTTATTGTGA GCGGAGGAGC GTTAGGCGTG GATATTATCG CTCAAGAAAA      60
CGCCTTACCA AAAACCATCA TGCTTTCGCT TGCAGTTTGG ATTTTATCTA TCCCACGAAC     120
AACCATAAAG TGATCCAAGA AATCGCGCAA AACGGTTTGA TTTTAAGCGA ACATGAAAAG     180
GATTTCATGT TTATTAAAGG TTTTTTTTTA GTTAGAAATT GTCTGGTGAT CGCTTTAACC     240
GACGCGGTGA TTATCCCCCA AGCGGATTTA AAAAGCGGCT CTATGAGTAG TGTGAGATTA     300
GCCCAGAAAT ACCAAAAACC CTTGTTTGTT TTACCCCAAC GCCTGAATGA GAGCGACGGC     360
ACTAATGAGC TTTTAGAAAA AGGGCAGGCT CAAGGGATAT TTAATATTCA AAATTTTATA     420
AACACCCTTT TAAAAGATTA CCATTTAAAA GAAATGCCTG AAATGAAAGA TGAATTTTTA     480
GAATATTGCG CGAAAAACCC TAGCTATGAA GAAGCGTATC TCAAATTTGG GGATAAGCTT     540
```

This Sheet Has Been Replaced



TTAGAATACG AGCTGTTGGG TAAGATTAAG CGCATCAATC ATCTCGTGGT GTTAGCA 597

(2) INFORMATION FOR SEQ ID NO:1189:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189

AGGTTAAAAA TGGCAACCAA GCTTACCCCC AAACAAAAGG CTCAATTAGA CGAACTTTCC 60
ATGAGTGAAA AAATCGCCAT TTTACTCATT CAAGTGGGCG AAGACACCAC AGGCGAGATT 120
TTAAGGCATT TAGACATTGA CTCTATTACA GAGATTTCTA AGCAAATCGT GCAATTAAAC 180
GGCACGGACA AGCAAATCGG CGCGGCGGTT TTAGAGGAAT TTTTTGCGAT CTTTCAGTCT 240
AACCAATACA TCAATACCGG CGGTTTAGAA TACGCTAGGG AGCTTTTAAC CAGGACTTTA 300
GGGAGCGAAG AAGCCAGGAA AGTGATGGAC AAACTCACTA AAAGCTTGCA AACGCAAAAA 360
AACTTCGCTT ATTTAGGCAA AATCAAGCCC CAACAACTCG CTGATTTCAT CATTAACGAA 420
CACCCTCAAA CCATCGCCTT GATTTTGGCC CACATGGAAG CCCCTAATGC GGCTGAAACT 480
TTGAGCTATT TCCCTGATGA AATGAAAGCC GAGATTTCCA TTAGAATGGC GAATTTAGGC 540
GAAATATCGC CCCAAGTGGT TAAAAGGGTT TCCACGGTGT TAGAAAACAA ACTAGAATCG 600
CTCACTAGCT ATAAAATTGA AGTGGGCGGC TTGAGAGCGG TGGCTGAAAT CTTTAACCGC 660
TTGGGCCAAA AGAGTGCCAA AACCACGCTC GCTCGCATTG AAAGCGTGGA TAACAAACTC 720
GCCGGCGCGA TTAAAGAAAT GATGTTCACT TTTGAAGATA TAGCCAAACT AGACAATTTT 780
GCTATCATGA GAGATTTTAA AAGTGGGGGA TTAAAAAAGA CTGGTCTT 828

(2) INFORMATION FOR SEQ ID NO:1190:

(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:1190

```
AGAAGTTTGG GAAAAGGGCG ACCAATGAAC AAGAAAAATA GCGTAATTTC TGGTTTGATG      60
AATTTTTTTA GCGAAAAGAA TGAGCGCTGG CTGTTAGCCC ACAGGCACAC GAGGGGGTTT     120
GTGATAGTGG CGTGGCTTTT TAGGTTTAAA AGCATTGCGT TTTCTATTTT AATCACTCTG     180
TTGGTTATTT TAGTGGATAT TTGGGTGTAT AGCGATGTGC GCCAGTTTTT ATTGGACACT     240
TCTAGCTCTT TTATTTGGCT TTTAATCGCT TTACTAATCA AGTGGGGCGT GATTGTTATA     300
AGTGCGCGCA AATGCTACCA ATTCAGCCAA AAAATGTTTG CGTTAATCCA AAGAAAAAGG     360
CAAATCAGAG AGAATTTAAA AAACCGCTCC AATCGCAAAG ATGCTAAAAA TTTTGAAAAA     420
CTCTCTAACA TCGCTGAAGA AATCATTTCA AAAAAACAAG AAGAGTCCCA CCACAAAGAA     480
GATTCTAATG ATGAAAACCA CAAAGACAAG CTTTCTAACA TTACCGAAGA AATGATTCTC     540
AAAAAACAAG AGGAACTGAA AGCTAGAAAG GATAAGGGGG AT                        582
```

(2) INFORMATION FOR SEQ ID NO:1191:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1617 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191

```
CTTATGGATA GAGCCAAATT TATATTCGTT ACAGGGGGCG TGTTAAGCTC TCTAGGGAAA      60
GGGATTTCAT CTTCTTCAAT CGCTACGCTT TTGCAGCATT GCAATTACCA GGTTTCTATT     120
TTGAAGATTG ATCCTTATAT CAATATTGAT CCAGGCACCA TGAGCCCTTT AGAGCATGGG     180
GAAGTGTTTG TTACTAGCGA TGGCGCTGAA ACGGATTTAG ACATCGGGCA TTATGAACGC     240
TTTTTGAACA GGAATTTAAC GAGGTTGAAT AATTTCACTA CCGGGCAGAT TTTTTCAAGC     300
GTGATAGAAA ATGAAAGGAA AGGGGAATAT TTAGGCAAAA CCATTCAAAT CGTCCCCCAT     360
GTAACCGATG AAATCAAAAG GCGCATTAAA AGTGCGGCTA AGGGGTTGGA TTTTTTAATC     420
GTGGAAGTGG GTGGAACCGT GGGCGATATG GAGGGCATGT TTTATGTGGA ACCGATCCGC     480
CAGCTGAAAC TGGAATTACG GAATAAAGCA CTCATCAATA TGCATGTAAC CTTGATGCCC     540
TATATCCGTG CCACTAGCGA ACTAAGAAGC AGACCCACGC AACACTCCGT CCAGGAATTA     600
CGGCGTCTTG GCGTAACCCC TCAAATCATT TTGGCGCGAT CGCCTAAGCC TTTGGATAAA     660
GAATTGAAAA AGAAAATCGC TTTGAGTTGC GATGTGGAAC AAGACAGCGT GATTGTAGCC     720
ACAGACACTA AAAGCATTTA CGCATGCCCT ATTCTTTTCT TGCAAGAAGG CATTTTAACC     780
CCCATTGCCA GACGCTTTAA TTTGAATAAG TTGCACCCTA AAATGGCGGC TTGGAACACT     840
TTAGTAGAAA AAATCATCGC TCCTAAACAC AAGGTCAAAA TTGGTTTTGT GGGCAAGTAT     900
TTAAGCTTAA AAGAATCTTA TAAATCCTTG ATTGAAGCCC TAATCCATGC GGGGGCGCAT     960
CTGGATACGC AAGTCAATAT TGAATGGCTG GATAGCGAGA ATTTTAATGA AAAGACTGAT    1020
TTAGAGGGCG TTGATGCGAT TTTAGTGCCG GGGGGCTTTG GAGAAAGGGG GATTGAGGGC    1080
AAAATTTGCG CCATTCAAAG GGCTAGGTTA GAAAAACTCC CCTTTTTAGG GATTTGTTTG    1140
GGCATGCAAT TAGCGATCGT TGAATTTTGT CGCAATGTTT TAGGCTTGAA AGGGGCTAAC    1200
TCTACGGAAT TTAACCAACG CTGCGAATAC CCTGTGGTGT ATTTGATTGA AGATTTTATG    1260
GATCAAAACC ACCAAAAACA GGTGCGCACC TATAATTCGC CTTTAGGAGG CACCATGCGA    1320
TTAGGCGAAT ACGAATGCGA AATCATGCCT AATAGCTTGC TAGAAAAAGC CTATAAAAAG    1380
CCTAACATCA AAGAAAGACA CCGCCATCGT TATGAAATCA ACCCCAAATA CCGCCAAGAG    1440
TGGGAAAATA AAGGCTTGAA AGTGGTGGGC TTTGGGGCGA ATCATTTGAT TGAAGCGATT    1500
GAATTAGAAG ATCACCCGTT CTTTGTGGGG GTGCAATTCC ACCCGGAATT CACCTCCAGG    1560
TTGCAAAGCC CTAACCCTAT TATTTTGGAT TTCATTAAGA GCGCTCTTCA TAAATCC       1617
```

(2) INFORMATION FOR SEQ ID NO:1192:

(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:1192

This Sheet Has Been Replaced



```
ATATGGCGTG GATGTGGAAG CCATGACAGG GTGCATGATG AGTTTGTTTT TGCTCGTTAC      60
ACGAAGGCTA ATTACGAAAA CACTTATTAC GATACAGAGT TTTCGCATTT AAAAGAAGCG     120
AGCGCGTATT TTCCGGACAT TGATGAAGCG AGCCTTTTTA CGGATTTGCA AGATTATTTT     180
AACTCATGGA AAGAATTGTC TAAAAACGCC AAAGACTCCG CTCAAAAACA GGCTCTCGCT     240
CAAAAAACAG AAGCTTTAAC GCACAACATT AAAGACACCA GAGAGAGGTT AACGACCTTA     300
CAGCATAAAG CGAGCGAAGA ATTAAAAAGC GTCATTAAAG AAGTCAATAG CCTGGGTTCT     360
CAAATCGCTG AGATCAACAA ACGCATTAAA GAAGTGGAAA ACAACAAGAG TTTAAAGCAT     420
GCGAATGAGT TAAGGGATAA GCGAGATGAA TTAGAGTTTC ATTTGCGAGA GCTTTTAGGG     480
GGGAATGTTT TTAAAAGCAG CATTAAAACC CATTCGCTCA CAGATAAAGA CTCAGCGGAC     540
TTTGATGAGA GCTATAACCT TAATATCGGG CATGGGTTCA ATATCATTGA TGGCTCTATT     600
TTCCATCCCT TAGTGGTTAA AGAATCCGAA AATAAAGGGG GTTTGAACCA GGTTTATTTT     660
CAAAGCGATG ATTTTAAGCT CACTAATATT ACCGACAAGC TCAATCAAGG GAAAGTGGGG     720
GCGTTATTGA ATGTGTATAA TGACGGCTCT AACGGGACTT TAAAGGGCAA GTTGCAAGAT     780
TATATTGATT TGTTGGATTC TTTTGCTAGG GGCTTGATAG AATCCACGAA TGCGATTTAC     840
GCTCAAAGCG CGAGCCATCA TATTGAGGGC GAGCCTGTGG AGTTTAATAG CGATGAAGCC     900
TTTAAAGACA CGAATTACAA TATCAAAAAC GGCTCGTTTG ATTTAATCGC TTACAACACC     960
GATGGTAAAG AAATCGCCAG GAAAACCATT GCTATCACGC CCATTACAAC CATGAACGAC    1020
ATTATCCAAG TCATTAACGC TAACACCGAT GACAATCAAG ACAACAACAC CGAAAACGAT    1080
TTTGATGAAT TATTTCACAG CGAGCTT                                        1107
```

(2) INFORMATION FOR SEQ ID NO:1193:

(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:1193

```
AAAACAAAGC TCGTTTTTAT GATAAAAGCG CGGTTTAAAA AACGCCTTTT AGGATCTAGG      60
GGCGCGTTTG ATTTGAATAT AGACTTAGAA ATTAAAGAAG CAGAAGTTGT CGCTTTATTA     120
GGAGAATCGG GAGCGGGTAA AAGCACGATC TTACGCATTT TAGCAGGGCT TGAAGCGGTG     180
AGTAGCGGCT ATATTGAAGC CAATCATTCA GTATGGTTAG ACACTCAAAA AAAGATTTTT     240
TTAAAACCAC AACAGCGAAA AATCGGCTTT GTGTTTCAAG ATTACGCCCT ATTCCCTCAT     300
TTAAACGTGT ATCAAAACAT CGCCTTTGCT CACCCTAAAG ATAAAAATAA AATCCACGAA     360
GTGTTACGCT TAATGCGTTT AGAAAACCTA AGCCAGCAAA AAATTCCCAA ACTCTCTGGC     420
GGGCAAGCCC AACGAGTCGC TTTAGCAAGA GCTTTAATCG CAGCCAAAAA TCTATTGCTT     480
TTAGATGAGC CTTTAAACGC CCTAGATAAC GCCTTAAAAA ACGAGGTGCA ACAAGGTTTG     540
CTTGATTTTA TCAAGCGTGA AAATTTAAGC GTGTTATTGG TAAGTCATGA TCCAAACGAA     600
ATAACCAAAC TCGCGCGAAC TTTCCTCTTT TTAAACAATG GCGTTATTGA TCCTAATCAA     660
GAAAATCGGC TTTTTTCAAA CCGCTTATTG GTAAAACCTC TCTTTGAAGA TGAAAATTAT     720
TGCCATTATG AGGTCATTCC TCAAACGATC AGTTTGCCCA AAGATTGTCT GAACCCAACT     780
TTTAAGCTTG ATTTCATTCA AAACAAAAAA TTT                                  813
```

(2) INFORMATION FOR SEQ ID NO:1194:

(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:1194

```
GGCTTATCCG CTACTATTCT TGGTATGTGG ATTATGTCTT CACTTTCTAG TTCATTCTTT      60
CATTCGCTCT TCTTCATCAA ATCAAACCCT GGCCAACTCT TAAAAGGTTG GGGTTCAAAA     120
ATCTTTTTCA TAAATAGAAA GTTTGTTTTA GCACAGTATA ATCCTAGCGT TTCAATTTTT     180
ATTTTACTCA ATAGGGTGTT TGGTGTTGGC GTT                                  213
```

(2) INFORMATION FOR SEQ ID NO:1195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature

This Sheet Has Been Replaced



(B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195

ATTCAGCGCT CGCACCAGCT CTTTAATTTG CAAGAAAAAA AAGGGATTCT TGGTTTTTTA 60
CACCAAAAAA ATATCTTAAA TATTGCTCAA AATGACATCC ACCAGCTCCT TATTCTCATG 120
GTGGTCTTTT CTATGTTAGC AACCCCTTTT ATTTTAAAAT ACCTAGAATC TATCGCTCAA 180
TTTATTTTGC ACCAAAAGAG CCAAGAAAAC GAGCCGGCTA AAAAA 225

(2) INFORMATION FOR SEQ ID NO:1196:

(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

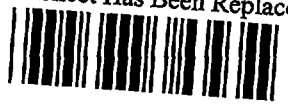
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196

GGCTTGATGC GCATTATCAT AAGGTTACTT TCATTTAAAA TGAACGCTTT TTTAAAACTC 60
GCGCTCGCTT CTTTGATGGG GGGGCTTTGG TATGCTTTCA ATGGCGAAGG CTCTGAGATT 120
GTCGCTATAG GGATTTTTGT GTTGATCTTG TTTGTTTTTT TTATCCGCCC TGTGAGTTTC 180
CAAGACCCAG AAAAACGAGA AGAATACATA GAACGGCTTA AAAAAAACCA TGAGAGGAAA 240
ATGATCTTAC AAGACAAGCA AAAAGAAGAG CAAATGCGCC TCTATCAAGC CAAAAAAGAG 300
CGAGAGAGCA GGCAAAAACA AGACCTTAAA GAACAAATGA AAAAATACTC A 351

(2) INFORMATION FOR SEQ ID NO:1197:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1197

AGGAAAAAAA TGGAAATCAT TTTATTAATT GTTGCGGCGG TTGTGTTGTT TTATTTTTAC 60

AACACCCTCA AAGAATATTT GAAAAACCCC CTAAACCCTA AAACCAAAAC CGAAGAATAC 120
GACTTGAAAA ATGACCCCTA TTTGCTGGTG CAATCTAGCC CCCTAGACAA ATTCAAGCAA 180
ACCCAAATAG GCGCGTATAT GCGTCTTTTA AAATTTTTAG ACATTCAAAA AAACGCCTTG 240
GATAACGCTT TAAGAACGCT TTTTATCCAT GAATTGGAGC AGCCCTTAAA CAGCGAACAG 300
CAAAATTTAG GCCAAAGAGC TTCTCAA 327

(2) INFORMATION FOR SEQ ID NO:1198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1629 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198

ATGCCTAATA ACGCTTTATT GCAAATCAAA CAAGACACCC TAAGTCTCAT TGACGATTTA 60
AAAGTCATTT GCAAGGATGC TGGTTTAGCG GGCGACGGCA ACGGATACAA GATCATCACG 120
CAATGCTTTT TGTATAAATT CTTATGCGAT AAGTTTGAAT TCTTTTTTGA ACAAAAATTC 180
CCCAACAAAA CGATACGAGA CTACAAAGAC TTTAACGAGG AAGAAAAAGA ATATTTTTTC 240
CTTACCTTAA GCGATAAAAA ACTCCCCAAA CTCGCTTATG ATGAGCTTTT AAACTATCTT 300
TTTGAAAAAC ATTTTTACGA TAACGATTTA CACCTAAAGC TAGATGCTAT TTTCAATCGC 360
ATTTCTAGCA ATAATGCCGA GCTTTTTAAC ACCAAAAGCA CGGATGAAAC CACTATCGCC 420
TTATTTGAAA GCGTCTCACA ATACATTAAT GAAGGGTCTA AAAGGGCTAA TTTTACAAGA 480
TCTTTATTAG ACAAACTCAA AAATTTTAAT TTCAAACAAG CTTTTTTAAA TTTACAAAAC 540
CAACAAGGCT ATGACTTTTT CGCCCCCATT TTTGAATACT TACTCAAAGA TTACAATAAT 600
AACAGCGGAG GGACATACGC CGAATACTAC ACCCCTTTAA GCATCGCTAG CATCATTGCC 660
AAGCTTTTAG TGAATAAACC CACTCAAAGC GTCAAAATCT ATGATCCAAG CGCTGGCACA 720
GGAACGCTTT TAATGGCATT AGCCCACCAA ATAGGCACCG ATTCTTGCAC CCTTTATGCC 780
CAAGACATTT CGCAAAAATC CTTAAGAATG CTCAAACTCA ACCTGATTTT AAACGACTTG 840
ACCCACTCTT TAAGACACGC CATTGAGGGA AACACTTTGA CTAACCCCTA CCACTCCAAA 900
GACCACAAAG GGAAAATGGA TTTCATCGTG AGTAACCCCC CTTTCAAATT GGATTTTTCC 960
AACGAGCATG CCGAGATTTC GCAAAACAAA AACGATTTTT TCTTAGGCGT GCCTAATATC 1020
CCTAAAAACG ATAAAAGCAA AATGCCCATT TACACGCTCT TTTTCCAGCA TTGCCTGAAC 1080
ATGCTCAGTC CAAAAGGTAA GGGAGCTATA ATCGTGCCAA CCGGATTCAT TAGTGCTAAA 1140
AGCGGGGTAA ATAATAAGAA TGTCCGGCAT TTAGTGGATG AAAGGCTCGT TTATGGGGTG 1200
ATTTGCATGC CCAGTCAGGT TTTTGCCAAC ACCGGCACTA ACGTGAGCAT CATCTTTTTT 1260
CAAAAAACGC CAAGCGCAAA GGAAGTGATC TTGATTGACG CTTCCAAACT CGGCGAAGAA 1320
TACACCGAAA ACAAAAACAA AAAAACGCGC TTAAGACCAA GCGATATGGA TTTGATTTTA 1380
GAAACTTTCC AAAATAAAGC CCCAAAATCG GATTTTTGCG CTCTGGTTTC TTTTGATGAA 1440
ATTACAGAAA AAAATTATTC TCTAAACCCC GGGCAGTATT TCACTATAGA AGACACGAGC 1500
GAGACAATCA GCCAAGCGGA GTTTGAAAAC TTGATGCAAC AATATTCAAG CGAACTAGCG 1560
AGCCTTTTTG ATGAAAGCCA AAATTTGCAA CAAGAGATTT TAGAAACTTT AAAAGGGGTT 1620
AGGTTTGAG 1629

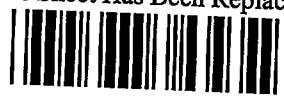
(2) INFORMATION FOR SEQ ID NO:1199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid

This Sheet Has Been Replaced



This Sheet Has Been Replaced



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

(ii) MOLECULE TYPE: DNA (genomic)

(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:1199

```
AAAGGGGATT TCATGAAAGA ACAAGAATGG GATTTAAGCG CTTTATTTGA AAATAAAGAA      60
AGCGCAGAAG AATTTTTAAA AACCTTACAA ACAGAAGTGC AAGAATTTGA GAACGCTTAT     120
CAAAATAACC TTAAGAATTT AGACGCTGCA AAATTTGCCA ACACTCTTAA ACATTACGAA     180
AATTTGTCAG AAAAGATCTC TAGAGCGATG GCTTACGCTC AATTACTTTT TGCCAAGAAC     240
ACTAAAGAAG CGAAGTTTTA TTCGCAATGC GAAATGGCTT GTGCAAATAT CCAACAACAC     300
CTTTTATTCT TTGAAATTGA ATTTAAGAAT TTGGACGCCA AAAAACAGCT CGCTTTCATT     360
AAAAAATGCA AAGATCATGC TTTTTATTTA AACAATCTCA TAGAAAAGAA AAAGCACACC     420
CTAAATTTAG ATGAAGAAAA GATCGCTCTA GCCCTTTCGC CTGTGGGAGT GGGTGCGTTT     480
AGCTTTGTTA TGGATGAACA TTTGTTTTCT TTGAACATCT CTTTACATAG AATAAACTTT     540
AAGCGAAGAA TAAATTTTAG CCCTCTTGCA CAACCC                               576
```

(2) INFORMATION FOR SEQ ID NO:1200:

(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:1200

```
GCCAAAGAGC TTCTCAATGA GCCTGTGGAT AAAAAAGAAA ATTTTGAATC CTTATGCCAA      60
GAAATCGCCG ACCACACGCA TGGAGAATAC ACCAAACGCC TGAAATTAGT GGAATTTCTT     120
ATGCTATTAG CCTATGCTGA TGGGATTTTG GACAGCAAAG AAAAAGAATT GTTTTTAGAT     180
GTGGGGGCGT TTTTGCAGAT AGACAATCAA GATTTTAACG AGCTTTATGA CAATTTTGAA     240
CACTTCAATT CAATAGAAAT CCCTATGTCT TTAGAAGAAG CAAAAAATCT TTTTGAAATC     300
CAAACCCACA CCACCATGCA AGATTTAGAA AAAAAAGCTT TGGATTTAAG CGCCCCCTAT     360
TACCATAAAA TGAATGACAA CAAACGCTAC AGCGAACAAG ATTTTATCTC TTTGAAAAAA     420
ATCGCCCTCG CTTCCCAACT TTTAGAAAAT GATTTAAAAG ACTCA                     465
```

(2) INFORMATION FOR SEQ ID NO:1201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1201

```
ATGCCCTTTT TAAAAGCCCT AGCATCTTTT GATGCGCCCT TTTTAGAAAA AGAAATTTCA      60
AAGCGTTTTA GGGATAATTT AGTTTTTTTC AAATCTTATC ACCCTAATCT GTTTAACGCC     120
CTCAATACGC CTTTTAAAAA TTACCAATTG CTTTTTGAAA CAAACCATCT TAATCTCTTA     180
CACACGCCCA CGAACGCTTT AAGCTACCCT AAACATCAAA TGATAGAAAC CGCTTTTAAC     240
ATGGCTAAAA ACCCCTTGAA TAATCCCAGA TGGTCATTAG ACAATAACCA CCTCTCTTTA     300
CATTATTTAA AATCTCAAAA CAACCACAAA CTCCCCCTAA CCCTTAAAGC CACGCATGCG     360
ATCTCAAACT TTTTAGATAA TCATCAAACG CCTTGCTCTT TAAAGAAATT CCTACCCCCT     420
ACCATGATTT ATGGCGTTTT AGACGGCTTG TTTTTGGCTA TTTTACAGGC TCAAAATTAC     480
CGCTTCCATT CGCTTTATTT GTTTGAAGAA AATTTAGACT TGTTTAAAAT CAGTTGCTAT     540
TTTGCGCGTT ATGAAGATTT GATTAAAAAA GGGGCTAAAC TTTTTATTCA AGGGTTTTTT     600
AACCCTAATG AATTGAAAAT GGATTTTTTG AAACGCCCTA TCACGCATTC TTTTTTAAAG     660
CTAGAAATCA TGCCCTATAA AAGCGCTTTT AATTTGCGCA TGCGAGAAAA CATTCAAAGC     720
TATTACAAAC AAGCCTTAAG GGGTTGGGGG AGTTTTGAAG ACGAATTGCT AGGGGTAAAG     780
AACACGCTTA AAAACTTACC CCTATGCCAA ACCCTAAAAA CCAAACCCAA AAAAATTAAC     840
GCCCCCATTT GCGTGGTGGG TAATGGGCCA AGCCTGGATT TATTGTTAGA TTTTTTAAAA     900
GAAAATGAAG AAAAATTCAT CATTTTTTCA TGCGGAACCG CTTTAAAGCC TTTAAAAGCG     960
CATGGCGTTA AAGTGGATTT TCAAATAGAA GTGGAGCGCA TAGACTATCT TAAGGAGGTT    1020
TTAGAAAGAG CCCCCCTAGA AGACACCCCC TTAATGGGCG CTAACATGCT CAATCCTAAC    1080
GCTTTTGATT TAGCCAAAGA AGCGTTGATG TTTATGCGTG GGGGGAGCGC TTGCGCATAT    1140
AAGCCCTTTG AGTATAGAAT ACGCAGCGCC TTTTGTGGGC AATGCCGGGG TGGCTTTAGC    1200
GGGTTTGATG AGCGA                                                     1215
```

(2) INFORMATION FOR SEQ ID NO:1202:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202

```
AAGGGGTTAG GTTTGAGTGA GTGGCAAACA TTTTGTTTAA AAGATTTAGG GAAAATAGTC      60
GGCGGCGCTA CCCCACCTAC CAATAACCCC AAAAATTATG GCAATAAAAT TGCTTGGATT     120
ACCCCTAAAG ATTTATCCAC TTTACAAGGG CGCTACATTA AAAAAGGCAG CCGCAGCATT     180
TCACGATTAG GGTTTAAATC ATGCTCTTGT GTGTTGCTCC CAAAGCATGC CATTTTATTT     240
TCTTCAAGAG CTCCCATAGG TTATGTGGCA ATTGCTGAAA AAAGGCTATG CACCAATCAA     300
GGTTTTAAAA GTATTATCCC TAACAAAAAA ATTTATTTTG AATTTTTATA TTACTTATTA     360
AAATACTATA AGGATAACAT TTCCAACATA GGGGGCGGAA CTACTTTTAA AGAAGTTTCA     420
GGGGCTACTT TAGGTCTATT CCAAGTTAAG ATACCCCCCA CTTATTACGA ACAACAAAAA     480
ATCGCCCACA CACTTTCTAT TTTAGATCAA AAAATAGAGA ACAACCATAA AATCAATGAG     540
CTTTTACACA AAATCTTAGA GCTTCTTTAT GAGCAATACT TCGTCCGTTT TGATTTTTTA     600
GATGAAAACA ACAAACCCTA TCAAACTAGC GGCGGGAAAA TGAAATTTTC TAAAGAATTA     660
AACCGCCTTA TCCCTAACGA TTTTAAAGTC AAAACGCTAG GGGAACTAAT AACTTGGATT     720
TCCGGAAGTC AGCCACCCAA AAGTTGTCAC ATATACGAGT ATAAAGAGGG TTACATTCGT     780
TTCATACAAA ACAGAGATTA TAGCTCTAAT AATTATGTTA CATATATTCC TATATCAAAA     840
AATAACAAGA TTTGTTATCA ATATGATATT ATGATGGACA AATACGGAGA AGCTGGATCC     900
GTGCGTTTTG GACTTCAAGG GGCTTATAAT GTTGCCTTAA GTAAAATTAG CGTATTAAAT     960
CAATCCATGC AGGAATATAT ACGCAGTTAT CTAAATTCAA AACCTATAAA AAAATATCTT    1020
TCTAATGCTT GCATGGCATC TACGAGAGCA TCACTAAATG AAAATCATAT TTATTCTTTA    1080
ATGCTCCCCA TACCACCTAT TAATCTATTA CAAAAATACG AAAAAATCGC AAAAAATATC    1140
ATAACAGCCA TTATTAAAAA CAATCAATCA ACCCAAACCC TAACCGCGCT CAGAGACTTT    1200
CTACTCCCCC TACTCTTAAA ACAACAAGTC AAACCACAA                           1239
```

(2) INFORMATION FOR SEQ ID NO:1203:

(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:1203

```
GGTGTAACTT TAATTCAACA AGAAGGATTT ATTATGATTA AAAGAATTGC TTGTATTTTA      60
AGCTTGAGCG CGAGTTTAGC GTTAGCTGGC GAAGTGAATG GGTTTTTCAT GGGTGCGGGT     120
TATCAACAAG GTCGTTATGG CCCTTATAAC AGCAATTACT CTGATTGGCG TCATGGCAAT     180
GACCTTTATG GTTTGAATTT CAAATTAGGT TTTGTAGGCT TTGCCAATAA ATGGTTTGGG     240
GCTAGGGTGT ATGGCTTTTT AGATTGGTTT AACACTTCAG GGACTGAACA CACCAAAACC     300
AATTTGCTCA CCTATGGCGG CGGTGGCGAT TTGATTGTCA ATCTCATTCC TTCGGATAAA     360
TTCGCTCTAG GTCTCATTGG TGGCGTTCAA TTAGCCGGAA ACACTTGGAT GTTCCCTTAT     420
GATGTCAATC AAACCAGATT CCAGTTCTTA TGGAATTTAG GCGGAAGAAT GCGTGTTGGG     480
GATCGCAGTG CGTTTGAAGC GGGCGTGAAA TTCCCTATGG TTAATCAGGG TAGCAAAGAT     540
GTAGGGCTTA TCCGCTACTA TTCTTGGTAT GTGGATTATG TCTTCACTTT C              591
```

(2) INFORMATION FOR SEQ ID NO:1204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1098 base pairs
(B) TYPE: nucleic acid

This Sheet Has Been Replaced



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

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204

```
TTTCGCTTTT ATTTCTTTAA AGCAAATCGA TCCTACTGGG GAAAGGTTTT TATGGTAAAC      60
AGCACACTTT ATATTGTTAT TGCCGGCTTA TGGCTTGCTG TAGGCTTTGG AATCTTTTTA     120
AAGAAATTAG ACATGCCCGT TATCATTGGC TACATTTGCA CAGGAACGGT CTTAGCGGCT     180
TTTTTTAAAA TTAATGATTT TAATTTGTTG TCTGATATTG GTGAATTTGG TATCGTCTTT     240
TTAATGTTTA TGATAGGCAT TGAGTTTAAT TTTGACAAGC TCAAGTCCAT CAAACAAGAA     300
GTGCTCGTTT TTGGGCTTTT ACAGGTTGTT TTATGCGCTT TAATCGCTTT TTTATTGGGG     360
TATTTTGTTC TGGGTCTTTC GCCCATTTTT TCCCTTGTTT TAGGCATGGG GCTTTCACTC     420
TCTTCAACCG CCATTGTGTT GAAATTCTTT GAAGATTCCA AACAGCTTAG CACGCCTATG     480
GGAAAGAGCG CGGTGGGGAT TTTGATTTTC CAAGATATTG CAGCCATTCC CATGCTTTTA     540
ATTTTGACGA TTCTAGGCAG TAAGGATTCT CATGTCAATT TGCTCATTCT TAAAACCCTT     600
ATTTCAGCGG GGATTATTTT AATTCTTTTA TTATTGCCTG AAAAAAAAGG GGCTAATCTC     660
ATCTTAGAGC AAGCGAAAGA CACGCGCTTG CCTGAAATCT TTATAGGCAC GGTTTTAGTG     720
ATTGTTTGCA GCGCGGCGGG GTTGAGCCAT TTTTTTGGGT TTTCTATGTC TTTGGGGGCG     780
TTCATTGTGG GCATGGCGAT TTCTAAATCG CGCTATAAAA TCAATGTCCA AGAAGAATTC     840
GCGCAATTAA AAAACCTCTT TTTGGCCCTT TTTTTCATTA CGATAGGGAT GCAGATTAAT     900
GTGAGTTTCT TCATGGAGAA ATTCTTTGTC GTCATCTTTT TACTCATTTT AGTGATGAGT     960
TTTAAGACTT TTATCATTTA TGCGCTATTG CGTTTTTTTA GAGACGCTAA AACCGCCATC    1020
AAAACCGCTC TTTCTTTGGC GCAAATTGGG GAGTTTTCTT TCGTGATCTT TTTAAATTCA    1080
GCGCTCGCAC CAGCTCTT                                                 1098
```

(2) INFORMATION FOR SEQ ID NO:1205:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205

```
TGTTTATGCG TGGGGGGAGC GCTTGCGCAT ATAAGCCCTT TGAGTATAGA ATACGCAGCG      60
CCTTTTGTGG GCAATGCCGG GGTGGCTTTA GCGGGTTTGA TGAGCGATGA AATTTATTTG     120
TGCGCTTTAG ATTGCGCTTA TATCAAAGGG TTTAAAAAGC ACGCTCAAAA TTCCTATTAT     180
```

```
GGAGATGAAA AAGAGATTGA CACCTCATCT TTAATCAGCG TAGAGGGTAA TGTTGAAGGT     240
TATGAAACTT TTAGCGACTC GCTTTTTTTG CTCTCTAAAG AAAGGATTGA AGAAGCCCTT     300
CATTATTACC AGCCTAAAAA AGTCTATAAT TTAAGCTATG GGGCGAAAAT CAAGCACGCC     360
GTTAGCCTCA ATCACTCTCA AGTGAAATTG AAACAAATCA ACAAACAAGA CGCTATCGTT     420
CGCATTAAAA GCATGTTTAG CCCTAGAAGT AATCATGCTA AGGATTTAAA AAATTTACAA     480
AAAAATCTGA TTCGTTTTAA AGAGGATTTT TTCACGCATT TAAACACGCC TTGTAAAACC     540
AAGCAAGAAG CATTTGAATG GGTGGATAGC TTGAGTGGAT TTTGCCAAAC AGCCAGCGCT     600
AAAACCCCCA CTATAGGCAT TTTATTTGAA GGGAGTGTCG CCCATATCTT ACAAAGCGTT     660
CTAATCGTTT CATTGCATCT TAAAGAAAAT GAGCTGACGC TTTTATCAAA TTCTCTCAAA     720
ACGCCT                                                               726
```

(2) INFORMATION FOR SEQ ID NO:1206:

(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:1206

```
ATCCTTCTTG TTGAATTAAA GTTACACCCT AAGATCGGTT ATTTTTCTAA AAGATTTAAT      60
TTTTTATCAA AGATGAGGGT TTTAGAGTGG AAATATTGGT TAAATACTGA TAAGTGGGAT     120
ACGCCCACCA ACAAACCGCC TCAAACTTTT AAAATACAAA TTTTTAAGAT ACAAATAGGT     180
ATAATCAATA ACTTCAATCA TTTAATCAAA GGGAGTTCTA TGAAAAACGC TTTCAAAGCG     240
TTTGCCTTGT TAATCGTATT TTTCTCAAAC GCTCTATTAG CGCAGGATTT AAAAATCGCT     300
GCTGCTGCTA ATCTCACGCG CGCTTTAAAA GCCCTTGTTA AAGAATTTCA AAAAGAACAC     360
CCAAAAGACG CTATTAACAT TAGCTTTAAT TCTTCAGGCA AACTCTACGC TCAAATCGCT     420
CAAAACGCCC CTTTTGATTT ATTCATTTCA GCGGATATTG CTAGACCCAA AAAACTTTAT     480
GATGAAAAAA TAACCCCTTT TAAAGAAGAA GTCTATGCTA AAGGCGTGTT GGTTTTATGG     540
AGTGAAAATC TAAAAATGGA TTCTTTAGAA ATTCTTAAAG ACCCTAAAAT TAAACGTATC     600
GCTATGGCTA ATCCTAAACT AGCCCCTTAT GGAAAAGCCA GCATGGAAGT CTTGGATCGT     660
TTAAAACTCA CTCCTAGTCT TAAATCTAAA ATCATTTATG GCGCTTCTAT TTCTCAAGCC     720
CATCAATTCA TCGCCACCAA AAACGCTCAA ATAGGCTTTG GAGCGTTATC TTTGATCGAT     780
AAAAAAGACA AAAACCTCTC TTATTTCATC ATTGATAAAA CCCTTTATAA CCCTATTGAA     840
CAAGCCTTAA TCATCACTAA AAATGGGGCT AATAACCCTT TAGCCAAAGT TTTTAAAGAT     900
TTTTTATTCA GCCCTAAAGC TAGAGCTATC TTTAAAGAAT ACGGCTATAT TGTGGAT        957
```

(2) INFORMATION FOR SEQ ID NO:1207:

(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

This Sheet Has Been Replaced



(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:1207

```
AAAAGGCGAA CAATGGATCA TGAGTTTTTG ATTACCATGC GTTTGAGCTT TTCTTTAGCT      60
TTGATTACCA CCCTTATTTT ACTCCCTATA GGGATTTTTT TAGGCTATTT TTTAAGCCTT     120
AAACGCAATC TTTTAACGAG CTTAACAGAA ACGCTTGTGT ATATGCCTTT AGTTTTACCC     180
CCAAGCGTGC TAGGGTTTTA TCTTCTTTTA ATCTTTTCGC CTTCTTCTTT TTTGGGAGCG     240
TTTTTACAAG ATGTGTTAAA TGTGAAACTC GTTTTTAGTT TCCAAGGGCT TATCTTAGGG     300
AGCGTGATTT TTTCCTTGCC CTTTATGGTA AGCCCTATTA AAAGCGCGTT AATTTCCTTG     360
CCCACTTCTT TAAAAGAAGC CAGTTATAGC TTGGGTAAAG GGGAATACTA CACCCTTTTT     420
TTTGTCCTAC TCCCTAACAT CAAACCCAGT GTGTTGATGG CTATCATTAC AACTTTTATG     480
CACACTATAG GTGAATTTGG CGTGGTGATG ATGCTTGGGG GTGATATATT AGGGGAAACA     540
AGAGTGGCTA GCATTACGAT CTTTAACGAA GCTGAAGCAC TCAATTATTC TAAAGCCCAT     600
CAATACGCCT TAACGCTCAC GCTTATTAGT TTTAGCCTCT TGTTTGTTAC CCTATTTTTA     660
AATAAAAAAC AAAGCTCGTT TTTA                                            684
```

(2) INFORMATION FOR SEQ ID NO:1208:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 561 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

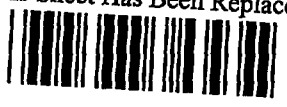
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208

```
AATTTTATTT TTGGAGAATT TATAATGAAG AGATCTTCTG TATTTAGTTT CTTGGTAGCT      60
TTTTTATTGG TAGTTGGCTG TAGTCATAAA ATGGATAATA AGACTGTGGC TGGCGATGTG     120
AGCACTAAAG CGGTTCAGAC TGCGCCTGTT ACTACAGAAC CAGCTCCAGA GAAAGAAGAG     180
CCTAAACAAG AGCCAGCTCC AGTGGTTGAA GAAAAGCCGG CTATTGAAAG CGGGACTATC     240
ATCGCTTCTA TTTATTTTGA TTTTGACAAG TATGAGATCA AAGAATCCGA TCAAGAGACT     300
TTAGATGAGA TCGTGCAAAA AGCTAAAGAA AACCACATGC AAGTGCTTTT GGAAGGCAAT     360
ACCGATGAAT TTGGCTCTAG CGAATACAAC CAAGCGCTTG GCGTTAAAAG GACTTTGAGC     420
GTGAAAAACG CTTTAGTCAT TAAAGGGGTA GAAAAAGATA TGATCAAAAC CATCAGTTTT     480
GGCGAAAGCA AACCCAAATG CGTCCAAAAA ACTAGAGAAT GTTACAGAGA AAACAGAAGA     540
GTGGATGTCA AATTAGTGAA G                                               561
```

(2) INFORMATION FOR SEQ ID NO:1209:

(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:1209

```
AAACGAATCA AAAGAGGGTT TTTTATGCAA GAAGCGTTGT TGCGTTTTCA AGAGGGCTTT      60
AAGGAGTGGG GTTATCTTAT TTTATTTTTG TATTCCTTGG GGGGTGGGTA TGTAGGGATT     120
GTCATCGCTT CCATTTTGAG CGCTACCACG CACGCTTTGG ATATAAAAAT AACCATTCTT     180
GTCGCTTTTT TAGGGAATTT AATAGGGAGT GGGGCTCTTG TAATCTTTGC CCGCTATCAA     240
AAAAGAGAGT TTTTAAAGTA TTTCCAAAAG CATAGAAGAA AGCTTGCTTT GGCGAGTTTG     300
TGGGTGAAAC GCTACGCCTT GCTCATGATT TTTGTCAATA AATATCTCTA TGGGATTAAA     360
AGCGTTGTGC CTTTGGCAAT TGGTTTTAGC AAATACCCTT TAAAAAAGTT TTTATGGCTT     420
AATGTTTTTT CCAGTTTTTT GTGGGCGTTA ATCGTGGGGA GCGTTTCTTT TCAAGCGAGC     480
GATTGGGTGA AAACGCTGTA TGAAAGGCTT TCTCATTACA CTTCGTTTTT TGTCATAAGT     540
TTTGTTCTTA TAGCGCTTTT AATATGGTTT TTATTGAAAC GATATTCGCG CAAAATGGGT     600
TTT                                                                  603
```

(2) INFORMATION FOR SEQ ID NO:1210:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210

```
GCTAGTTTTA ATTACAATTT TCAAATGTTA AGGAAAAACA TTTTAGCTTA CTATGGGGCG      60
AATTTTCTCT TAATCATCGC TCAAAGCTTG CCCCATGCGA TTTTAACCCC CTTGTTGCTT     120
TCTAAAGGGC TTAGTTTGAG TGAAATCTTG CTCGTGCAAA CCTTTTTTAG TTTTTGCGTG     180
CTGGTGGCTG AATACCCAAG CGGCGTTTTA GCGGATTTGA TGAGCCGGAA GAATTTATTC     240
CTGGTTTCTA ATGTGTTTTT AATCGCTAGT TTTTCGTTTG TGCTGTTTTT TGATAGTTTT     300
ATCCTCATGC TTTTAGCGTG GGGGTTGTAT GGTTTGTATA GCGCATGCTC TAGCGGCACG     360
ATTGAAGCTT CACTCATCAC AGACATTAAG GAAAACAAAA AAGATTTATC CAAGTTTTTA     420
GCCAAAAACA ATCAAATTAC TTATTTGGGC ATGATTATAG GGAGTTCTTT GGGATCGTTT     480
TTGTATCTCA AAGTCCATGC GATGCTGTAT GTCGTGGGGA TTTTTTTAAT CATGCTCTGT     540
GCGCTAACAA TCATCATTTA TTTTAAAGAA AAAGAAGGGG ATTTTAAAAG CCAAAAAAAT     600
TTGAAACTCC TTAAAGAGCA AGTCAAAGGC AGTCTTAAAG AGCTTAAAGA TAACCCCAAG     660
```

```
CTTAAAATTT TGTTAGTGGG GCATTTGATT ACGCCTGTCT TTTTTATGAG CCATTTCCAA     720
ATGTGGCAAG CGTATTTTTT AAAACAAGGC GTTAAAGAGC AATACCTTTT TGTGTTCTAT     780
ATCGCTTTTC AAGTGATTTC CATCCTCATT CATTTTTTAA AAGCCAAAAA TTACAGCCAA     840
AAAATCGCCC TGAGTTCGCT TTTGGTGTTG CTAGGCGTTA GCCCCTTGTT GCTTAGCAAT     900
ATCCCTTATT GTTTCATAGG GGTGTATGCG CTCATGGTGG CGTTTTTTGC TTACATGAGT     960
TATTGCTTGG GGTATCAATT CTCCAAATTC GTTTCTAAAA ACAACATTTC ATCGCTCTCA    1020
TCGCTTTTAT CAAGCTGTGT GCGCGTGGTC TCTGTGCTAA TCTTGTCGCT CAGTAGCCTA    1080
GAGTTGCGTT ACTTCTCACC CCTAACTATC ATAACCATGC ATTTTGCCCT AACGCTTATC    1140
ATCCTCTTTT TCTTTTTGTA TAAGGCTAAG CCGTTTGATG AG                       1182
```

(2) INFORMATION FOR SEQ ID NO:1211:

(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:1211

```
CGCAGAAATC TTACTAGACA ACATGGAAGT GTTAAAAAGC GTGAGAAGCG TTTTAAAACG      60
CATGCGAGCC TTTGCGATAG CGTGAGGAGC GGTAAAAGAT TAGGCTATAC CAATCAAGTG     120
ATCACCGATA TTGTCAATAT CGGTATTGGG GGGTCAGATT TAGGCGCTTT AATGGTTTGC     180
ACCGCCCTAA AACGCTACGG CCACCCAAGA TTAGAAATGC ATTTTGTGTC TAATGTGGAT     240
GGCACGCAGA TTTTAGACGT T                                               261
```

(2) INFORMATION FOR SEQ ID NO:1212:

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

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1212

```
CAGCATTATC CTAATAACCT AAAAGATATA GAGATGAATA CAGAAATTTT AACCATCATG      60
```

```
TTAGTTGTCT CCGTGCTTAT GGGATTGGTA GGCTTAATAG CGTTTTTATG GGGGGTTAAA     120
AGCGGTCAGT TTGACGATGA AAAACGCATG CTTGAAAGCG TGTTGTATGA CAGCGCGAGC     180
GACTTGAACG AAGCGATTTT ACAAGAAAAA CGCCAAAAGA AT                        222
```

(2) INFORMATION FOR SEQ ID NO:1213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 726 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1213

```
GAAATGCAGT TTTTACATGC GCATCTTTTA AGCGTGGTGA TCTTTTTCCC CATGCTGAGC      60
GCTCTATTAG CGTTCTTTAT GAGCGATCAA GCGAGCAGGG CGTATGCGAT CGTCATCGCC     120
TTGATTGAAT TGTTATTGGT CTTGTTGTTA TGGCATGGGT TTGATATTCA AACCGCAGGC     180
ATGCAGTTTG AAGAAATGAA AGAATTAGCC TATCAAATTG GCGTGAATTA CCATGTTGGC     240
GTTGATGGCA TCGCGCTCTT TTTGTTGCTC TTAAACGCTA TCGTGGTGTT ATTGTCCGTG     300
ATTTATGTCA AAGAGCGTCG TAAAGACTTT GTGATTTGTC TTTTATTGTT AGAAGGGATC     360
TTAATGGGCG TGTTTTCTTC TCTTAATGTG ATCTTTTTCT ACGCTTTTTG GGAAATCTCG     420
CTCTTGCCGG TTTTATACCT CATCGGTCGT TTTGGCCGTA ATAACAAAAT CTATTCTGGC     480
ATGAAGTTTT TCCTCTACAC CTTTTTAGCG TCGTTGTGCA TGCTTTTAGG CATTTTATAC     540
ATCGGGTATG ACTACGCCAA TAATTACGGC ATGATGAGTT TTGATATTTT AGACTGGTAT     600
CAGTTGAATT TTTCTAGCGG GATTAAAACC TGGCTCTTTG TAGCTTTCTT AATAGGGATT     660
GCGGTTAAAA TCCCGCTCTT TCCCTTCACA CATGGCTGCC TTATGCGTAT TCTAACGCCC     720
CCACTC                                                               726
```

(2) INFORMATION FOR SEQ ID NO:1214:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1488 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214

```
AAGAGGTCTC TTATGTTAAT AGATATTCTC CACATCTCTT TTGATAGCTT TAGTTTTGAG      60
AGCATTTTAC CCATGCTGGT GTTGGTGTGT GGGGGGATTT TCACGCTCTT AATCAACGCT     120
TTCACTTCCA GGTTTTCGCG CAATTTGAAT GTGTTTTTAT GCATGCTCTT TTTGGTTTTG     180
GATTTTTTAG TGGTTTCAGG GTTAGAAGAG CAAGAAAACG CCTTTTTTGG GTTTTTAAGC     240
CTAGATACTC TCTCGCTCAT CTCTCAAAGC ATTGTCTTGA TTTCAGCTTT TTTTCTCATT     300
TTCTTAGCCC TTTCAAAAGA ACGCTTCAAC GAATTTCAAA CCGCTGAATT TTATTCCCTA     360
TACTTGTTTA TTGTCGCTGG CTTTCAGTTC ATGGTTTCAA GCAACCAGTT TGTTGTAATC     420
CTTATTGGGT TAGAAACAGC GCCTTTGCCC CTTTGTGTGT TAATGGCGTT GAGCGATAAA     480
CGCTACGGCT TAGAAGCAGG GATCAAGTAT TTCACCATGG GGGCGATGGC GAGCGCGTTT     540
TTTGCTATGG GCGCGATGGC TTTTTACCTG CTTACAGGGA GCTTGAATCT TGAAGTCATT     600
ACCCTATACT TACACACTGA GGGCATCACA AACCCCATGC TCTTTGCGAT GGGCACTATT     660
TTTTTGATTG GAGCGATTGG CTTTAAGGTT TCTTTAGTGC CTTTCCATAC CTGGATGCCT     720
GATGTGTATG AGGGCAATAA CCCAGTCTTT GCGAGCTATA TTTCCATTGT GCCTAAAATC     780
GCTGGCTTTG TGGTAGCGAC TCGCCTTTTT GGGGCGTTTA TAGACACTCA TACCGCTTGG     840
GTAGAAGACA TTTTTTATGT TTTGATCCTT ATGACTATCA CCATCCCTAA TTTCATTGCT     900
TTATGGCAAG AAGATGTCAA AAGGATGCTC GCTTATAGTT CTATTTCGCA TTCTGGGTTC     960
GCTTTAGCGT GCGTGTTTAT CCACACTGAA GATAGCCAAC AAGCGATGTT TGTTTATTGG    1020
TTCATGTTTG CCTTCACTTA CATTGGGGCT TTTGGCCTTT TATGGCTCTT AAAAAGCCGG    1080
GAAAAAACAT GGGATGAACG CTACGATCAC CCCTATTCTA AATTCAACGG CCTTATCAAA    1140
ACCCACCCCT TAGTGGCGAT CTTGGGCGCT ATTTTTGTTT TTGGGCTTGC AGGGATCCCG    1200
CCTTTTAGCG TGTTTTGGGG GAAATTTTTA GCCGTTGAAA GCGCGTTAGA GAGCAATCAC    1260
ATTCTTTTAG CGGTGGTGAT GTTAGTTAAT AGCGCGGTGG CTGCGTTTTA TTATTTCCGT    1320
TGGCTCGTGG CGATGTTTTT CAATAAGCCC TTACAAACCC AAAGCTACGC TCAAAACGAT    1380
ATTTACACCC AAAACGCCAC CATGCCCATT TATGCGGTCA TTATTGCCAT GGCGTTAGCG    1440
TGCTTGTTCT CTGTGTTTAT GATGCGAGGG CTTTTAGAGT TTGTGGCT                 1488
```

(2) INFORMATION FOR SEQ ID NO:1215:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215

```
AATCCCGCTC TTTCCCTTCA CACATGGCTG CCTTATGCGT ATTCTAACGC CCCCACTCTA      60
GGCTCTGTCA TGCTTTCAGC CTTGCTTTCT AAAATGGGGA CTTACGCCTT ATTACGCTTC     120
TTGCTCCCGC TTTTTCCTGA ACTTTCAGAA ATTTATTTAA CCCCCATAGC CATTGTGGCG     180
CTGTGCATGA TCATTTATGG AGGTTTTCTA GCCTACGCTC AAAAAGATTT AAAAACCCTC     240
ATCGCTTATA GCTCTTTCTC GCACATGGGA GTCGTGGTGC TTGGGGTTTT TTCTTTCAAT     300
GTTGAAGGGG TTTCAGGGGC GGTGTTTATG ATGTTTGCGC ATGGCGTTAT CGTCATGGGA     360
TTATTTTTAC TCGCTGGTAT CTTGGAAGAA CGCGCCAGCA GTTTAGAAAT CGCTCGCTTT     420
GGATCGATCG CTAAAAGCGC TCCTGTTTTT GCAGCCTTTT TTATGATCGT TTTAATGGCG     480
AATGTGGGCA TGCCTTTAAG CATTGGTTTT GTGGGAGAGT TTTTGAGCTT GTTAGGGTTT     540
TTTGCCACTT ACCCTCTTTT GGCTATCATT GCCGGGACAA GCATCATTCT ATCAGCGGTT     600
TACATGCTCA CTTCATATAA AGATGTGTTC TTTGGCAACT TAAAAACCGG GAACAACCAA     660
ATCAGCGTGT TTGAAGATTT AAACGCTCGT GAGGTAGGGG TTTTAAGCGT GATTTTAGCT     720
TTGATCTTAA TTTTAGGGAT TTATCCTAAA GCGCTTTTAA AACCGATTGA GCAAGGCTTT     780
AAGCAGCTTT TAGAGGTGAT AGAAATCCGC TCGCTCCTTT TTTTAGGTTC ATTGGACACT     840
```

AAGATAAAAG AGGTCTCTTA TGTTAATAGA TATTCTCCAC ATCTCTTT 888

(2) INFORMATION FOR SEQ ID NO:1216:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1404 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216

ATTTATTCAA AAACAAGGAG TCATGACATG GACATTAGCA TTTTTAGAGA ATACGATATT 60
AGAGGCATTT ACCCCACCAC TTTAGATGAA AATACGGCTT TTAGTATCGG CGTGGAGTTG 120
GGAAAAATCA TGCGAGAATA CGATAAAAGC GTGTTTGTAG GGCATGACGC AAGGGTGCAT 180
GGGCGTTTTT TGTTTGAAGT TTTGAGCGCG GGGCTGCAAT CAAGCGGCTT GAAAGTGTAT 240
GATTTAGGGC TAATCCCCAC ACCGGTAGCG TATTTTGCGG CCTTTAATGA AATAGACAAT 300
ATCCAATGCC CTAATTCCAT CATGATCACT GGCTCTCACA ACCCCAAAGA ATACAACGGC 360
TTTAAAATCA CGCTCAATCA AAACCCGTTT TATGGCAAGG ACATTCAGGC TTTAAAAAAC 420
ACGCTTTTAA ACGCAAAGCA TGAAATAAAG CCCCTAAAAG AAACGCCAGA GAAAGTCAAT 480
GCCCTAGAAG CGTATCATCG CTATTTGATC AAGGATTTTA AGCATTTAAA AAATCTTAAA 540
TACAAAATCG CCCTGGATTT TGGTAATGGC GTGGGGGCGT TAGGATTAGA GCCGATTTTA 600
AAGGCTTTAA ACATTGATTT TAGCAGCCTT TATAGCGATC CTGATGGGGA TTTTCCTAAC 660
CACCACCCAG ACCCTAGCGA AGCGAAAAAC TTAAAAGACT TAGAAAAACA CATGCGAGAA 720
AACGCTATTT TAATAGGCTT TGCTTTTGAT GGCGATGCGG ATAGGATTGC GATGCTAAGC 780
TCTCATCATA TCTATGCGGG CGATGAATTA GCGATTTTAT TCGCTAAACG CTTGCATGCT 840
CAAGGCATCA CCCCTTTTGT GATCGGCGAA GTCAAATGCT CTCAAGTGAT GTATAACGCA 900
ATCAATACTT TTGGTAAGAC GCTCATGTAT AAAACCGGGC ATAGCAATTT AAAAATCAAG 960
CTCAAAGAAA CTAATGCGCA TTTTGCGGCT GAAATGAGCG GGCATATCTT TTTTAAAGAA 1020
CGCTATTTTG GCTATGATGA CGCTCTTTAC GCATGTTTAA GGGCTTTGGA GTTATTGCTT 1080
GAACAAAGTC CAAGCGACTT GGAAAACACC ATTAAAAACC TCCCCTATTC CTACACCACG 1140
CCTGAAGAAA AAATCGCCGT GAGCGAAGAA GAAAAATTTG AAATCATTCG CAACTTACAA 1200
GAAGCGCTTA AAAACCCGCC AAGCCATTTC CCTACAATCA AAGAAATCAT CAGCATTGAT 1260
GGCGTGAGAG TGGTTTTTGA ACATGGCTTT GGGCTTATTC GCGCAAGCAA CACCACCCCC 1320
TATTTAGTCA GCCGCTTTGA AGGCAAGGAT GAAACAACAG CGTTAGAATA TAAAAGGGCG 1380
TTGCTTGGGC TATTAGAAAA ACTT 1404

(2) INFORMATION FOR SEQ ID NO:1217:

(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:1217

```
GGAATTTTTA TGAATGAGAT CATTTTAATC ACCGGCGCTT ATGGCATGGT GGGGCAGAAC      60
ACGGCGTTGT ATTTTAAAAA AAACAAGCCT GATGTTACCT TACTCACCCC TAAAAAGAGC     120
GAATTGTATT TGTTGGATAA AGACAACGTT CAAGCCTATT TGAAAGAATA CAAGCCTACA     180
GGCATTATCC ATTGTGCCGG GAGAGTGGGG GGCATTGTGG CAAACATGAA CGATCTTTCA     240
ACTTACATGG TTGAGAATTT ACTCATGGGT TTGTATCTTT TTTCTAGCGC TTTAGATTTG     300
GGCGTGAAAA AAGCCATTAA TCTAGCGAGC TCTTGCGCTT ATCCTAAATA CGCCCCTAAC     360
CCTTTAAAAG AGAGCGATTT ATTGAACGGC TCTTTAGAAC CAACGAATGA AGGCTACGCT     420
TTAGCCAAAC TCTCTGTGAT GAAGTATTGC GAATACGTGA GCGCTGAAAA AGGCGTTTTT     480
TATAAAACTC TAGTGCCTTG TAACCTTTAT GGCGAGTTTG ACAAGTTTGA AGAAAAGATA     540
GCGCACATGA TACCAGGGCT TATTGCTAGG ATGCACACCG CTAAATTAAA AAATGAAAAA     600
AATTTTGCGA TGTGGGGCGA TGGCACGGCC GAAGAGAGTA TC                        642
```

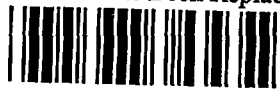
(2) INFORMATION FOR SEQ ID NO:1218:

(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

This Sheet Has Been Replaced



(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:1218

```
GCTCACGCCA ACCGCACCAT CATCCACAGG ATTGATGATA GCATCGCGCA GCGCGTGGAT      60
AATGCCATTC GCCCCATGCG TTTGGTTAGA GGGTTTGCCC CCCTTTACCT CACTTTACCC     120
AAACGCTCTT TTAATGCGCC CAAAAAGATT TTAGCGCTTG GAGCGGAGCA AAAAGGGCAT     180
TTTAGCTTAC TAGATAGCGA AACTTCTGTT CTTTTACTCT CGCCTTTTTG TGGGGATTTG     240
AGCGTTTTAG AAAATGAAAA ACACTTTAAA GAAACTTTGA ATTTTTTCTT AAAAACCTAT     300
GATTTCAAAC CCACGCTCTT AGCTTGCGAT GAGCATCAAA ACTACACCAC CACCAAAATG     360
GCTTTTGATT TTAATACGCC CTTGTTGCAA GTCCAGCACC ACCATGCCCA CTTTTTAGCG     420
AGCGTCTTAG ACGCATTATT ACAAGATCCG CATTTAAATC ACCCCTTTAT AGGTATTGTT     480
TGGGACGGGA GTGGGGCTTA TGAAAATAAG ATTTATGGGG CGGAGTGTTT TGTGGGGGAT     540
TTGGAACGCA TTGAAGAAGT GGCTAGATTT GAAGAATTTT GGCTTTTAGG GGGGCAAAAA     600
GCGATCAAAG AGCCTAGAAG ATTGGTTTTA GAAATCGCTT TAAAACACCA GCTCAACAAG     660
CTTTTAAAAC GCGTTCAAAA GCATTTCAAA GAAGACGAAT TAGGAATTTT TAAACAAATG     720
CATGACAAAA AAATTCAAAG CGTCGCCACC AATTCCATAG GGCGTTTGTT TGATATAGTG     780
GCGTTTAGTT TGGGCGTGGT GGGAACGATT AGTTTTGAAG CCGAGAGCGG GCAGGTTTTA     840
GAAAATCTAG CCCTACAAAG CGATGAGATC GCTTTTTACC CTTTTGAAAT CAAAAACAGC     900
GTGGTGCGTT TGAAGGAATT TTATCAAGCG TTTGAAAAGG ATTTGGGCGT TTTAGAACCC     960
AAACGCATCG CTAAGAAATT TTTTAACAGC TTAGTAGAAA TCATTACCGC TTTGATTGCG    1020
CCTTTTAAAG GGCATGTCGT GGTGTGCAGT GGGGGCGTGT TTTGCAACCA ATTGTTGTGC    1080
GAACAATTAG CCAAGCGATT GAAAAAGCTT CAAAGGGAGT ATTTTTTCCA CAAGCATTTC    1140
```

CCCCCTAATG ACAGCAGTAT CCCTGTCGGT CAAGCCTTAA TGGCGTATTT CAACCCTACA 1200
ATCATCAAAA AAGGA 1215

(2) INFORMATION FOR SEQ ID NO:1219:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219

CGCTTTGAGT GCGGAGCGAG CGACATGAGC GGGTGGCTTT TAATGGGATT ACCGGGAGCT 60
TTATATGTGG GGGGGCTTAT CAATTCACAC ATCGCCATAG GCTTGAGTTT GGGCGCACTC 120
ATTAACTGGG TTTTTGTGGC TAAGCGCTTA CGCATTTATA CGAGCGTGAT CGCTAATTCT 180
ATTACCATTT CAGATTATTT TGAAACGCGC TTTAGCGATG ATAAACACAT CTTGCGCTTG 240
ATTTCAGCTT TTGTGATTTT AATCTTAAAG ATTTTTTATT TTTCTTCAGG GCTAGTGAGT 300
GGGGCTAAAC TCTTTGAACC GACCTTTGGC ATTCAATACA CCTACGCTTT AAGCATTGGC 360
ACGCTGATTA TTGTTTCTTA CACCTTTTTA GGAAGGTATA AGGCGGTGTG CTGGACGGAT 420
TTGATTCAAG GGCTTTTGAT GATGAGCGCT TTAATCGTGG TGCCGATCGT TATGATAATC 480
CATCTTGGAG GGATTGGAGA GGGGATTAAA ATCATTAAAG AGATCAAGCC TGAAAACCTT 540
TCTTTCTTGC AAGGCTCTAG CGTAGTCGCT ATTATTTCAA GCCTTGCTTG GGGGTTAGGC 600
TATTTTGGGC AACCCCATAT TTTAGTGCGC TTCATGTCTA TCCGCTCCAT TAGAGATGTG 660
CCTAAAGCGA CCACTATTGG GATTTCTTGG ATGGTTATTT CTTTAATTGG GGCATGCGTT 720
ATGGGGCTTT TAGGCGTTGC TTATGTACAT AAATTTGACT TGAGTTTAGA AGACCCTGAA 780
AAGATTTTCA TTGTAATGAG TCAATTGCTC TTTAACCCTT GGATCACAGG CATTTTATTG 840
AGCGCGATTT TAGCGGCGGT GATGAGCACG GCCAGTTCGC AACTGCTTGT AAGCTCTTCT 900
ACCATTGCTG AAGATTTCTA TGCGACGATT TTCAATAAAA ACGCCCCCCA AAAATTAGTG 960
ATGACGATTT CTAGGCTTTC GGTTTTAGGG GTGGCTTGCA TCGCTTTTTT CATTTCAACG 1020
GATAAAAACG CTAGCATCCT CAGCATCGTG AGTTACGCAT GGGCTGGCTT TGGCGCGAGT 1080
TTTGGCTCTG TGATTTTGTT TTCACTTTTT TGGTCAAGAA TGACGCGCAT TGGCGCGATT 1140
GCTGGCATGC TCTCTGGGGC TAGCACGGTG ATTTTATACG ATAAATTTGG CAAAAGCTTT 1200
TTGGATATTT ATGAAATCGT TCCGGGCTTT ATTGTAGCGA GCGTAGCTAT TGTTGCGTTT 1260
AGTTTGTTTT CTAGCGTGCG ATCAGGCACT AAAGAGGCCT TTGAAACCAT GCTTAAAGAA 1320
ATTGAGAGCT TAAAGCAT 1338

(2) INFORMATION FOR SEQ ID NO:1220:

(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

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220

```
AATAAGTGGA TTAAAGGGGC GGTTGTTTTT GTAGGGGGTT TTGCAACGAT TACAACCTTT      60
TCTTTAATCT ACCACCAAAA GCCAAAAGCC CCCCTAAATA ACCAGCCTAG CCTTTTGAAT     120
GACGATGAGG TGAAATACCC CTTACAAGAC TACACTTTCA CTCAAAACCC ACAGCCAACT     180
AACACGGAAA GCTCCAAAGA CGCTACCATC AAAGCCTTAC AAGAACAGCT CAAAGCCGCT     240
TTAAAAGCCC TAAACTCCAA AGAAATGAAT TATTCCAAAG AAGAGACTTT TACTAGCCCT     300
CCCATGGATC CAAAAACAAC CCCCCCTAAA AAAGACTTTT CTCCAAAACA ATTAGATTTA     360
CTGGCCTCTC GCATCACCCC TTTCAAGCAA AGCCCTAAAA ATTACGAAGA AAACCTGATT     420
TTCCCTGTGG ATAACCCTAA TGGCATTGAT AGTTTCACTA ACCTTAAAGA AAAAGACATC     480
GCCACTAATG AAAACAAGCT TTTACGCACC ATTACAGCTG ACAAAATGAT ACCCGCTTTT     540
TTGATTACGC CCATTTCTAG CCAGATCGCT GGTAAAGTGA TTGCGCAAGT GGAGAGCGAT     600
ATTTTTGCAA GCATGGGCAA AGCCGTCTTA ATCCCCAAAG GCTCTAAAGT CATAGGCTAT     660
TACAGCAACA ATAACAAAAT GGGCGAATAC CGCTTGGATA TTGTATGGAG TCGAATCATC     720
ACTCCCCATG GCATTAATAT CATGCTCACT AACGCTAAAG GGGCGGACAT TAAAGGCTAT     780
AACGGCTTAG TGGGGGAATT GATTGAAAGG AATTTCCAAC GCTATGGCGT GCCGTTACTG     840
CTTTCTACGC TCACTAACGG CCTATTGATT GGGATCACTT CGGCTTTAAA CAACAGAGGC     900
AATAAAGAAG AGGTGACTAA TTTCTTTGGG GATTATCTTT TATTGCAATT GATGAGGCAA     960
AGCGGCATGG GGATCAATCA AGTGGTCAAT CAAATTTTAA GAGACAAGAG CAAGATCGCC    1020
CCCATTGTGG TGATTAGAGA GGGGAGTAGG GTCTTCATTT CGCCCAATAC TGACATCTTC    1080
TTCCCTATAC CCAGAGAGAA TGAAGTCATC GCTGAGTTTT TGAAG                    1125
```

(2) INFORMATION FOR SEQ ID NO:1221:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221

```
AAAGCGGCGT TTTGTATAGG GATTTTTTTC TATGGCGCTT ATTATTTCCT AGATGAATTT      60
TTAATCAAGC TTTATTTGCA GCCAAGCGAG CAAGACGCGC TCTTTATGCA AGAGACTAAA     120
AGAGCGATGA ATATTTATTA TGTGGGCTAT GTTTTTTTAG GCATGACTTT GTTGTGCGCG     180
GTGTTTTTCC AATCTATTCA ACGCACTAAA AGTTCGTTTA TCATCACGAT TTCGCACACG     240
CTAGGGTTTA TCGTTATCCT ATTGCCGATT TTAAGTCATT TTTATGGGGT TAATGGCATT     300
TGGGTAACTT ACCCTATTGC GCAATTTTTA GCCGTTTTTG GTAGCGTTAG GGGTAACTTA     360
TTA                                                                  363
```

(2) INFORMATION FOR SEQ ID NO:1222:

(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:1222

```
ATGCTCAAAA AAAAGATTGA TTTGCATAAA GATTCTATTA GGAAGCTCTT TTTTTATTAC      60
TTCATCCCTT TAGTTTTTTC TATGATCTCA CTTTCTACTT ACTCTATGGT AGATGACATG     120
TTTGTGGGCA AAAAACTGGG TAAAGAAGCT ATCGCTGCGG TCAATATCGC ATGGCCTATT     180
TTTCCAGGAC TCATTGCGTA TGAATTGCTT TTTGGTTTTG GGGCAGCGAG CATTGTGGGG     240
TATTTTTTAG GTCAAAATAA AACCCATAGG GCTAGGCTTG TGTTTAGCAG CGTGTTTTAT     300
TTTGTCGCTC TAAGCGCCTT TATTTTGAGC ATGGCGTTAT TGCCTTTTAG CGAAAATATC     360
GCGCGTTTTT TGGGAGCAAT GACGCTTTAT                                      390
```

(2) INFORMATION FOR SEQ ID NO:1223:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223

```
AATCATTTTA ATGGTTGTGT TTTTAGGGTT CAGCACCTTT TAGCGGATGT CTTTGTGGTG      60
AATGACAAAC GGCCCGTTTT AGCGATGGTA GCGATGTTGA TTGGCTCGTT AGCGAATATC     120
TTTTTCAATT ACTTGTTTAT TTTTGTGTTG GAAGTGGGGG TTCAAGGCAG CGCGATAGCC     180
ACCGTGATAG GGCATGCGAT AGGGGTTTTA GTCTTAATGC AGCATTTTTG GCGCAAAAAA     240
GGGCAGTTGT ATTTTATCAA ACGATTTTCT TTATCTTCAG TCATTTCTTC AGCTAAAAGC     300
GGTGTGCCTC AAAGCACGGC GGAATTTAGC GCTTCTATTA TGATTTTATT GTTTAATACC     360
GCTATCATGC ACACGGCGGG GGAAAGGTTT GTGAGCATGT ATGGGATCGT TATGTATAAT     420
GCGATTATCT TTTTTACGAC TTTGTTTGCG ATTTCTCAAG GCATCCAACC GATTGCAGAG     480
CTT                                                                  483
```

(2) INFORMATION FOR SEQ ID NO:1224:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224

TTTCTTAACA TTAGGGATTT GACGATGATT TTTAGCTCTC TTTTTAGTGT TGTAGGGATG 60
GCGGTGCTTT TTCTTATTGC TTGGGTGTTT TCTGGCAATA AAAGGGCTAT AAATTATCGC 120
ACGATTGTCA GCGCCTTTGT GATTCAAGTG GCTTTAGGGG CGTTGGCTTT ATATGTGCCT 180
TTGGGCAGAG AAATACTGCA GGGTTTAGCT AGCGGCATAC AAAGCGTGAT TGGTTACGGC 240
TATGAGGGGG TACGCTTTTT ATTTGGCAAT CTCGCTCCAA ACGCTAAGGG CGATCAAGGG 300
ATAGGAGGCT TTATCTTTGC GATCAACGTT TTAGCGATCA TTATCTTTTT TGCTAGCTTG 360
ATTTCACTTC TATATTATTT AAAAATCATG CCTTTAGTGA TCAACCTCAT CGGCGGGGCG 420
TTGCAAAAAT GCTTAGGCAC TTCTAAAGCA GAAAGCATGA GCGCAGCGGC TAATATTTTT 480
GTGGCGCACA CCGAAGCGCC CTTAGTCATT AAACCCTATT TGAAAAGCAT GAGCGATTCA 540
GAGATTTTTG CGGTCATGTG CGTGGGCATG GCTAGCGTTG CGGGGCCTGT GTTAGCCGGG 600
TATGCGAGCA TGGGCATTCC TTTACCTTAT TTAATCGCCG CATCGTTTAT GTCCGCTCCT 660
GGGGGGTTGT TGTTCGCTAA AATCATTTAC CCGCAAAACG AAACCATTTC TAGCCATGCA 720
GATGTTTCTG CAGAAGAGCA TGTCAATATT ATAGAAGCTA TCGCTAATGG GGCAAGCACA 780
GGGCTTCATT TAGCCTTGCA TGTGGGGGCG ATGCTTTTAG CCTTTGTGGG GATGCTCGCG 840
CTCGTTAACG GGCTTTTAGG GGTTGTAGGG GGATTTTTAG GCATGGAGCA TTTGTCTTTA 900
GGGGTGGTTT TAGGCACGCT TTTAAAACCT TTGGCCTTTA TGTTAGGCGT TCCTTGGAGC 960
CAAGCCGGGA TTGCCGGGGA AATCATAGGC ATTAAAATCG CGCTCAATGA ATTTGTGGGC 1020
TATATGCAAT TATTGCCTTA TTTGGGCGAT AACCCTCCTT TAATCTTGAG CGAGAAAACC 1080
AAAGCGATCA TCACCTTTGC GTTGTGCGGA TTCGCTAACT TAAGTTCAGT CGCCATGCTC 1140
ATTGGGGGGC TTGGCAGTTT AGTGCCTAAA AAGAAAGATT TCATTGCCAG GCTTGCTTTA 1200
AAAGCGGTGC TTGTAGGCAC GCTTTCTAAT TTCATGAGCG CGACTATCGC CGGGTTATTC 1260
ATAGGGTTAA GCGCCAAT 1278

(2) INFORMATION FOR SEQ ID NO:1225:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 948 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature

(B) LOCATION 1...948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225

```
ACGCTATCCA AAGAAGAGGG ATTGATGCCA CAAAACCAGC TTGTGATCAC CATCATTGAT      60
GAATCAGGCT CTAAGCAACT CAAATTTTCT AAAAATTTAA AACGCAACCT CATCATTTCT     120
GTTGTCATTC TTTTATTGAT CGTGGGGCTT GGCGTGGGGT TTTTAAAATT TTTAATCGCT     180
AAAATGGATA CGATGACAAG CGAGAGGAAT GCGGTTTTAA GGGATTTTAG GGGTTTGTAT     240
CAAAAAAATT ACGCCCTAGC GAAAGAGATT AAAAACAAGC GAGAAGAGCT TTTTATTGTG     300
GGGCAAAAGA TCCGTGGGCT AGAATCCTTG ATTGAAATCA AAAAGGGGGC TAATGGGGGA     360
GGGCATCTCT ATGATGAAGT GGATTTAGAA AATTTGAGCT TAAATCAAAA ACATTTAGCA     420
CTCATGCTCA TTCCTAATGG CATGCCCCTA AAAACTTATA GCGCTATCAA ACCCACTAAA     480
GAAAGGAACC ACCCCATTAA AAAGATTAAG GGCGTTGAAT CCGGGATCGA TTTTATCGCG     540
CCATTGAACA CGCCTGTGTA TGCGAGCGCT GATGGGATTG TGGATTTTGT GAAGACTCGT     600
TCTAATGCGG GGTATGGGAA CTTGGTGCGC ATTGAACATG CGTTTGGTTT CAGCTCCATT     660
TATACGCACT TAGATCATGT CAATGTGCAG CCTAAAAGCT TCATCCAAAA AGGGCAGTTG     720
ATTGGCTATA GCGGGAAGAG CGGTAATAGC GGCGGCGAAA AATTGCATTA TGAAGTGCGG     780
TTTTTGGGTA AAATTTTAGA CGCAGAAAAA TTCCTAGCAT GGGATTTGGA TCATTTTCAA     840
AGCGCTTTAG AAGAAAATAA ATTTATTGAA TGGAAGAATC TGTTTTGGGT TTTAGAAGAC     900
ATCGTCCAGC TCCAAGAGCA TGTGGATAAA GACACCTTAA AAGGTCAG                  948
```

(2) INFORMATION FOR SEQ ID NO:1226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 945 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

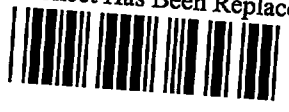
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226

```
GGGTTTTTGG TGTTTTTAGA CAGGCGTTTG ATTGTGATGG TTACGGACTC TAAAGGGAGT      60
CGTTATATTA ATGTGCATAT CTTATTCCGC CAAATCAGTT TGTATGCGCT GTTGAGCGTT     120
GTGGGATCTT TATTGTTTTT AGGCGTTTCA TTACTGGTTT TAAATAAAGA AATTAAAAAC     180
ATTGAAAAAC AGCATGCTTT AATCACTAAG GAATTTGAGA AAAAAAGAGA GACGAATGAA     240
AAGCTTTCTT TGCAAATGGA TGAGTTTTTA GACGATTTGC AACTTTCAGG GGAGCGCATC     300
AACGATTTAG AAGAAGTGGT GGGGGTGAAT AGGCCTGAAG AAGAAAAAGA AGAGGGCAAT     360
TTTTCCAGCC GCTTGGATGT GGCTGGGATT ACCGGGCTTC AAAAAAGCTT TATCATGCGC     420
CTTATCCCTA ATGACTACCC GCTAGAATCC TATCGGCGCG TTTCAGCCGC TTTTAATAAA     480
AGAATGCACC CTATTTTGCA TGTGTTGCAC AACCATACCG GGCTTGATTT AAGCACCGCT     540
ATTAACACGC CTGTGTATGC GAGCGCGAGC GGGGTAGTGG GGTTAGCGAG CAAGGGGTGG     600
AATGGGGGGT ATGGGAATTT GATTAAGGTT TTCCACCCTT TTGGTTTTAA AACCTACTAC     660
GCCCATTTGA ATAAAATCGT CGTAAAAACG GGCGAATTTG TCAAAAAAGG GCAGTTGATT     720
GGGTATAGTG GTAATACAGG AATGAGCACA GGACCGCATT TGCATTATGA AGTGCGCTTC     780
TTAGATCAAC CCATAAACCC CATGAGTTTC ACCAAATGGA ACATGAAAGA TTTTGAAGAA     840
GTTTTTAATA AAGAAAGGAG CATCAGATGG CAATCTTTGA TAACAATAAT AAATCGGCTA     900
ATGCAAAAAC AGGACCAGCG ACTATCATCG CTCAAGGCAC CAAAA                     945
```

(2) INFORMATION FOR SEQ ID NO:1227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1380

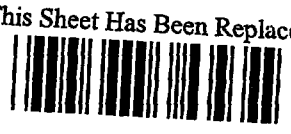
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227

```
GATATTGAAT TCGCCAATCT TTATCATATT CCTATTAAAG TGATCACGCA AAGCCCTCAA      60
AATTTGCCCC ACACCAAAGA AGAGATTTTA AAAAATAGCG GGGAGTGGAG CGATCTTTCT     120
AGCTCACTGG CCAGAAAAAA AATCCTCCCT TATTTTGACA AAGAAAATCT CGGTAAAAGG     180
GTCATCAACT ACCGCTTGCA AAATTGGGGG GTGAGCCGTC AAAGGTATTG GGGAGCGCCC     240
ATTCCTATGA TTCATTGCAA ACATTGCGGA ATCGTGCCTG AAACCCAACT GCCGGTAACT     300
TTACCTGAAG ACATTGTGAT TGATGGGGAA GGCAATCCAT TAAAAAAGCA TGCGAGTTGG     360
AGATTCGCTC AATGCCCCAG ATGCCATAAA GACGCTTTAG TAGAAACAGA CACCATGGAC     420
ACTTTTATCC AATCCAGCTG GTATTTCTTG CGTTATACCA CCCCCAAAAA TCAGCGTGAA     480
AATCAAGCGT TTGATCAAAA TTACTTGAAG TATTTCATGC CGGTGGACAC TTATATTGGC     540
GGCATTGAAC ATGCGATTTT GCACTTGTTA TACGCGCGCT TTTTCACTAA GGCTTTAAGG     600
GATTTGGGCT ATCTTCATTT AGATGAGCCT TTCAAACAGC TTATCACTCA AGGCATGGTC     660
TTAAAAGATG GTGCTAAGAT GAGCAAATCT AAAGGCAATG TCGTTAGCCC TAAAGAGATA     720
CTCAAAAAAT ACGGGGCTGA TGCCGTAAGG CTCTTTATCC TTTTTGCTGC CCCGCCGGCT     780
AAAGAATTGG AATGGAATGA CAACGCTTTA GAAGGCGCGC ACCGGTTTAT CAAGCGCTTA     840
TACGATAAAG CGAACGCCAT TACCCCTACC ACTTCTAAGC CTGAATTTAA AGAAGTTGGC     900
CTGAATGAAG CGCAAAAATT AGCCCGCAAA AAAGTCTATG AGGCGTTGAA AAAATCGCAT     960
GAGATTTTCA ATAAGGCTGA AAGCGCTTAC GCGTTTAACA CTTTGATCGC AAGCTGCATG    1020
GAGGCTTTAA ACGCTTTGAA CGCGCAAAGT GATGAGCAAA TTTTATGCGA GGGTTATTTT    1080
GTGTTGTTGC AAATCTTAGA GCCTATGATC CCGCACACGG CATGGGAATT GAGCGAGAGG    1140
CTTTTTAAAA GAGAGAATTT CAAGCCTATA GAAGTAGATG AAAGCGCTTT GATAGAAGAC    1200
TTTATGACTT TAGGGCTTAC CATTAATGGC AAAAGGCGCG CGGAATTGAA AGTCAATATT    1260
AACGCTAGCA AAGAAGAGAT TATTATTTTG GCTAAAAAAG AATTAGAGAA ATATTTAGAA    1320
AACGCGAGCG TTAAAAAAGA AATTTATGTG CCTAATAAAC TTGTTAATTT TGTTACCGCA    1380
```

(2) INFORMATION FOR SEQ ID NO:1228:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature

(B) LOCATION 1...1209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228

```
CTAAATTTGT GGCTCAAATC GCTTATGAGG GGAAATTCAA TAATGAAAAA TAGTCATGGG      60
TTAAAGGCGT TTTTAGAAAC AAAGCCTAAG GAATACCATA AGTTCGACCC TAGCCGTTTC     120
ATTCAAATTT ATAAGGATTT TAAAAACGCT TTTTTTGAGA TTCAAGCCAA AGTCATTCAT     180
GTGGTAGGGA CTAATGGTAA GGGCAGCACA GGGCGGTTTT TAACCCTTTT ATTAGCCGAT     240
CAAGGGTTTA AAGTGTTGCA TTTCACCTCC CCTCATGTTT TTGAATTCAG GGAGCGCTTT     300
TATTTGAATG GCTCTGTTGT TAAAGAAAGC GTTTTAGAAA ACGCCCACCA GCAATTGCAA     360
TCGCACGCTT TCAGTAACGC TTGCTCGTAT TTTGAATACG CTACCTTATT AGCTGTCATG     420
CTCGCTAAAG ATTGCGATTA TTTGGTTTTA GAAGCAGGGC TTGGGGGGGA GTTTGACAGC     480
ACGAACGCTT TGGAAAAAAC CCTAAGCGTT TTCACCCCCA TTGATTACGA TCATAAGGAA     540
TTTTTAGGGG ATAGTTTAGA AAGCATTGCG ACTACTAAAT TAAAAGCGAT GGGCTCTCTT     600
AATATCATCG CTCCCCAACA AGAACTGGTT TTAAATGTGG CTCAAAAAAT CGCTAAAGAC     660
AAACACGCGC AATTGATTGT GGTTCAAAAT GAAATTTCAA AAGGAGTGAG CGATTATATT     720
GAACGCCACC ATTTAGCCCA TTTTTTAGCG ATGAATTTAG AAGTGGCTCT AAAGGCGTTT     780
GAAACGCTAT TGCCATGCAA TAAACAAGAA GTTTTAAAAA ACCTAAAGCC CCTAGATTTA     840
ATCGGCCGTT GCGAGCTTTT AAGCCCTAAC ATTTTAATAG ATGTGGGGCA TAACCCCCAT     900
AGCGCTAAAG CCTTAAAAGA AGAAATCAAA CGCATCTTTA ACGCTCCAAT CGTTTTGATT     960
TATAATTGCT ATCAAGATAA AGACGCTTTT TTGGTGCTAG AAATTTTAAA GTCTGTGGTT    1020
AAAAAGGTTT TGATTTTAGA ATTGCATAAT GAAAGAATTA TCCAATTAGA AAAACTTAAA    1080
GGGATTTTAG AAACTTTAGG GTTAGAACAC GCCTTGTTTG AAGAACTGAA AGAAAATGAA    1140
AATTATTTGG TGTATGGCTC ATTTCTGGTA GCCAACGCTT TTTATGAACG CTATCCAAAG    1200
AAGAGGGAT                                                            1209
```

(2) INFORMATION FOR SEQ ID NO:1229:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229

```
AGCGTGTCCA GTCATAGCGG GAGCGCGGAT TTGTTGGAAA ATTTGGGCGT GAATATTGAA      60
ATGAACCCCA TGCAATTAGA AAATTGCTTC AAACAATCGC ATTTTGGGTT TTTATTCGCG     120
CCTTTATACC ATCAAAGTTT TAAAAAATCC GCCCCTTTAA GAAAAGAGCT TTTCACTAAA     180
ACGATTTTCA ATTGCTTAGG GCCTTTAATC AACCCCTTAA GGCCAAAAAT CCAGCTTTTA     240
GGCGTGTATG ACAAATCCTT GTGTAAGACC ATGGCGCTAG CGTTGAAGGC TTTAGGCGTT     300
AAAAGGGCGA TGGTGGTTAA TGGAGGGGGG ACAGATGAAA TCGTGTTGCA TGACATTACG     360
CATGCGTGCG AATTGAAAAA TAACGAAATT TTAGAGTATG ATTTGAGCGC TAAAGATTTT     420
GATTTACCCC CCTATGATTT GAAAGAATTA CAGATTGAAA ACGCCAAAGA AAGCGTTCAA     480
GCGTGTTTAG ATATTTTAGA AAATAAAGGC AAAGATTCGC ATACAATGGT GGTTGCGGCG     540
AATGTGGCGA GTTTGTTGTA TTTGAGCCAT AGGGCTAAAG GATTTAAAAG AGGGCGTGAG     600
CATGACTTTA GAGCATTTAA AAACCAAAGC GCATTATGTG CATTTACAAA AAATCATAAG     660
GCTAAGCCAT GCCTAGCGTG T                                               681
```

(2) INFORMATION FOR SEQ ID NO:1230:

(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:1230

```
AATTTGGTAG TGAGTGTTCC TGCAACGAGT GCGAATTTAG GCCCCGGTTT TGATTGCTTG      60
GGTTTGAGTT TGAATTTACG CAATCGTTTT TTTATTGAGC CTAGTAATAT CCATGCGGTG     120
AAATTGGTTG GGGAGGGTGA AGGGATCCCT AAATTTTTAA CCAACAATAT TTTCACCAAA     180
GTGTTTTATG AGATTTTAAA AAAGCATGGG AATGACGGCT CGTTTAAATT TTTATTGCAT     240
AATAAAGTCC CTATTACAAG GGGCATGGGG TCTAGCTCAG CGATGATTGT GGGGGCGGTC     300
GCTTCAGCGT TTGCGTTTTT AGGGTTTGCT TTTGATAGAG AAAACATTCT CAATACTGCT     360
CTAATTTATG AAAACCACCC GGATAATATC ACCCCGGCGG TGTTTGGGGG GTATAATGCA     420
GCGTTTGTGG AAAAAAAGAA AGTGATAAGT TTAAAAACCA AAATCCCTTC TTTTTTAAAA     480
GCGGTGATGG TGATCCCTAA TAGGGTCATT TCTACCAAGC AATCGCGCCA TCTCTTGCCC     540
AAGCGTTACA GCGTGCAAGA AAGCGTGTTT AACCTTTCGC ATGCGAGTTT GATGACGATG     600
GCGATTGTGC AAGGGAAGTG GGACTTGTTG CGTTGTTGTT CTAAAGACAG GATGCACCAA     660
TATAAGCGCA TGCAAACTTA TCCCGTGTTG TTTGCGATCC AAAAGCTCGC TTTAGAAAAT     720
AACGCCTTAA TGAGCACGCT TTCAGGGAGT GGTTCGTCGT TTTTTAACAT GTGTTATGAA     780
GAAGACGCTC CTAAATTAAA GCAGGTTTTG AGCAAGAAAT TCCCTAAATT TAGGGTAGCG     840
GTTTTAGATT TTGACAATGA TGGAGTCCTT ATTGAGAAAG AC                        882
```

(2) INFORMATION FOR SEQ ID NO:1231:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231

```
TTAGTATTCA AAAAGCCCTT TTTTAAAAAT AGGTTACTAA ACGTTACTAA TAAGTTAAAA      60
TTCGTGAAAA TAACCATAAT GATTAAAGAT TTTAACCACT ATTGTAGAAA AATAACGAGA     120
GGGTTTGTAA AAATTCCCAC CAAAAAACAA GGAGCAAAAA AGATGAAAAA AGCGGGTTTT     180
```

```
CTTTTTTTGG CGGCGATGGC TATCATTGTT GTGAGTTTAA ACGCCAAAGA TCCGAATGTG      240
TTGCGTAAGA TTGTTTTTGA GAAATGTTTG CCTAATTATG AGAAAAATCA AAATCCTTCA      300
CCATGCATAG AAGTCAAACC CGACGCCGGC TATGTGGTTT TAAAAGATAT TAACGGTCCG      360
TTGCAATATT TGTTGATGCC AACGACTCAC ATTAGTGGCA TTGAAAACCC TTTGTTGCTT      420
GATCCTTCTA CGCCTAACTT TTTTTACTTG TCATGGCAAG CGCGCGATTT TATGAGTAAA      480
AAATACGGAA AACCCATTCC TGATTATGCG ATCTCTTTGA CGATCAATTC TAAAAAAGGG      540
CGATCGCAAA ACCATTTTCA CATCCATATT TCTTGCATTA 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:1232:

(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:1232

```
TATCATCGCA CTAATACCAC GATAAGGATA ATTATCATGC AAGATTTACC CCCATGCCCT       60
AAACGCAACG ACGCCTACAC CTACCATGAT GGCACGCAGT TCGTTTGCTC TAGCTGTTTG      120
TATGAATGGA ATGGAAATGA AATTAGTAAT GAAGAATTGA TCGTTAAAGA TTGCCATAAT      180
AATCTTTTAC AAAATGGGGA CTCGGTCATT CTCATTAAAG ATTTAAAGGT TAAAGGCTCA      240
TCTTTGGTGC TTAAAAAAGG CACTAAAATC AAAAATATCA AGCTTGTCAA TAGCGATCAC      300
AATGTGGATT GTAAAGTGGA AGGGCAGAGC TTGTCTTTAA AATCTGAATT CCTTAAAAAA      360
GCT                                                                    363
```

(2) INFORMATION FOR SEQ ID NO:1233:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

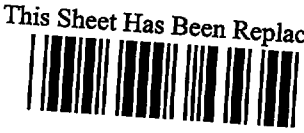
(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature

This Sheet Has Been Replaced



(B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233

```
AAGGGTTGTT TTATGCGAGA ATTTTTTAAG AAACTTGGCA CAGAATACGC TTCCAAGCTG      60
TTTTTGGTTT ATTGGCTTAG ATGGATGTTG AGTGCGTTGG TGATGCTGCC TTTTATGGAG     120
GTTTTTTATT ATTTCAATTT TCCGTTGTGG CTCAATCTTT TCTTAGGGCA AACCATTGGA     180
GCGGTGATTT TTTTCAAGTT GGATAAGTTG ATTTTTTCTA AAAAA                     225
```

(2) INFORMATION FOR SEQ ID NO:1234:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1491 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234

```
TTCTTTAAAC GCTATGAAAG GTTAAGCATG CAATATTCTT CTTTGCTGTC AGTGGTGTTG      60
TTTTTGCCTT TAATCGGTGC GGTTTATGCG GGGCTGTTTG GGGCTAAAGC TAAAGCGTTG     120
CATGTGGGCG TTTTCAATTC TTTGTGCGTG CTGGTTTCTT TCATTGGCGC GGTGGTTCTT     180
TTCATTCAAG CATGGCATCA TCAAAGCTAT GAAAAATATT TGTTTGACTG GATCGTGGTA     240
GGGAATTTTA AAGTCGGCTT TTCCCTCATG CTGGATAATA TCAATGCGGT CATGATTGTC     300
GTGGTCACTC TAGTTTCTTT CTTAGTGCAT GTGTATTCTA TAGGCTATAT GGAGCATGAT     360
ACAGGGTTTA ACCGCTATTT TTCCTACCTT AGCGGCTTTG TGTTTTCCAT GCTGGTGTTG     420
GTGTTGAGCG ATAATTTTTT AGGGCTTTTC ATTGGCTGGG AAGGGGTGGG GCTATGCTCT     480
TACTTGCTCA TTGGCTTTTG GTATCATAAA AAAAGCGCGA ATAACGCTTC TATTGAAGCC     540
TTTGTGATGA ATCGAATCAC GGATTTAGGC ATGCTCATGG GGATTATTTT GATCTTTTGG     600
AATTTTGGCA CCCTCCAGTA TAAAGAAGTC TTTAGCATGC TCAATAACGC CGATTATTCC     660
ATGCTCTTTT ACATTAGCGT GTTTCTTTTT ATTGGCGCTA TGGGGAAGAG TGCTCAATTC     720
CCTATGCACA CATGGTTAGC CAACGCTATG GAGGGGCCTA CCCCTGTATC CGCTCTCATC     780
CATGCAGCGA CGATGGTAAC CGCTGGGGTG TATCTAATCA TCAGAGCCAA TCCTTTGTAT     840
AGTGCGGTGT TTGAAGTGGG TTATTTTATC GCATGCTTAG GAGCGTTTGT GGCTCTTTTT     900
GGAGCGAGCA TGGCTTTAGT CAATAAGGAT TTAAAACGCA TCGTGGCTTA TTCCACGCTT     960
TCTCAATTAG GCTATATGTT TGTAGCGGCC GGGCTTGGGG CTTATGCGAT CGCGCTTTTC    1020
CACCTCTTTA CGCATGCGTT CTTCAAATCC CTCCTTTTCT TAGGCTCAGG CAATGTCATG    1080
CATGCGATGG AAGACAATCT GGATATTACT AAAATGGGCG CTTTATACAA GCCTATGAGG    1140
ATCACAGCTG TCTTTATGAT TATAGGGTCA GTGGCTTTGT GTGGGATCTA CCCCTTTGCG    1200
GGCTATTTCT CCAAAGACAA GATTTTAGAG GTCGCCTTTG GGATGCACCA CCACATTTTA    1260
TGGTTTGTTC TTTTGATTGG GGCGATCTTT ACCGCTTTTT ATAGCTTCAG ACTCATCATG    1320
CTGGTGTTTT TTGCACCCAA ACAACATGAA ATCAACCACC CCCATGAAGG CCAAAAATTT    1380
CATGCTTTTG AGCATGCTAC CGTTAGGGGT TTTGGCGGTC ATTGCCGGTT TTTCAGAAGA    1440
GCCGTTTTTT CATTTTATCT CTCAAGTGAA TTCCTAGTGT TGGAGAGTAT C              1491
```

(2) INFORMATION FOR SEQ ID NO:1235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 base pairs
(B) TYPE: nucleic acid

This Sheet Has Been Replaced



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

(ii) MOLECULE TYPE: DNA (genomic)

(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:1235

```
AACAAGCCGA ACAAGGGTGC AGTATTGGAG AAAACAAAGA AGAGGCAGTT GCTTCAAAAG      60
AAAACAAAGA AGAGAATAAA ACAGAAGCGG CTGCCCCAAA AGAAAATCAA ACAGAAAACA     120
AGACAGAGGT TAAAGAGAAA AATTGAAGTC CCTACCAAAA CCACTTACTT GTTGCTTGAA     180
GAAGCGGGCA TCAATTTAGA AACTTATGAA AAAATTCTCG CTCTTTTGCA AAAATCAAAT     240
AACACCTTGC TAGTGGTTGG CGAGGAAATT TATAGCCACA AACAAGCCCA TAACATCGCT     300
AAAATGTTGC GTTTATTAGC CCAAAAAAGC GCTATTAAAC TCATTCTTAT CCCCCCAAGC     360
GCGAACGCTT TAGGCATCGC TTCTATTTGC GAATTGAGCG AAGAAGTTTT TGAACATGAA     420
AAAATCGTAG GCATTCGCGC TCAAGGGGAT TTCACTATCA ATAGCGACGA TAGGGTTTTT     480
GGGAAAGACG CTGTCAGTAA AGTGGATTTT ATTCTGCCCA GTCTCAACCA ACTAGAAGGC     540
ACGATCACTA ATGTTGAAGG GCGTGTGTTG CCCTTAAAAC CGGCTTTAAG GTTTGAAGGC     600
TATGACTTGA GCGATATCAT GCAAGGCTTT GGCTTTGTGG AAGAAAACCT CACAGAATGC     660
ACCCACAAAC TCCCTACAGA AGCGGGCTTT AAAGCCTTAG AGTTTGATCA TCTAACCAAC     720
TATTTCACTA ACGACAGGGC TAATCACAGA GGCTATTTAT TAGGAACAAG CCATTTTGAA     780
AATAGCGCTA AAGAATCGAA GCCACAGAAT GCGAGCCTAT CAAGCCTT                  828
```

(2) INFORMATION FOR SEQ ID NO:1236:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236

```
GGAGGTTTTA TGGCCAAACA AGAATACAAG CAACTTCCTA AACGAGCCGA AGTCCATAGC      60
GCGACCGAGC AGTTTAAAGA CACCATTAAA ACGAGCTTGG GTTTGGATCT ATTCAAAGGG     120
TTAGGGCTTA CGATCAAGGA ATTTTTTAGC CCAAGCGTAA CCATCCATTA CCCTATGGAG     180
CAACTCCCCT TAAGCCCACG CTATCGCGCG GTGCATCATT TGCAACGGCT TTTAGACTCA     240
GGCTCTGAAA GGTGTATAGG CTGTGGGCTG TGCGAAAAGA TTTGCACGAG CAACTGCATA     300
AGGATCATCA CGCATAAGGG CGAAGACAAC CGCAAAAAGA TCGATTCTTA CACGATCAAT     360
TTGGGGCGTT GCATTTATTG CGGGTTGTGT GCGGAAGTTT GCCCAGAATT GGCGATCGTT     420
ATGGGGAATC GGTTTGAAAA CGCCAGCACC CAACGCTCCC AATACGGCTC TAAAAGCGAG     480
```

TTTCTAACGA GCGAACAAGA CGCTAAAAAC TGCTCGCATG CCGAATTTTT AGGCTTTGGT 540
GCGGTAAGCC CTAATTATAA CGAACGCATG CAAGCCACCC CTTTAGATTA TGTCCAAGAA 600
CCTTCAAAAG AAGAATCCAA AGAAGAGTCT CCAACAAGCC CAGAAAGCCA TAAGGGAGAT 660
GAAAATGTT 669

(2) INFORMATION FOR SEQ ID NO:1237:

(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:1237

ATTATGTCCA AGAACCTTCA AAAGAAGAAT CCAAAGAAGA GTCTCCAACA AGCCCAGAAA 60
GCCATAAGGG AGATGAAAAT GTTTGAAACC ATTGCCTTTT ATTTCTTTGC GATCCTTACT 120
TTAAGCATGG CGTTAGTGGT GATCACAACC ACAAATATCC TCTATGCCAT TACCGCTCTC 180
GCTAGTAGCA TGGTTTTTAT TTCTGCTTTT TTCTTTTTAC TGGACGCTGA GTTTTTGGGC 240
GTGGTGCAAA TCACGGTGTA TGTGGGTGCG GTCATTGTGA TGTATGCGTT TGGCATGATG 300
TTTTTCAACT CCGCTGCAGA AGTAGTTGAA CGCAAGCAAA GCCCTAAAAT CTTGTGCGTT 360
CTTTCATTTG GCGTGGCGCT GTTGCTCACC TTGATTTTAA GCGCTCCTAG CATTGGCGAA 420
AACCTTTCTA AGCAAGTCAA TTCCAACGCT ATTGATGCGC AAATCCCTAA CATTAAAGCG 480
ATTGGTTATG TGCTTTTCAC CAATTACCTC ATTCCCTTTG AAGCGGCGGC TTTAATGCTT 540
TTAGTCGCTA TGGTTGGAGG CATCGCTACA GGGATTCAAA AAATCCATGG GAAAAATCAC 600
ACGCAATTTA TAAAGGAATC TCTA 624

(2) INFORMATION FOR SEQ ID NO:1238:

(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:1238

This Sheet Has Been Replaced



```
ATGAAACAAT TTAAAAAGAA ACCAAAAAAG ATAAAACGAT 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 TAACTACTAC     300
CACTCTCAAA ACAACCAAGA CATCACAGCC AATTTAAAAA ATGATAACGG CACTTATTTT     360
TTAAGCGGTC TGTATAACTA CACCGGAGGG GAATATAATG GGGGGAATTT AGACATTGAA     420
TTAGGCAGTA ACGCTACTTT TAATCTAGGT GCGAGTAGTG GGAATAGCTT CACTTCTTGG     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 ACCATTAATT CGGTTTCTTT AAATGGGGAA     720
TACTTGCAGT TCTTTAGC                                                   738
```

(2) INFORMATION FOR SEQ ID NO:1239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239

```
GTTTTCACGC CAAGGGTGAA GCGCTTTTTC ATCTTCTTAT TCCTCTTTTT AATCTTGCAT      60
GAAATCTTAA ACACAGAATT AGCCCCTTTA AATGGGATTT CGCTCGCGCT GGGCTATTTG     120
TGTTTGTTCA TACTCGTTTT GAGCGCTTCT TTAATCTTTG AAAAAGTCTT ATCCAAGCAG     180
TATTTGCAAA CCGCTAAAGA TAAAATCGCC TCTTTAAAAA ATTTAAAAGT CATCGCCATT     240
ACAGGAAGCT TTGGGAAAAC CAGCACCAAA AATTTCTTGC ATCAAATCTT ACAAACCCAA     300
TTCAACGCGC ATGCAAGCCC TAAAAGTGTC AACACCCTTT TAGGCATTGC GAACGATATT     360
AACCAGAATT TAGACGACAG GAGTGAAATT TATATCGCTG AAGCTGGGGC AAGGAATAAG     420
GGCGATATTA AAGAAATCAC CCGTCTCATT GAACCGCACC TTGCCGTGGT CGCAGAAGTG     480
GGCGAACAGC ATTTAGAATA TTTTAAAACT TTAGAAAATA TTTGCGAGAC TAAAGCGGAA     540
TTATTGGATT CCAAACGCTT AGAAAAAGCC TTTTGCTACT CTGTGGAAAA AATCAAACCC     600
TATGCCCCTA AAGATAGCCC TTTAATAGAC TATTCTAGCC TAGTTAGAAA CGTCCAATCC     660
ACTTTAAAAG GCACTTCTTT TGAAACGCTT ATCAATGGCG TTTGGGAAAG CTTTGAAACG     720
AAGGTTTTAG GGGAGTTTAA CGCCTATAAT ATCGCTTCAG CGATTTTAAT CGCTAAGCAT     780
TTAGGCTTAG AGACAGAAAG GATCAAACGG CTTGTTTTTG AGCTTAAGCC TATTAACCAT     840
CGTTTGCAAC TGTTGGAAGC GAATCAAAAA ATCATTATAG ACGATAGCTT TAATGGGAAT     900
TTAAAGGGCA TGTTAGAGGG CATTCGTTTA GCGAGCTTGC ATCAAGGGCG TAAGGTCATT     960
GTAACACCGG GATTAGTGGA AAGCAATACA GAAAGTAATG AGGCTTTAGC GCAAAAAATA    1020
GACGGGGTTT TTGATGTCGC TATCATCACA GGGGAGTTGA ATTCCAAAAC GATTGCTTCC    1080
AAATTGAAAA CCCCCCAAAA AATCTTACTC AAGGATAAGG CGCAATTGGA AAATATCTTA    1140
CAAGCCACCA CGATTCAAGG CGATTTGATT TTATTCGCTA CTGACGCCCC TAATTACATT    1200
```

(2) INFORMATION FOR SEQ ID NO:1240:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2151 base pairs
(B) TYPE: nucleic acid

This Sheet Has Been Replaced



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

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240

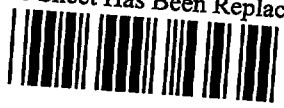
TATGCCTTAA AGTCGTTGAG ACAGGCTTAT TTCTTTTCTC AAAGCGTGTT TGTAGGGCTT 60
TATCATGGGG CAAGCATCTT TGATTTAAAA TTTGAAGTCT ATCTTACTAT GCTAATCTCT 120
TTAATGCCCT TTGTGGCTAC GATTTATATC AATTTCCCAA AAACCACAGA AACTTCGCAT 180
GGCTATGCGA GATGGGCTAA TGTTAAAGAT ATAGAATGCT TTAAAATTTT TAGCAAAGAG 240
GGCTTTTGTA AAGTGGTGCA TAGATTAGGG GTGCAATTTG ATAATGGCTT TATTCTAGGT 300
AAATTTGGTT TTCCAAAGCT TAGAAATGTG TGCTATGACA AGCCCTTAGG AACGATGATT 360
GTTGCACCCC CTGGTGCTGG AAAAACTGCA TGTGTGGCTT TGCCAAATTT ATTGACTTTG 420
CCTAATAGCT GTATTATCAC TGATATTAAA GGCGAACTAA GAGATAAGAC CGCAGGTTAT 480
AGACAAAAAT TCTTAAACAA TAGAATTTTA ATTTTTAATC CTTATGGTGA TGATAACACT 540
TGCTATTTCA ATCCTTTTGA TAAAAGGATT GTTGAAAAGA TGACCTTTGC GGAGCAATTA 600
AGGCATGTTA AAGCAGTAGG CGATGGTATT TTTGTAGATG AAGAAGACCA TTGGGTATCT 660
AAAGCTAAAG AGCTTTTTGT CTTTTTTGCT CTTTTACAAG TAGTAACCAA AGGGCATAGC 720
TCTTTTTATG ATGTCTCTAT CGCACCAGCT AATGATTATG CCCCCTTAAT ACACCCTAAA 780
AGCCCTTATT ACAAGCAACT TTACCAACAC GATAAAAAGA CAGGCGAAGT TATCTTAGAC 840
CCACAAACTA ACGCCCCTAT GAAAAATCCC CAAGCTAATG TTTTAAAACT CTTTTTAAAT 900
CAAGTGGCTG ACCAAAAATA CATAGATATG AATGATGAAA AAAACTATGA CCCAAGAGAA 960
CCTGAACCCC CTTATGGAAC AAAAGGGGCG TTAGATGAGA TTATAAGGAC AGATGCTAGG 1020
AGTTGGGCAA ACACTCCTGA TGATGAATTT GGGAGCATTA TGTCTTCTTT TAAGCGTTTT 1080
ATGTATGTCT ATAAAGACCC AAAAGTGCGT GAAGCTACTT CTAAAATGAG CTTTGATTAT 1140
GAAGAATTAA GAACGGGCAA TATCAGTATT TACATTGTAA TCGCTCAAAT TGATATAGGC 1200
ACACTTTCTT CTTTAGTAAG AGCCTTTTTA GAGAGTATTG CTAAAAACCT TATGGTCAAA 1260
GAAAGCTCTA AACCTGAAGA GCGTATTTTT ATCATTGCTG ATGAATTTGT TAGATTTGGT 1320
AAGTTGCCTT TCTTGTTAGA AATGCCAGCA CTTTGTCGCT CTTATAATGT TGTCCCCTTA 1380
TTCATCACGC AAGATTATGC TATGATTAGA AAATACTATA GCGATGATGA TTTGAAAATC 1440
TTAAAAGGCG TGGTGCATTA TAACATTGTC TTTAAGATGA ATAGTGCTGA AGATGCTGAG 1500
ATTGTCTCTA AGGAAGTGGG CGAATTTACA AGACGATCTA AAAATTATTC TACCGAAAAA 1560
GGTCAATTGG TCTTTGGAGG TAGCTCTTCT TATAGCCATG AGGGTAGAAA CTTACTCACA 1620
GCCCAAGATA TTATGAATAT CAATTCAGAT GAAGTCATTG TTATTGTTAC AGGGGCTAAA 1680
GCTACCCCCT TAAAACTCAA AGCTAATTAT TGGTTCAAAG ATAAAGAGCT TTTAAAAAGA 1740
GCTAATTTGC CTATTGATTT AGAAGTAGAG AGACAAAGAG TTGAAGAGCC TATACAACCC 1800
ACTACAGAGA TTGAAACAAC CCCTAATCAA AACAAAGCTG ACTTAGAACC AAGTAATAAG 1860
GGGGAAAAAG TAGAGAATGA GAGCAATGAG AGAAACACTA ACGAGAATAA TCCCACTACA 1920
CCACAAGAGC TTGAAAATTC AAACTTAAAA GAAAGCGAGA AAGACAATGA AAGTCCCATT 1980
ACCTTAGAAA ATGCTAATGA AAATATAGAG CAAGGAAATC ACAATGAAAT TGATGAGATT 2040
TTAAAAAAGC CACTGAGTGA AATCAGTATG GAAGAGAAAA GAGCCTTGTT TAAGAAAATG 2100
CAACAAAGCG ATGAAGAAAG CGAACAAGAA GTTACACAAA GCACCCAAAG T 2151

(2) INFORMATION FOR SEQ ID NO:1241:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7320 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...7320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241

TATAATCATC CAAATTTAAG CGTTGCTGAT TTAGAATTAG AGCAACAGAA TTTAGGAGAA 60
CAAAATGGAA AAGAGAGAAC AAATCGCGCA GATGAGCCGA ATGGAACTAG AGCAGGAATT 120
CCGCAAGAAA TTCACCGCAG AAGCGAACCT AGAGGACAGC AAGAGGGAAT GGAGCGATCG 180
AGTGATGAAG ATCTTTCACA CCAAGACCCT AGTTTATTTA TTGAGTCTAG AGAGCAGGGA 240
GGAACAAGAG GAGTTTATCG ATCTAGCGAC CAACAGGCAG TTTCAGAAGA ATCCCATAGA 300
GAGCGAGATA GAATACATGA ACATGTATCT AGAGGAGATG GAGTATCAGC AAGAGCGGAT 360
GCAAGAGCGA ATAGCAATGG AGCATCAAGT CCAGCAAGCC GAATGGAAAA TGGAGCAAGA 420
AGCGAAGAAA AGGGGGATAA TCCCAGCGAT GAGAGAGGAA TACCACAGAC ACCGCAATCC 480
CCATCTCATC AACAAAATAG CTCCAGAGAT TTGGGGCTTT CTCTCTCTAG AGAACAGCCA 540
GGACAGACTG GACGCTTACG CCTTTTTGAT CATGGACAGA TGGGCTCATT ATTTCCCACA 600
GACCATGAAA ACCAAAGAAA AAGGAGCGAT AATGAGCTTG ATAGACGCAG TGATAAAGCA 660
AACGAAAATG GAGACAAAAG CCCTAGACAG AATGGAAGCG CAAATCAAGA GAGCGCAAGG 720
AGTGAGCGAT ATGGAATTGC TCAAGGAAGC TCAAATCAAT CAGTATTATT ACCTGCTCAA 780
AGCCGATTAC ATCATGCAGG ACTCAGCGCA CAAAATGGAC TTAGAGACCT TGAAGAAAAC 840
AGGGATCAAG AGGGAAGACT TTTATCAAAT TTAGATAATT TAGAAAGCTT GCTTAACGCT 900
ATTAGAAACA ACACTATAGC GAGTGAGCCT GATTTTAGAT CCAGGCTCTT AGAAGCCATT 960
CAAAACAACG ATCCTTTAAA AGATAGCATT GTGGGGGCGC AACTCCTTAA AGACCCTACG 1020
ACTAAAATCT TTTATGACAA ATTCCAATTA AAAATCAGCC CTAAAAAAGT CTTAGAGATT 1080
TTAGAAAATC GCCTTAAAAA ATCCATTGAA ACAACGAACG AAACGCTAAA CGCATTCAAT 1140
GTGCTGGATA GTCAAGCCAT TGATTTAAAC GCTATCTCTA ATAGCGTAGG ATTAAATCCC 1200
ACACAAGAGA GCAAAATAAC AGACAATAGC GTAGAGTTGA ATAACGCTCA AGAACAAACC 1260
GCGCAAGAGC AAACCACACA AGAACAAACC ACACAAGAAC AAACCACACA AGAACAAACC 1320
ACACAAGAAC AAACCACACA AGAACAAACC ACACAAGAAC AAACCACACA AGAGCAAGAC 1380
ACGCAAGAAA ACGCGCCAAC CACGATAAAA CAAGAAACAC CAATTACGCC AGCCATCCCC 1440
CTTAATCCTA AAATAGATTT TAAACCGAGC GAAGAAGTTT TAATCAAGGG AGCTAAAACT 1500
CGCTACAAGG CTAACATTAA AGCCATTGAG CTTTTAAAAG AATTGCAAGC CAAACAAGAG 1560
ATCTTAAAAG GCGATTACTA CGCCACTTTA AAAGAGCAAG AAATCCTAGC GCAATTTAGC 1620
GGATGGGGCG GGTTAGAGAG CTACTTTAAA AAGGCTCAAC ACCCTGAGGA ATTTAAAGAA 1680
TTAAACGCCT TACTCACTAA AGATGAATTC AGAAGAGCTT ATTTGAGCGC AAGAGACGCT 1740
TACTACACCC CTAAATTAGT TATTGATAGC ATTTATCAAG GTTTAGATCA ATTAGGGTTT 1800
AATAACGACA ACCATCCAAA AAAAATCTTT GAACCCAGTT TAGGCACAGG CAAATTTATC 1860
GCTCATGCGC CAAGCGATAA GAATTACCGC TTCATCGGCA CAGAATTAGA TCCTATTAGC 1920
GCTAATCTTT CTAAATTCCT TTACCCTAAT CAAGTCATCC AAAACACCGC TTTAGAAAAC 1980
TACCAATTCT ATCAAGAATA CGATGCGTTT GTGGGCAATC CTCCTTATGG CAATCATAAA 2040
ATCTATAGCT CCAATGACAA AGAATTGAGT AACGAGAGTA TTCATAATTA CTTTTTAGGG 2100
AAAGCTATCA AAGAATTGAA AGATGATGGC ATAGGAGCGT TTGTGGTGAG TTCTTGGTTT 2160
ATGGATGCTA AAAACCCTAA AATGAGAGAA CACATCGCAA AAAACGCCAC CTTTTTAGGC 2220
GCGATAAGAC TGCCTAATAG CGTGTTTAAA GCAACAGGCG CTGAAGTTAC GAGCGACATT 2280
GTGTTTTTTA AAAAAGGCGT TGAAAAAGCA ACCAATCAAA GCTTCACTAA AGCTATGCCT 2340
TATTATGACA AGATACTCAA TAGCTTGGAT GATGACACCC TTTTTGCCTT GCAAAACAAC 2400
CGCTTTGATA GTTTTATTCC TAGCGATCAA CTTAAGATTG TCAATGCGGT TGCAAACCAT 2460
TTTGGTTTCA AACAAGAAAA ATTGCAACGC TGGTATGAAA AAATAGACAC CGCTAACTTT 2520
GGCTACAGCA CGCAAGATTA TAAGATCATC AAAGACTTCA TTGATAAAGT TGGAAAGAAT 2580
AGCATCAATC TCAACGAACA AACCCTAAAT GAATACTTTA TCCACCACCC TGAAAACATT 2640
CTAGGGCATT TGAGTTTGGA AAAAACCCGC TATAGATTTG AAACAAATGG CGAACAAATT 2700
TACAAATACG ACTTGCAAGC CTTAGAAGAT GAGAGCTTGG ATTTATCCCA AGCGCTTAAA 2760
CAAGCGATAG AAAAATTGCC TAAAGACGTC TATCAATACC ATAAGACTAC CCTTAAAACA 2820
GACGTTCTTA TTATTGATTC AAGTAACGAA CGCTATCAAG AAGTTCAAAA GCTTATCAAA 2880
AATTTAGAAA GGAGGGAATT AGTCAAGTGG GATAATCTTT ATTTCCAACT AGAACAAAAT 2940
AATGAAATGG GCATTTTTTT AAAACCCACT AAAATCAACT CTAAAGTCCA AGATTCACGA 3000
CTAAAAGCCT ATTTTAAAAT TAAAGACGCT TTGAATGATT TAACGAGCGC GGAATTAAAC 3060

CCCTTTAAGCT CTGATTTAGA GCTAGAAAAC AAGAGGGCTA AACTCAATCT TGTTTATGAT 3120
GAATTTGTCA AGAAATTTGG CTATCTCAAT GAGAATAAAA ATCGTAAGGA CATCAGACAA 3180
GATTTGTATG GCGCTAAAGT CTTAGGATTA GAAAAAGACT TTGAAAAAGA AATAACCCCT 3240
AGAAGCGCTA AAATGCAAAA CATAGAACCA AGGCAAGCTC AAGCCAAAAA AGCTCAAATC 3300
TTTTTTGAAA GGACTTTAAA CCCTAAAAAA GAACTTATTA TCACTAACGC TAAAGAGGCA 3360
TTAATTGCAA GCATCAATCA AAAAGGGGGT TTGGACTTGC ATTTCATTAG GGATCATTTC 3420
ACAACCCAAA GTTTAGAAAC CACGATTAAA GAACTTTTAG AGCAAAAACT TATCTATAAA 3480
GACCACAAGG ATAATGGCGG CTATATTTTA GCGAACGATT ATTTGAGCGG CAACGTGAAA 3540
AGAAAACTCA AAGAAGTTAA AGAAGCCATC AATCAAGGCG TGGAGGGATT AGAGGCTAAT 3600
GTGAAAGATT TAGAGCTGAT TATCCCTAAA GATTTGAAAG CCACTGAAAT CATGGCTAAT 3660
ATCAACAGCC CTTGGATACC CACTCAGTAT TTAGAAGAGT TTTTAATGGA ATTGAGCGCT 3720
AACCATTATG AAAAGCAATA CGGCGATAAA ATGACAGATT ACCAACTAAG CAATCTCAAA 3780
GAAGACATCA AAATAGAACA CCTAAGCGGT GCTTATGAAG TTTTTGTTAG AAACAATGAA 3840
TTAAACGAGC TTTATGGTAT CAGGCATAAA GACAAGCCGC ATTCTTATAA AGTGCCTTTT 3900
GAAAGCCTTT TAAATAAAGT CTTAAACAAC AAGGATTTGA GCGTTAAATA CGCCCAAGTT 3960
GATCCTAATG ACCCTAAAAA AGAAATATTC ATCACTGATG AAGAGCAAAG CAATCTCGCC 4020
AGACAAAAAG CAGAAGAATT GAAAGAAGCT TTTAAAGACT GGATTTATAA AGATTATTCA 4080
AGAAGAACCC ATTTAGAGCA AATCTATAAT GACACTTTCA ACAACTTTGT TTTAAAAACC 4140
TATGATGGCT CGCAATTAGA ACTAGAGGGC TTTAACTACC ATATCAGCTT GCGCCCCCAC 4200
CAAAAGAACG CTATTTTTAG AACCATCCAA GACAGGGCGG TGTGTTTAGA CCATCAGGTT 4260
GGAGCAGGCA AGACTTTGTG CGCTATAGCC AGCTGCATGG AACAAAAACG CATGGGATTA 4320
GTGAATAAAA CGCTCATTGC CGTGCCTAAC CATTTAACCA AGCAATGGGG CGATGAATTT 4380
TATAAGGCTT ACCCTAACGC TAATGTGTTA GTTGTTGATA GCAAGGACAC CACTGAAAAA 4440
GAAAGAGAAC TTTTATTCAA TCAAATCGCT AACAACAATT ATGACGCTGT GGTTATCGCG 4500
CACACCCATT TGGAATTATT GTCTAACCCT AGAGGAATCA TAGAAGAATT GAAAGAAGAA 4560
GAGCTAGTGA ATGCTGAAAA AAACTTTGAA AGGCAAGAAT TAGCTTATAA AAATAACCCT 4620
AGAGAAACTA AAAAACCCAA TGAAAGAGCC TTTAAAAACA AGTTGGATAA AATCCGTGCT 4680
AAATACGATG CGATTTTAGA AAAACAAGGC TCTCATATTG ATATTAGTCA AATGGGGATT 4740
GACAATTTGA TTGTGGATGA AGCCCACTTA TTCAAAAATC TAGCCTTTGA AACTTCTATG 4800
GAAAAAATTG CAGGACTTGG TAACCAACAA GGCTCTAATC GCGCTAGAGA TTTGTTTATT 4860
AAAACGCGCT ACTTGCATCA AAACGATAAG AAAATCATGT TTTTAACCGG CACGCCTATA 4920
GCTAATTCCT TGAGTGAAAT GTATCACTTG CAACGCTATT TAACCCCTGA TGTGTTAAAA 4980
GAAAGAGGGT TAGAATTCTT TGATGATTGG GCTAAGACTT ATGGGGAAGT GGTGAATGAT 5040
TTTGAATTAG ACACTTCCGC TCAAAGTTAT AAAATGGTTA ATCGCTTTTC TAAATTTAGC 5100
GATGTGCAAG GCTTAAGCAC CATGTATAGA GCTTTTGCGG ATATTGTCTC TAATGATGAT 5160
ATTTTAAAGC ATAACCCCCA CTTTGTGCCT AAAGTGTATG GGGATAAACC TATCAATGTG 5220
GTGGTGAAAA GAAGCGAAGA AGTGGCTCAA TTCATTGGAG TGGCTTTAGA AAATGGAAAA 5280
TATAATGAAG GCTCTATCAT TGATAGGATG CAAAAATGCG AGGGCAAGAA AAGCCAAAAA 5340
GGGCAAGACA ATATCCTTTC TTGCACCACA GACGCTAGAA AAGTGGCTTT GGATTACCGC 5400
TTGATTGACC CTAACGCTAA AGTAGAAAAA GAATTTTCTA AAAGCTATGC TATGGCAAAA 5460
AATATCTATG AGAATTATTT AGAAACTCAT GCCACTAAAG GCACACAACT TGGTTTCATA 5520
GGGCTATCCA CACCCAAAAC CCATAGCCAA AAAGTCAGTT TAGAAGCGCT AGATAACGCT 5580
CACGAAACTG AAAATAAAAA TCCCCTAGAT AAAGCTCAAG AACTTTTAGA AAGCTTGTCT 5640
AGTTATGATG AAAAGGGCAA TCTTATCGCT CCTAGCAAGA AAGAATTAGA GAACGAGCTC 5700
AAAGAGAAAG AAGCTAAAAG CGTCAATTTA GATGAAGAGA TAGCTAAAGG CTGTTCGTTT 5760
GATGTTTATA GCGATGTTTT AAGGCATTTA GTCCAAATGG GTATCCCACA AAATGAAATC 5820
GCTTTCATCC ATGACGCTAA AACCGAAGAG CAAAAGCAGG ATTTGTTTAA AAAGCTCAAT 5880
CGTGGCGGAG TCAGGGTATT ATTGGGCAGT CCTGCTAAAA TGGGCGTAGG CACTAATGTG 5940
CAAGAAAGAT TAGTCGCTAT GCATGAATTA GATTGCCCAT GGAGACCTGA TGAATTGTTG 6000
CAAATGGAAG GGCGTGGGAT AAGGCAAGGC AATATTTTAC ACCAAAATGA TCCTGAAAAC 6060
TTTAGAATGA AAATCTATCG TTACGCCACT GAAAAGACTT ACGATAGCCG TATGTGGCAA 6120
ATCATAGAAA CTAAATCTAA AGGCATAGAG CAATTTAGAA ACGCGCACAA ATTAGGCTTG 6180
AATGAATTAG AAGACTTTAA TATGGGTAGC TCTAATGCGA GCGAGATGAA AGCAGAAGCG 6240
ACAGGCAATC CCTTGATTAT TGAAGAAGTC AAATTGAGAG CGGAGATTAA AAGCGAAGAA 6300
TCAAAATACA AAGCCTTCAA TAAAGAGCAT TACTTCAATG AAGAAAGCTT AAAAAACAAC 6360
GCTTCTAAAT TGGATTATCT AAAACAGGAA TTGAAAGATT TAGAAACGCT TCAAAGATCC 6420
GTAATAATCC CCACTCATAC AGAGATCAAG CTCTATGATT TGAAAAATGA AGAAAGTAAG 6480
GATTATGAGC TTATCAAAGT TAAAGAGGTA GAGCCTTTAA AAGAAAACGC CTCTATGAGT 6540
GAAGAATTAA CGCACAAGAA ACTCAAAGAA CAAAACAAGC AAATAGCCGA ACAAAATAAA 6600
GAAAAGCTAG ACGCTATTAA AAAGCAATTT GCAAGCAATT TGAACACCTT GTTTGTGAAT 6660
GAAGAAGAAG ATTATAAGCT TTTAGAATAC AAGGGCTTTG TGGTGAATGC TTATAAAACT 6720
AAGTATCAAG TGGAGTTTAG TTTAAGCCCT AAAGACAATC CCAATATTGC CTATAGCCCT 6780
AGCAATATGG TTTATAAAAA CGATACTATC AACATGTTTA GCTCTTATAA TTTCTGCGCT 6840
GAGATCAAGT TTGATGGGTT TTTAAAAAGG TTGGATAACG CTATCACTAA ACTCCCTGAA 6900
AAAATCAAGG AATTAGAAAA CTCCATTGAA ATCACGAAAA AAAATATCGC TAAATACACA 6960

```
AGATTAGTGG AGCAAAAACC TTCTTACCCA CGACTAGAAT ACCTGCAAGC TTTAAAATGG    7020
GATCATAAAA CTCTAATAGA TGATTTAGCT AAAATGAGCA AAGACAGAAA TTATAAGCCT    7080
GCGTTCAACC CTAAATCTAA AGAAGTCTTA AAGAATTTGA ACGCTGAAAA AAGAGCGAGT    7140
TTAGAGAATG AGAGGGAAGA GCAAGGGGTT AAGGGGAACA CAAAGAGTCA TGATGAAATA    7200
GAGCCAGCTA CAGAACAAGT GATTGAAAAA GAAATAGAAA AAGGAGATGA AATCGCTAAT    7260
AATGTTGATT ACTACGAGAA CGAACAAGAA GTGGAAATTA CTAAATCAAT GGGTAGAAGA    7320
```

(2) INFORMATION FOR SEQ ID NO:1242:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242

```
AGGGAGGGGG CGATGAATTT TTTTGACACC CTTATGGGTA TGTTTGTTGA GCCATCTCAA      60
AAAGTAGCCA AAAGTCTTGC TGAACATGTG GGTAGCTTTT TTCATGCACA ACTCATTTTA     120
AACACAATTA TTACTATTTT ATTTATGATA TGGGCGTATA AGCGTGTGAA AGAGGGCGAT     180
ATGTTTGAGT TTAAAACCGC TATGGGTGTG GTTGTATTTA TAGCGTTTGT AGGATTTATC     240
AATTGGGGGA TTAAAAATCC TAATGATTTT AACACTTATT TTATCAATAC GATATTCTAC     300
CCATCTGAAA AACTAGCCAT ACTTATCGCT CAAAGCCTAA ATGATGGCTT AGAAATCCCC     360
ACTAACACTA ATTTAAGTCC TAGTGAAATT TTTAGCATAG GAAATTTAGC CTCAAGTGCG     420
TATGCAATGA TAGTTAATCT GTGGGATAAT GCTTTTGATG GTATTAACAT GTTTAATTGG     480
CTCACAATGA TACCTAAAAT AATTATGTTT TTTTTAGTGA TTTTAGGGGA ATTATTGTTT     540
TTAGGCTTAT TGCTTATTAT TGTGTTATTA GTTACAGCAG AAATTTTTAT GTGGTCAGCA     600
TTAGGTTTAA TTGTATTGCC TTTAGGTTTA ATCCCCCAAA CCAAAGGCAT GTTATTTAGC     660
TATCTTAAAA AGCTCATTTC CCTTACTCTT TATAAACCTT GTATGATGTT AGTAGCTTTT     720
TTTAATTATG GAATAATCTA TAAAGTCAAT ACTTTAATCC CCACTAAACA CGAAGTCACA     780
CAAGGCTTTT ATGGCAATGC GGATAAAATG GCAAATGAGG GAAAAATTAT TGATGTCTTT     840
GGCAATGTCT TAAAAGGAGA TTGGAACTCT TATATAGCCC ATAGTTCTAT TGTAGGCTTT     900
TTAACCATTA TTGTTTTAGG TTCTGTGATT TGTTTCTTTC TAGTCAAACG AGTGCCTGAT     960
TTTATCAATA ATATCTTTGG CACAAGTGGA GGCGTGGGGG CAGTAACAGA AATGATGCAA    1020
AAAATTGGCA TGACAATAGG CGGAGCTGTA TTTGGGGGTA GTGCAGTTAT GGTTGCTAAT    1080
CAAGTTAAGC AAGCCTATCA GAGTGCTGGG GGCGGACTAG CAGGACTTCA AGCTGGAGCT    1140
AAAGCTTTTG GGCTTGGAGC AATCAGTGGA GGGGCAAGTG CTATGGCAAA CCACAGGAGT    1200
GTTAAAGCTG GGGTGAAACA CTTTGTAGCA AGTGTTAAAA GTGGCTTTGG ATTTGATAAT    1260
GATAAAAATA ATAAA                                                     1275
```

(2) INFORMATION FOR SEQ ID NO:1243:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(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:1243

```
AAGGAGCAAC AAATGGCTTA CAAACCTAAC AAAAAGAAGT TAAAAGAATT AAGAGAGCAA      60
CCGAATTTAT TTAGCATCTT AGATAAGGGC GATGTTGCAA CAAACAATCC TGTTGAAGAG     120
TCAGACAAGG CCAATAAAAT ACAAGAGCCA CTCCCTTATG TCGTGAAAAC GCAAATCAAT     180
AAAGCAAGCA TGATTTCTAG AGATCCTATT GAATGGGCAA AGTATTTAAG CTTTGAAAAA     240
CGAGTCTATA AGGATAATAG TAAAGAAGAT GTCAATTTCT TTGCCAATGG TGAGATAAAA     300
GAAAGTTCTC GTGTTTATGA AGCGAATAAA GAAGGGTTTG AAAGGCGCAT CACTAAAAGA     360
TACGATCTGA TTGATAGAAA TATTGATAGA AATAGAGAAT TTTTTATAAA AGAAATTGAA     420
ATTCTAACCC ACACAAACAG CTTAAAAGAA TTGAAAGAGC AAGGGTTAGA AATCCAATTG     480
ACCCACCATA ATGAAACGCA TAAGAAAGCC TTAGAAAATG GCAATGAAAT CGTTAAAGAA     540
TACGACCATC TTAAAGATAT TTACCAAGAA GTAGAAAGAA CAAAAGATGG TGGATTGGTA     600
AGAGAAATAA TCCCCAGTAT TTCTAGCGCT GAGTATTTCA AGCTTTACAA CAAACTGCCT     660
TTTGAATCAA TAAACAATGA AAATACCAAA CTGAATACTA ACGACAATGA AGAAGTTAAA     720
AAACTAGAAT TTGAATTAGC TAAAGAAGTG CATATTTTAA TCCTAGAGCA ACAATTGCTT     780
TCAGCAACAA ATTATTATTC TTGGATAGAT AAAGATGATA ATGCGAATTT TGCTTGGAAA     840
ATGCATAGGC TTATCAATGA AAATAAACTC AAAGAAAACC ATCTCAGCGC CAATAACGCT     900
AATAAGATTA AGCAATTTTT CTTTAATAAT GGTTCTATTT TAGGCTGGAC TAAAGAAGAA     960
CAAAGCGCTA TACAAGAAAA CAGAGATTAT TCTTTAAGAA GCGCTCTTTT AAGTTTAGAA    1020
GAAATCGCTC AAGCAAAAAT TGAATTGCAA AAATACTATG AAAGCGTTTA TGTTAATGGT    1080
GATGGGAATA AAAGAGAAAT CAAGCCTTTT AAAGAAATTT TAAGAGACAC CAACAATTTT    1140
GAAAAAGCTT ATAAGGAGCG TTATGACAAA TTGGTAAGCT TGAGTGCAGC AATCATTCAA    1200
GCTAAAGAGG GTGGTAATGA GCGACAAAAT TCTAGTGCAA ATAACAATAA CCCTATTAAA    1260
AATACAATAG AGACTAATAC TTCTAACAAT ATTATTCAAA ATAATGATAA TATAATCATC    1320
CAAATT                                                               1326
```

(2) INFORMATION FOR SEQ ID NO:1244:

(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

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244

```
ATCAAACATT ACAAACAATA TGGCACAGGC TTACATCTAT TTAGGCATAG TTTTGCAACA      60
CTCATTTATC AAGAAACCCA AGACTTAGTT TTAACTTCAA GGGCGTTAGG GCATAGCTCC     120
TTACTCTCTA CTAAGATTTA TATTCATACC ACACAAGAGC ATAACAAGAA AGTGGCTCTT     180
GTGTTTGATA GTTTGATAGA GAACAAGAAG                                      210
```

This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:1245:

(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:1245

```
AAAAAGAGAA AATACATGCG TTTTAGAAGA GTTAAAAAGC ACAAAAATAA ACACAATAAG      60
GAGCATACAA GTATGGATTT ACAACAAATT GATGAGCTAG AAAAGAAGTT TGAAGAACAA     120
GAAGAACAAG CCCAAGATAC CCCCCTAAAA CAAGAGCCTA GCACAAAGGA AGTAAAAATC     180
CCTAAAAAAA GGGGGCGTAA AAAAAGCTTG TTAGATGAAG ATAAGAAAAA GAGCTTTAAC     240
ATTGCCTTTA GTCCTTGTGT GATAAAAGAA CTTAATGAAT TTTTGCTAGA ATTTGGCTCA     300
TTTAAAGAGA CACGAAGCAC TTTTATTGAA GAAGCGCTTA TTAGGCATTT AAAACACAGA     360
AAAAACACCC AAGAGCAAAA GCTTTTAAAG CAACTAGAAA GATTACAAAA CAAAGAAAAG     420
GGCAATAATG AAAACAATGA ACTTGAA                                         447
```

(2) INFORMATION FOR SEQ ID NO:1246:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246

```
CTTAATACTG ATAAAATAAC TAAATACTTG ATTATTATTG ATATATTTTT AAAACTTTAT      60
GTTATAATGA TAAGTGAGAT TATTAAGTTT CAATTAAAAG GAATAAAAAT GATTAGATTA     120
AAAGGTTTGA ATAAAACTTT AAAAACAAGC TTATTAGCTG GGGTTTTACT AGGTGCTACT     180
GCTCCCTTAA TGGCAAAGCC TTTATTAAGC GATGAAGACT TATTGAAACG AGTAAAACTA     240
CACAATATCA AAGAAGATAC GCTGACTAGC TGTAATGCTA AGGTGGACGG CTCTCAATAC     300
TTGAATAGTG GTTGGAATTT ATCTAAAGAA TTTCCGCAAG AATATAGAGA AAAGATTTTT     360
GAATGCGTAG AAGAAGAAAA ACATAAACAA GCCCTTAATT TAATCAATAA AGAAGACACT     420
```

```
AAAGATAAAG AAGAACTTGC AAAAAAAATC AAAGAAATTA AAGAAAAAGC TAAAGTTTTA     480
AGGCAAAAAT TTATGGCTTT TGAAATGAAA GAACACTCTA AAGAATTCCC AAATAAAAAG     540
CAACTTCAAA CCATGCTTGA GAACGCTTTT GATAATGGAG CTGAAAGTTT TATTGATGAT     600
TGGCACGAAC GCTTTGGGGG TATAAGTAGA GAGAATACTT ATAAAGCACT TGGCATTAAA     660
GAATATAGTG ATGAAGGAAA GATATTAGCC TTTGGCGAAA GAAGTTATAT TAGACAATAT     720
AAAAAAGATT TTGAAGAAAG CACTTATGAT ACTAGACAAA CCTTATCTGC TATGGCTAAT     780
ATGAGTGGCG AAAACGATTA TAAAATTACT TGGTTAAAAC CCAAATATCA GCTCCATAGT     840
TCAAATAATA TTAAACCCTT AATGTCAAAC ACAGAGTTGT TAAATATGAT AGAGCTAACC     900
AATATCAAAA AAGAATATGT TATGGGCTGT AATATGGAAA TAGATGGTTC TAAATATCCC     960
ATTCATAAAG ATTGGGGATT TTTTGGTAAG GCAAAAGTCC CAGAAACTTG GAGAAATAAG    1020
ATTTGGGAAT GTATTAAGAA TAAAGTAAAG TCCTATGACA ACACTACCGC TGAAATAGGA    1080
ATAGTTTGGA AAAAAAATAC TTATTCTATC TCTCATCAC                           1119
```

(2) INFORMATION FOR SEQ ID NO:1247:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 693 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1247

```
AAAGATTACA AAACAAAGAA AAGGGCAATA ATGAAAACAA TGAACTTGAA TGAATTTTTT      60
ACGCATAAGA TAATCTATAA AGACACCCCT TTAAAGTTTA AGGATACACT AGAACAAGAA     120
ATCAGCCAAG CTAGTTTAGT AGAGAAGTTA ATCTTAGCTA ATATCTTAGC CAATATGGTG     180
TTTGCTAAGA TAAGCAATGA GAATGCCCCT AAAATTCTTA TTTCACGCTT GATGTGTAAG     240
TTTAGTCCTA TTGATTATGA AAGCACTATT CCTAGTGATT TTAAGCCTAT AGATGAAGAA     300
GAATATGAAG ATGATTTAGA ATGGCTAAAT GAAGAAAAAG AAGATAGGCT CTTTAATTAC     360
TATCTATTTT TAAATGGTAT TAAAGAAAGT GATGTAGAAG AAGTGTTTAA TGAAAGTGTA     420
GAAATCTATG ATGAGTGCTT AATAGAAATC GCTCAAAATG TCCTTAAAGA TAAATTTTCT     480
TATGACATTG ACTTATTGCA AGTTTTAGTA AAAGGTTATG CTAAAGAGAT TAGAGAATTT     540
TTGAGTTATA AACCTATAAA AGAAATCAAA GACTTTAAAG ACAAAGACAC CGCACTTTAT     600
ATCAGCTTAG GAAAAGACTA TGACAAAGAA AAAGAGCCAT TTTCTAAAAA ATTGCAACAA     660
TGTTTTAAAG AGATTTTAGA GAGCAAGGGT ATT                                  693
```

(2) INFORMATION FOR SEQ ID NO:1248:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1263

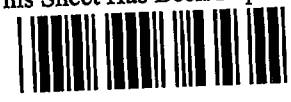
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248

```
ATGAAAGGTT TAACAATGAA AAAATTAGTT TTTAGCATGC TTTTATGTTG TAAAAGCGTG      60
TTTGCAGAGG GGGAAACTCC TTTGATTGTC AATGACCCAG AAACCCATGT AAGTCAAGCC     120
ACTATCATAG GCAAAATGGT AGATAGTATC AAAAGATACG AAGAGATTAT TTCTAAGGCT     180
CAAGCTCAAG TCAATCAGTT ACAAAAAGTC AATAACATGA TAAATACGAC TAATTCTTTG     240
ATTAGTAGTA GTGCTATCAC TTTAGCCAAT CCTATGCAAG TTTTACAAAA CGCTCAGTAT     300
CAAATAGAGA GCATTAGATA CAACTATGAG AATTTAAAGC AAAGCATAGA AAATTGGAAC     360
GCACAAAATT TGTTAAGAAA CAAATACTTA CAGCAACAAT GCCCTTGGCT TAATGTCAAT     420
GCTCTTACTA ACAATAAGAT TGTCAATCTT AAAGATCTCA ATAACCTAAT CACCAAAAAT     480
GGCGAACAAA CCCAAACCGC AAGAGATGTG CAAAATCTCA TTCAGTCCAT TAGTGGCAGT     540
GGCTATGGAA ACATGCAATC ACTTGCTGGG GAATTGAGTG GTAGAGCGTG GGGGGAAATG     600
TTGTGTAAAA TGGTAAACGA TAGTAATTAT GAAAGCGAGC AAGCTCTTTT AGCAACAGGC     660
AATAACCCAG AAGAGCAAAA ACGAAGATTT TTGCTTAGAG TAAAGAAAAA GGTTAATGAT     720
AATAAGCAGT TAAAAGATAA ACTTGACCCA TTTCTAAAAA GACTTGATGT CCTACAAACT     780
GAGTTTGGTG TAACTGACCC TACAGCTAAC CATAATAAGC AAGGGATACA TTATTGCACA     840
GAAAATAAAG AGACAGGTAA ATGCGACCCT ATTAAAAATG TATTTAGGAC AACTCGCTTA     900
GATAACGAAT TAGAACAAGA AATCCAAACG CTCACACTTG ATTTAACCAA AGCCTCCAAT     960
AAAGACGCTC AAAGCCAAGC CTACGCAAAT TTCAATCAAA GGATTAAATT ACTTACTCTA    1020
AAATATTTAA AAGAAATTAC CAATCAAATG CTCTTTTTAA ATCAAACAAT GGCAATGCAA    1080
AGCGAGATTA TGACAGATGA TTATTTTAGG CAAAATAATG ATGGCTTTGG GGAAAAAGAA    1140
AACCATATAG ACAAACAATT AACGCAAAAA AGAATAAACG AAAGAGAAAG AGCTAGAATA    1200
TACTTTCAAA ACCCTAATGT TAAATTTGAC CAATTTGGCT TTCCCATTTT TAGTATATGG    1260
GAT                                                                 1263
```

(2) INFORMATION FOR SEQ ID NO:1249:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249

```
AAGCGTTGGT GGTATTTCGT GCGAGCGTTT TTAAACAGGA GTTTTGCTCC CTTACTCAAC      60
CCTAACGAGA ACCTTTTAGA TCAAGTTAAG TCTAGCATTA TTTTAAAAAA AGGGGTGTCT     120
TATTTTGACT GGGGGGCTTC AGGTTTGGCG AGTGCTTTAG TGGAAAAGCG CGTGAAATCC     180
TTACTGCCTT ATTATGCGAA CGCTCATTCT GTCGCTTCTA AACATGCGAT TTTAATGGGC     240
ATGCTTTTAA AAGAATGCCA AGAAAAGTTA AAGCGTTCTT TAAATTTGAG TGCTAATCAT     300
TGCGTCTTGA GCGCGGGGTA TGGGGCGAGT TCAGCGATTA AGAAATTTCA AGAAATTTTA     360
GGGGTGTGTA TCCCTTCAAA AACGAAGAAA AATTTAGAGC CGTATTTGAA AGATATGGCT     420
TTAAAGCGTG TGATTGTAGG GCCTTATGAG CATCATTCTA ATGAAGTTAG CTGGCGTGAA     480
GGCTTGTGTG AAGTGGTGCG TATCCCTTTA AATGAACATG GTTTATTGGA TTTAGAAATT     540
```

SUBSTITUTE SHEET (RULE 26)

```
TTAGAGCAAA CTTTAAAAAA AACCCCTAAC AGCTTGGTTT CTGTGAGCGC GGCTTCTAAT      600
GTAACGGGAA TTCTTACGCC TTTAAAAGAA GTTTCATCAT TGTGTAAGGA ATATAGGGCT      660
ATTTTAGCTT TGGATTTAGC GAATTTTAGC GCGCATGCTA ACCCTAAAGA TTGCGAATAC      720
CAAACCGGTT TTTATGCGCC TCATAAGCTT TTAGGGGGCG TTGGAGGGTG CGGTCTTTTA      780
GGCATTTCTA AAGATTTGAT TGACACGCAA ATCCCTCCGA GTTTTAGCGC AGGGGGCGTG      840
ATTAAATACG CTAATCGCAC ACGGCATGAA TTTATTGATG AATTGCCTTT AAGAGAAGAA      900
TTTGGCACGC CAGGATTGTT GCAATTTTAC AGGAGCGCTC TAGCGTATCA ATTAAGAGAT      960
GAATGCGGTT TGGATTTTAT CCATAAGAAA GAAAACAACC TTTTAAGGGT GCTTGTGTAT     1020
GGCTTAAAAG ACTTGCCCGC TATTAATATT TATGGGAATT TAACGGCGAG TCGTGTGGGG     1080
GTAGTGGCTT TTAATATTGG AGGGATTTCG CCCTATGATT TAGCGAGGGT TTTAAGCTAT     1140
GAATACGCTA TTGAGACCCG GGCGGGTTGC TCTTGCGCGG GGCCTTATGG GCATGATTTG     1200
TTGAATCTTA ACGCTCAAAA GTCAAGCGAT TTTAACGCTA AACCCGGATG GCTTAGAGTG     1260
AGTTTGCACT TCACGCATTC CATAAACGAT ATTGATTATT TGCTAGACAG CTTGAAAAAA     1320
GCGGTGAAAA AATTGCGT                                                   1338
```

(2) INFORMATION FOR SEQ ID NO:1250:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250

```
TATGTGATAG AGCTTGACAT TAACGCCAGC GATAAATCGC TCTCGCACAG AGCCGTTATT       60
TTTAGCCTGC TCGCTCAAAA ACCTTGTTTC GTGCGGAATT TTTTAATGGG AGAAGATTGT      120
TTAAGCTCTT TAGAAATCGC TCAAAATTTA GGGGCTAAAG TGGAAAATAC CGCCAAAAAT      180
TCTTTTAAAA TCACACCCCC AACAACTATA AAAGAGCCTA ATAAGATTTT AAATTGCAAC      240
AATTCTGGCA CTAGCATGCG TTTATACAGC GGGCTTTTAA GCGCTCAAAA AGGCCTTTTT      300
GTTTTAAGCG GGGACAATTC CCTAAACGCA CGCCCCATGA AAAGAATCAT TGAGCCTTTA      360
AAGGCGTTTG GGGCAAAGAT TTTAGGGAGA GAGGATAACC ATTTTGCCCC CTTAGCGATT      420
GTAGGGGGTC CTTTAAAAGC TTGCGATTAT GAAAGCCCTA TCGCTTCAGC TCAAGTCAAA      480
AGCGCTTTTA TTTTAAGCGC CTTACAAGCT CAAGGCATAA GCGCCTATAA AGAAAGCGAG      540
CTTAGCCGTA ACCACACAGA AATCATGCTT AAAAGTTTGG GGGCTAACAT TCAAAATCAA      600
GACGGCGTTT TAAAAATTTC ACCCCTAGAA AAACCCCTAG AATCCTTTGA CTTTACCATA      660
GCCAATGATC CGTCTAGCGC GTTTTTTTTA GCTCTCGCTT GCGCGATTAC GCCAAAAAGC      720
CGCCTTCTTT TAAAAAATGT CTTGCTCAAC CCCACTCGCA TAGAAGCTTT TGAGGTTTTG      780
AAAAAAATGG GCGCTCATAT AGAATATGTT ATCCAATCCA AAGATTTAGA AGTTATTGGC      840
GATATTTACA TAGAGCATGC CCCTTTAAAA GCGATCAGTA TTGATCAGAA TATCGCCAGC      900
CTTATTGATG AAATCCCCGC TTTAAGCATC GCTATGCTTT TTGCAAAAGG CAAAAGCATG      960
GTGAGAAACG CTAAAGATTT ACGAGCCAAA GAAAGCGATA GGATTAAAGC GGTTGTTTCT     1020
AATTTCAAAG CTTTAGGGAT TGAGTGCGAA GAATTTGAAG ACGGGTTTTA TATAGAGGGA     1080
TTAGGAGATG CGAGTCAATT AAAGCAGCAT TTTTCTAAGA TTAAACCCCC TATTATCAAG     1140
AGTTTCAATG ATCACAGGAT TGCGATGAGT TTCGCTGTTT TAACTTTAGC GTTGCCTTTA     1200
GAAATTGATA ATTTAGAATG CGCGAACATT TCTTTCCCAA CCTTTCAGCT TTGGCTCAAT     1260
CTATTCAAAA AAAGGAGTCT CAATGGAAAT                                      1290
```

(2) INFORMATION FOR SEQ ID NO:1251:

This Sheet Has Been Replaced



(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:1251

```
AATGCGCGAA CATTTCTTTC CCAACCTTTC AGCTTTGGCT CAATCTATTC AAAAAAAGGA      60
GTCTCAATGG AAATTAAAAT GGCTAAGGAT TATGGTTTTT GTTTTGGCGT CAAAAGAGCG     120
ATACAAATCG CTGAAAAAAA TCAAAACAGC TTGATTTTTG GCTCGCTCAT TCATAACGCT     180
AAAGAAATCA ATCGTTTGGA AAAAAATTTC AATGTGAAAA TTGAAGAAGA TCCTAAAAAA     240
ATCCCTAAAA ATAAGAGCGT GATCATAAGA ACCCATGGCA TTCCTAAACA GGATTTAGAA     300
TACTTGAAAA ATAAGGGGGT TAAAATCACT GACGCGACTT GCCCGTATGT GATCAAACCT     360
CAGCAAATTG TGGAATCCAT GAGTAAAGAA GGGTATCAAA TCGTGCTTTT TGGGGACATT     420
AACCACCCTG AAGTCAAGGG CGTGATCAGC TATGCCACTA ACCAGGCTTT AGTCGTCAAT     480
TCGTTAGAAG AATTGCAAGA AAAAAAATTG CAACGGAAAG TGGCTTTAGT CTCTCAAACC     540
ACCAAGCAAA CCCCAAAACT CTTGCAAATC GCTTCT                               576
```

(2) INFORMATION FOR SEQ ID NO:1252:

(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:1252

```
AAATTACCAA TCCACGCATT CGTTTTAATG TGTTTAGCGA TCCCCTCTAA AGTCATAGCC      60
ATTAACGATA ATGTGGCACT CTTAGAGACT TTGGGCGTTC AAAGAGAAGC GAGCTTGGAT     120
TTAATGGGCG AGTCCGTTAA AGTGGGCGAT TATGTGCTAC TACACATCGG CTATGTGATG     180
AGTAAGATTG ATGAAAAAGA AGCCCTAGAA TCCATTGAGC TTTACCAAGA AATGATCGCC     240
GAAGTGAACG AAACGCATGA A                                               261
```

(2) INFORMATION FOR SEQ ID NO:1253:

This Sheet Has Been Replaced



(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:1253

```
AAAGGAACAA GCATGAGCGA ACAACGAAAA GAATCGTTAC AAAATAACCC TAATTTGAGT     60
AAAAAAGACA TCAAAATCGT GGAAAAGATT TTGAGCAAGA ACGACATTAA AGCCGCTGAA    120
ATGAAAGAGC GCTACCTTAA AGAAGGGTCT GTATGTGTGA ATTTCATGAG TTCTCCCGGT    180
AGCGGTAAAA CCACGATGTT AGAAAATCTA GCGGATTTTA AAGACTTTAA GTTTTGCGTG    240
GTAGAGGGCG ATTTGCAAAC CAACAGGGAT GCGGACAGGT TGCGTAAAAA AGGCGTGAGC    300
GCGCATCAGA TCACCACCGG CGAAGCGTGC CATTTGGAAG CGAGCATGAT TGAGGGGGCG    360
TTTGATTTAT TAAAAGATGA GGGAGCGTTA GAAAAAAGCG ATTTTTTAAT CATTGAAAAC    420
GTGGGGAATC TGGTTTGCCC CTCAAGCTAT AATCTAGGGG CGGCGATGAA TATCGTTTTA    480
CTCTCTGTCC CAGAGGGCGA TGATAAGGTG CTAAAATACC CTACGATGTT CATGTGTGCG    540
GATGCGGTCA TTATCAGTAA GGCGGACATG ATTGAAGTGT TTAATTTTAG GGTTTCTCAA    600
GTCAAAGAAG ACATGCAAAA ATTAAAGCCT GAAGCGCCCA TTTTTTTAAT GAGCTCCAAA    660
GACCCTAAAA GCTTGGAAGA TTTTAAAAAT TTCCTTTTAG AAAAAAAGCG TGAAAATTAC    720
CAATCCACGC ATTCGTTT                                                  738
```

(2) INFORMATION FOR SEQ ID NO:1254:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2871 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254

```
GGAAAAATAA TGGCAAAGAA AAAACAAGAA GTAAGGAATA ATGAAATTTT TGTCGCTCAA     [illegible]
AAACTCGCTG AAGAGGAATT GAACGCTAAC GAGATTAACG ATCCGTTAGA AATGCTGGAC     [illegible]
TTTAAAAGCT TTGATGATAA TAAGGAGCTT TTAGATTACC AACAGCAAGC TTTGATTAAC     [illegible]
GCTTTTAGAG TGCTTGTTGC TTATTTTAGA GACTTCAAAG AAAGTAAAAA AGAATTTTAC     [illegible]
GCTTTTTATC AAAAGCATTA TTCATTCGCT AATTGCGATT TCGCTAAAAA GAAACTCAAT     [illegible]
CATTTGTTAA AGAGCCATTT TAAGGTAGAA AATCATTGCG TGCGTTTTGA AAATTTCATC     [illegible]
```

```
AACCGCCTAG CCTTTTACAT GGCCACAGGG AGCGGTAAAA CGATCGTCAT TATCAAACTG     420
GTAGAGCTTT TAAGCGTGGC TATGGGAATG GGTTTGATCC CTAAGAAAAA TATCATGTTT     480
TTTAGCGCGA ACGAGCATTT AATCAAGCAA TTTGAAAAAG AAATTGAAAA ATACAACCGC     540
AATAAGGACT ATTCCAAACA AATTGATTTC AAAAACCTTA AAAGCGTTAA GAATAAGGAT     600
TTTTATCGTG CTCCAAAAGA TTCTTTAATG AAAGAAATCG CTCTTTTTTA TTACCGCGCA     660
GATTTAATGA GCGATGAAGA AAGCAAGGAA AACCTTTTAA ATTATAAGGA TTGTTGGGAT     720
AATGGGGAAA ATTATGTGAT TTTAGATGAA GCGCATAAGG GGAATAAGAC TGAAAGCAAA     780
AGACAGGCGA TTTTTAGCCT GCTGTCTTTA AAAGGGTTTT TATTCAATTT CAGCGCCACT     840
TTCACTGAAG AAAGCGATCT CATCACTGCG GTGTATAATT TGAGCGTGGG CGAGTGGGTG     900
AAACTTGGCT ATGGTAAAGA GTCTGTTTTA TTGAAGAAAA ACAACTTAAA CGCTTTTAAG     960
GAATTGAAAG ATTTAAACGA CAGGGAAAAA GAAATCGCTC TTTTAAAGGC GTTATTGCTT    1020
TTAGGCATGC AAAAACGCTA TAAAGTAGAA GGCTATTTTC ATGACCCTTT AATGCTCGTG    1080
TTCACGCATT CTGTGAACAT GGAAAACAGC GATGCGGAAA TCTTTTTTAA AACTTTAGCG    1140
CGCGTGATTG AAAATGATGA TGAGAGCGAT TTTTCAAAAG CTAAAGACGA TTTATTAGAG    1200
GAATTAAAGA ATCCGGAATT CCTTTTTAGC GATGGCAAAG ATAAAGAAAA AGACTATAAA    1260
ATTGAGGTCT TTAAAGAGAG TTTAAAGGGC ATGGATTTTA AAGGCTTAAA AGAAGCAGTT    1320
TTTTATGCCA GTAATGGGCA TATTGAAGTC ATCATTAACC CTAAAAACAA CCAAGAAATC    1380
GCTTTCAAGC TCAACACGAG CGATAAAGTC TTTTGCCTGA TTAGAATAGG CGATATTACA    1440
GAATGGATCC GTGAAAAATT AAAGAGCGTG AAGGTGGTGA GTAAGAATTT GAGCTTCAAA    1500
GAAGAGAGCT ATTTCAGCCA GATTGATAAG AGCAGTATCA ATATCTTAGT GGGGTCTCGT    1560
GCTTTTGACA CTGGGTGGGA TAGCACAAGG CCTAGCGTGA TTTTATTTTT AAATATAGGG    1620
CTTGATGATG ACGCTAAAAA GCTGGTGAAA CAATCTTTTG GCAGGGGCGT AAGGATTGAA    1680
AGCGTCAAAA ACCAACGCCA AAGGTTAGCG TATTTAGAGA TAGATGAAGC CATTAAAGAC    1740
AAGCTGAAAC CAAACGCTGC AATGCTGGAA ATGCTTTTTG TGATACCTAC CAACCATGCA    1800
AGCCTTGAAG CGATTTTAAA GTTCCAAAAA GAGAGCGAAA ATGGGGGTGA GAATAGAGGT    1860
CCTTGGCGTG AAATCAAATT AGAAAAAACG CGCATAGAGC ATGCCTTATT CGTGCCTTGC    1920
TACCGAAAAG AACAAACCAA CGCTCTTAAA ATTTCTCAAA GCGCTTCGTT TAAAATGAGC    1980
GAAAAAAATT TTAAGGATTT AAAAGAGCAT TTTCATTTAA TGAGTGAAAA GCATTTTATT    2040
TTAAAGCATG AAATTTATGA CCCTAAAGAT TACGCGCTGT TAAAAGAAAT GATACAAACA    2100
GCGCATTTTA AAAAGGTATC AACCTGGCAT TATAAAGATT TAGATTACAT GATTTCTGAA    2160
ATTAAAGGCA AGCTATACCC TAATCAAAAA GTGCCTAAAG ACGAGTTTAA CGCCCTAGAT    2220
AATGAGAAAA TCGTGCATTT TAAAAGGGTT AAAGTTAAGG CGGATAAAAA AGAAAAATTG    2280
ATTCAAACCA TCCAAGAAGT GAAAGAGCAT GCGCCTTTGG ATAAAGAAAC TTTAAGAAAA    2340
AAAATCGCGC AAGGCGAGAT CGATCCTTAT GATACAGAAA AACACAAACA AGACAGAACG    2400
TTCAAAGTTG GTGATGCAGA GCTGTTAAAA CTCAAAGAGC ATTACTACAC CCCGCTCATT    2460
AAAGCCAAAA ACTGCGATTG GCTTAAGCAT GTGGTTAAGG TAAAGAGCGA GAGCGATTTT    2520
TTAGAAGAGT TGTTAAAGAT TACCGAAACG CTGCAAGAAA ACTATGATTT TTGGGCGTTC    2580
AGCAAGATTG ATGAGCATTT AGACAATTTG TTTATTCCCT ATATAGACAA CGCTACAGAA    2640
AGGCGCTTTT TCCCTGATTT TATCTTTTGG CTGCAAAAAG GCGGCACGCA GATCATTTGC    2700
TTCATTGATC CTAAAGGGAG CAAACACACT GATTACGAGC ATAAGGCAGA TGCGTATCAA    2760
CTTTTTGAAG ATAAGGTTTT TAACCCTAAA GACGATCCCA ATCTCAAAAT CAAAGTGGTT    2820
TTAAAATTTT ATGGGGATAA GGATGATGTG GGGGAGCGTT ATAGGGATCT T              2871
```

(2) INFORMATION FOR SEQ ID NO:1255:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 747 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255

```
TGCATGCGTT TTTATTTTAA ATTCCTTTGG CTTTTAGGGA TTTTTCTTAT TTTTTATTTT      60
TTAGACATTA AAGGCAGCTC TTCTTATATC AGCGACCGGG TTAAAAGCGC CTTGATGAGC     120
GCGAAAAACA GCTTACTAGA CAACGTTCAA GCGTATTTTT TTCAAGCCCA AAACATTAAG     180
GAATTTCAAA AAGAACGCTT GATTTTAGAA GCTTTTAAAC TAGAAAACGC TGATTTGAAA     240
GAGCGTTTGA ATAGTATTTA TCCTTTAGAA AATCCAAAAA TGACTTATAC CCCTACTTTC     300
ATGACTTCAT TCATCAATTT AGAAGACACA CACAGCGTTT CTCTCAACCC TATTGTGAAT     360
TTAGAAGAAA ACAAGATTTA TGGCCTTGTC TCTCACAACC AAGCCATAGG CATTGCCGTG     420
CTAGAAAAAG GGCGCTTGAA CGGGTTTTTG AACGCCCACA AGCGGTGTGC TTATAGCGTG     480
ATGATAGGCC AAAATCAAGT CTTAGGCTTT ATAGGGACTA ATTTCAAGCA AGAATTAGTC     540
GTGGATTTCA TTGTCCCAAG CGCTGAAATC AACATAGGCG ATCAAGTGCT AACGAGCGGG     600
CTAGATGGGA TTTTTGGAGC GGGGGTGTTT GTGGGTGAAG TTTCAAGCGT TGAAGATCAT     660
TACACTTATA AAAGCGCGGT GTTGAAAAAC GCTTTTTTAA GCGAAGCCAA ACTTTTAAGG     720
CATGTGTTTT TAAGCGGTGT GAAAAAC                                         747
```

(2) INFORMATION FOR SEQ ID NO:1256:

(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:1256

```
TGGTATTTTA AAAAAGAAAG AAATCCCATG GTTATACATG AAAAAATCAA AAGCCGCTTT      60
TCTAGGAATT GGTCTTTAAG GAATAGGGGC AGGCATTTTG CATCTTCAAG CGTGTATTTT     120
TTCTCACTTC TTGTCATTAC AGCGGTTAAT AGAAGTAGTG CAGTTGCTTG GTTATTGATG     180
CCTGAACATT TGATTGGGTG GTTTTTGATT TCTTTTAGTG GGGAATTTGT AGCAGACATG     240
GCGTTTGGCA AAAAAAGTAA GATTTTTAAA ACCCGCTTTG GAATTTCTAT TGTGAGCGGC     300
GTTTCACTAT TGCTTGGCGC TTTACCAGCG CATTTATTTT TTGTATGGTT TGGCTTTATT     360
AATTGGTGGG CTGTCTTTTT TATAGAAGCG GGAGCTGATC TATTGGTGGG CTGTGTGATA     420
CAAAAGATTT TTTTTGGTAA ATATTGGGTG GATCGCTATT AT                        462
```

(2) INFORMATION FOR SEQ ID NO:1257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1257

```
TGGGCGAAAG GCGCTGGGGC TTTAGTGCTT GAAGAATACG AGAGCGCGAA AAAAAGAGGG      60
GCTAAAATTT ATGCAGAATT TGCCGGGTAT GGCGAGAGCG GCGATGCTAA CCACATCACA     120
GCCCCAGCCC CTGAGGGTGA AAGGGCTTTT AAAGCCATGA AAATGGCTTT AGAAATGGCG     180
AAAGTGGAAG TATGCTATGT GAACGCCCAT GGGGACAAGC ACGCATTA                  228
```

(2) INFORMATION FOR SEQ ID NO:1258:

(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:1258

```
ACGCCCATGG GGACAAGCAC GCATTATAAC GATTGGTATG AAAGCATTGC GTTAAAAAAT      60
GTGTTTGGCT CTAAAGAAAA AGTCCCTCCT GTTAGCTCCA CTAAAGGGCA GATTGGGCAT     120
TGCTTGGGTG CTGCGGGCGC GTTAGTAGCC GTTATTTCTA TCATGGCCAT GAATCAAGGG     180
ATCTTACCTC CTACCATTAA TCAAGAAACG CCTGACCCAG AATGCGATCT GGATTATATC     240
CCTAATACAG CCAGAGAAAA GCAAGTGAAT GCGGTGATGA GTAACTCATT TGGTTTTGGT     300
GGCACTAATG GTGTTGTGAT TTTCAAAAAA GCC                                  333
```

(2) INFORMATION FOR SEQ ID NO:1259:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 567 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259

```
GGCCCAATAC AAAGCGCTCC AGCAATGAAC AAGCTTTTTT TAGCTTTTAT TGTTGGGGGA      60
ATGCTTTTAA GTGCTGATGC TTTAAACGAT AAGATTGAGA ATTTAATGGG GGAGCGATCC     120
TACCACATGA ACAAGCTTTT TTTAGAGCGT TTGTTTAAAA ATCGTAAGGA TTTCTATGAA     180
ATGGGGCGTT TGGATTCCTT AAAACTACTC AACACTCTCA AAGAAAACGG GCTTTTATCG     240
TTTAATTTTG ACAAACCAAG CGTGTTAAAA ATCACTTTCA AGGCTTCAAG TAATCCCCTA     300
GCGTTTGCCA AAAGCATCAA CAATTCTTTG AATATGATGG GGTATTCGTA TGTTTTGCCT     360
ATTAGAATGC AAAGCTCTTC AGGCGAGAAT GTTTTTTCAT ACGAGCTTAA AACGGAATAC     420
GTTTTAGACC CTAACATTTT GATAGAGACG ATGAAAAGGC ATGGTTTTGA TTTTATGGAT     480
ATTAGACGGG TGTCTTTAAA GGAGTGGGAA TACGACTTTG CCTTACAAAA GATCAAGCTC     540
CCTAACGGCG AGAGCCTTAG TTTTGAG                                         567
```

(2) INFORMATION FOR SEQ ID NO:1260:

(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:1260

```
ATGGAACAGA ATAAAAAAAG TTTAGAAAAT TTAGATCTTT CTGATGTTCA AAACATTTCT      60
AAAGATATTT CTGGAACGGC TTTAGAAGAA TTATCGCTTA AAAATTTAGA TAAAAATTTG     120
CAGATTCTAA AAGAAGTTGG AGCGGCAGAA ATTTGCAAGG CGACTAAAAT CGCTTCTAAA     180
AATATCCATT CTATCTTGGA AAAGCGCTAT GAGTCTTTAT CAAGGGTGCA TGCTAGGGGT     240
TTTATACAGA TTTTAGAGCA CGAGTATAAA ATTGATTTGA GCGCATGGGT GAAAGAATTT     300
GACAAAGTGT GTGTTTTTAA AGAGGGCGTG GGAGAAGAGC AAAAACAAGA AACAAGCCCT     360
GAAGAAACAG CAAAAAAACC CCTTAAGGTT GAATTGGATT ACAGCATCAA TCAAGCCAAT     420
ACTTCATTAT CCAAAAAATC TTCCAAATGG AAACCCTTTG TTATCGTTTT AGGGGTGGTT     480
GTCATTATTT TAGTGGTCGT TATCATTCAA AACAGCTCTT CTTTAAAAGA AGAGAGAGAG     540
CAAGAACGCG CTATTAAGCC CGACACCAAA AATAATTCTT TCAATGAAAC TAATCCTACA     600
GAAGAAAAAA AGTTAGAGCC AACGCCTAAA TTAGAAGAAA AACACAAAGA ACAAGACAAG     660
CAAGGCAAAG AAGCGATCAA AGAAAATCCT AATACCATTT ACATTATCCC TAAACGAGAT     720
ATTTGGGTAG AAGTGATTGA TTTAGATGAG AAAAAAAACT CTTTTCAAAA GGTTTTTAAA     780
AAAAGTTATC CTTTAGAGGC TAAAAACCAC CGCTTGTTGT TACGCTTTGG GCATGGGCAT     840
CTTATTCTTA AAAACAACCA TCAAGAACAA GATTATAACG ACAGCAAAAC TAGGCGGTTT     900
TTATACGAGC CAAATAAAGG TTTAACGCTC ATCAATGAGG CCCAATACAA AGCGCTCCAG     960
CAA                                                                  963
```

(2) INFORMATION FOR SEQ ID NO:1261:

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

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1261

```
AGGAGTGGGA ATACGACTTT GCCTTACAAA AGATCAAGCT CCCTAACGGC GAGAGCCTTA      60
GTTTTGAGTA GCGATCCTGT GGAGTTTAAG GAAGCGAGCG GGAAATATTG GCTGAGCGTG     120
AATCAAAACG CGTATTTAAA AATAAGCTCC AATAACCCTT TGTGGCAACC CAAAATCATT     180
TTTTATGATG AAAACTTAAA GATCATTCAA ATCATTGCTA AAGAAAACAG ACAACAAGAA     240
ATCGCTCTTA ACTTGCTTGA TGGCGTGCGT TTTATCCATA TCACTGACGC AAAAAACCCT     300
ATCATTTTAA AAAATGGGAT TAGCGTGGTT TTTGATGCGA TGCCT                      345
```

(2) INFORMATION FOR SEQ ID NO:1262:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 615 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262

```
CGGTCTCTAG CGTGCTGGCT AAGATTGAGT CTCTTTAAGG GGATAATCAT GTTCGATTCA      60
ATCGTTTATT TTTTCAATAA GAGCGGGTTT GTTACCACGC TTGTTTTAGT TTGGATTTCG     120
CTTTATTTGG TGATGACTTT ATGGGTCTTT TTGTATAAAA GCATTGTATT AAAGATTGAA     180
CTCAGGCGCG AGATGCAATC TTTGTCTAAC ATTCTTAATG GAGCGCAAGA CGCTCAGAGC     240
ATTTTATGTT TAATAAAAAA AGAAATGATG AGACCAAAAG GTATTCTAAT GAATTGTTGC     300
AGGGCTTGGA AACACCAGGT TCTTAAGCAA AGCACGACAG GTTTAGTGGT GTTGAGCATT     360
ATCTCTTCTA CAGCCCCCTT TATTGGTTTG TTTGGGACGG TAGTTGAAAT TTTAGAAGCG     420
TTTAACAATT TGGGCGCGTT AGGTCAAGCT TCTTTTGGAG TGATCGCACC CATTATTTCT     480
AAGGCGCTTA TCGCCACCGC TGCAGGGATT TTAGCAGCCA TTCCAGCCTA TTCTTTTTAC     540
TTGATCTTAA AGCGCAAGGT GTATGATTTA TCGGTTTATG TGCAGATGCA AGTGGATATT     600
TTGTCTTCTA AAAAA                                                      615
```

(2) INFORMATION FOR SEQ ID NO:1263:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 408 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1263

```
AAGGTTTTTA TGAATTACGA TAACTATTGG GATGAGGACA AACCAGAACT CAATATCACG      60
CCTTTAGTGG ATGTGATGCT TGTTTTATTG GCTATTCTTA TGGTAACGAC GCCCACTCTC     120
ACCTATAAAG AAGAGATTGC CTTGCCTTCT GGTTCAAAAA CTGCTAGAGC CACTCAAGAT     180
AAAGTGATAG AGATACGCAT GGATAAAGAC GCAAAAATCT ATATAGATAG TCAAACCTAT     240
GAATACAACT CTTTCCCGGA CACTTTCAAT TTGCTTTCTA AAAAATACGA TAAAGATACT     300
AGGGTGAGTA TCCGTGCGGA CAAGCGATTG ACCTATGACA AAGTGATTTA TTTGTTAAAA     360
ACGATTAAAG AAGCGGGGTT TTTGAAAGTT TCTTTAATCA CAAGTCCT                  408
```

(2) INFORMATION FOR SEQ ID NO:1264:

(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:1264

```
AAAGTAGGGC CAATTTGCAT GAGTAAGAGC GCGATTTTTG TTCTTTCTGG CTTTTTAGCG      60
TTCTTGCTCT ATGCTTTGTT ATTATATGGT TTGTTGTTAG AAAGGCATAA TAAAGAAGCA     120
GAGAAAATCC TTTTAGATTT AAATAAAAAG GACGAACAAG CCATTGACTT GAATTTAGAA     180
GATCTGCCAA GCGAGAAAAA GAATGAAAAA ATTGAAAAAG TAACGGAAAA ACAGGGCGAT     240
TTTTTAGAGC CTAAAGAAGA ACCCAAAGAA GAGCCTGAAG AAAGCCTTGA AGATATTTTT     300
TCTTCACTCA ATGATTTTCA AGAAAGACAG ACAAAAACGC TCAAAAAGAC GAGCAAAAAA     360
ATGAACAAGA AGAACAAAGG CGTT                                            384
```

(2) INFORMATION FOR SEQ ID NO:1265:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 645 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1265

```
GGAAGAACAA TGAAATATTT ATGGCTTTTT TTAATATACG CTATAGGGCT TTTTGCAACA     60
GATAAAACGC TAGATATTAT TAAAACCATT CAAAAACTTC CTAAGATTGA AGTGCGCTAC    120
TCCATAGATA ACGATGCCAA TTACGCTTTA AAATTGCATG AAGTCTTAGC GAACGATTTA    180
AAGACTAGCC AGCATTTTGA TGTTTCTCAA AACAAAGAGC AAGGTGCTAT CAATTACGCA    240
GAACTCAAGG ATAAAAAAGT CCATCTTGTA GCGCTTGTGA GCGTGGCGGT AGAAAACGGC    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:1266:

(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:1266

```
TTCCTGAGGG GGAAGTTTAT ACAGGAGAGG TTAAAAGCGT TGTGTTGCCA AGGAGTGGAA     60
GGGGAATTTG GGGTGCTTTA TGGGCATAGC AACATGATCA CCTTGCTTCA GGCGGGAGTG    120
GTTGAGATTG AAACCGAAAA CCAAAAAGAG CACATTGCTA TCAATTGGGG TTATGCAGAA    180
GTTACTAATG AACGGGTGGA TATTTTAGCC GATGGAGCGG TCTTTATTAA AAAAGGATCA    240
GATGACAGAG ATGATGCTAT CTCTAGGGCT AAAAAGCTTT TAGAGGACGC AAGCTCTGAC    300
AGGTTAGCGG TCTCTAGCGT GCTGGCTAAG ATTGAGTCTC TT                       342
```

(2) INFORMATION FOR SEQ ID NO:1267:

(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:1267

```
AAGCTTAGCA TGAGAGCGAT CGCTATTGTT TTAGCCAGAA GTTCCAGTAA AAGGATTAAG      60
AATAAAAATA TGATTGATTT TTTCAATAAA CCCATGCTCG CTTACCCTAT TGAAACAGCA     120
CTAAATTCCA AGCTCTTTGA AAAAGTGTTT ATCTCTAGCG ATAGCATGGA GTATGTCAAT     180
TTAGCCAAAA ATTATGGGGC GAGTTTTTTG AATTTACGCC CTAAAAATTT AGCAGACGAG     240
CAGGGCCACG ACTTTAGAAG TGATGGCCTA TCACATGAAA GAATTAGAAT TAAAAGA        297
```

(2) INFORMATION FOR SEQ ID NO:1268:

(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

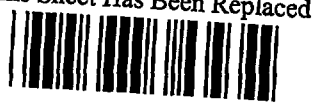
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268

```
ATCCCTCCGA GCACACCATT TCTTAACATT CTGCATGTTT TTAAACATTA TCGCTCCCAT      60
TATGGTAAAA TAAATACTTG CTTAAACACG CTAGGAGATT TGATTTTGGC ATTACCCGTT     120
TATTATGATA AAGACATTGA TTTAGGCGTT ATCCAATCCT TACAAGTGGG CATTATTGGC     180
TATGGCGTGC AAGGAGAGGC TCAAGCACTC AATTTGAGGG ACTCTAAAGT GAAGGTGCGT     240
ATTGGCTTGT ATCAAGGGAG TTTGAGCGTT TCAAAAGCAA AAAAAGAGGG CTTTGAGGTG     300
CTAGGAGTCA AGGAATTAGT CCAACAATCT GATGTGATCA TGGCGTTACT TCCGGATGAA     360
TTGCATAAAG AAGTGTTAGA AAAAGAAGTG ATCCCTTTTT TAAAAGAGGG GCAAATTATA     420
GGCTTTGCTC ATGGTTTTAG CGTGCATTTC AATCAGGTTG TTCTCCCAAA AGGCGTGGGC     480
GCGATTTTAG TCGCACCAAA AGGGCCCGGG AGCGCTTTAA GAGAAGAATA CCTTAAAAAT     540
AGGGGTTTAT ACCATCTAAT CGCCATAGAG CAAGAAAGCT CAATTCATAA CGCTAAAGCG     600
GTGGCTTTAA GCTATGCTAA AGCGATGGGT GGGGGGAGAA TGGGGGTTTT AGAAACGAGT     660
TTTAAAGAAG AATGCGAGAG CGATTTATTC GGCGAGCAAG CGGTCTTGTG CGGGGGGTTA     720
GAAGCGATCG TAAGAATGGG GTTTGAAACT TTAATCAAGG CAGGATAC                  768
```

(2) INFORMATION FOR SEQ ID NO:1269:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(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:1269

```
CAGACGAGCA GGGCCACGAC TTTAGAAGTG ATGGCCTATC ACATGAAAGA ATTAGAATTA      60
AAAGATGAAG ACATTGCGTG TTGTTTGTAT GGCGTTTCAG TATTTTTACA AGAAAAGCAT     120
TTACAAAACG CTTTTGAAAC TTTAAAACAA AATCAAAATA CGGATTATGT TTTCACATGC     180
TCTCCCTTTA GCGCTTCGCC TATCGTTCTT TTAGCCTTGA AAACGGCGTT CAAATGGCTT     240
TTAAAGAGCA TTCAAACACG CGCACGCAAG ATC                                  273
```

(2) INFORMATION FOR SEQ ID NO:1270:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 936 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270

```
ATGAAAAGCG ATAAACCCTT TTTAGAACGC TATTTTTATG ACCCCACTCT TTTGCAAAAG      60
GGGTTGATTT TCGCGCTCTA TCCTTTTTCT TTAATCTATC AATGTATTGC CACAATTAAA     120
CGAAAAACCG CTAAAAAGCA TGATTTTAAA ATCCCCATTA TCAGCATAGG CAACTTGATC     180
GCTGGGGGAA GCGGTAAAAC GCCCTTCATT TTAGAAATCG CTCCAAGATA CCAAGAAGTG     240
GCGGTTGTTT CTAGAGGGTA TCAACGGGAT TCTAAAGGTT TAGTGGTGGT GAGCGTTAAA     300
GGAAACATTT TAGTTCCTCA AAAAACAGCG GGCGATGAAG CCTATCTTTT AGCCTTAAAT     360
CTAAAACAAG CGAGCGTGAT TGTGAGCGAA AAAAGGGAGC TAGGCGTTTT AAAAGCCCTT     420
GAATTAGGAT CAAAGATCGT GTTTTTAGAC GATGGTTTTA GGTTTAATTT CAACCAATTC     480
AATGCGCTTT TAAAACCCAA AGTCCCCCCC TACTACCCTT TTTGTTTGCC TAGCGGGTTG     540
TATAGAGAAA ATATTAAAAG CTATAAAGAA GCCCATTTAG TCATTACAGA AGATAAGGAT     600
TATCAAAGAA TCACCTCTAT CACTAACCCC ACCAAACGCA TGCTTTTAGT AACGGCTATC     660
GCTAACCCTA GCAGGCTTGA TGCGTTTTTA CCCAAAGAAG TGGTTAAAAA ATTGTATTTT     720
AGAGACCATG CCCCTTTTGA TTTGAAGCTT TTAGAAAAAG AGTTTTATCA AAATAACGCC     780
ACCTCCTTAT TGGTTACTTC AAAAGATCTC GTCAAATTAC AAGATTGCAA ATTGCCTTTA     840
```

AGCGTATTGG ATTTAAAACT AGAAATTTGC CCTAAAGTTT TAGAGGAGAT TGATCGTTAT 900
ATCCTTTCTT ATCCTTGTAA TATAAAAGAA CATCTA 936

(2) INFORMATION FOR SEQ ID NO:1271:

(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

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271

AAAGTGTTGT GGGTGCTATA TTTTTTAACC AGTTTATTTA TTTGCTCTTT GATTGTTTTG 60
TGGTCTAAAA AATCCATGCT CTTTGTGGAT AACGCTAATA AAATCCAAGG CTTCCATCAT 120
GCAAGAACCC CACGAGCCGG GGGGCTTGGG ATCTTTCTTT CTTTTGCGTT GGCTTGTTAT 180
CTTGAACCTT TTGAGATGCC TTTTAAGGGG CCTTTTGTTT TCTTAGGGCT ATCGCTAGTG 240
TTTTTGAGCG GTTTTTTAGA AGACATTAAC CTTTCATTAA GCCCCAAAAT ACGCCTTATT 300
TTGCAAGCTG TAGGGGTCGT TTGCATCATT TCATCAACGC CTTTAGTGGT GAGCGATTTT 360
TCGCCCCTTT TTAGCTTGCC TTATTTCATC GCTTTTTTAT TCGCTATTTT TATGCTGGTG 420
GGTATCAGTA ACGCTATTAA TATCATTGAC GGGTTTAACG GGCTTGCATC TGGGATTTGC 480
GCGATCGCGC TTTTAGTCAT TCATTATATA GACCCTAGCA GTTTGTCTTG TTTGCTCGCT 540
TACATGGTGC TTGGGTTTAT GGTGTTAAAT TTCCCTTCAG GAAAGATTTT T 591

(2) INFORMATION FOR SEQ ID NO:1272:

(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:1272

CAGTTTGTCT TGTTTGCTCG CTTACATGGT GCTTGGGTTT ATGGTGTTAA ATTTCCCTTC 60
AGGAAAGATT TTTTAGGCGA TGGGGGGGCG TATTTTTTGG GTTTGGTGTG CGGGATTTCT 120
CTCTTGCATT TGAGTTTGGA GCAAAAAATC AGCGTGTTTT TTGGGCTCAA TTTAATGCTT 180

```
TATCCGGTCA TAGAGGTGCT TTTTAGTATC CTTAGGCGCA AAATAAAACG CCAGAAAGCC     240
ACCATGCCGG ATAATTTGCA TTTGCACACC CTTTTATTTA AATTCTTGCA ACAACGCTCT     300
TTCAATTACC CTAACCCTTT ATGCGCGTTT ATCCTTATTC TATGCAACCT GCCTTTTATT     360
TTAATAAGCG TTTTGTTTCG CTTGGACGCT TATGCGCTCA TTGTGATTAG CCTAGTCTTT     420
ATCGCATGCT ATTTAATAGG CTATGCTTAT TTGAATAGGC AAGTTTGCGC TTTAGAAAAG     480
CGGGCGTTT                                                             489
```

(2) INFORMATION FOR SEQ ID NO:1273:

(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:1273

```
ATGAATAAAA CCATAAAAGC CGCCGCCCTA GCCTATAACA TGGGGCAAGA TCATGCCCCA      60
AAAGTGATCG CAAGCGGGGT GGGCGAAGTG GCTAAAAGGA TCATTCAAAA AGCTAAGGAA     120
TACGATATAG CGCTCTTTTC TAACCCCATG CTGGTGGATT CGCTCTTAAA GGTGGAATTA     180
GACTGCGCGA TACCTGAAGA ATTGTATGAA AGCGTGGTGC AAGTGTTTTT ATGGCTCAAC     240
AGCGTGGAAA ATAACGCGCA AATGTCCAAG                                      270
```

(2) INFORMATION FOR SEQ ID NO:1274:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274

```
GTCAAAAAGT CAAATAACAT GGTAGTAGAA TTAAAAAACA TTGAAAAGAT TTATGAAAAC      60
GGGTTTCATG CTCTAAAAGG CGTGAATTTG GAATTGAAAA AAGGCGATAT TTTGGGCGTG     120
ATAGGCTATT CAGGGGCGGG GAAATCCACG CTCATTCGCT TGATCAATTG TTTAGAGCGC     180
CCCAGTTCTG GCGAAGTTTT AGTCAATGGG GTCAATCTGT TAAACTTAAA GCCTAAAGAA     240
```

```
TTGCAAAAAG CGCGCCAAAA AATAGGCATG ATTTTCCAGC ATTTCAATTT ATTGAGCGCT     300
AAAAACGTGT TTGAAAACGT CGCTTTCGCT CTAGAAATCG CCCGATGGGA AAAAACTAAG     360
ATTAAATCAA GGGTGCATGA ATTGTTGGAA TTAGTGGGGT TAGAAGATAA AGTGCATTTT     420
TATCCTAAAC AGCTCAGCGG CGGGCAAAAA CAACGAGTGG CGATCGCTAG GAGTTTAGCG     480
AATTGCCCTA ATTTGTTGCT TTGCGATGAA GCCACATCCG CTTTGGATTC TAAAACCACG     540
CATTCTATTT TAACGCTTCT AAGCGGCATT CAAAAAAAGT TTGATTTGAG CATCGTTTTC     600
ATCACACACC AGATTGAAGT GGTTAAAGAA TTGTGCAATC AAATGTGTGT GATCAGCAGC     660
GGCGAAATCG TAGAAAGAGG CTCGGTGGAA GAAATTTTTG CTAACCCTAA ACATGCTGTT     720
ACTAAAGAAT TGCTTGGCAT CAAAAACGAA CATGCGGATC AAAAATCGCA AGACATTTAT     780
CGCATCGTGT TTTTAGGGGA GCATTTAGAC GAGCCGATCA TTTCTAATTT GATCAGGCGT     840
TTTAAAATAA GACGT                                                     855
```

(2) INFORMATION FOR SEQ ID NO:1275:

(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:1275

```
TTATTTTGCT CCTGCCTTTA TCAGCGCTTT TTGATTGGCA CAAGCATTGG ATCTAGCGCG      60
AGCATTATCC CGTTAGCCAT TTCGGCCATT CCTTTTGTTG TAAAGCTTTT TGAAAATTCT     120
TTAATGGAAG TAGAGCATGG CAAGATTGAA ACCACTTTAA GCTTGGGGGC GTCTCATTTG     180
GAAGTCATTA AAATGATGCT TTTAGAGAGC CTGCCTTCTT TAGTGAATAA TATCACCATC     240
ACTTTAATTT CTCTAATAGG CTATTCGGCT ATGGCTGGAG CGTTAGGGGC TGGGGGATTG     300
GGGGATTTAG CCATTAGGAT TGGCTATCAA AGTTATAGGG GCGATGTGCT TTTTTATGCG     360
GTGGTCGTGA TCATCGTTTT AGTGCAAATC ATTCAAAGCG CGGGGGATTA TGTGGTGAAA     420
CGCTTGAGAA AGAATAAGTA T                                               441
```

(2) INFORMATION FOR SEQ ID NO:1276:

(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

This Sheet Has Been Replaced



(B) LOCATION 1...837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276

```
TCTTATTTTT GTTATAATCT TAGGTTGTTA AGTTTAGTTA AAGGGAAAAC CATGCTCCGC      60
TCTCTCTATA GTGCCACTTC AGGGATGCTC GCCCAACAAA CGCACATTGA CACCACTTCA     120
AACAACATCG CCAATGTCAA TACCACCGGG TTTAAAAAAT CTCGCGCGGA TTTTAACGAC     180
TTGTTTTACC AAGCGATGCA ATACGCCGGC ACCAACACAA GCAACACGAC TTTATCGCCA     240
GATGGCATGG AAGTGGGCCT TGGCGTACGC CCTAGTGCGA TTACCAAAAT GTTTTCGCAA     300
GGCAGCCCTA AAGAAACGGA GAATAATTTA GATATTGCTA TTACAGGTAA AGGCTTTTTT     360
CAAGTCCAGC TTCCTGATGG CACTACCGCT TACACAAGGA GCGGGAATTT CAAGCTAGAC     420
GAGCAGGGCA ATCTTGTAAC AAGCGAGGGC TATCTCCTCA TCCCTCAAAT CACTTTACCC     480
GAAGACACCA CGCAAGTGAA TATCGGTGTG GATGGCACGG TGAGCGTGAC TCAAGGCTTG     540
CAAACGACTT CTAACGTGAT CGGGCAAATC ACTTTGGCTA ATTTTGTCAA TCCGGCGGGG     600
CTTCATTCTA TGGGGGATAA TTTGTTTTCC ATCACCAACG CTAGCGGCGA TGCGATTGTG     660
GGCAACCCGG ATTCTCAAGG CTTAGGCAAG TTAAGGCAAG GCTTTTTGGA GCTTAGTAAC     720
GTGAGATTGG TAGAAGAAAT GACAGATCTA ATCACCGCTC AAAGGGCTTA TGAAGCCAAT     780
TCTAAAAGCA TTCAAACCGC TGATGCCATG CTCCAAACAG TCAATTCCCT CAAACGC        837
```

(2) INFORMATION FOR SEQ ID NO:1277:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 948 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277

```
AAATGGCGCA ACTCATCAAG CGATAAAATG GCTAAAAAGA AAATTGCGAT CAGCTGTGGG      60
GATATTCAAG GCGTAGGCTT AGAATTGATC TTAAAAAGCC ATAAGGAAGT GAGTGCACTT     120
TGTGAGCCGT TGTATCTCGT TCATAGCGAA CTTCTAGAAC GAGCCAATCA ATTGCTTGAT     180
AACGCTTATG AAACTAAAAC GCTTAATGCG ATCGCTATTG ATGCCCCTTT ACCCTTATTA     240
AACTCTAGCA CGATAGGCAA AGTCAGCACT CAAAGCGGGG CGTATAGCTT TGAGAGTTTT     300
AAAAAGGCTT GCGAGTTGGC GGATAGTAAA GAAGTGGATG GCATTTGCAC TTTGCCTATC     360
AACAAACTCG CATGGCAACA AGCTCAAATC CCTTTTGTGG GGCATACCGA TTTTTTGAAA     420
CAACGCTACA AAGATCATCA AATTATTATG ATGCTTGGGT GTTCAAAACT CTTTGTGGGG     480
CTATTTAGCG ACCATGTGCC TTTAAGCGCG GTTTCTCAAC TCATTCAAGT GAAAGCGTTA     540
GTTAAGTTTT TATTAGCGTT TCAAAAAAGC ACTCAAGCCA AAATCGTTCA AGTGTGTGGT     600
TTCAACCCCC ATGCGGGCGA AGAGGGATTG TTTGGGGAAG AAGATGAAAA GATTTTAAAA     660
GCCATTCAAG AGAGCAACCA AACGCTAGGT TTTGAATGCT TTTTGGGGCC ACTGCCCGCT     720
GATAGCGCTT TTGCCCCCAA TAAACGCAAA ATAACCCCCT TTTATGTGAG CATGAGCCAT     780
GATGTAGGGC TAGCCCCTTT AAAAGCGCTC TATTTTGATG AAAGCATCAA TGTGAGTTTG     840
AACGCTCCCA TTTTACGCGC TTCCACTGAC CACGGCACGG CGTTTGATAT TGCTTATCAA     900
AATAAGGCGA ACCATAAAAG CTATTTGAAC GCGATCAAAT ACTTGGCT                  948
```

(2) INFORMATION FOR SEQ ID NO:1278:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1062 base pairs

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

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278

```
CAAGGTATAA TTCAAGCAAA AACACCACCC AAAGATAAAG ACATGATTTT AAGCATTGAA      60
AGTTCTTGCG ATGACAGCTC TTTAGCCCTT ACAAGAATAG AGGACGCCAA GCTCATCGCT     120
CATTTTAAAA TCTCTCAAGA AAAGCACCAC AGCTCTTATG GGGGCGTTGT GCCTGAGATT     180
GCATCGCGCC TGCATGCTGA GAATTTGCCG CTTTTATTAG AACGCGTTAA AATAAGCTTG     240
AATAAGGATT TTTCCAAAAT TAAAGCCATC GCTATCACTA ATCAGCCAGG TTTGAGCGTT     300
ACTTTAATAG AGGGTTTGAT GATGGCAAAA GCCTTGAGCT TGTCTTTGAA TTTACCCTTG     360
ATTTTGGAAG ATCATTTGAG AGGGCATGTG TATTCGCTCT TTATCAATGA AAAACAAACC     420
CGCATGCCTT TAAGCGTGCT GCTAGTCTCT GGGGGGCATT CTTTAATTTT AGAGGCTAGA     480
GATTATGAAG ACATTAAAAT CGTTGCCACG AGTTTAGACG ATAGCTTTGG GGAGAGTTTT     540
GATAAGGTTT CAAAAATGCT TGATTTAGGC TATCCAGGAG GCCCCATAGT GGAAAAATTA     600
GCCCTTGATT ATGCACACCC AAACGAGCCT TTAATGTTCC CTATCCCTTT AAAAAACAGC     660
CCGAATTTGG CTTTTAGTTT TTCAGGTTTA AAAAATGCGG TGCGTTTGGA GGTTGAAAAA     720
AACGCCCATA ATTTGAACGA TGAGGTAAAA CAAAAGATTG GCTATCATTT TCAAAGCGCG     780
GCTATCGAGC ATTTAATCCA GCAGACTAAA CGCTATTTTA AAATCAAACG CCCTAAAATT     840
TTTGGCATTG TGGGGGGAGC GAGCCAAAAT CTAGCCTTAA GAAAGGCGTT TGAGGATTTG     900
TGTGCTGAGT TTGATTGCGA GCTTGTTTTA GCCCCTTTAG AATTTTGCAG CGACAATGCC     960
GCCATGATAG GGCGATCAAG CCTAGAAGCT TATCAAAAAA AGCGCTTTAT CCCTTTAGAA    1020
AAAGCCGATA TTTCGCCAAG AACGCTGTTA AAAAATTTTG AG                       1062
```

(2) INFORMATION FOR SEQ ID NO:1279:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 768 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1279

```
AGGAATAATA TGGCATACAA ATATGATAGA GACTTGGAAT TTTTAAAGCA ACTGGAATCT      60
AGTGATTTAT TGGATTTGTT CGAGGTGCTT GTTTTTGGTA AAGACGGCGA AAAAAGACAC     120
AATGAAAAAC TCACAAGCTC CATAGAATAC AAAAGGCATG GCGATGATTA CGCTAAATAC     180
```

GCAGAAAGAA TCGCTGAAGA GTTGCAATAC TATGGGAGCA ATAGTTTTGC GAGTTTCATT 240
AAAGGTGAAG GAGTCTTATA CAAAGAGATT TTATGCGATG TGTGCGATAA ATTAAAGGTC 300
AATTACAACA AGAAAACTGA AACGACTTTA ATTGAACAAA ACATGCTTTC TAAAATCTTA 360
GAAAGAAGCC TAGAAGAAAT GGATGATGAA GAAGTGAAAG AAATGTGCGA TGAATTGTCC 420
ATAAAAAACA CGGACAATTT GAACAGACAA GCCTTAAGCG CGGCGACTTT AACGCTGTTT 480
AAAATGGGAG GCTTTAAATC TTATCAATTA GCTGTCATTG TTGCGAATGC GGTTGCAAAA 540
ACCATTCTAG GGCGTGGTTT ATCGCTTGCG GGCAATCAAG TGCTTACAAG AACTCTGAGC 600
TTTTTAACAG GCCCTGTTGG CTGGATCATT ACAGGCGTAT GGACAGCGAT TGATATTGCA 660
GGGCCGGCTT ATAGGGTAAC CATACCGGCA TGCATTGTGG TCGCCACTTT ACGCCTAAAA 720
ACGCAACAAG CCAATGAAGA TAAGAAGTCG TTGCAAATAG AATCCGTT 768

(2) INFORMATION FOR SEQ ID NO:1280:

(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:1280

GTTATAATAT TTTTGCTATT GTTTTTTTTA GGAAATAAAG TTTTCAGTAT TTATTTGCTT 60
TTAGAGTCAT TTTTGTGGGT AATATTGACC ACTTGGTGTT GTTTGGTCAT GCATGAAGAT 120
CAGAGACAAA AAGACATGGA ACAACTTATC AATGGGATTG ATAGGATTAT TAAAGCAAAT 180
TCCGGTAAAT CTTTACACCA AGAAACACAA CAAGCAAATA AAACCGATAA AGCATGGGAT 240
TTGGCGGCTA ATGTTTTTCT CATTGGTCTG GTTGTTTTGG CTGTTTTTCA CATGATCAAG 300
CGA 303

(2) INFORMATION FOR SEQ ID NO:1281:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281

GCGGTGAAAA AAGTAGAATC CATGAATGTG GTGCCTTTCA TTGACATCAT GCTTGTGTTG 60
TTAGTGATCG TGCTCACAAC GGCGTCTTTT GTGCAAACTT CAAAGCTTCC TATTAGCATT 120
CCTCAAGTGG ATAAGGATAG CACTGATTCT AAAGATGTGT TGGACAAAAA ACAAGTTACG 180
ATCGCTATTT CTAATAAGGG TTCTTTTTAT TTTGACGATA AAGAAATCAG CTTTGAAAAT 240
TTAAAACACA AGGTTTCCAC TTTGGCTAAA GACACCCCTA TTGTCTTGCA AGGCGATAAG 300
AAAAGCAATT TGGACAACTT TATCAAAGTG GTGGATTTAT TGCAACTAAC AATC 354

(2) INFORMATION FOR SEQ ID NO:1282:

(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

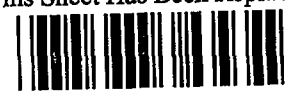
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282

CTACACAGAC AGGCGCAAGT TAGAATTAGC CTTACACAAA CGACGACTTT AGTGGCCACT 60
ATTGGCTCAA ACGCCCCTTA TATCGGTCTT TTAGGGACGG TTATGGGGAT CATGCTCACC 120
TTTATGGATT TAGGCTCAGC TTCTGGCATT GACACTAAGG CGATCATGAC TAATTTAGCC 180
CTTGCTTTAA AAGCGACCGG CATGGGGTTA TTGGTAGCGA TCCCTGCGAT TGTGATTTAT 240
AACTTGTTAG TGAGAAAAAG CGAGATTTTA GTTACCAAAT GGGATATTTT CCACCATCCG 300
GTTGATACGC AATCCCATGA GGTTTATAGC AAAGCC 336

(2) INFORMATION FOR SEQ ID NO:1283:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 417 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1283

AACCATAAGA TTAGGGGTTA TGAAAAACGC ATGGCATTAG ACAAAAGGAT TTGGATGCAT 60
TTTGATCTTT TGCCTTTTGT GTTTATCATC CCCTTGTTGG TGGTTTCTTT TTTGTTGATT 120

```
TTTGAGAGTA GTGCGGTTTT GAGCTTGAAG CAAGGGGTTT ATTATGCCAT AGGGTTTCTT     180
CTCTTTTGGG TAGTGTTTTT TATCCCTTTC AGGAAACTCG ATCGGTGGCT CTTTGCGCTT     240
TATTGGGCGT GCGTTATTTT ATTAGCGTTA GTGGATTTTA TGGGATCGAG CAAGCTTGGA     300
GCGCAGCGAT GGCTAGTCAT TCCTTTCACT TCTATCACCT TACAGCCTAG CGAGCCTGTG     360
AAAATCGCTA TTCTTTTATT GTTGGCGCGA TTTGATCAAA ATCAACCCAC CTCCTTT        417
```

(2) INFORMATION FOR SEQ ID NO:1284:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 930 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...930

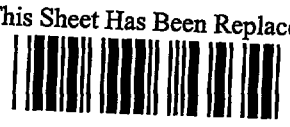
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284

```
TTTTGTGGGA CACTAAAGGC ATTGAAGATA AAGATTACCA CGACACCATG CAAAGCATTA      60
AAAAAGAAAT GGAAGATTCT TTTAAAACAC TTGATGAAAA AGAAGCCATT GATGTGGCGT     120
ATCTGTGCGT TAAGGAGACT TCTTCTAGGG TTCAAGAGAG AGAGAGAGTT ATTAAGCTTC     180
GCTAAACATT GGAATATCCC AACGATTGTC GTTTTCACAC ACACTCAAGC CGAAGCCGGC     240
GATGCGTTTG TCCAAGAAAC TAAAGGGATC ATAGACGAAG AATGGGGGTT TAAAGGTTTT     300
GTCAGAGCCT ATGTGAGGGT CAATTCCGTT GCCTTTTCAT TTAGGGGGTT GAAAGTCCCT     360
GTTGAAGGTT TAGAAGAATT GGTAGATGAA ACGAAAAAAT GCCTTTCAGA CGCTGAAAAA     420
AATAAGAAAA GGCATTTCTT GAGTATTCAA AGAGTTAAGA TTCAAGAAAG AAAACAGGCT     480
ATGATAGAGG AATGTAAAAC CATTATCCAT GTTGCATCAG GCGCTGCAGG AGTTGCTGGG     540
CTTATCCCCA TACCTTTTAG CGATGCGCTC GCTATCGCAC CCATTCAAGC AGGGATGATC     600
TATAAAATGA ATGACGCTTT TGGAATGGAT TTGGATAAAT CTGTGGGCGC GAGTTTGGTC     660
GCAGGATTGT TAGGCGTAAC CGCTGTCGCG CAAGTGGGGA GGACTCTCGT TAATGGTTTC     720
CTTAAATTCA TTCCTGTTGT GGGGAGTGTT GCAGGGGGCG CAACCGCTGC TGTTATCACA     780
GAAGGCATTG GGTTTGCGTA TTTGAAAGTG CTAGAAAAGT GCTTTAATGA TGAGACGGGT     840
GAAGTCAATT TGCCTGGTGA AGTTGGCATG ATCACTTCTC TCTTTAAGGA GAATTATCTC     900
AACTTGGATA CAATCAAAAA ATTAAAACCA                                      930
```

(2) INFORMATION FOR SEQ ID NO:1285:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1285

```
ATGAGGTCTT GGATGAAGAA AAAATACTTC ACGCTTTTAT TGCAAAGTAG TGTGGTATTA      60
GCGGTTTTTA TAGGGTGTTC TTCTACCAGG AATCATACTT TTTCAGCCCT TAGTAATCAA     120
GAAAATACAG ACGATAAGCT CCCAGTGGTC CATTCCATTA AAACGATTAA CGATGTGAGT     180
TCAGTGGGCT TTGAATGGTC TAAAGTCGCT GACACTTATG ACATTGACGG GTTTGTTTTG     240
TATCGTTTGA AAAAAGACTC CAAGCTTAAA AGAATCGCCA CCATTAAAAA CCCTTATGCG     300
ACCCACTATT ATGATGAGGG GTTAGAAACA GAGAGTTCCT ACACTTACCA ATTAGCCACC     360
TACAAGGGCG ATAAAATTTC CAAACTTTCA GAACCCATTT TAGTAAAAAC CTCCTTTATC     420
AATCCTGTAG AAAGCGTGTT TGCAAGCCTT GAATACCCTA AAAGCGTGAA AGTCTTTTGG     480
AGCCCGCACC CAAATCCCAG CGTTTCTAAA TACATCATTC AAAGGCAGAA TAAAGACGGC     540
AAATTTTTAA ATGTGGGGGC TGTAAAAAAC CGCTTATTCG TGGAGTTTTT TGATAAAGAT     600
TTAGAAGATG GGCAAAAATA CCGCTACCAA ATCATCGCCG AAAATTTCAT GGGGGATAAA     660
TCCAGGCCTA GCGTGATAGT GGAGGGGAAA ACCAAAGACT TGCCCAAAGA AATCGCTAAT     720
GTTAGAGTGA GTCAAAACCT CACACGACAA ATTGAATTGA GTTGGGATAA ATCCCCAGAA     780
GAAGATGTGA TAGCTTATCG CATTTACGCT TCCAATAACC GCAACGATAA ATACAAATTC     840
ATCGCTCAAA CCACCAACAC TTCCTATGTG GATAAGATAG AAAAAGACAA TCTCACTCGT     900
TATTATAAAG TCGTCGCCGT AGATAAAACG CATCTTGAAG GGGCGTTACC CAAAGAGCCT     960
GCCATGGGTG AAACCTCTGA TAGGCCTGAA GCCCCTATCA TCACTAAAGG GACTATTCAA    1020
GACTCTTCGG CCTTGATCCA ATGGGAAAAC AACCCAAGCC CTAAAATAGC CACTTATGCG    1080
GTGTATCGTT TTGAAGCCAA CTCCAAAACC CCTTTGCGTT TTGGGAATAT CACACAAAAC    1140
CAGTTCGTGG ATAAGGACAT GAAAGTGGGC GTGGCTTATC GCTATCAGGT GGTGAGCGTG    1200
GATAAAGATG GTTTAGAGTC GCACCCAAGC AAAGAAGTGC GTTTGTTTTT AGAGCGC       1257
```

(2) INFORMATION FOR SEQ ID NO:1286:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286

```
CTTAAAAACA CTCTAAAAGG GTTATTGATG CTGGATTTTG ATTTGGTTCT TTTTGGCGCG      60
ACTGGGGATT TAGCCATGCG AAAGCTCTTT GTTTCGCTTT ATGAAATTTA TATTCATTAT     120
GGTTTTTAAAA ACGATTCTAG GATTATCGCA TCGGGGCGTA AGGAGCTATC CAATGAAGAG     180
TTTTTAGCGC TTCTTTGTGA AAAAACACAA CTGCATTCAA GAGAAAAGGG TGAGGAATTT     240
TTAACCCATA TCAGTTATTT GCGCGTCCGT TTGGATAACC CTAAAGACTT TGAAGAATTG     300
AGTAAAATCG CCACAAACAA TAAGCCCTTG ATTTTCTACT TTTCTATCTC CCCTAGTTTT     360
TTTGCAACGA CCGCTCAAAA TTTAGCCCAA AACGCGCTCA ATCACGCTAA CACTCGTTTG     420
ATTCTAGAAA AGCCTTTAGG GCATGATTTA AAGACTTGTA AAGAGATTTT CCAAAGCATT     480
AGCGCTTTTT TTAAAGAAGA ACAAATTTTT AGAATCGATC ATTATTTAGG GAAAAAGGGC     540
GTTCAAAATA TCCTTGAATT GCGCCTGAAT AACCCTATCT TAAACATTTT ATGGGATCAA     600
ATCAGCGCGG TTGAAATCTG CGTGTATGAG ACTTTAGGGG TGGAAGAAAG GGGCGAATTT     660
TACGATAAAA TCGGGGCTTT AAGGGATATG GTTCAAAACC ATCTCTTGCA AGTTTTATCC     720
CTTATCGCTA CAGATTTACC CAACGATTTA AAAGATTTGA GGCAAGAAAA ATCAAAGTTT     780
```

(2) INFORMATION FOR SEQ ID NO:1287:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1038 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287

```
GGCATGGTTA AACACTATCT TTTCATGGCG GTTTCGCAGG TCTTTTTCTC CTTCTTTTTA      60
GTGCTGTTTT TTATCTCTTC CATTGTGTTA TTAATCAGTA TTGCAAGCGT AACGCTCGTG     120
ATTAAAGTGA GCTTTTTGGA TCTGGTGCAA CTCTTTTTGT ATTCCTTGCC AGGAACCACT     180
TTTTTTATTT TGCCGATCAC TTTTTTTGCG GCTTGCGCTT TGGGGCTTTC AAGGCTTAGC     240
TATGACCATG AATTGTTAGT GTTTTTCTCT TTAGGGGTTT CGCCTAAAAA AATGACTAAA     300
GCGTTTGTGC CTTTAAGTTT GTTAGTGAGC GCGATTTTAT TAGCGTTTTC GCTCATCTTA     360
ATCCCCACTT CTAAGAGCGC TTATTACGGG TTTTTGCGTC AAAAAAAAGA CAAGATTGAC     420
ATTAACATCA GAGCGGGTGA ATTCGGGCAA AAATTAGGCG ATTGGCTCGT GTATGTGGAT     480
AAGACTGAAA ACAATTCCTA TGATAATTTG GTGCTTTTTT CTAATAAAAG TCTCTCTCAA     540
GAAAGCTTTA TTTTGGCTCA AAAAGGCAAT ATCAACAATC AAAACGGCGT GTTTGAATTG     600
AATTTGTATA ACGGGCATGC GTATTTCACT CAAGGCGATA AAATGCGTAA GGTTGATTTT     660
GAAGAATTGC ATTTGCGCAA CAAGCTCAAG TCTTTCAATT CTAATGATGC GGCTTATTTG     720
CAAGGCACGG ATTATTTGGG TTATTGGAAA AAAGCCTTTG GTAAAAACGC TAATAAAAAT     780
CAAAAACGCC GTTTTTCTCA AGCGATCTTA GTTTCCTTGT TCCCTTTAGC GAGCGTGTTT     840
TTAATCCCCT TATTTGGCAT CGCCAACCCG CGATTCAAAA CGAATTGGAG TTATTTCCAT     900
GTCCTTGGAG CGGTTGGGGT TTATTTTTTA ATGGTGCATG TGATTTCTAC GGATTTGTTT     960
TTGATGACCT TTTTCTTCCC CTTTATTTGG GCGTTTATTT CTTATTTATT GTTTAGAAAA    1020
TTCATTTTAA AGCGTTAT                                                  1038
```

(2) INFORMATION FOR SEQ ID NO:1288:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1845 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1288

```
ATCTTAATTG AAGGGGTGTT CATGCCTAAG CATTCTTTAG AACAAATCAA AGAAAAAATT      60
ACAGAGCGTA GCAAAAAAAC CAGAGAGCTT TATTTAGAAA ATACCTTCAA CCCTAAAAAC     120
CAGCCCAAGA TTGAGAGCTT GGGTTGCGCG AATATTGCGC ATGTTACGGC GAGCATGCCA     180
GAGCATTTAA AAATGCCTTT AGGTTCGCAT AAAAGAAAGC ATTTTGCGAT TATCACCGCT     240
TATAATGACA TGCTTTCAGC CCACCAACCT TTTAAAAATT ACCCTGATCT GATTAAAAAA     300
GAGTTGCAAG AGCATAACGC CTATGCGAGC GTCGCTAGTG GGGTGCCAGC GATGTGTGAT     360
GGTATCACGC AAGGTTATGA GGGAATGGAA TTGAGCTTGT TTAGTAGAGA TGTGATCGCA     420
TTAAGCACCG CCGTAGGGTT AAGCCATAAT GTTTTTGACG GGGCGTTTTT TTTGGGCGTG     480
TGCGATAAAA TTGTGCCAGG CTTGCTCATA GGAGCGTTAA GCTTTGGGAA TTTAGCGAGC     540
GTGTTTGTGC CAAGCGGGCC TATGGTGAGC GGGATAGAAA ATTATAAAAA AGCCAAAGCG     600
CGCCAAGATT TTGCAATGGG AAAGATCAAC AGAGAAGAGC TTTTAAAAGT GGAAATGCAA     660
AGCTATCATG ATGTGGGCAC TTGCACTTTT TATGGCACGG CTAATTCTAA TCAAATGATG     720
ATGGAGTTTA TGGGGTTGCA TGTGGCCAAT TCTAGCTTTA TCAACCCTAA CAACCCCTTA     780
CGAAAGGTTT TAGTAGAAGA GAGCGCTAAA AGATTAGCGA GCGGGAAAGT CCTGCCTTTA     840
GCCAAACTCA TTGATGAAAA AAGCATTCTT AACGCTCTTA TAGGCTTAAT GGCAACAGGG     900
GGTTCTACTA ACCACACTTT GCATTTGATC GCTATCGCTA GATCTTGTGG GGTGATCCTC     960
AATTGGGACG ATTTTGACGC AATCTCTAAT CTCATACCCC TTTTAGCTAA AGTCTATCCT    1020
AACGGATCAG CGGATGTGAA CGCTTTTGAA GCGTGTGGGG GCTTAGCGTT TGTGATCAAA    1080
GAATTGCTAA AAGAGGGGCT TTTATTTGAA GACACTCATA CCATTATGGA TACAGAAACG    1140
CAAAAAGGCA TGCAAAATTA CACCAAAACC CCCTTTTTAG AAAACGACCA ATTGGTGTAT    1200
AAAGACGCTG TTAGTCATAG CCTGAATACG GATATTTTAC GCCCTGTTAG TGAGCCTTTT    1260
GCCGCTAATG GAGGGCTTAA AATCTTAAAA GGTAATTTGG GGCGGGCCGT GATTAAAATC    1320
TCAGCCATTA AAGATGAGCA TAGGAAAGTT AAAGCTAGAG CGATTGTTTT TAAAACCCAA    1380
AGCGAATTTT TAGAACGCTT TAAAAATAAA GAATTAGAAA GGGACTTTGT GGCGGTCTTG    1440
CCTTTCCAAG GGCCTAAGTC TAACGGCATG CCAGAATTGC ACAAACTCAC CACGAATTTA    1500
GGGGCTTTGC AGGATATGGG CTACAAGGTC GCGCTCGTTA CGGATGGGCG CATGAGTGGG    1560
GCGAGCGGGA AAGTGCCTAG CGCGATCCAT TTAAGCCCTG AGGGGGCGTT AAACGGGGCG    1620
ATCATTAAGA TTAAAGATGG CGATTTGATA GAATTAGACG CTCCTAATAA CGCCTTGAAT    1680
GTGCTTGAAA AGGATTTTGA AAAGAGAGGC ATCAACCCCT TGTTTTTAGA AACCTTAGAA    1740
AATTTAGAAA AGCCTACTTT TGGGTTGGGT AGGGAATTAT TTACAAGCTT GAGATTGAAT    1800
GCCAATACCG CTGAAGAGGG TGGCATGAGT TTTGGCATAA AGGTA                    1845
```

(2) INFORMATION FOR SEQ ID NO:1289:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 642 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1289

```
AAATATAAAG GAGATAAAAT GCAAGATAAA ATAATAGAAA TTTTACAAAT CAGCCCCATT      60
GTCCCTGTGG TGGTGGTTGA GAATATAAAA GACGCTGTGC CTTTAGCGCA AAGCCTGATA     120
GAGGGGGGTA TTCCAATCAT AGAAGTAACT TTGCGATCAA ACTGTGCTTT AGAGGCCATA     180
GAGCTTATCG CTAAGAATGT GCCAAAAATG CGCGTGGGTG CTGGCACGAT ACTCAATCTC     240
ACTCAATTAG AGCAGGCTCA AAATAGGGGG GCAGAGTTTT TGATTAGCCC GGGTCTTACG     300
ATAAAGCTTT TAGAACACGC AAAGAAAAAA GACATGCCTT TAATACCTGG GGTTTCTAGC     360
```

```
AGCAGTGAAG TCATGCAAGC TTTAGAATTG GGTTATAACG CTTTGAAATT TTTCCCGGCG     420
GAGTATTGCG GGGGCGTTAA ACTTTTAAAC GCTTTTAACG GCCCTTTTAA AGGGGTGAAA     480
TTTTGCCCCA CTGGGGGGAT TAGCGCAGAT AACATGCGTT CTTATTTGGC TTTAGAAAAC     540
GTTGTGTGCG TGGGGGGGAG CTGGCTTACC CCTAAAGATT TAATTCAAAA CAAAGAGTGG     600
GATAAGATCA CAGAAATTTG CAAGAGAGCG TTAGCTTTAA GA                        642
```

(2) INFORMATION FOR SEQ ID NO:1290:

(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:1290

```
AATACCGCTA TTGTATCGTT TTTATGGTTT GCTTATGTTT CTATAGGTTT AACTAATTTT      60
GTAGCTGTTG GTTATATGGT ATCGTTGCTT GGCGCGCTTA AACGCACCCC TTGCACTAAT     120
CGCTTTTATC TTAAAGCACT ACTATTTGCT ATATTCTATC ATGCAGTAAA TAATTTTCTA     180
ACGCAATGCC CGCCCCATCA AGTCCGGGAG TTTTTTTCAT CACGACATGC ACAGGGATGG     240
AAGCGAGAAA CGCTCCCATG CGCCCTTTCG TTTCAAAACG CGCTC                     285
```

(2) INFORMATION FOR SEQ ID NO:1291:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1080 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291

```
AAGAAAACGC CCCCTATTCT CTGCCGATTG CTCGGATTTT ACATTCTAAA AAAGTTACCA      60
CAGAGGTGTT TTATGCCAAA AACTGAAACT TACCCAAGAC TATTAGCCGA TATTGGCGGC     120
ACAAATGCGC GTTTTGGTTT GGAAGTCGCC CCACGACAGA TTGAATGCGT TGAAGTCTTC     180
AGGTGCGAAG ATTTTGAGAG CTTGAGTGAT GCGGTGCGAT TTTACCTTTC TAAATGCAAA     240
GAAAGCCTTA AACTGCACCC TATTTATGGC TCTTTTGCTG TGGCTACGCC CATTATGGGC     300
```

This Sheet Has Been Replaced



```
GATTTTGTCC AAATGACGAA CAACCACTGG ACTTTTTCTA TTGAAACGAC ACGGCAATGT     360
TTGAATTTAA AAAAACTGCT TGTCATCAAT GATTTTGTCG CGCAAGCCTA TGCCATTAGC     420
GCGATGCAAG AAAACGATCT AGCCCAAATA GGCGGGATTA AGTGTGAAAT CAACGCTCCT     480
AAAGCGATTT TAGGGCCAGG AACCGGGCTT GGGGTAAGCA CTCTTATCCA AAACAGCGAT     540
GGCTCTTTGA AAGTCTTGCC CGACGAAGGT GGGCATGTGA GCTTTGCCCC TTTTGATGAT     600
TTAGAAATTT TAGTGTGGCA ATACGCCCGC TCTAAATTCA ACCATGTGAG CGCGGAAAGG     660
TTTTTGAGCG GTAGCGGCCT GGTGTTGATT TATGAAGCCC TGTCTAAACG CAAAGGCTTA     720
GAAAAAGTGG CGAAGTTGAG CAAGGCTGAA TTAACCCCAC AAATCATTAG CGAACGCGCT     780
TTGAATGGGG ATTACCCTAT ATGCCGATTG ACCTTGGACA CTTTTTGCTC CATGCTTGGC     840
ACGCTCGCTG CTGATGTGGC TCTCACTTTG GGGGCTAGAG GGGGGGTGTA TTTGTGTGGG     900
GGGATTATCC CACGATTCAT TGATTATTTT AAAACTTCGC CCTTTAGAGC GCGTTTTGAA     960
ACGAAAGGGC GCATGGGAGC GTTTCTCGCT TCCATCCCTG TGCATGTCGT GATGAAAAAA    1020
ACTCCCGGAC TTGATGGGGC GGGCATTGCG TTAGAAAATT ATTTACTGCA TGATAGAATA    1080
```

(2) INFORMATION FOR SEQ ID NO:1292:

(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:1292

```
TCCCAGGGAC TGATTTTTGA TAAAAAGAAA CAAAAATTTC TAAAAGATTT TAAAGCAGGA      60
GAATTATTGT ATCAATCCCA TTTCAAACCA TTAGTAGAAT TTATAGCCGA AGAGCTTCTT     120
AAAAACTCGC GCGCCAAAAT CATTCAATCA AACTGCAATA AAGCCTTAAA AGTGGTAGAA     180
GAATTACAAA ATACGATAAA AACCACGATT GAAAAACAGA TCAATCCAGG GATGAAAGAA     240
ACACAAGACC CCCAACAAGA AGCTCGCTTT AATTTGGATC GTTCTACAGA TAAATTTATA     300
TCAGATTTGG AAAAATCAGC GTTCAGCAAA ATCAATCAAT TCGAATTTAA TTTTAGAAAA     360
GAAATGCATG AACGCATTGA AAGAGGTATT GGAAATAATG AATGTAAAGA AATTTTTGGC     420
AATGAACTCA AACAAAGAAA GACAAAATTG ATTGAAGACA TAGAACGGCG GTTCAAAGAA     480
TGCGAGGAAC AATTCCGTGG AAGTGTAGGA AAAAATATTG AACAACTTGA AGAAAGAGTT     540
AAAGATTCTC TAGCGATTAT AAAACGCATC AATAACCTTG GTCTTAATCC TAATTCTAAT     600
TTTAATATGG ATAGCGGCAT TGATACAATA GGCTTATTTA GTTCAATAGG AGGTTTGGTG     660
TTGCTTCTAT TGACGCCTGT AGTAGGTGAG TTTGCGTTAA TTGCAGGAGT GGGTTTAGCA     720
TTAGTGGGGG TAGGTAAATC AATATGGAGT TTTTTTGATT CAGATTATAA AAAATCCCAA     780
CAAAGAAAAG AAGTGGATAA GAATTTACAT CAAATTTGCG AAAAAATTGT GCAGGATGTG     840
AAAAGCCGCA TTGAAAGTTA TAAAAATGGT GCATTGGGAA TGATTGAAGA ACTCAACGCC     900
GGTTTTAACA AACTTGTTGA TCATTACGAA CGCATGAAAA GACAATTGGA AGAAGCCCAT     960
GAAAAACTAG GATACATCTA TAATAGTATC CATCTTACAA TATCTAACCG CCGCATACAA    1020
```

(2) INFORMATION FOR SEQ ID NO:1293:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 657 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1293

```
AGTGCCTTAT GGCACAAAGA CCCCACCACG ATCAAGCAAT TTGGCTTAGA GGCTTTGGAT      60
TTTTTCAAAC CGCATGAGAT TGAATTATTG ATTGTGGCAT GCAACACCGC GAGCGCTCTG     120
GCTTTAGAAG AGATGCAAAA GTATTCTAAA ATCCCTATTG TGGGCGTGAT TGAGCCAAGC     180
ATTTTAGCGA TCAAGCGGCA AGTGGAAGAT AAAAACGCCC CTATTTTAGT GCTAGGGACA     240
AAAGCGACGA TTCAATCCAA CGCCTATGAC AACGCCCTGA AACAACAAGG CTATTTGAAC     300
ATTTCGCATT TAGCTACTTC TCTTTTTGTG CCTTTGATTG AAGAAAGTAT TTTAGAGGGC     360
GAATTGTTAG AAACTTGCAT GCATTATTAT TTCACTCCCT TAGAGATTTT ACCCGAAGTG     420
ATCATTTTAG GTTGCACGCA TTTTCCCTTA ATCGCTCAAA AAATTGAGGG CTATTTCATG     480
GGGCATTTTG CCCTTCCAAC GCCCCCCCTA CTCATCCATT CGGGCGATGC TATTGTAGAA     540
TATTTGCAAC AAAAATACGC CCTTAAAAAC AATGCATGCA CATTCCCTAA AGTGGAATTT     600
CATGCGAGCG GCGATGTGAT CTGGCTAGAA AGACAAGCTA AAGAATGGCT CAAATTG        657
```

(2) INFORMATION FOR SEQ ID NO:1294:

(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:1294

```
GGTATTAAAC TAGGGGGTAT TAACATGGCA GGCACACAAG CTATATATGA ATCATCTTCT      60
GCAGGATTCT TATCGCAAGT CTCCTCAATC ATCTCAAGCA CAAGTGGTGT CGCAGGGCCA     120
TTTGCAGGAA TAGTAGCGGG CGCTATGACA GCAGCGATTA TTCCTATTGT TGTGGGATTT     180
ACTAATCCGC AAATGACCGC TATCATGACC CAATACAATC AAAGCATCGC TGAAGCTGTA     240
AGCGTGCCTA TGAAAGCCGC TAACCAACAA TACAGCCAAT TGTATCAAGG TTTTAACGAT     300
CAAAGCATGG CTGTGGGAAC AATATCT                                         327
```

(2) INFORMATION FOR SEQ ID NO:1295:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 366 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

This Sheet Has Been Replaced



(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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:1295

```
TTTCAATTTG AAAGGAAACG CATGAAATTT TTTACAAGAA TCACTGACAG CTACAAGAAA      60
GTTGTAGTAA CTTTAGGGCT AGTGGTAACA ACCAATCCTT TAATGGCGGT CACCAGTCCT     120
GCAACAGGCG TTACTGAGAC TAAAAGTTTG GTTATTCAGA TCATTTCTGT TCTAGCGATC     180
GTAGGTGGTT GCGCTTTAGG GGTCAAAGGC ATAGCAGATA TTTGGAAAAT CTCTGATGAC     240
ATCAAAAGAG GTCAGGCGAC TGTTTTTGCT TACGCGCAAC CCATAGCTAT GTTAGCGGTG     300
GCAGGTGGCA TTATCTATTT GAGCACTAAG TTTGGCTTCA ATATTGGCGA GAGTGGAGGA     360
GCTAGC                                                                366
```

(2) INFORMATION FOR SEQ ID NO:1296:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2973 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2973

This Sheet Has Been Replaced



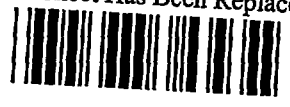
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296

```
AGCGGTATAT CTATAAAGAG AGGGGTGTTT GTGGCAAGCA AACAAGCTGA CGAACAAAAA      60
AAGCTAGTTA TAGAGCAAGA GGTTCAAAAG CGGCAGTTTC AAAAAATAGA AGAACTTAAA     120
GCAGACATGC AAAAGGGTGT CAATCCCTTT TTTAAAGTCT TGTTTGATGG GGGGAATAGG     180
TTGTTTGGTT TCCCTGAAAC TTTTATTTAT TCTTCTATAT TTATATTGTT TGTAACAATT     240
GTATTATCTG TTATTCTTTT TCAAGCCTAT GAACCTGTTT TGATTGTAGC GATTGTTATT     300
GTGCTTGTAG CTCTTGGATT CAAGAAAGAT TACAGGCTTT ATCAAAGAAT GGAGCGAGCG     360
ATGAAATTTA AAAAACCTTT TTTGTTTAAG GGCGTGAAAA ACAAAGCGTT CATGAGCATT     420
TTTTCCATGA AGCCTAGTAA AGAAATGGCT AATGACATCC ACTTAAATCC AAACAGAGAA     480
GACAGGCTTG TGAGCGCTGC AAACTCCTAT CTAGCGAATA ACTATGAATG TTTTTTAGAT     540
GATGGGGTGA TCCTTACTAA CAACTATTCT CTTTTAGGCA CAATCAAATT GGGGGGCATT     600
GATTTTTTAA CCACTTCCAA AAAAGATCTC ATAGAGTTAC ACGCTTCTAT TTATAGCGTT     660
TTTAGGAATT TTGTTACCCC TGAATTCAAA TTTTATTTTC ACACTGTTAA AAAGAAAATT     720
GTTATTGATG AAACCAATAG GGATTATGGT CTTATTTTTT CTAATGATTT CATGCGAGCG     780
TATAATGAGA AGCAAAAGAG AGAAAGTTTT TATGATATTA GTTTTTATCT CACCATAGAG     840
CAAGATTTAT TAGACACTCT CAATGAACCC GTTATGAATA AAAAGCATTT TGCAGACAAT     900
AATTTTGAAG AGTTTCAAAG GATTATTAGA GCCAAGCTTG AAAACTTCAA AGATAGGATA     960
```

```
GAGCTCATAG AAGAGCTACT GAGTAAATAC CACCCCACTA GATTAAAAGA ATACACTAAA    1020
GATGGCATTA TTTACTCCAA ACAATGCGAA TTTTACAATT TTCTTGTGGG AATGAATGAA    1080
GCCCCTTTTA TTTGCAACAG AAAAGACTTG TATCTCAAGG AAAAAATGCA TGGTGGGGTG    1140
AAAGAAGTTT ATTTTGCCAA TAAGCATGGA AAAATCTTAA ATGACGATTT GAGTGAAAAA    1200
TATTTTAGCG CTATTGAGAT CAGTGAATAC GCCCCTAAAT CACAGAGCGA TTTGTTTGAT    1260
AAAATCAACG CTCTAGACAG CGAATTTATC TTTATGCATG CTTATTCGCC TAAAAACTCA    1320
CAAGTTTTAA AGGACAAACT AGCTTTCACC TCTAGAAGGA TTATTATTAG TGGAGGCTCC    1380
AAAGAGCAAG GCATGACTTT GGGTTGCTTG AGCGAATTAG TGGGTAATGG TGATATTACG    1440
CTAGGCAGTT ATGGTAATTC TTTAGTGCTG TTTGCTGATA GCTTTGAAAA AATGAAACAA    1500
AGCGTTAAGG AATGCGTCTC TAGTCTTAAC GCTAAAGGTT TTTTAGCCAA CGCAGCGACT    1560
TTCTCTATGG AAAATTACTT TTTTGCCAAA CATTGCTCTT TTATCACGCT TCCTTTTATT    1620
TTTGATGTAA CTTCTAACAA TTTTGCTGAT TTCATAGCGA TGAGAGCGAT GAGTTTTGAT    1680
GGCAAAGAAG ACAATAACGC TTGGGGCAAT AGCGTGATGA CGTTAAAAAG CGAGATCAAT    1740
TCGCCTTTTT ATTTGAACTT CCACATGCCC ACTGATTTTG GTTCAGCTTC AGCAGGACAC    1800
ACTTTGATAC TTGGCTCAAC CGGTTCAGGT AAGACAGTGT TTATGTCCAT GACTCTAAAC    1860
GCTATGGGGC AATTTGCCTA TAATTTTCCT GCTAATATCA GCAAAGACAA GCAAAAGCTC    1920
ACTATGGTTT ATATGGATAA AGATTATGGC GCTTATGGGA ATATTGTTGC AATGGGTGGG    1980
GAGTATGTCA AGATTGAGCT AGGGACAGAT ACAGGATTAA ATCCTTTTGC TTGGGCAGCT    2040
TGTGTGCAAA AAACAAATGC AACAATGGAG CAAAAACAAA CAGCTATTTC TGTTGTCAAA    2100
GAGCTTGTGA AAAACTTAGC AACTAAAAGC GATGAAAAAG ATGAAAATGG CAACAGCATC    2160
TCTTTTAGCC TAGCAGATTC TAATACGCTT GCAGCGGCAG TAACCAACCT TATCACAGGA    2220
GATATGAACC TAGATTATCC TATCACTCAA CTTATTAATG CTTTCGGGAA AGACCACAAT    2280
GATCCTAATG GGCTTGTCGC GCGATTAGCG CCTTTTTGCA AATCAACCAA TGGTGAATTT    2340
CAATGGCTTT TTGACAATAA AGCAACAGAT CGCTTAGATT TTTCAAAAAC GATTATTGGC    2400
GTTGATGGGT CAAGTTTCTT AGACAATAAT GACGTTTCGC CTTTTATTTG TTTTTACCTT    2460
TTCGCTCGTA TCCAAGAAGC AATGGATGGG CGTAGATTTG TCTTAGATAT TGATGAAGCG    2520
TGGAAATATT TAGGCGATCC AAAGGTCGCT TATTTTGTGA GAGACATGCT AAAAACTGCA    2580
AGGAAAAGAA ACGCTATTGT TAGACTTGCG ACTCAAAGCA TCACTGATCT TTTGGCTTGC    2640
CCTATTGCTG ATACGATTAG AGAACAATGC CCTACAAAGA TTTTTTTGAG AAACGATGGG    2700
GGTAATCTTT CTGATTACCA AAGATTAGCC AATGTTACAG AAAAAGAATT TGAAATCATC    2760
ACTAAGGGGC TGGATAGGAA AATCCTCTAC AAACAGGATG GAAGCCCTAG CGTTATCGCT    2820
AGTTTTAATT TGAGAGGCAT TCCTAAAGAA TATTTGAAAA TTTTATCCAC AGATACTGTA    2880
TTTGTCAAAG AAATTGACAA GATTATCCAA AACCATAGTA TCATAGATAA ATATCAGGCC    2940
TTGAGGCAAA TGTATCAACA AATAAAGGAG TAT                                 2973
```

(2) INFORMATION FOR SEQ ID NO:1297:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3549 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...3549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297

```
TTTTTAGTAG CATTAATGAT ACCAAATTTA GATATAGAAG GAGAAACAAT GACTAACGAA      60
GCCATTAACC AACAACCACA AACCGAAGCG GCTTTTAACC CGCAGCAATT TATCAATAAT     120
CTTCAAGTGG CTTTTATTAA AGTTGATAAT GTTGTCGCTT CATTTGATCC TAATCAAAAA     180
CCAATCGTTG ATAAGAATGA TAGGGATAAT AGGCAAGCTT TTGAGAAAAT CTCGCAGCTA     240
AGGGAGGAAT TCGCTAATAA AGCGATCAAA AATCCTACCA AAAAGAATCA GTATTTTTCA     300
AGCTTTATCA GTAAGAGCAA TGATTTAATC GACAAAGACA ATCTCATTGA TACAGGTTCT     360
```

```
TCCATAAAGA GCTTTCAGAA ATTTGGGACT CAGCGTTACC AAATTTTTAT GAATTGGGTG     420
TCCCATCAAA ACGATCCGTC TAAAATCAAC ACCCAAAAAA TCCGAGGTTT TATGGAAAAT     480
ATCATACAAC CCCCTATCTC TGATGATAAA GAGAAAGCGG AGTTTTTGAG GTCTGCCAAA     540
CAAGCTTTTG CAGGAATTAT CATAGGAAAC CAAATCCGAT CGGATCAAAA ATTCATGGGC     600
GTGTTTGATG AATCTTTGAA AGAGAGGCAA GAAGCAGAAA AAAATGGAGA GCCTAATGGA     660
GATCCTACTG GTGGGGATTG GCTTGATATT TTTTTATCAT TTGTGTTTAA CAAAAAACAA     720
TCTTCCGATC TCAAAGAAAC GCTCAATCAA GAACCAGTTC CTCATGTCCA ACCAGATGTA     780
GCCACTACCA CCACTGACAT ACAAAGCTTA CCGCCTGAAG CTAGGGATTT GCTTGATGAA     840
AGGGGTAATT TTTCTAAATT CACTCTTGGC GATATGAACA TGTTAGATGT TGAGGGAGTC     900
GCTGACATTG ATCCTAATTA CAAGTTCAAC CAATTATTGA TCCACAATAA CGCTCTGTCT     960
TCTGTGTTAA TGGGGAGTCA TAATGGCATA GAACCTGAAA AAGTTTCATT GTTGTATGGA    1020
AACAATGGTG GTCCTGAAGC TAGGCATGAT TGGAACGCCA CCGTTGGTTA TAAAAACCAA    1080
CGAGGCGACA ATGTGGCTAC ACTCATTAAT GTGCATATGA AAAATGGCAG TGGGTTAGTC    1140
ATAGCAGGTG GTGAGAAAGG GATTAACAAC CCTAGTTTTT ATCTCTACAA AGAAGACCAA    1200
CTCACAGGCT CACAACGAGC ATTGAGTCAA GAAGAGATCC AAAACAAAGT GGATTTCATG    1260
GAATTTCTTG CACAAAATAA TGCTAAATTA GACAACTTGA GCAAGAAAGA GAAAGAAAAA    1320
TTCCAAAATG AGATTGAAGA TTTTCAAAAA GACTCTAAGG CTTATTTAGA CGCCCTAGGG    1380
AATGATCACA TTGCTTTTGT TTCTAAAAAA GACAAAAAAC ATTTAGCTTT AGTTGCTGAG    1440
TTTGGTAATG GGGAATTGAG CTACACTCTC AAAGATTATG GGAAAAAAGC AGATAAAGCT    1500
TTAGATAGGG AGGCAAAAAC CACTCTTCAA GGTAGCCTAA AACATGATGG CGTGATGTTT    1560
GTTGATTATT CTAATTTCAA ATACACCAAC GCCTCCAAGA GTCCTGATAA GGGTGTGGGT    1620
GCTACGAATG GCGTTTCCCA TTTAGAAGCA GGCTTTAGCA AGGTAGCTGT CTTTAATTTG    1680
CCTAATTTAA ATAATCTCGC TATCACTAGT GTCGTAAGGC AGGATTTAGA GGATAAACTA    1740
ATCGCTAAAG GATTGTCCCC ACAAGAAGCT AATAAGCTTG TCAAAGATTT TTTGAGCAGC    1800
AACAAAGAAT TGGTTGGAAA AGCTTTAAAC TTCAATAAAG CTGTAGCTGA AGCTAAAAAC    1860
ACAGGCAACT ATGACGAGGT GAAACAAGCT CAGAAAGATC TTGAAAAATC TCTAAAGAAA    1920
CGAGAGCGTT TGGAGAAAGA TGTAGCGAAA AATTTGGAGA GCAAAAGCGG CAACAAAAAT    1980
AAAATGGAAG CAAAATCTCA AGCTAACAGC CAAAAAGATG AGATTTTTGC GTTGATCAAT    2040
AAAGAGGCTA ATAGGGATGC AAGAGCAATC GCTTACGCTC AGAATCTTAA AGGCATCAAA    2100
AGGGAATTGT CTGATAAACT TGAAAATATC AACAAGGATT TGAAAGACTT TAGTAAATCT    2160
TTTGATGAAT TCAAAAATGG CAAAAATAAG GATTTCAGCA AGGCAGAAGA AACACTAAAA    2220
GCCCTTAAAG GCTCGGTGAA AGATTTAGGT ATCAATCCAG AATGGATTTC AAAAGTTGAA    2280
AACCTTAATG CAGCTTTGAA TGAATTCAAA AATGGCAAAA ATAAGGATTT CAGCAAGGTA    2340
ACGCAAGCAA AAAGCGACCT TGAAAATTCC ATTAAAGATG TGATCATCAA TCAAAAGATA    2400
ACGGATAAAG TTGATAATCT CAATCAAGCG GTATCAGTGG CTAAAGCAAC GGGTGATTTC    2460
AGTGGGGTAG AGCAAGCGTT AGCCGATCTC AAAAATTTCT CAAAGGAGCA ATTGGCTCAA    2520
CAAGCTCAAA AAAATGAAGA TTTCAATACT GGAAAAAATT CTGCACTATA CCAATCCGTT    2580
AAGAATGGTG TAAACGGAAC CCTAGTCGGT AATGGGTTAT CTAAAGCAGA AGCCACAACT    2640
CTTTCTAAAA ACTTTTCGGA CATCAAGAAA GAGTTGAATG CAAAACTTGG AAATTTCAAT    2700
AACAATAACA ATAATGGACT CGAAAACAGC ACAGAACCCA TTTATACTCA AGTTGCTAAA    2760
AAGGTAAAAG CAAAAATTGA CCGACTCGAT CAAATAGCAA GTGGTTTGGG TGATGTAGGG    2820
CAAGCAGCGA GCTTCCTTTT GAAAAGGCAT GATAAAGTTG ATGATCTCAG TAAGGTAGGG    2880
CTTTCAGCTA ACCATGAACC CATTTACGCT ACGATTGATG ATCTCGGCGG ACCTTTCCCT    2940
TTGAAAAGGC ATGATAAAGT TGATGATCTC AGTAAGGTAG GGCTTTCAAG GGAGCAAAAA    3000
TTGACTCAGA AAATTGACAA TCTCAACCAG GCGGTATCAG AAGCTAAAGC AAGTCATTTT    3060
GACAACCTAG ATCAAATGAT AGACAAGCTC AAAGATTCTA CAAAAAAGAA TGTTGTGAAT    3120
CTATATGTTG AAAGTGCAAA AAAAGTGCCT ACTAGTTTGT CAGCGAAATT GGACAATTAC    3180
GCTACTAACA GCCACACACG CATTAATAGC AATGTCAAAA ATGGAACAAT CAATGAAAAA    3240
GCGACCGGCA TGCTAACGCA AAAAAATTCT GAGTGGCTCA AGCTCGTGAA TGATAAGATA    3300
GTTGCGCATA ATGTGGGAAG TGCTCCTTTG TCAGCGTATG ATAAAATTGG ATTCAACCAA    3360
AAGAATATGA AAGATTATTC TGATTCGTTC AAGTTTTCCA CCAGGTTGAG CAATGCCGTA    3420
AAAGACATTA AGTCTGGCTT TGTGCAATTT TTAACCAATA TATTTTCTAT GGGATCTTAC    3480
AGCTTGATGA AAGCAAGTGT GGAACATGGA GTCAAAAATA CTAATACAAA AGGTGGTTTC    3540
CAAAAATCT                                                            3549
```

(2) INFORMATION FOR SEQ ID NO:1298:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 672 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298

```
GCACTAAGTT TGGCTTCAAT ATTGGCGAGA GTGGAGGAGC TAGCTAAATT GATCAACAAT      60
AATAATAACA ATAAAAAACT GAGAGGCTTT TTTTTGAAAG TTCTCTTAAG TCTCGTTGTT     120
TTCAGTTCGT ATGGGTCAGC AAATGACGAT AAAGAAGCCA AAAAAGAAGC GCTAGAAAAA     180
GAAAAAAACA CTCCCAATGG GCTTGTTTAT ACGAATTTAG ATTTTGATAG TTTTAAAGCG     240
ACTATCAAAA ATTTGAAAGA CAAGAAAGTA ACTTTCAAAG AAGTCAATCC CGATATTATC     300
AAAGATGAAG TTTTTGACTT CGTGATTGTC AATAGAGTCC TTAAAAAAAT AAAGGATTTG     360
AAGCATTACG ATCCAGTTAT TGAAAAAATC TTTGATGAAA AGGGTAAAGA AATGGGATTG     420
AATGTAGAAT TACAGATCAA TCCTGAAGTG AAAGACTTTT TTACTTTCAA AAGCATCAGC     480
ACGACCAACA AACAACGCTG CTTTCTATCA TTGCACGGAG AAACAAGAGA AATTTTATGC     540
GATGATAAGC TATATAATGT TTTATTGGCC GTATTCAATT CTTATGATCC TAATGATCTT     600
TTGAAACACA TTAGCACCAT AGAGTCTCTC AAAAAAATCT TTTATACGAT TACATGTGAA     660
GCGGTATATC TA                                                        672
```

(2) INFORMATION FOR SEQ ID NO:1299:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 462 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

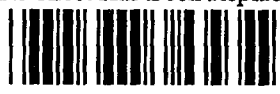
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299

```
AATAATGCTA AAAATAAGAA TAAAGGAGTC AAAAGTATGA AAACGAACTT TTATAAAATT      60
AAATTACTAT TTGCTTGGTG TCTTATCATT GGCATGTTTA ACGCTCCGCT TAACGCTGAC     120
CAAAACACGG ATATAAAAGA TATTAGTCCT GAAGATATGG CGCTAAATAG CGTGGGGCTT     180
GTTTCTAGAG ATCAGCTAAA AATAGAGATC CCTAAAGAAA CCCTAGAGCA AAAAGTGGCC     240
ATACTCAATG ACTATAATGA TAAGAATGTT AATATCAAGT TTGACGACAT AAGTTTAGGG     300
AGTTTCCAAC CTAATGATAA TCTAGGTATC AATGCGATGT GGGGCATTCA AAATCTTCTC     360
ATGAGCCAAA TGATGAGCAA TTACGGTCCA AACAATTCTT TCATGTATGG CTATGCGCCA     420
ACATACTCAG ATTCATCGTT TTTACCACCG ATCTTAGGGT AT                        462
```

(2) INFORMATION FOR SEQ ID NO:1300:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1554 base pairs

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

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300

```
CCTTTGGTTA AAATAAGGTT ATTTGATTTT ACTATAAGGT TGTTTAAACC TGAATTTCAC      60
ATTTTTGATT TTTTAAAAGG GATTAGAGTT CTTATGATTG AATGGATGCA AAATCATAGA     120
AAGTATTTAG TGGTTACGAT ATGGATAAGC ACGATCGCTT TTATTGCCGC CGGAATGATA     180
GGTTGGGGGC AATACAGCTT TTCTTTAGAT AGCGATAGCG CTGCCAAAGT GGGACAGATT     240
AAGATTTCTC AAGAAGAATT AGCCCAAGAA TACCGCCGCC TTAAAGACGC CTATGCTGAG     300
TCTATCCCTG ATTTTAAAGA ACTCACCGAA GATCAAATCA AAGCCATGCA TTTAGAAAAA     360
AGCGCGCTAG ATTCGCTCAT CAATCAAGCT TTATTGAGGA ATTTCGCTTT AGATTTAGGG     420
CTTGGTGCTA CCAAGCAAGA AGTGGCCAAA GAGATCAGAA AAACGAACGT TTTTCAAAAA     480
GATGGCGTTT TTGATGAAGA ATTGTATAAA AATATCTTAA AACAAAGCCA TTACCGCCCC     540
AAGCATTTTG AAGAAAGCGT TGAAAGGCTT TTAATCCTTC AAAAAATCAG CGCTCTATTC     600
CCCAAAACCA CCACCCCTTT GGAGCAATCC AGTCTATCGC TTTGGGCAAA ATTGCAAGAC     660
AAATTAGACA TTCTTATCCT AAATCCTAAT GATGTTAAAA TCTCTCTCAA TGAAGAAGAG     720
ATGAAAAAAT ATTATGAAAA CCATAGAAAG GATTTTAAAA AGCCCACAAG CTTTAAAACA     780
CGCTCTTTAT ATTTTGACGC TAGTTTAGAA AAAACTGATT TGAAAGAGTT GGAGGAATAC     840
TACCATAAAA ACAAGGTGTC TTATTTGGAC AAAGAGGGGA AATTACAGGA TTTTAAAAGC     900
GTTCAAGAGC AAGTCAAGCA TGATTTAAAC ATGCAAAAGG CGAATGAAAA AGCCTTAAGG     960
AGCTATATCG CTCTAAAAAA GGGGAACGCA CAAAACTACA CCACGCAAGA TTTTGAAAAA    1020
AACAACTCCC CCTATACTGC TGAAATCACG CAAAAACTCA CCGCTCTCAA GCCCCTTGAA    1080
GTCCTAAAAC CAGAGCCTTT TAAAGATGGT TTTATCGTGG TGCAGCTTGT CTCTCAAATT    1140
AAAGACGAAT TGCAAAATTT TGATGAAGCC AAAAGCGCTC TTAAAACCCG TCTGACTCAA    1200
GAAAAAACCC TTATGGCGTT GCAAACTTTA GCTAAAGAAA AGCTTAAGGA TTTTAAAGGG    1260
AAAAGCGTGG GTTATGTAAG CCCTAATTTT GGAGGCACTA TCAGTGAACT TAACCAAGAA    1320
GAGAGCGCGA AGTTTATCAA CACCCTTTTT AACCGCCAGG AAAAAAAAGG GTTTGTAACC    1380
ATAGGTAATA AAGTGGTGCT TTATCAAATC ACAGAGCAAA ATTTCAATCA CCCCTTTAGT    1440
GCAGAAGAAA ACCAATACAT GCAGCGTTTA GTCAATAACA CTAAAACGGA TTTTTTTGAT    1500
AAAGCGTTGA TAGAAGAATT GAAAAAACGC TATAAGATAG TCAAATACAT TCAA          1554
```

(2) INFORMATION FOR SEQ ID NO:1301:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 471 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1301

```
AAAGGTAAGC TAGGCCTATT TTACTATTTT TCAGACTTAC TAGAGTCGCT AATTTGCTTT      60
TCAAACTCTT GTTGTAAGGC CTGTTGTTGC TTTTCTTTCT TTGAAAGGCG TCGTTTTTTC     120
TTGGGCTTTT TTTCCTTTTT TGAAGAAGTC TCTGGCTCTT TTGAAGCTGT TTCTTTGAGC     180
GTGTTAGCGT TAGTCATAGG GTCTAGATCT GGGTTAGAAG AATTCTGTGT CTTAGAAGAG     240
CTTATAAATT CAGGGCTATC AGTATGGCTT TCAAGCTCCC CACTGCTCCT CTTTTGGAAT     300
GCTGCCTTAG TGTCTTTCTC AGCTTGTTCT TCCATTTTTT TAAGAACGAT TGCATCCACT     360
TTTCTAGCCT TTTGTTTTTG GCTCACCCTA ACCATGCTGA TCAAGTATTT GATATACCCA     420
TCATACATGT CCCCAAACTG CTCATGCAAA GCCCCAAAAT CTGAGCCTTT G              471
```

(2) INFORMATION FOR SEQ ID NO:1302:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302

```
GGGCTTTTGA AGCCTTTAGA AGAAACCGAA ATCAAGGCGT GTAACAAAGA TATTTTACCC      60
TTAAAGCCTT ATGAAAAAGC CAAATTGATT GCTTATATCC CCCAAGTGGA ATATTATGCG     120
TTTAATTTCA GCGTGTTGGA TTTTGTCTTA ATGGGGAAAG CGACGCATTT GAATCTGTTC     180
GCTATGCCTA AAGCTAAGCA CATTAAAGAA GCCACGAGCG TTTTAGAGCG CTTGGATTTA     240
GAGTCCTTAA AAGATCAAGG CATTAACGAT TTGTCCGGCG GTCAAAGGCA GATGGTACTT     300
TTAGCCAGAA GCTTGTTGCA AAGAACGCCC TTATTGTTAC TGGATGAGCC TACGAGTGCG     360
TTAGATTTAA AAAACCAAGC CCTTTTTTTT GATGCGATTA AAGATGAGAT GAAAAAACGA     420
GAATTGAGCG TTTTAGTCAA TATCCATGAT CCCAATTTGG TTGCCAGGCA CTCCACGCAT     480
GTGGTCATGC TCAAAGATAA AAAACTTTTT TTGCAAGCTT CCACGCCAAT CGCTATGACT     540
TCACACAATT TAAGCGCGCT TTATGACACG CCCCTAGAAG CGATCTGGCA TGATGATAAG     600
CTTGTGGTGT ATGCGTTG                                                  618
```

(2) INFORMATION FOR SEQ ID NO:1303:

(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:1303

AAAAAAAAAA AAAACGATGA AAAGCATATC GCTAAGCACT TTGTAGCGGT ATCCACCAAT 60
AAAGAAGCCG TGCAACAATT TGGCATTGAC GAGCATAACA TGTTTGGATT TTGGGATTTT 120
GTAGGGGGGC GTTATAGCTT GTGGTCGGCT ATTGGCTTAT CCATTATGAT CTATTTAGGG 180
AAGAAAAATT TTAACGCCCT TTTGAAAGGG GCGTATTTAA TGGATGAGCA TTTTAGAAAC 240
GCCCCTTTTG AAAGCAATTT ACCCGTTTTA ATGGGATTAA TCGGCGTGTG GTATATCAAT 300
TTTTTCCAAT CCAAAGGCCA CTTGATCGCC CCTTACGAC 339

(2) INFORMATION FOR SEQ ID NO:1304:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304

CACAACAAGA CACGAATGAA AAGAGCGAAA CGGAGGAAAT TTATCACTAA ATTTTCACGC 60
TACTACACCC CAAGCGTTTT ATTCATCGCC TTAATGATCG CTGTATTACC GCCCTTGTTT 120
TCTATGGGGA GCTTTGATGA GTGGATTTAT AGGGGGCTTG TGGCTTTAAT GGTGAGCTGT 180
CCTTGCGCGT TAGTGATTTC TGTGCCTTTA GGGTATTTTG GAGGCGTGGG AGCGGCGAGC 240
CGAAAGGGGA TTTTAATGAA AGGAGTGCAT GTTTTAGAGG TGCTTACCCA AACTAAAAGC 300
ATCGCCTTTG ATAAAACCGG CACTTTGACT AAAGGCGTTT TTAAAGTGGT GGATATTGTG 360
CCGCAAAACG GGCATTCTAA AGAAGAAGTT TGCATTACGC TTCTTGCTCG CAGCTTTTAT 420
CCACGCACCC GATCGCTTTA TCCATTCAAA AAGCATGCGA AGAAATGT 468

(2) INFORMATION FOR SEQ ID NO:1305:

(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:1305

```
CGCTCCACTC TAGCGAGCGC TGATGTGGGG ATTGGCATGG GGAAAGGATC AGAATTGAGC      60
AAGCAAAGCG CGGACATTGT GATCACTAAT GACTCCTTAA GCTCTTTAGT CAAAGTTTTA     120
GCGATCGCTA AAAAAACTAA AAGCATTATT TGGCAAAATA TCTTGTTCGC TTTGGGGATT     180
AAGGCGGTTT TTATCGTGCT AGGGCTTATG GGGGTAGCGA GCTTGTGGGA AGCGGTCTTT     240
GGCGATGTGG GGGTTACGCT TTTAGACTTA GCCAATTCCA TGCGCACGAT GAGGGCT        297
```

(2) INFORMATION FOR SEQ ID NO:1306:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1083 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

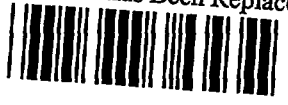
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306

```
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 TCCCCCCCTT GCTTTGCACT TTCCATCGTT TTGGTTTGCT GTTTTTAAGG     360
CAACACATGA ATCTTTTAAA AAGGGCGTGC GATTTTTCGG TGCTAGATAG CGATGAAGTG     420
AAAACGCTCT GCAAACAGCT CAAAATTTCA AATTTCAGGG CGAGCATTTC TCAAATCAAA     480
AACGGCATGA TGGATTTGAG CGTGCAAGAT AGCGAATGTT ACAAAGCGTA TGAGCTTTAT     540
CAAAACGCGC TCAAAAAAGA CAATTTAGTG GATTTTGACG ATTTGCTTTG TTTGAGCGTT     600
AAGATTTTAC AAGATAATGA AAAACTCGCC AAAGAGACCA GCGAACGCTA CCATTACATT     660
ATGGTAGATG AGTATCAAGA CACGAACGCC CTGCAACTGG AATTTTTAAA ACAATTGAGT     720
TTCACGCACC ATAATTTGTG CGTGGTGGGC GATGACGATC AGAGCATTTA TGGGTTTAGG     780
GGGGCTGATA TTTCTAACAT TTTAAATTTT TCCAAGCATT TTAAAGGGGC TAAAATAGTG     840
AAATTAGAGA CCAACTACCG CTCTAGCGCT GAAATCTTAG CGTGCGCTAA TTCCCTGATC     900
AGCCATAACC AACACCGCCA CATTAAAACG CTTCAAAGTT TCAAAGGTTC GCACAAAAGC     960
GTGATTTGTA AAGAATACCC CACGCAAAAA GAAGAGAGCC TGGATGTGGC TTATCAGATT    1020
CAAAGCCCTT TTAAAGAAGG GCGAGAATTT AGAAAATATC GCTATTTTGT ATCGTTTAAA    1080
TGG                                                                 1083
```

(2) INFORMATION FOR SEQ ID NO:1307:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2526 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

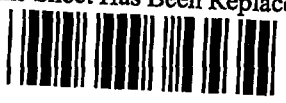
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307

```
TTTGTGCTGA ATGAAGAGCA AAATTCATTA GAAGAAAAAG GGGGCGAAAA CAAAAACGAA      60
AAAGAAACCC CCCTAAAGGG CATTCATTCT AAAATCCCCT CTTTGAAGCA GGCTTTGGAG     120
CAGACGATTA GTAAAATCAA AAGCTCTAAA GAGTTTTTCA AACAGCTTCT ACACAATAAA     180
AAAAAGCTTT ATATCGCGCT TGGAATATTG CTTTCACTCA TCGCGCTCAT TGTGGCTTTG     240
AGTTTGTTAC TAGGGCATAA AAAAGAAAAT AAACAAACTT CTTTACAAAC TAATACCGCC     300
ACCACCAATA ACGAAACGCC TAACGACACC AATAACGCAG AAGCCGAAGG GCAAATAGAA     360
AATTTAGACT TGCCTGATTT AATCGGCAAA GACTCTTTGA AAAGAAACGA TGAAAGCCAA     420
GTGGATGCGA TGATGCAAAA AGCGAGCCTT TTGTATGAGC AAGGGCAAAA AGATGAAGCC     480
TTGCATTTGT TTGATAAGAT CGCTTCTTTC TCGCAAGGGA TTGCGAGCCA TAATCTAGGG     540
GTGATTAAAT TCAAAGAAAA GGATTTTAAT GGGGCGTTGG ATTTGTTTGA TTCCAGTATC     600
GCTTCTAAAG AAAACGCGAG CGTGAGCGCG ATTGATGCGT TAGTTACGGC TTATCATTTG     660
CAAGATGCGG ATTTGTATTA TCATTATCTA AAAATTGTAA GAGACACTTT GTATAAAGAT     720
TACAAAAAGT CTTTTTATTC CTACGCTTAC GCACTCAAAT CCTACTACGC TGGAGAGTAT     780
TTTGAAGCCC TTTCGCCTTT AATGCACCCT AATTCCAACG CCTTTTTAAA GCCTAATGCG     840
CGCTTAGCGT CTAAATTGTT TTTGATGTTT AAAGATGAAA CGAACGCTTA CAAGCAATTG     900
CAAAAAAGTG CGAACGCCCA AGATGAGCTT GCTTTAGGGC TTTTGCAGGC CCGTTTGGGT     960
ACTTACAAGC AGGCTTTGGA GCATTTGCAG CATTATTTGC ACAACTACCC TAAAGATTTA    1020
AACGCTTTAA TGGCTTTGGA ATTGGTGAGT TTGAAAATGG GCGATACCCT TAAAGCGAGC    1080
GAAGCCTTAA AATTAGCCAG CCATACGCAA GAAGACACGC TATTAGCCAA CTCTTTTTAC    1140
CCCATCAAGC CCACTATAAA CCCTATGTTT TTAGACAAAG AAAGGGCCAA AGAGCGTTTT    1200
TGGAACACGC AATATTTTGA AGGTAAAAGG GATTTTATCT ACCGCTTGCT GTTTTATTAC    1260
GCTCCTTTTA AGGTTTTAGA CTCTAAAGAA ACCTTAGGCG TGATTGAAGA GGGGCTGTTT    1320
CTTTTAGATT CTGACACGCA AAAGGATTTA GAGGGGGCAA GCCTTGCTTT TAAAAGGGGG    1380
CGTTTGATGG CGATAGCGGA TAAAAACGCG CTCAAGGGGT TGAAAGAATT AGAAAAGAAG    1440
CGTCTAAAAA AAGCCCTTTC TTTTTTTGAT TTGTCTTTAA AAAATAGCCC CAATAACGCG    1500
CTTTTGCATT ATAATGTGGG CTTGATTTAT GCGCAATTGG AAAATTACCA CAAAGCTTAT    1560
TTCCATTTTT TAAGGGCTTT CCATTTGAAT TCTGCGGATT ATTTGAGCGC GGTTTTTGCG    1620
GTTTTAGCCT CGCATTTCAC CCATGAAGAC ACCACGGAGT TTTTAAGAGA AATCACCGAG    1680
AATTTTTATA GTCATGATTT TTCTAGCCCC ACGCAAAAAG CTTTACTCTC TTCGCTCATC    1740
GCTTATTTGA ATTACCGCAC CAATTGGGAT ATGGACTGGC TCAAAAACGC CCCTAAAAAG    1800
CTCCCTTTTT ATTACGCGCT AGAAGCGGTG TTCGCTAAAG AGAGCAAGGA TAAAAAATTG    1860
ATGGTGCAAT CTTTTGGGAA TTTAAAAAAA ATGCTCCCTA AAGATCTCAT CTCTAATATT    1920
TTTTATGAAA TCGTCTCGTA TTACGATGCG AGCATCCGCC ACACTTTAAG CATTTACACC    1980
CTTTTAGATT CGCATAAAAT CAGTTGGGAT CAAACCATGC AAGGGCCCAT TTTAGGGCGT    2040
CATTTCTACA CTTACATGGG ATTTATGGTC AATGATCTGG ATCATCAAGA AAGATTGTTA    2100
GAGCAAAAAA TCGCCAGTTT AGAAAGGGGC GAAGCCCCTA ACGATTGGTT GGAAAATTTA    2160
GCGCTAGTGA GTTTGTTTCA AGGCCAGTAT GAAAAAGCGA GCGCGTTGTA TCAAAACTTA    2220
ATTGATGGGC TTAAGGATAA CGAGGCGCGT TTAAAAATCC TAGCGGGTTT AACCTATATC    2280
GCGCAAAATA ATTACAATAA CGCCGCTTTA TGGCTAGAGC TTGGGAAATT AGACGATCCG    2340
AATAATGAAA ATATCCGTTA CGCTTTAGGG TTGTTGTATC AAAGAAAGGG AGACTTGAAA    2400
TCAGCGCTAA ACCATTTTTT AGCCATTAAA ACCTCTGATT TTTCGTCGCC TTATTTTGAT    2460
TTTGAAATTG ACACCAATCT TTTAAAAGAG CGTTTGAACC AAGAAGAAAA GGGCGAGTTT    2520
TTAGAA                                                               2526
```

(2) INFORMATION FOR SEQ ID NO:1308:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1068 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308

```
AAGGTTACTA CTACCATGAT AAAAGCAATC ATTGGAAAAA TCATCGGCAC TAGAAACGAT      60
CGCTGGATCA AACAATACAA AAAAAAAGTC CTAGCCATCA ACGCCTTAGA GCCTACTTAT     120
GAAAAAATGA GCGATGTTGA GCTGCAAAAC GCTTTTGAAG AATTAAAAAA ACGAGTGCGA     180
TCCGTAGAAA AAGATTTGCA AGAAAAAACC CTTTTAGAAG TTTTACCAGA AAGCTTTGCT     240
ATCACTAGAG AAGCGAGCAA AAGGATCTTA AAGATGCGCC ATTTTGATGT GCAACTCATT     300
GGGGGCATGG TCTTAAACGA TGGCAAGATC GCTGAAATGA AAACCGGAGA GGGTAAGACT     360
TTGGTCGCTA CTTTAGCGGT GGCTTTGAAC GCTATGAAAG GCGAGAGCGT GTATGTGGTA     420
ACCGTTAATG ATTACTTAGC CCATAGGGAT TCTAAAGAAA TGGAGCCGTT GTATCAATTC     480
TTAGGTTATA GCGTAGGCAC GATCACTGCG AGCGTGCGAG ATGATGATGA GCGCTTAGAA     540
ATTTATTCTA AAGACATTGT TTATGGCACT AATAATGAAT TTGGCTTTGA TTATCTAAGG     600
GATAACATGA AATATTCTTT AGAGCATAAA GTGCAAAAAT CCCATGCGTT CGCCATTGTT     660
GATGAAGTGG ATTCCATTTT AATTGATGAA GCGAGAACTC CTTTAATCAT TTCAGGGCCT     720
GTGGATAGGC GCATGGAAAA TTACAACAAG GCTGATGAAG TCGCTAAAAG CATGCAAGTG     780
GAAGTGGATT TCACCATAGA CGAAAAAAAC CGCGCGATTT TAATCACTGA AGAGGGGATT     840
AAAAAAGCCG AAAATCTCTT TGGCGTGGAT AATTTATACA AAATTGAAAA CGCCGCCCTA     900
TCGCACCATT TAGACCAAGC CTTGAAAGCG AATTACCTCT TTTTTATTGA TAAAGATTAT     960
ATTGTAGCCA ATAATGAAGT GGTGATTGTA GATGAATTTA CCGGCCGTTT GTCTGAGGGG    1020
AGGCGCTTTA GTGAGGGCTT ACACCAGGCT TTAGAGGCTA AAGAGGCG                 1068
```

(2) INFORMATION FOR SEQ ID NO:1309:

(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

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309

```
AAGGTTTTTC TAAAACCCCT AAAAGAAACG AGCCTTGCCC TTGTGGGAGT GGCAAAAAAT      60
ATAAAGATTG TTGCGCTAAA AGCGGGCCTA AAAAGGGCTT ATTTGCCAAA TAGATCCTTA     120
```

```
ATCTTTTTCC TTATCAAGCG TTATTTGCGT TTTGATAAAA GCCAGCCTTT CATTAGTATC     180
ACTGCTTTGT TAGCCTTTTT TGGCGTGGCG GTTGGCGTGA TGGTTTTAAT TGTGGCTATG     240
GCGATCATGA ACGGCATGAG TAAGGAATTT GAAAAAAAGC TTTTTGTGAT GAACTACCCC     300
TTAACGCTCT ATACCACAAG CCCTTATGGG ATCAGCGAAG AAGTGGTTCA AGCTTTAGAA     360
AAAAAGTTCC CTAATTTGCT TTTTAGCCCC TATTTGCAAA CCCAAAGTCC GATTAAAAGC     420
GCGCATTCCA TGAATGGCGG CGTGGTGTTT GGGGTTGATT TTTCTAAAGA AAGGCACATC     480
AATGAAGTTT TAAATGACGC CTTAAAAAAC ATTAATGAAA ACGATCTCTT CAAAAACCCT     540
TTTAATTTGA TCGTGGGGAA AAGCTTGAGA TACAGCTTGA ATTTAGATCT CAATCAAAAA     600
GCCGATTTGT TTTTCACCGA ATTAGAGCCA ACAGGTCTCA CGCTCTCCCC CATCATGAAA     660
CGCTTTACTA TCAAAGGCGA TTTTGATTCA GGGCTAAAAT CCTATGACAT GAGCTACATG     720
TATGCGAGCC TTCAAGCTAT AAGCGCGATC AGGAGATTAC CCTTAGGGCT TTATGATGGG     780
GTGCATGTCT ATTCTAAAAC GCCCATGAAG GATATTGAAA AATTACGCAA CGCTTTAAAA     840
ACAATCAACC ACCATGGCAT AGGCATTGAA GGGTGGTGGC AACAAAACGG GAATTTTTTC     900
TCGGCGATGG AATTGGAAAA AAGAGCGTTA TTCATTGTGC TCATGCTCAT TATTTTAATG     960
GCGTCTTTGA ATATCATCAG CTCGCTTTTA ATGGTGGTGA TGAACAGGCG TAAAGAAATC    1020
GCCCTACTCT TTAGCATGGG GAGCAGTCAA AAAGAAATCC AAAAAACCTT TTTTTATTTG    1080
GGTAATATCA TTAGT                                                    1095
```

(2) INFORMATION FOR SEQ ID NO:1310:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1062 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310

```
AGAGGCGTGA GCATTAAAGA AGAGAGCCAA ACCTTAGCCG ATATTACTTT CCAAAATTAT      60
TTCAGGATGT TTTCTAAACT TTCAGGCATG ACAGGCACGG CTCAAACCGA AGCCACAGAA     120
TTTTTAGAAA TCTACAATTT AGAAGTGGTG TCCATCCCTA CTAATCTAGC GATCAAGCGA     180
AAAGATTTGA ACGATCTGAT CTATAAGAGT GAAAAAGAAA AATTTGACGC TGTGATCCTT     240
AAAATTAAAG AATTACACGA TAAGGGTCAG CCCGTTTTAG TCGGCACGGC TAGCATTGAA     300
AAGAGTGAAA CCTTGCACGC TTTACTCAAA AAAGAGCGCA TCCCTCACAC CGTTTTAAAC     360
GCCAAGCAAC ACACTAAAGA AGCTGAAATC ATCAAAGACG CCGGGCTTAA AGGGGCGGTT     420
ACGATTGCGA CCAACATGGC AGGCAGGGGC GTTGATATTA AGCTCACTGA TGAAGTTAAA     480
GAACTTGGGG GGCTGTATAT CATTGGCACT GAAAGGCATG AGAGCCGTAG GATTGACAAT     540
CAATTAAGGG GGCGAAGCGG GCGTCAAGGC GATCCGGGAG TGAGTCAGTT TTATTTGAGC     600
TTAGAAGACA ATCTGTTACG CATTTTTGGG AGCGATAGGA CTAAGGGGGT GATGGAAAAA     660
TTAGGGCCTA AAGACGGCGA ACACATTGAA TTCAAGCTCG TTACAAGAGC GGTGGAAAAC     720
GCGCAAAAAA AAGTGGAGAA CTTGCATTTT GACAGCCGTA AGCATTTGTT AGAATACGAT     780
GATGTGGCTA ATGAGCAACG AACAAGCGTG TATAATCTTA GAGATGAATT ATTAGACATC     840
AATTACGATA TTAGCGCTAA AATCGCTGAA AACAGAGAAT ACGCGCTCAA TCAAATCTTT     900
TCTAAACTCA AAGCCTTTGA CCATCAAAAC CTGTCTGAAG AGGAACTTTT AGGGCTTAAA     960
AACATTTTAA AAGAAGATTT TAACGCTAGC GTTGAATTAG AAGATTTAGA AAAAGCCTCC    1020
CCTATTGAAA TATTTGTGGC TGAAAAACTC AAAAGCGGAT TA                       1062
```

(2) INFORMATION FOR SEQ ID NO:1311:

(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:1311

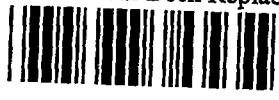
```
ATGCAGAAGT TTTTCTCTCG TTTTAGAAGG TGGGCGTTGC CCTTTTATTT TGTGAGCGCT      60
TTAGCAGCGA TTGATATTGA TGAAGTAACA GAAGCTCAAG CTAATAGCAT TAAATTAAGC     120
GATCAGTTAG TGAGCCTGAG CGATAAGCTT TTAGAAAAAG CGGTGGATAG GGGGCGCAAT     180
ACCGATCACT TAAAAGATCT TAACGATTTG CATGAAAAAA TCAAACATTT GCGCTTGATT     240
TTAGAGCCTA AGCCTAAGGG CAAAGAAGAT AGTCCTAACT TGGGAGGTAA TAAGGATATG     300
AAAACGGTTG AAATCGGAAG C                                               321
```

(2) INFORMATION FOR SEQ ID NO:1312:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312

```
AAAAACCAAA TACTTCAAAT CCCACTGCTT CCACCCCCCC CCAATAATGA AGAGCTTTTA      60
AAATCTATTA CAGATCTTAA AGATCGCCTT AAAAAATTAG AAGATCTTAA ATTAGAAGAC     120
TTTGAACCCC TTAGAAAACT CTCTCATTTT ATAGTTATAG GTAATTTGTT TGGAAAATCC     180
TCTAACGACA CCCAAGAAAA CCCAAAAGAC GCTTTAAAAT CCACCAATTT CCACGAGAAA     240
CACACCAAAC CGACTGAAAC CACCGAACTA GTTGAAGAAA ATAAAGCGCT AACCACAGAA     300
AAAGAAAGGC TAGAAAGAGA AAATAAAAAC CTAACTGCAG ACAAAGAAAA CCTAACTAAA     360
GAAAAAACCG AATTACAAAA ACAAGTGAAT GAGTTAAAAA ACTCTAAGCA AGTTTTAGAA     420
AATGAAAAAG CCGATTGGCT AAGAGAAAAA GAAAATCTAA CCAAAGACAG AGAAAACCTA     480
ACTAAAGAAA AAACAGAGCT GACTGAAAAA AATAAAGTGC TAACCACAGA AAAAGAAAGG     540
TTAGCCACAG AAAAAGAAAA CCTAACTAAA GAAAAAACCG AATCACAAAA ACAAGTGAAT     600
GAGTTAAAAA ACTCTAAGCA AGTTTTAGAA AATGAAAAAG CCGATCTGAC CAACGAAAAC     660
ACCAAGCTAA AAACAGATAA AACAGATCTG ACTGAAAAAA ATCAAAGGCT AACCACAGAA     720
AAAACAGAAT TAAATAACAA GATTACTGGG TTAGCCACAG AAAAAGAAAG GTTAGCCGCA     780
GACAAAGAAA ACCTAACTAA AGAAAGCAGA CAAAGAAAAC CTAAC                     825
```

(2) INFORMATION FOR SEQ ID NO:1313:

(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:1313

```
GCGCTTTCTA ATTGTTTGAG CTTGTCAGTT AGGCGTTGGT TTTCTTTCTC TAAATTGGTG    60
CATCGTTTTT CTAGAAACCC ATGCGCATCT TGCAATCGCG CTCGCTCTTG TTCGAGACTA   120
TCTCGCTCAT TAGTGAGCGC GGTAACTTGG TGGTTGAGCT TGTCGTTTTC GGTGGTTAGT   180
GCTTTATTTT CTTTAGTCAG CTCGGTGATT TTATGGGTTA GCTCGGTGTT TTCTCTTTTT   240
AGCCTTTCTT TTTCTGTTGT CAATTCTCTT TTTTCTTCAG TCAGCCGATC TCTGGCTGCT   300
AATAAGCGTG TGTTTTCTTT AGCTAAAATG TCTTTTTCCG TTTTCAGTTC TGCTTTTTCT   360
TTAGTGAGCT TGTTATTGTT TTGCCATAAT                                    390
```

(2) INFORMATION FOR SEQ ID NO:1314:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 981 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314

```
ATGGGAACGC TCATTGAAAA ATGGTTTGGC TTCTCTCAAA TCAGAGAAGA ATTAGAAGCT    60
CGCATCAGTG AGTTAGAAGA CGAAAACACC GAATTGTTAA GAGAAAGAGA ATACTTAGCT   120
GCAGAAACTA GCGAGTTAAA AGACGCTAAC GATCAATTAC GGCAAAAAAA CGACAAGTTA   180
TTCATAACAA AAGACAAGCT AACCAAAGAA AACACCGAGT TATTCGCAGA AAACGAAAGC   240
TTATCTGTAA AAATCAGCGG GTTAGAACAC TCTAACGATC AATTATGGCA AAACAATAAC   300
AAGCTCACTA AAGAAAAAGC AGAACTGAAA ACGGAAAAAG ACATTTTAGC TAAAGAAAAC   360
ACACGCTTAT TAGCAGCCAG AGATCGGCTG ACTGAAGAAA AAAGAGAATT GACAACAGAA   420
AAAGAAAGGC TAAAAAGAGA AAACACCGAG CTAACCCATA AAATCACCGA GCTGACTAAA   480
```

```
GAAAATAAAG CACTAACCAC CGAAAACGAC AAGCTCAACC ACCAAGTTAC CGCGCTCACT      540
AATGAGCGAG ATAGTCTCGA ACAAGAGCGA GCGCGATTGC AAGATGCGCA TGGGTTTCTA      600
GAAAAACGAT GCACCAATTT AGAGAAAGAA AACCAACGCC TAACTGACAA GCTCAAACAA      660
TTAGAAAGCG CTCAAAAAAG CTTGGAAAAC ACTAACAATC AATTACGGCA AGCTTTAGAA      720
AACTCTAATG TCCAATTAGC ACAAGCTAAA GAAAAAATAG CCATAGAGAA AAGCGAGCTG      780
GAGCGAGAAA TCGCACGCTT GAAGAGCTTA GAGGGTATGG AAGCCAAAAG CGATCTGGAC      840
TTACACAACA GGCGTTTAGC GAGCGCAAAC GAGGATTTAA AACGCCAAAA CCGAAAATTA      900
GAAGAAGAGA ACATCGCCCT CAAAGAGAGG GTTGATGGCT TGAACGAGCA GCTCTCCAAA      960
TTGCAACCAC AAAAACCACA A                                                981
```

(2) INFORMATION FOR SEQ ID NO:1315:

(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:1315

```
TTTAAAACCA TTGAACGAAA CGATTTTAAA TTAAACGGAT TGACAAAAAT TTTACAAAAC       60
AAAGGATATA AAATGAAAAC AATTAAAAAT GGTATTATGA TCGGCACACT CGGTGCGTTG      120
TTATTGAGCG GTTGTTCTAG CTTTGATGCT CAGCGTTTCG CTTGTCTCCC TAAAGACCAT      180
TCTTCAAAAG ACGCTTCTAC CAAAAAAGAA GCGCAATACA TTCCTAAGGG CTTTTTTGAC      240
CCTTATTCTT CTAACTTAAA CCATTGGGAT TCTACATTC                              279
```

(2) INFORMATION FOR SEQ ID NO:1316:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 909 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316

```
AGCTTAAATA AGGGTCTGGC ATTGTTTTTA GTCAAAAAAA TAGGCGTGGT AATAATGATT       60
```

```
TTAGTCTGCT TTTTAGCTTG CTCGCAAGAG AGCTTTATCA AAATGCAAAA AAAAGCCCAA     120
GAGCAAGAAA ATGACGGCTC TAAACGCCCC AGCTATGTGG ATTCGGATTA TGAAGTCTTT     180
AGCGAAACGA TTTTTTTACA AAACATGGTG TATCAGCCTA TAGAGGAAAG AAACGCTTTT     240
TTCCAACTGA CTAAAGATGA AGACAATTCT TTTAACCCTG AAAATTCCGT GATTTTACTG     300
AATGAGCCAA GCGATAATAG TGAAAAAAAC CTACTCTCAT ACCCAAACGA TCCCAATAAC     360
AATGAAGACA ACGCTAATAA TAGTCAAAAA AATCCGTTCC TTTACAAGCC CAAAAGAAAA     420
ACAAAAAACC CAAAACTCAT TGAATATTCC CAACAAGATT TCTACCCCCT AAAAAATGGG     480
GATATTATCA TGAGTAAAGA AGGGGATCAA TGGTTGATAG AAATCCAATC CAAAGCCTTG     540
AAGCGTTTTT TAAAAGATCA AAACGATAAA GATCGCCAGA TCCAAACTTT CACTTTTAAT     600
GACACTAAAA CGCAAATCGC GCAAATTAAG GGCAAAATTT CTTCGTATGT TTATACCACC     660
AATAACGGTA GCTTGAGTTT AAGGCCTTTT TATGAATCGT TTTTGTTAGA AAAAAAGAGC     720
GATAATGTTT ATACGATAGA GAATAAGGCT TTAGATACTA TGGAGATTTC AAAGTGTCAA     780
ATGGTGTTAA AAAAGCATTC AACCGATAAA TTAGACAGCC AGCATAAAGC CATCAGTATT     840
GATTTGGATT TTAAAAAAGA GCGCTTTAAG AGCGATACGG AACTCTTTTT AGAATGTCTT     900
AAGGAAAGT                                                             909
```

(2) INFORMATION FOR SEQ ID NO:1317:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1317

```
GCATGGTTAA AAAGTAGGGT TTTAATGAAA CGCCTTGCTG TTGCGCTTAT TTTGGTGTTG      60
GGAGTGGTGT GGGGGAAATC CTTGCCTAAG TGGGCAAAAG ATTGCTCAAA AGAGATGCGG     120
ATTGAAAAGA CCCAAACCAA AGATGAAAAA ATTTTAGTGT GTGGGATGAG CGATATATTG     180
CTTTCAGATA TGGATTATAG CTTGTCCTCA GCCAGACAAA ACGCCTTAGA GAAAGTGATG     240
GAAGCTTTCA AGGGGGATAG AATAGAGATT AAGGCTGGTG AGCTAAAGGC CACTTTTATT     300
GATACGGATA AAGTTTATGT GCTTCTAAGA ATCACTAAGA AGCATGTCGC TTTAATGAAT     360
GAG                                                                   363
```

(2) INFORMATION FOR SEQ ID NO:1318:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

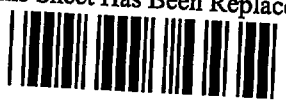
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318

```
GGATTGATAA TGAAAAAGAT TATTCTTGCA TGCCTTGTGG CTTTTGTGGG TGCCAATTTA      60
AGCGCAGAGC CTAAGTGGTA TAGCAAGGCC TATAACAAAA CAAACGCCCA AAAAGGCTAT     120
CTTTATGGGA GTGGTTCAGC CACTTCTAAA GAGGCTTCTA AACAAAAAGC GTTAGCGGAT     180
TTAGTGGCGT CTATTAGCGT GGTGGTCAAT TCACAAATCC ACATTCAAAA AAGTCGTGTG     240
GATAATAAGT TAAAATCCAG CGATTCACAA ACGATCAACT TAAAAACCGA TGACTTGGAA     300
TTGAATAATG TAGAAATTGT CAATCAAGAA GCGCAAAAAG GGATCTACTA CACCAGAGTG     360
AGGATCAATC AAAACTTGTT TTTGCAGGGT TTAAGGGATA AGTATAACGC TCTTTATGGG     420
CAGTTTTCCA CCTTAATGCC TAAGGTTTGC AAAGGGGTTT TTTACAAACA ATCCAAGAGC     480
ATGGGGGATT TATTGGCTAA AGCGGCGCCT ATGGAAAGGA TTTTAAAAGC GTATTCTGTC     540
CCGGTGAGTT CGTTAGAAAA TTATGAAAAA ATCTATTACC AAAACGCTTT CAAACCTAAA     600
GTGCGAATCG CTTTTGATGA TAACAGCGAC ACAGAGATTA AAAACGCTCT CATGAGTGCT     660
TACGCTAGAG TGCTAACCCC TAGCGATGAA GAAAAACTTT ATCAAATCAA AAATGAAGTT     720
TTCACGGACA GTGCTAATGG CATCACACGC ATTAGAGTGA TTATTAGCGC GAGCGATTGT     780
CAAGGCACGC CTGTATTGAA TAGGAGTCTT GAAGTGGATG AAAAGAATAA GAATTTTGCT     840
ATCACGCGCT TGCAATCTTT ACTTTATAAA GAATTGAAAG GTTATGCCAA TAAAGAAGGA     900
CAAGGCAATA CAGGGCTA                                                  918
```

(2) INFORMATION FOR SEQ ID NO:1319:

(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:1319

```
CCCCAAAGAG TTGTTTTTAG GGTGCGATTC TTGCTCGCTA TCCCCCAAAT TTTAGTGGGC      60
TTAAGGATTG CGGTGGTGAT GCTAGTAGCG ATGGCTGGAA TCGGGGCACT CATTGGGGCT     120
GGGGGTTTGG GGCAGGCGAT TTTTAGAGGG CTAAACACGC AAAATACCAC GATTTTAGTG     180
GCGGGCAGCT TTATTATTGC TCTTTTTAGC GTTTTAGCGG ATCAATTTGT GAGCGTGTTT     240
CAGCATGAAA ACGCCTTGCA ACGCCTATTT TCTCAAAACG CCACCCAAAA ACAAAAAAGA     300
AGAGTTTATG TTAATTTAGC GGTGTTTCTT TTTTTATTGC TAGCGAGCGC TTTATGGCTC     360
ATTCCTAGAA GTGCCATAGA AGAAAAGCCC TTAGTCGTGG CGACAAAACC TAGCAGCGAG     420
CAGTATATTT TGGGCGAAAT TTTAAGCCTT TTGTTAGAAA AACACCATAT CCCTATCAAG     480
CGAGCGTTTG GCATTGGTGG GGGGACGATG AATATCCATC CGGCATTGAT TAGGGGCGAT     540
TTTGATTTGT ATGTGGAATA TACCGGCACC GCTTGGGTGA ACACGCTCAA AAACCCTTTG     600
ACTCAAAAAG TGGATTTTGA AACGATTAAA AAGCGTTATG AGAAGGAATT TAATCTTTTG     660
TGGGTGGGAC TTTTGGGCTT TAATAACACC TATTCTTTAG CGATTTCTAA AGAAGACGCT     720
CAAAAATACG CAATTGAAAC TTTCAGCGAT TTAGCCTTTC ATAGCCCGAA TTTTGATTTT     780
GGAGCGGAGT TTGATTTTTT TGAAAGAGAG GACGCTTTTA AGGGCTTAAT CAAAGCTTAT     840
CGCTTTCATT TTAGAAGTTT GCATGAAATG GATATTAATT TGCGTTATAA AAGTTTTGAA     900
TCCCATAAGA TCAACGCTTT AGACGTCTTC ACTACAGACG CTCAAATCAA AGAGCTGGAT     960
TTAAAGGTGC TGAAGGACGA TAAAGGGTTT TTTCCTAATT ATCAGGCCGG TATTGTT       1017
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1320:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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:1320

```
GGAGCAAAAA TGAAAAAAAT TGGTTTGAGC TTGTGTTTGG TTTTGAGTTT GGGTTTTTTA     60
AAAGCCCATG AAGTGAGCGC TGAAGAGATT GCGGATATTT TCTACAAACT CAACGCCAAA    120
GAGCCTAAAA TGAAAATCAA CCACACGAAG GGGTTTTGCG CTAAAGGCGT GTTCCTCCCT    180
AACCCGCAAG CAAGAGAGGA TTTAGAGGTG CCACTACTCA ATGAAAAAGA AATCCCTGCG    240
TCTGTAAGGT ATTCTTTAGG GGGCGTGGCG ATGGACGATA AAAGCAAGGT TAGGGGAATG    300
GCGTTAAAAC TAGAAAATCA AAACGCTAGT TGGACAATGG TGATGCTCAA TACAGAAATC    360
AATTTTGCCA AAAACCCTGA AGAATTCGCC CAATTTTTTG AAATGAGACT TCCTAAAAAT    420
GGCCAAGGTA GA                                                        432
```

(2) INFORMATION FOR SEQ ID NO:1321:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1584 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321

```
CATGAGTTTT TAGCTATTAA TGAATTGATG TTTGACGTGT TTTTGCCCAG CAGATTGAAA     60
CAAAAAGAGC TTTTAGAAAA AATTGAGGTG ATCCAAAAGT TTTTCCCTAA TTTTCCCAAA    120
GAAACGCTTT TAAACAATTA CCAAAAAGAA AATTCGCTCT ATAACCATAA CCTCATTAAA    180
GTGGTGGGCT TCATTCCCTA TGCCACCATG CAATCCCTTT ATACCAAACT CATCCAAACT    240
CAAGGCATTT TTGTGCGCCC TTTAGACAAG CGCTACTACC CTAATAACGC TTTAGCTTCG    300
CATGTTTTAG GTTATGTGGG GGTGGCAAGT TTACAAGATT TAAAAGACGA TGAAGAGAAT    360
CAATACAGCC AGATTGTAGG CAAAACCGGC ATTGAAAAAG AATACAACAA GTTTTTACAA    420
```

GGCAAGGTGG GTTATAAAAT CATACATGTC AATGCGCTCA ATCAAGAATT AGCCACCTTA 480
GAGGTCGTGC CACCACGCTC CAATAACCAC TCGCAATTGA GTTTAGACAA ACGCTTCCAA 540
AAAGAAGCAC ACAAGCTCTT TGTAAATAAG AGAGGGCCTA TTTTAGTGAT GGATGCAGAA 600
AATGGGGAAT TGCTCGTTGC AGGAAGTTAC CCTGAATACA ATTTGAACGA TTTTGTAGGC 660
GGGATCAGTC AAGACAAATG GCAAAAACTC CAAGATGATA TTTATAACCC TTTATTAAAC 720
CGCTTCGCTA ATGCCTTGTA TCCGCCGGGA TCTGTGGTTA AAATGGGCGT GGGGTTAAGC 780
TTTTTAGAAA ACCTTCATAT CACAGAAAAC ACCACTATCC CCACACCGCC TTTTATTGAA 840
GTGGGCAAGC GCAAATTCAG GGACTGGAAA AAAACAGGGC ATGGCAATTC TAATTTGTAT 900
AAAGCCATTA GGGAGTCCGT GGATGTGTAT TTTTATAAGT TTGGGCTTGA AATCTCTATA 960
GAAAAACTCT CTAAAACCTT AAGGGAAGTG GGCTTTGGGG AAAAAACGGG CGTTGATTTG 1020
CCGAATGAAT TTGTGGGGAT TGTGCCGGAT AATTTGTGGA AGCTCAAACG CTTCAATCAA 1080
GACTGGCGCG TTGGGGACAC GCTCATTACT GCTATTGGGC AAGGCTCTTT TTTAGCCACG 1140
CCTTTGCAGG TGTTAGCCTA CACAGGACTC ATTGCGACAG GCAAACTGGC AACGCCTCAT 1200
TTTGCTATCC ATAACCAACA ACCGCTCAAA GACCCCCTGA ATAGTTTTCA AAAAAAGAAG 1260
CTCCAAGCCT TGCGCGTGGG CATGTATGAA GTGTGTAACC ATAAAGACGG CACCGCTTAT 1320
CATTCCACAA GAGGTTCTAA GGTTACCTTA GCGTGTAAAA CCGGCACCGC GCAAGTCGTA 1380
GAAATCGCTC AAAACATCGT CAATCGCATG AAAGAAAAGG ATATGGAATA TTTCCATCGA 1440
TCCCATGCGT GGATTACGGC ATTCTTGCCC TATGAAAAAC CCAAATACGC TATCACTATT 1500
TTAGTAGAAC ATGGGGAGGG AGGGTCAAAA CTAGGGGGCT TGTTAGTGAA AATGAGCAAC 1560
AAACTCTATG AGCTTGGCTA TCTT 1584

(2) INFORMATION FOR SEQ ID NO:1322:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 840 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced

(ii) MOLECULE TYPE: DNA (genomic)

(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:1322

ATTAATTTTG TTAATAAAGG GGTTTTTATG AACATATTCA AGCGTATTAT TTGCGTAACC 60
GCTATTGTTT TAGGTTTTTT TAACCTTTTA GACGCCAAAC ACCACAAAGA AAAAAAAGAA 120
GACCACAAAA TCACTCGTGA GCTTAAAGTG GGCGCTAACC CTGTGCCGCA TGCGCAAATC 180
TTGCAATCAG TTGTGGATGA TTTGAAAGAG AAAGGGATCA AATTAGTGAT CGTGTCTTTT 240
ACGGATTATG TGTTGCCTAA TTTAGCGCTC AATGACGGCT CTTTAGACGC GAATTACTTC 300
CAGCACCGCC CTTATTTGGA TCGGTTTAAT TTGGACAGAA AAATGCACCT TGTTGGTTTG 360
GCCAATATCC ATGTGGAGCC TTTAAGATTT TATTCTCAAA AAATCACAGA CATTAAAAAC 420
CTTAAAAAAG GCTCAGTGAT TGCTGTGCCA AATGATCCGG CCAATCAAGG CAGGGCGTTG 480
ATTTTACTCC ATAAACAAGG CCTTATCGCT CTCAAAGACC CAAGCAATCT ATACGCTACG 540
GAGTTTGATA TTGTCAAAAA TCCTTACAAC ATCAAAATCA AACCCCTAGA AGCTGCGTTA 600
TTGCCTAAGG TTTTAGGGGA TGTGGATGGG GCTATCATAA CAGGGAATTA TGCCTTGCAA 660
GCAAAACTCA CCGGAGCCTT ATTTTCAGAA GATAAGGACT CGCCTTATGC TAATCTTGTA 720
GCCTCTCGTG AGGATAATGC GCAAGATGAA GCGATAAAAG CGTTGATTGA AGCCTTACAG 780
AGCGAAAAGA CCAGGAAATT CATTTTGGAT ACCTATAAGG GGGCGATTAT CCCGGCTTTT 840

(2) INFORMATION FOR SEQ ID NO:1323:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 978 base pairs

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

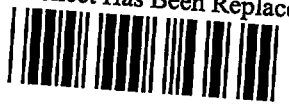
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323

```
ATGATGATAA CCAAACAATC GTATCAAAGA TTCGCTTTAA TGCGGGTTTT TGTGTTTTCG      60
CTTTCGGCGT TTATTTTTAA CACCACGGAG TTTGTCCCTG TTGCACTTCT GTCAGACATT     120
GCGAAAAGCT TTGAAATGGA GAGCGCAACA GTGGGGCTTA TGATCACTGC TTATGCATGG     180
GTGGTGTCTC TTGGCTCATT GCCCTTGATG CTGCTTAGCG CTAAAATTGA AAGGAAACGC     240
TTATTGCTTT TTCTTTTCGC TCTTTTTATT TTCAGCCATA TCCTTTCAGC GTTAGCGTGG     300
AATTTTTGGG TGCTTCTCCT TTCTCGTATG GGTATCGCTT TTGCCCACTC TATTTTTTGG     360
TCCATCACGG CTTCTTTAGT CATTCGTGTC GCGCCAAGAA ACAAAAAACA ACAGGCCTTA     420
GGGCTGTTAG CGTTAGGGAG TTCGTTAGCG ATGATTTTAG GGTTGCCGCT TGGGAGGATC     480
ATTGGGCAAA TTTTGGATTG GCGATCCACT TTTGGCGTGA TTGGGGGCGT TGCGACTCTT     540
ATAATGCTGC TTATGTGGAA ATTGCTCCCG CATCTACCGA GTAGAAACGC CGGCACGCTC     600
GCAAGTGTCC CTATATTAAT GAAACGCCCG CTTTTAGTGG GGATTTATTT GCTTGTGATC     660
ATGGTTATTT CTGGGCATTT CACCACTTAT AGCTATATTG AGCCTTTTAT CATTCAAATC     720
AGCCAATTTT CTCCTGACAT TACAACGCTA ATGTTGTTTG TGTTTGGGTT AGCAGACGTG     780
GTGGGGAGTT TTTTGTTCGG CCGTTTGTAT GCGAAAAATT CAAGAAAATT TATCGCTTTT     840
GCAATGGTTT TAGTCATTTG CCCGCAACTC TTGCTTTTTG TGTTTAAAAA CTTAGAGTGG     900
GTGATCTTTT TGCAGATTTT CTTGTGGGGG ATTGGGATTA CTTCACTCAC CATTACGTTA     960
CAAAATGAGG GTATTCAC                                                  978
```

(2) INFORMATION FOR SEQ ID NO:1324:

(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:1324

```
AAGGGCATTC AAAAGAAACA AAATCTTAAA GAGGTGGCTT TAGACGCTTT CTTGCCTAAA      60
AGCATCAATT ACTACCATTT TAACGGCTCT CTCACCGCTC CTCCTTGCAC AGAGGGGGTG     120
GCATGGTTTG TCATAGAAGA ACCTTTGGAA GTTTCTGCCA AACAATTGGC TGAAATCAAA     180
AAACGCATGA AAAATTCGCC CAACCAACGC CCCGTCCAGC CTGACTACAA CACCGTGATC     240
```

ATTAAAAGCT CGGCTGAGAC CCGC 264

(2) INFORMATION FOR SEQ ID NO:1325:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325

This Sheet Has Been Replaced



AGGATAATTA AAATGAAAAA AACTTTTTTG ATCGCTTTAG CGCTTACGGC TTCTCTTATA 60
GGCGCTGAAA ACACCAAATG GGATTATAAA AATAAAGAAA ATGGCCCGCA CCGCTGGGAC 120
AAATTGCACA AAGATTTTGA AGTGTGCAAA AGCGGTAAAA GCCAATCGCC CATCAACATT 180
GAGCATTACT ACCACACGCA AGATAAAGCC GATTTGCAAT TCAAATACGC CGCTTCTAAA 240
CCTAAAGCGG TCTTTTTCAC CCACCATACT TTAAAGGCTT CGTTTGAGCC GACTAACCAC 300
ATCAATTATA GAGGGCATGA CTATGTGTTG GATAATGTGC ATTTCCACGC CCCTATGGAG 360
TTTTTAATCA ATAATAAAAC CAGGCCTTTG AGCGCGCATT TCGTGCATAA AGACGCTAAA 420
GGGCGTTTGT TGGTGTTAGC GATTGGGTTT 450

(2) INFORMATION FOR SEQ ID NO:1326:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326

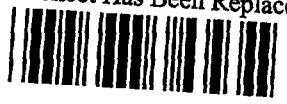
ATGCCTGTTA TAAGAGTTTT AGTAATGCTT GCAACAATGA TGATGAAATT AGTAAAAACG 60
GCAAAAGAAA AGAAAGTTTT TAAGAATGTG GGAATATCTA TAATGGGGAT TGCTTTTTGG 120
GAAGCGATAA AAGACTCGAT AAAAAAACAA ATTAAAAAAA GCGATTGGAT ATGCGGGAAT 180
GTTAAGACTG CGGATGATTA TTTAAAAACG CATCCTAACT CATGGTTTAA TTCAGCAATA 240
GGTGTAACAG CGATAACAGC CATGCTTATG AATGTGTGTT TTGCTGATGA CCAATCCAAA 300
AAAGAAGTGG CTCAAGCTCA AAAGGAAGCT GAAAACGCTA GGGATAGAGC GAACAAGAGT 360

```
GGGATAGAAC TGGAACAAGA AGAGCAAAAG ACAGAACAAG AAAAACAAAA GACAGAACAA     420
GAAAAACAAA AGACAGAACA AGAAAAACAA AAGACAGAAC AAGAAAAACA AAAGACAGAA     480
CAAGAAAAAC AAAAGACAAG CAATATAGAG ACTAACAATC AAATAAAAGT AGAACAAGAA     540
CAACAAAAGA CAGAACAGGA AAAACAAAAG ACAAACAATA CGCAAAAAGA TTTGGTTAAC     600
AAAGCAGAAC AAAATTGCCA AGAAAATCAT AATCAATTCT TTATTAAAAA ATTAGGAATT     660
AAGGCTGGCA TTGCTATAGA AATAGAAGCT GAATGCAAAA CCCCTAAACC CACAAAAACC     720
AATCAAACCC CTATCCAGCC AAAACACCTC CCAAACTCCA AACAACCCCA TTCTCAAAGA     780
GGATCAAAAG CGCAAGAGCT TATCGCTTAT TTGCAAAAAG AGCTAGAATC TCTGCCCTAT     840
TCACAAAAAG CTATCGCTAA ACAAGTGGAT TTTTATAGGC CAAGTTCTAT CGCTTATTTA     900
GAACTAGATC CTAGAGATTT TAACGCTACA GAAGAATGGC AAAAAGAAAA TTTAAAAATA     960
CGCTCTAAAG CTCAAGCTAA AATGCTTGAA ATGAGGAGTT TAAAACCAGA CCCACAAGCC    1020
CACCTTTCAA CCTCTCAAAG CCTTTTGCTC GTTCAAAAAA TATTTGCTGA TGTTAGTAAA    1080
GAAATAAAAG TAGTTGCTAA TACCGAGAAA AAAGTAGAAA AAGCGGGTTA TGGTTATAGT    1140
AAAAGGATG                                                            1149
```

(2) INFORMATION FOR SEQ ID NO:1327:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 996 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1327

```
AATAAAAGGA AGAACATTAA AGAAGTTTAT GCGGGCGAGA TTTGCGCGTT CGTGGGCTTG      60
AAAGACACGC TGACTGGGGA CACGCTTTGC GATGAAAAGA ATGCGGTGGT TTTAGAGAGA     120
ATGGAATTTC CTGAGCCGGT CATTCACATC GCTGTGGAGC CTAAAACGAA AGCAGACCAG     180
GAAAAAATGG GCGTAGCGTT AGGCAAGCTT GCTGAAGAAG ATCCAAGCTT TAGGGTGATG     240
ACTCAAGAAG AAACCGGTCA AACCCTTATT GGTGGTATGG GTGAATTGCA CCTAGAAATC     300
ATCGTGGATA GATTGAAGAG AGAATTTAAG GTGGAAGCTG AAATCGGTCA GCCGCAAGTC     360
GCCTTTAGAG AGACTATCCG CTCAAGCGTG AGCAAAGAGC ATAAATACGC TAAGCAAAGT     420
GGTGGCCGTG GGCAATACGG GCATGTGTTT ATCAAGCTTG AGCCTAAAGA GCCTGGCAGT     480
GGGTATGAAT TTGTGAATGA AATTTCTGGG GGCGTGATCC CTAAAGAATA TATCCCTGCG     540
GTGGATAAGG GTATCCAAGA AGCGATGCAA AATGGCGTTT TGGCAGGCTA TCCGGTGGTG     600
GATTTTAAAG TTACCCTTTA TGATGGGAGC TACCATGATG TGGATTCTTC AGAAATGGCG     660
TTTAAAATCG CTGGCTCTAT GGCGTTTAAA GAAGCGAGTC GTGCGGCTAA CCCGGTTTTA     720
CTAGAGCCTA TGATGAAAGT GGAAGTGGAA GTCCCTGAAG AATACATGGG CGATGTGATT     780
GGCGATTTAA ACAGAAGAAG AGGGCAAATC AATTCTATGG ACGATAGATT AGGTTTGAAA     840
ATCGTGAATG CTTTCGTGCC GTTAGTGGAA ATGTTTGGTT ATTCTACGGA TTTGCGATCA     900
GCCACTCAAG GGCGTGGGAC TTACTCTATG GAGTTTGACC ACTATGGCGA AGTGCCTAGC     960
AATATCGCTA AGGAAATCGT GGAAAAACGC AAAGGC                               996
```

(2) INFORMATION FOR SEQ ID NO:1328:

(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:1328

```
TCTAAAAGGG CGTTCGCAAG CTCTTTAGTG TCTTCTAAGC TGTTTTTGAG GGACAAAGAA      60
ACTCGTAAAA GGGGTTTAGA AACCGTAGGG GGGCGGATAG CCCCCACTAA AAACCCCTTT     120
TCTTTCAAAA AATATTGGGC GTTTAAAAGA GCGGGATTGT TTTCAAACTC TAGGGTAAAA     180
AATCCTGTAG GCGTTCTAAC GCCTAAAGTT TCAAAAATAA TCTGTTGGTG TTTGCTAAGC     240
TCATTTTTTA ATTCTTGTTT TTGCGCGATA AAGTATTCTA AATGGGCCAA AGTCAAAGCG     300
GTGTCTAACA GGCTTAAAGC GGTGGTA                                         327
```

(2) INFORMATION FOR SEQ ID NO:1329:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329

```
ATAAGGAATG CCACCATGTT TGGGAATAAG CAGTTACAGC TTCAAATCAG TCAAAAAGAT      60
TCTGAGATTG CGGAGTTAAA AAAAGAAGTC AATCTCTATC AAAGCCTTTT AAATTTGTGC     120
TTGCATGAGG GTTTTGTAGG TATTAAAAAC AATAAAGTCG TTTTTAAAAG CGGGAATCTT     180
GCAAGCTTAA ACAATTTAGA AGAACAAAGC GTTCATTTTA AAGAAAACGC AGAAAGCGTT     240
AATTTACAAG GGGTTTCTTA TTCTTTGAAA AGCCAAAATA TTGACGGCGT GCAGTATTTT     300
TCATTGGCTA AAAAAACAGG GGGTGTGGGG GAATACCATA AAAATGATTT GTTTAAGACT     360
TTTTGCACGA GCTTAAAAGA GGGCTTAGAG AACGCGCAAG AAAGCATGCA GTATTTCCAT     420
CAAGAAACAG GCTTGCTCTT GAATGCGGCT AAAAATGGCG AAGAGCATTC TAATGAAGGA     480
TTAATAACCG TTAATAAAAC GGGTCAAGAC ATTGAATCGC TTTATGAAAA GATGCAAAAC     540
GCCACTTCGT TAGCGGACTC CCTCAACCAA CGGAGCAATG AAATCACTCA AGTCATTTCT     600
TTGATTGATG ATATTGCAGA GCAAACCAAT CTCTTAGCCC TAAACGCCGC TATTGAGGCC     660
GCACGAGCGG GTGAACATGG CAGAGGGTTT GCGGTGGTGG CTGATGAGGT GAGAAAGCTC     720
GCTGAAAAAA CCCAAAAAGC CACTAAAGAA ATCGCTGTCG TGGTTAAAAG CATGCAACAA     780
GAAGCGAACG ATATTCAAAC CAACACCCAC GATATTAATT CTATTGTAGG CTCTATTAAG     840
GGTGATGTGG AAGAGCTTAA ATCCACCGTA AAAAATAACA TGATTGTCGC GCAAGCCGCA     900
AAATACACCA TCTACAATAT CAATAACCGG GTGTTTTGCG GTCTGGCTAA ACTCGATCAT     960
GTGGTCTTTA AAAACAATCT TTATGGCATG GTCTTTGGTC TCAATTCCTT TGACATTACC    1020
AGCCATAAGA GTTGCCGTTT AGGCAAATGG TATTATGAGG GTGCGGGTAA AGAAAACTTT    1080
```

GCTAACACTT CAGGCTATAG AGCTTTAGAA AGCCACCATG CGAGCGTGCA TGCTGAAGCT 1140
AATGATTTGG TTAAAGCCGT TCAAGAAGAT CACGTCACCG ATTCAAAATA CCTAGAACAT 1200
AAAGTGCATT TAATGGAAGA TAGCGCTAAG CATGTCAAAG AAAATATTGA TAAGATGTTT 1260
TATGAAAAAC AAGATGAACT CAATAAAATC ATTGAAAAAA TTCAAAAAGG CGAA 1314

(2) INFORMATION FOR SEQ ID NO:1330:

(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:1330

GAGTGGTTAA TGCTAAAAAA GATTTTTTAT GGTTTTATCG TTTTATTTTT GATTATCGTA 60
GGGTTGTTGG CCGTTCTTGT CGCTCAAGTT TGGGTAACTA CGGATAAGGA TATTGCTAAA 120
ATTAAAGATT ATCGCCCCAG TGTCGCTTCA CAGATTTTAG ACAGAAAAGG GCGTTTGATC 180
GCTAATATTT ATGATAAGGA ATTTCGTTTT TATGCGCGTT TTGAAGAAAT CCCCCCACGA 240
TTTGTTGAAA GCCTTCTAGC GGTAGAAGAC ACCCTCTTTT TTGAGCATGG GGGGATCAAT 300
TTAGACGCTG TCATGCGCGC TATGATTAAA AACGCTAAAA GTGGTCGTTA CACTGAAGGG 360
GGTAGCACTC TAACCCAACA ACTCGTTAAA AACATGGTGC TCACACGGGA AAAAACCCTA 420
ACCAGAAAAC TCAAAGAAGC TATCATCTCC ATACGCATTG AAAAAGTCTT AAGCAAAGAA 480
GAAATTTTAG AGCGTTATTT GAACCAAACT TTTTTTGGGC ATGGGTATTA TGGCGTGAAA 540
ACCGCAAGTT TAGGGTATTT TAAAAAACCC CTTGACAAAC TCACGCTTAA AGAAATCACC 600
ATGTTAGTCG CCTTACCTAG GGCTCCAAGT TTTTATGACC CTACCAAAAA TTTAGAATTT 660
TCACTCTCTA GGGCTAATGA TATTTTAAGG CGGTTGTATT CTTTAGGCTG GATTTCTTCT 720
AACGAGCTCA AATCCGCTCT CAATGAAGTG CCAATCGTCT ATAACCAAAC TTCCACGCAA 780
AATATCGCTC CCTATGTCGT GGATGAAGTG TTGAAGCAAT TGGATCAATT AGACGGGTTA 840
AAAACTCAAG 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:1331:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1779 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331

```
ATACGAACAC CAATGGATAC CATAAAAAGC ATTCCCATAA GAACTTTTAT TTTACTCTAT      60
AAAAGCTCAC CAAAATGTGT TGTGTTGGCA TCAATTACAG TGCTATTTGT CGGCATTCTT     120
CCATCTCTGA ATATTCTTGT TATGATAAAA TTGATTGATA TTGTGGTGAA TCTATTACAA     180
AAGCATACGC ATTTTGAATA CAGCTTGCTG TTACCAACTT TACTACTATG GGGAGCCTTG     240
CTGTTTTTAA CGCATGTGTT CTCAGGAATT TTATCAAGCT TGCAAACCAT TATTGCCGAA     300
CAATTTTCTA TAAATATCAT CACTCAGCTT GCTAATAAAC TCACACAAGT TAAAAATCTA     360
AATTTTTTTG AGAATAAAGA CCATACTATC AAGCTTAACA CTATCCATAA CGGACTGCAC     420
ATCCGCCCCC TAAATTATGT CAGTAATCTT TTTTTCAATC TACAACGCAT TATAGGGCTT     480
ATCAGTCTGT TTGGGATATT ATTTTCCATT AGTATTTATC TACCCTTTAT AATGATTTTT     540
GCAACAGTGC CTTGTATTCT CATTTCCAAC CATATAGCAA AAAAACATAG TGCTTCCATA     600
GATAAACTTC AAGACCAAAA AGAAAGCATG CAAAATTACT TATACTCTGG ACTAGATAAC     660
CAAAAGAACA AGGACAACCT ATTATTTAAC TTCATGCTAA ATTTTCACCA TAAATTTATT     720
GAAACAAAAG AATTGTATCT CAATAATTTT GTGAAAGTAG CCCAAAAAAA CTTAATATTT     780
ACCATATATG CTGATGTTTT AATCACCACT CTAAGTATTG CACTATTTTT TCTAATGGTT     840
TTTATTATCC TTTCAAAATT AATTGGTGTG GGAGCAATTG CTGGGTATAT CCAAGCATTT     900
AGCTCTACCC AACAACAACT ACAAGATTTA TCATTTTATG GAAAGTGGTT TTTTGCTATC     960
AATAAATACT TTGAAAATTA TTTCTGTATT TTAGATTACA AAATACCGAA ACCAGAAACA    1020
CAAATCAAAT TAGAAGAAAA AATCCATAGC ATTACATTTG AAAATATTAG TTTCTCTTAT    1080
CCTAATTCAA AACTTATTTT TGAAAACTTT AATCTCTCTT TACACTCTAA TAAAATTTAT    1140
GCATTAGTCG GCAAGAATGC TAGCGGAAAA AGCACGCTGA TTAATTTATT ATTAGGTTTT    1200
TATACCCCAA ATTCAGGTCA AATTATCATT AATAACAAAT ACCCATTACA AGACTTGGAA    1260
CTAAATAGCT ACCATCAACA AATGAGTGCC ATATTTCAAG ATTTTTCTCT TTATGCTGGG    1320
TATAGCATTG ATGATAATCT TTTTATGCAA AACAATATCA CTAAAGAGCA ATTGAAGCAA    1380
AAAAGAGAAA TACTAAAATC TTTTGATGAG AATTTTCAAA ATTGTCTTAA TGATTGCAAC    1440
AACACACTAT TTGGAGCGCA ATATAATGGG GTAGATTTTT CTTTAGGTCA AAAGCAACGC    1500
ATAGCTACCA TGAGAGCCTT TTTAAAACCA AGTAATTGCA TTGTTTTAGA TGAGCCAAGC    1560
AGCGCCATCG ATCCCATTAT GGAAAAAGAG TTTTTAGATT TTATTTTTAA AAAATCGCAA    1620
TCTAAGATGG CTTTAATTAT TACACACCGC ATGAATAGTG TCAAGCAAGC TAATGAAATT    1680
ATCGTGTTAG ATCAAGGCAA ACTAATAGAA CAGGGCAACT TTGAAACCCT TATGAAAAAA    1740
CAGGGATTAT TTTGCGAATT GTTTTTGAAA CAACAATAC                            1779
```

(2) INFORMATION FOR SEQ ID NO:1332:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1332

```
ACGCCCAGCA TGATAGTTAC AGAAACGAGC ACCGGTAAGA TTTTAGCCTT AGTGGGGGGG      60
ATTGATTATA AAAAAAGCGC TTTCAATCGC GCCACGCAAG CCAAACGGCA GTTTGGGAGC     120
GCGATCAAGC CTTTTGTGTA TCAAATCGCT TTTGATAATG GCTATTCCAC CACTTCCAAA     180
```

ATCCCTGATA CCGCGCGAAA TTTTGAAAAT GGCAATTATA GTAAAAACAG CGTGCAAAAC 240
CACGCATGGC ACCCTAGCAA TTATACTCGC AAATTTTTAG GGCTTGTAAC CTTGCAAGAA 300
GCCTTGAGCC ATTCGTTAAA TCTGGCTACG ATTAATTTAG CGATCGCTTG G 351

(2) INFORMATION FOR SEQ ID NO:1333:

(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:1333

CAAGGAGTTA CAACAATGGC TTTTCAGGTC AATACAAATA TCAATGCGAT GAATGCGCAT 60
GTGCAATCCG CACTCACTCA AAACGCACTT AAAACTTCAT TGGAGCGATT GAGTTCAGGT 120
TTAAGGATCA ATAAAGCGGC TGATGACGCA TCAGGCATGA CGGTGGCGGA TTCTTTGCGT 180
TCGCAAGCGA GCAGTTTGGG TCAAGCGATT CCCAACACGA ATGACGGCAT GGGGATTATC 240
CAGGTTGCGG ATAAGGCTAT GGATGAGCAA TTAAAAATCT TAGACACCGT TAAGGTTAAA 300
GCGACTCAAG CGGCTCAAGA TGGGCAAACT ACGGAATCTC GTAAAGCGAT TCAATCTGAC 360
ATCGTTCGTT TGATTCAAGG TTTGGATAAT ATCGGTAACA CAACGACTTA TAACGGGCCA 420
AGCGTTATTG TCTGGTCAAT TCAC 444

(2) INFORMATION FOR SEQ ID NO:1334:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 744 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334

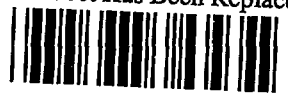
TTCAAGGTTT GGATAATATC GGTAACACAA CGACTTATAA CGGGCCAAGC GTTATTGTCT 60
GGTCAATTCA CTAACAAAGA ATTCCAAGTA GGGGCTTATT CTAACCAAAG CATTAAGGCT 120
TCTATCGGCT CTACCACTTC CGATAAAATC GGTCAGGTTC GTATCGCTAC AGGCGCGTTA 180
ATCACGGCTT CTGGGGATAT TAGCTTGACT TTTAAACAAG TGGATGGCGT GAATGATGTA 240

```
ACTTTAGAGA GCGTAAAAGT TTCTAGTTCA GCAGGCACAG GGATCGGCGT GTTAGCAGAA     300
GTGATCAATA AAAACTCTAA CCGAACAGGG GTTAAAGCTT ATGCGAGCGT TATCACCACG     360
AGCGATGTGG CGGTCCAGTC AGGAAGTTTG AGTAATTTAA CCTTAAATGG GATTCATTTG     420
GGTAATATCG CAGATATTAA GAAAAACGAC TCAGACGGAA GGTTAGTCAC AGCGATCAAT     480
GCGGTCACTT CAGAAACCGG TGTGGAAGCT TATACGGATC AAAAAGGGCG CTTGAATTTG     540
CGCAGTATAG ATGGTCGTGG GATTGAAATC AAAATTGACA GCGTCAGTAA CGGGCCTAGT     600
GCTTTAACTA AACGATGGTC AAAGAGCGGT CAAGATGAAA CGAAGGGATC TACTAACTAC     660
GGAAGGTATT CTCGGACACG CCTAGACGTA AGAGCATCAA TGTCGATTCG GTATTTAAAT     720
CACGCTTGCT TGCTTCAGAG CTAT                                            744
```

(2) INFORMATION FOR SEQ ID NO:1335:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1335

```
TCACCTCTTT GGTTAAAAAC ACGATTCCCA AATATTTGGC TCGCTAAAAT CCTTTATATG      60
GCTATCTTGC TTTGCGCGAT CGCTCATTCT GTGGGGCTAA TCTTGCGCTG GTATGTGAGT     120
GGGCATTCGC CTTGGAGTAA CGCTTATGAG TCCATGCTCT ATATCGCATG GGCTTCTGTT     180
ATCGCAGGGT TTGTTTTACG ATCCAAACTC GCGCTATCGG CTTCTAGCTT TTTGGCCGGT     240
ATCGCGCTCT TTGTGGCTCA TTTAGGCTTT ATGGACCCTC AAATTGGCCC TTTAGTGCCG     300
GTGTTAAAAT CCTATTGGCT CAATATCCAT GTCTCTGTCA TCACCGCTAG TTATGGCTTT     360
TTGGGCTTGT GTTTTGTGCT AGGGATTTTA                                      390
```

(2) INFORMATION FOR SEQ ID NO:1336:

(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:1336

```
AAAAGGCTTG AAATGGGCTT GTCTGTAGGC ATTGTGGGTT TGCCTAATGT GGGCAAATCC      60
AGCACCTTTA ACGCGCTCAC CAAAACCCAA AACGCCCAAA GTGCGAATTA CCCTTTTTGC     120
ACCATTGAAC CCAATAAAGC CATTGTGAAT GTGCCTGACA GGCGGCTTGA TGCGTTGGCT     180
CAAATCGTAA AGCCTGAACG AATCTTGCAT TCTGTGGTGG AATTTGTGGA TATTGCCGGA     240
TTGATTAAGG GGGCGAGCAA GGGGGAGGGT TTAGGCAATC AGTTTTTAGC CAATATCAAG     300
GAATGCGAAG TGATCTTGCA AGTGGTGCGC TGTTTTGAAG ATGACAATAT CACGCATGTG     360
AACGATAAAA TTGACCCCCT AAATGATATA GAAACCATTG AATTGGAATT GATTTTGGCG     420
GATATTGCCA CTTTAGACAA AAGGATCGAT CGCTTGCAAA AAGCCCTAAA AAGCTCAAAA     480
GACGCTAAAA ATCTTTTAGA ATGCGCTTTG AGTTTAAAAA CGCATTTAGA AGAATTGAAG     540
CCGGCGAAAA CTTTCCCCTT AAACACGAGC GAGGCTTTTT TGGAATTAGA CAAGGAATTG     600
CGTTTTTTAT CCCATAAAAA AATGATCTAT GTCGCTAATG TGGGCGAAGA AGATTTAAAT     660
ATTCTCAACG AGCATGCCAA AAAAGTTGAA AACCATGCGA AAGTCCAAAA TAGCGAGTTT     720
GTCGCCTTGT GCGCTAAATT GGAAGAAGAA ATGGTTTCTA TGAGTGGAGA TGAAGTCAAA     780
GAATTTTTGC AAAGTTTGGG CGTAGAAGAA AGCGGGCTAG AAAAAACCAT TCGTTTGAGT     840
TTTAAGGAAT TAGGCTTGAT CAATTATTTT ACCGCTGGAG TCAAGGAAGT GCGATCATGG     900
ACGATTAAAA AAGGTTCTAG TGCGCCTGTG GCTGCTGGGG TGATCCATAA GGATTTTGAA     960
AAAGGCTTTA TTAGAGCTGA AACCATCAGT TATGACGATT TTATCGCTTA TAAGGGCGAA    1020
GCCGGGGCGA AAGAAAAGGG AGCGTTACGC ATTGAAGGTA AGGATTATAT CGTTCAAGAT    1080
GGCGATGTGT TGCATTTTCG CTTCAATGTC                                     1110
```

(2) INFORMATION FOR SEQ ID NO:1337:

(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:1337

```
AGGAATAAAA CCATGCAAGC GTTAAAATCA TTGCTTGAAG TGATTACAAA ACTCCAGAAT      60
CTAGGCGGCT ATTTGATGCA TATAGCTATT TTCATCATTT TTATTTGGAT TGGAGGGCTT     120
AAGTTTGTGC CTTACGAAGC TGAAGGGATC GCCCCTTTTG TGGCCAACTC CCCTTTCTTT     180
TCTTTCATGT ATAAATTTGA AAAACCTGCA TACAAACAAC ACAAAATGTC TGAATCCCAA     240
TCCATGCAAG AAGAAATGCA AGATAACCCT AAAATCGTTG AAAACAAAGA ATGGCATAAA     300
GAAAACCGCA CTTATTTAGT GGCTGAAGGT TTAGGGATTA CGATCATGAT CCTAGGCATT     360
TTGGTGCTTT TGGGGCTTTG GATGCCTTTA ATGGGCGTAG TTGGGGGCTT CTTGTCGCTG     420
GAA                                                                  423
```

(2) INFORMATION FOR SEQ ID NO:1338:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338

```
CGATCACCAC CCTATTCTTT TTTATTCACA ACGCCAGAAG TGTTTGTCAA TCAGCATTTC      60
CCATGGCTTT CTGGGGCTGG AAGGCTAGTG GTTAAAGACT TGGCGTTATT TGCTGGAGGC     120
TTGTTTGTGG CCGGATTTGA TGCGAAACGC TATTTGGAGG GTAAAGGGTT TTGCTTGATG     180
GACCGCTCAT CGGTAGGGAT TAAAACTAAA TGCTCTAGCG GGTGTTGCTC T              231
```

(2) INFORMATION FOR SEQ ID NO:1339:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339

```
TGGTGTTTTA CAAATATTCA GGAAATCGGG AATGATTTTT TAATCCCTCA AAGTTTCAAA      60
AAAAAAGATT TTTCCAATTT AGCCCAACAG GTGTGCCATA GGCATGAGGG TTTTGGGGCA     120
GATGGGCTTG TGGTCGTCTT ACCGAGTAAA GATTATGACT ACGAATGGGA TTTTTACAAT     180
TCAGACGGCT CTAAAGCCGG CATGTGTGGG AATGCGAGCC GTTGCGTGGG GTTATTTGCC     240
TACCAACATG CTATAGCCCC TAAAGAGCAT GTTTTTTTAG CCGGAAAAAG AGAGATTTCT     300
ATCCGCATAG AAGAGCCCAA CATCGTAGAG AGCAATCTCG GTAATTATCA AATCCTAGAC     360
ACCATACCCA ATTTAAGATG CAAAAAATTT TTTACTAATA ACAGCGTTTT AGAAAATATC     420
CCTATGTTCT ATCTTATCAA TACAGGAGTG CCTCATTTAG TGGGATTTGT GAAAAATAAA     480
GGGTTATTAA ATTCTCTTAA CACACTGGAA TTAAGGGCTT TAAGGCATGA ATTTAACGCT     540
AATATTAACA TCGCTTTTAT AGAAAATAAA GAGACGATTT TTTTACAAAC TTATGAGAGA     600
GGGGTTGAAG ATTTCACGCT AGCTTGCGGG ACAGGCATGG CAGCGGTTTT TATCGCCGCG     660
CGCCTTTTTC ATAACACCCC TAAAAAAGCC ACTCTCATCC CTAAAAGCAA CGAATTTTTA     720
GAGCTTTCTT TAAAAAATGA TGGAATTTTT TATAAAGGAG TCGCGCGTTA TATCGGCATG     780
AGCGTTTTAG GCATGGGTGT TTTTAAAAAT GGGTGTTTT                            819
```

(2) INFORMATION FOR SEQ ID NO:1340:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1077 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340

```
TTTTTGGTTC AGTTTAATGG GGATAATTGC ATGAAAGCTC AGTATTTCTT TTGGATTCTT      60
TTTTTGATTG GTTTTTATTG GATGCTTTAT CTGTATCAAG ATTTTTTAAT GGACGCACTG     120
ATCGCTGGGC TTTTGTGTGT GGGGCTTTTT CAAGTGAAAG TTTTTTTGAA TAAACGCTTT     180
TCTAATGTTA TCAGTTCGTT TTTATGCGTT TTGGTTTTAG CGAGCGTTGT GATCGTGCCG     240
TTGTATTTTA TTGTTTATAA GGGTTCTAAT GTCATTTTTG AAATCAATTT TGAAAAACTT     300
TCAGCCTTAA TCAAATGGCT TAAAGGGACA ATCACCGAAA ATTTGTCGCA TTTTCCTGCC     360
ATTCATGATG GGGTTAGCAA GTTTTTAGAA AATTTTAGCG CCGCTTCCAT CACGGGCTAT     420
TTGTTGAAAG TGAGCAGTTA TATTGGGAAA TACAGCTTGA AACTCGTTAC AGACGCTTTA     480
TTTATCTTGG GGTTATTGTT TTTCTTTTTT TACTATGGGG AGAAATTTTA TCGTTATTTT     540
TTAGGGGTCT TGCCTCTTGA AATGAATCAA AGTAAAAAAA TTTTTGAAGA AGTGGCTGGG     600
ATTTTACGAA TCGTGCTTTT AACTTCTCTC ATCACGGTTA TTTTAGAGGG CGTGGCGTTT     660
GGGACGATGA TAATATGGTT TGGGCATGAT GGCTGGTCTT TAGGGATTTT ATACGGCCTA     720
GCGTCTTTGG TGCCGGCTGT TGGGGGGGCT TTGATTTGGA TCCCTATAGC GATTTATGAG     780
CTTTATCATG GGCATGTGAA TGAGGCTATT TTTATCGTTT TGTATTCCAT TTTGTTAATT     840
GGTGTGTTGA TTGATAGCGT GATCAAGCCA ATTTTAATCG TTTTTATCAA AAAAAGAATC     900
TTTAAAACCA CCCTTAAAAT CAATGAAATA TTGATTTTCT TTTCTATGAT TGCTGGGATT     960
TCTCAATTTG GTTTTTGGGG GATTATCGTA GGGCCTACCA TCACGGCGTT TTTTATCGCG    1020
TTACTGCGAT TGTATGAAAA TTACTTTATT CAAAAGGAGC AAAAAACATG CGAATGT       1077
```

(2) INFORMATION FOR SEQ ID NO:1341:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 645 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1341

```
AGGTTAAACA TGAACTACAA AGTTGCATCT GCTAGAAATA TCGCAACGCT TCTTTTCTTA      60
TTCTTTTCTC AAAGTGAAGC TTTTGATTTG GGTAAAATCG CTAAAATCAA AGCGGGTGCT     120
GAAAGTTTCT CTAAAGTCGG TTTCAATAAC AAACCTATCA ACACTAATAA AGGGATTTAC     180
CCTACCGAAA CCTTTATGAC GATTATGGCT TACATGCAGG TGGATTTTAC GGAGCTCTTG     240
CCCAAAAGCG CTACGGCTAA CGGGCACCAT TTAGACGGGA GCCTTGGGGG TTGGGGGGGT     300
GCTGTGATTT ATGATAGCAC TAAGGATTTT ATTAACGAAG TTACAGGAAA ACCCTATGGG     360
```

```
GCTATGACGT GGAACTACGT GGGCTATTGG GGCGGTCTTG TAGGGCAAAA ACCATGGGCT     420
AGTTGCGGGT TAGCCACAGG GAATTTGACC CAAGGCCAAT ACGATAAGAT GACTCAAGCT     480
GAAATGACGC AGTTGTCTAA TCAAGAAGCT TTAGCGGCTT CCACTTGCGC AAAAACCTAT     540
GCCGATCACA CGAGAAACTA TGTGATTTAT AACGCTTACT TGCGCTACAA CTACAAAGAT     600
ATTTTTGAAA TTAGGGGCGG AAGGTACGAA TCCCAGCGGA TTATA                     645
```

(2) INFORMATION FOR SEQ ID NO:1342:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 795 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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

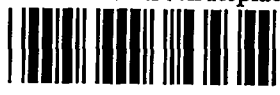
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342

```
ATTTTCTATC CAAATGGGTA TAATAATCGC ATGGGTTTTT TAAAAGTTTT AAAACATGAC      60
GCTTTAGGGC AAGTAGGGAA TATTGTTATA GGGAATTTCT TAATAACGCT CACTGTTTTA     120
GCGGTTTGTT TTTCCTCTCA AAGCGCTGAA GAAACGACCA TGCTCACCCT AAGCTACACG     180
CTCTTTTTTA TTTTAGGGGC GTTTTTATTA GTCGCAATCA GCGTGGGAGC GATCAAAAAC     240
CTCAACGCGC TTTTTTCTAA AAGAGGGGTT TTAAGCTTTT CCTTACCCAT TAGTTTGGAA     300
TCTTTATTGC TCCCTAAAAT CTTGCTCCCC ATGGTGTTTT TTATCTTCAG TTTGTTCTGG     360
TTTGTGGCGA GCGTGCGTTT GGGCTATTAC CTTTTTAACG CGCAATCCAG CGTGCTGTTT     420
ATCTTGCACA CCGCTTTAAA AACCTTTGCG TTAAAACCCA CTAAAACTAT AGGCGTTGCG     480
CTGTTTTTAG GGCTTGTTTT AATGAAATTT TTATTTGTTT TGAGCGTTTT AAACGCTACT     540
AGGATCAAAA AAGCGCGTTT TTTACTCGGG GGGTTGTTGT TCATTCTGGT GGGGGTTGTT     600
TTGGAATTGG CTTTCAATTC GTTACTGCCC TTAATGAGTT CTAGTTTGAG CATCAATGAG     660
GGGTTTTATT ATTTCTTGCA ACAACAAGAA TTACAAGAAA ATAAATACTA TCTTTTATGG     720
GGGGTGGATT TTTTAAAAAT CCTTTTATTG TATGGGGTGA TCCGTTACTT GCTCACGCAT     780
AAATTAGAAT TGGAT                                                     795
```

(2) INFORMATION FOR SEQ ID NO:1343:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 594 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1343

```
CACATGAAAG GCTTATGGCT TGTAATCTCT TTAGTTTTTG TTGGTTTTTT GTGGGCTAAT      60
GAATCTTATG TTTTTAACAA TTCTAAGGGG CGTTTAACAG AAAAAAGCGT TGCGTTTATA     120
GAGGGCGTTT CTAAAGAGCT TTATCTTAAA ACCGGCGTGC GTTTTGCGAT TGATATGACG     180
GATTTTGAAA AAAATCCTAT CGCTCTAGCG AATAAAAAAG AGCGCCAAAG CTATCAAGAG     240
GGCTTTTTAA AGCAGCTCAA ACCCCCTTTT GTGGTATTCT TTTTCTACCA TGACGCTCAA     300
AAAATAGAAT TAGTGGCTAA CCCTAAAGAT TTGCTAGACA CTGATAAAAT CTTTTTTGAA     360
AAAATCGCTC CCTTACTCCC CACAAACGCT AAAGAATACA CGCCCCAAAG AATTTCAGCC     420
ATGCTCATTA ACGGCTATTC GGTCGCAGTA GATGCTTTAG CGGAAAAATA TCATGTGAAT     480
ATCACGCAAA ATTTTAGCGC TCCTAAGGGA GTAACTTTTG TAAAGGTGGT TATTTATATT     540
TTGTTATTGA CGCTTTTGGG CGCGTTTTTG GGGCTTTATT TTTTTAAAAA ATCT           594
```

(2) INFORMATION FOR SEQ ID NO:1344:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 591 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1344

```
GAGGGAAAAT CAATGAAAGA AAAAAACTTT TGGCCTTTAG GAATCATGAG CGTGCTTATT      60
TTTGGGCTTG GGATCGTGGT GTTTTTAGTG GTGTTTGCCC TAAAAAATTC GCCTAAAAAT     120
GATTTAGTGT ATTTCAAGGG TCATAACGAA GTGGATTTAA ACTTTAACGC CATGCTTAAA     180
ACTTATGAAA ACTTTAAATC CAATTATCGT TTTTCAGTGG GTTTAAAGCC TCTTACCGAA     240
AGCCCTAAAA CCCCCATTTT GCCCTATTTT TCTAAAGGCA CGCATGGGGA TAAAAAAATT     300
CAAGAAAACC TTTTAAACAA CGCTTTGATT TTAGAAAAGT CCAACACGCT TTATGCACAA     360
TTGCAACCGC TCAAACCCGC TTTAGATTCG CCAAATATTC AAGTGTATTT AGCGTTCTAT     420
CCCAGCCAAT CCCAGCCCAG ATTATTAGGA ACGCTTGATT GTAAAAACGC ATGCGAACCT     480
TTAAAATTTG ATTTGTTAGA GGGCGATAAA GTGGGGCGCT ATAAGATCCT TTTTAAATTT     540
GTTTTTAAAA ATAAAGAAGA ATTGATTTTG GAGCAACTGG CTTTTTTTAA G              591
```

(2) INFORMATION FOR SEQ ID NO:1345:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345

```
GCAAATCAAT TTGCGCTACA ATTTTCCTTT TCTAATTTCA AGCATGGCGA TTTTACCACA      60
AGGGATTTTA TGCTCTATTC TTTATTATAT GGCTATTTTA ATATCAATCT TTTCCAGTAT     120
TTGACCTTTA GAGCAGGGTT AGGGTTTTTC ATAGCCTTTT TTCTCACGCT TTTTTTAATG     180
CCTAAATTCA TTCTATGGGC CAAGGCTAAA AAGGCTAACC AGCCCATTTC TAGCTTCGTG     240
CCAAGCCACC AGAATAAAAA GGATACCCCT ACGATGGGGG GCATTGTGTT TGTTTTTGCA     300
ACCATTGTTG CGAGCGTGTT GTGCGCGTCT TTGAGCAATC TTTATGTGTT GTTAGGGATA     360
ATCGTGTTAG TGGGCTTTAG TTTTGTGGGT TTTAGAGACG ATTACACTAA AATCAACCAG     420
CAAAATAACG CCGGGATGAG TGCGAAAATG AAATTTGGCA TGCTGTTTAT CCTTTCGCTT     480
ATAGTGTCTG TTTTATTGAG CCTTAAGGGG TTGGACACTT TTTTATACGC GCCGTTTTTG     540
AAAAACCCCT TGTTTGAAAT GCCCACGATG TTAGCGGTTG GTTTTTGGGT GTTGGTTTTT     600
TTATCCACGA GCAATGCGGT GAATTTAACC GACGGGTTAG ACGGATTAGC GAGTGTGCCT     660
AGCATTTTCA CCCTCTTAAG CCTTTCTATC TTTGTGTATG TGGCAGGGAA TGCGGAATTT     720
TCTAAATACT TGCTCTATCC TAAAGTCATA GATGTGGGGG AATTGTTTGT GATTTCGCTA     780
GCATTAGTGG GATCGCTCTT TGGCTTTTTG TGGTATAACT GCAACCCGGC AAGCGTGTTT     840
ATGGGCGATA GCGGGAGTTT GGCAATAGGA GGGTTTATCG CTTATAACGC TATTGTTTCG     900
CATAATGAAA TCTTGCTCGT TTTAATGGGG TCTATTTTTG TAATAGAAAC TCTGTCTGTG     960
ATCTTGCAAG TAGGGAGCTA TAAAACCCGT AAAAAACGCC TTTTTTTAAT GGCACCCATC    1020
CATCATCATT TTGAACAAAA GGGTTGGGCA GAAAATAAGG TGATCGTGCG TTTTTGGATC    1080
ATTTCTATGC TGAGTAATTT AGTCGCTCTT TTGAGCTTGA AGGTGTGT                  1128
```

(2) INFORMATION FOR SEQ ID NO:1346:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 909 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346

```
GCAAGATTTA TTAAAATATT TGGCATGGGA AAATTTTCTA AATTAGGCTT TATTTTAGCC      60
ACTTTGGGTA GCTCTATCGG TTTAGGGCAT ATTTGGCGCT TTCCTTATAT GGTAGGTCAT     120
AATGGGGGGA GCGCGTTTGT GCTTTTATAC CTAGCACTAA CCTTGAGTTT AGGCATTGCT     180
ATGCTTTTAG TGGAAATGCT GATTGGAAAT TTGGGTAAAA AAGACGTTGT TTCCAATTAT     240
CAAATCTTAG ATCCTAAAAG GAAAAAATAT TACCCTTTCA CTTCTTTTTT TATTTTAGGC     300
GGCCCTCTCA TTCTATCTTT TTATGCGGTG GTGTTAGGCT GGGTGCTTTA CTATCTTTTT     360
GTAGTAACTT TTGATTTGCC TAAAGATTTA GAGCAGGCTA AAATGCAATT CAGCATGCTT     420
CAAAATGGCA GTTTGATCTG GCCTGTTATT GGCTTTAGCG CATGCTTGTT GCCGACAATA     480
TGGTTTGTTT CTAGGGGGAT TGAAGAGGGG ATTGAAAAAT TAAATGTCGT GCTGATGCCC     540
TTATTGTTTG TGATTTTCAT AGGGCTTTTA ATCTATGCGA TGACTTTAGA AAGCATGCCT     600
AAAGCTTTGC GTTTTTTATT TAATTTTGAG ATTCAAAAGA TTGATTTTAA GGTTGTGATG     660
GACGCTTTAG GGCAGATGTT TTTTTCTTTG AGTTTAGGGG TAGGCACGAT CATTACTTAT     720
```

```
TCGGCTTTTA CGCCTAAAAA AGAAAACCTA CTCAAAAGCT CTCTGTTTAT TGTTTTACCG     780
GGTATTTTAA TTTCTTTGAT TGCCGGGGTG ATGATTTTTA CCTTTGTGTT TGAATACCAT     840
GCAGACGTGT CTCAAGGGCC AGGGCTTGTT TTTATTTCCT TACCTTTAAC TTTCGCTAAA     900
ATGGGATCA                                                             909
```

(2) INFORMATION FOR SEQ ID NO:1347:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347

```
AGGTGTGTTA AAATGAAAAT TTCTTTATTG GGGCATGGAA AAACCACTCT AGCCCTAGGG      60
CGTTTTTTTA AAAAAAACCA TAATGAAGTC AAATTTTTTG ATGATAAATT CCCTGCATTT     120
TTTAAGGATA GCGAGGGTTT TCTTTGCTAC CCTAGTAAGG ATTTTAACCC TAATGATTCC     180
CAACTAGAAA TCGTCAGCCC TGGCATTAGT TTCACGCACC CTTTAGTCAT GAAAGCCAAG     240
CATTTAATGA GCGAATACGA TTATATTGAT AGTTTGTTTG ATCATTCTTT CACGCCTACG     300
ATGATAAGTA TTAGCGGCAC TAACGGGAAA ACCACCACGA CCGAAATGCT CACCACACTT     360
TTAGAAGATT TTAAGGCTGT GAGTGGGGGG AATATCGGCA CGCCCTTGAT TGAATTGTTT     420
GAAAAACGAT CGCCCTTGTG GGTGCTAGAA ACAAGCTCCT TTTCTTTGCA TTACACTAAT     480
AAGGCTTACC CTTTAATCTA CTTGCTCATC AATGTGGAAG CCGATCATTT GACTTGGCAT     540
TGCAATTTTG AAAATTATTT GAACGCTAAA CTCAAGGTTT TAACATTGAT GCCTAAAACT     600
TCGCTCGCTA TCCTCCCTTT AAAATTCAAA GAACACCCTA TTGTTCAAAA CTCGCAAGCG     660
CAAAAAATCT TTTTTGACAA AAGCGAAGAG GTTTTAGAGT GTTTAAAAAT CCCTTCTAAC     720
GCCCTTTTTT TTAAGGGAGC GTTTTTATTA GACGCGGCTT TAGCCCTTTT AGTTTATGAG     780
CAATTTTTAA AAATAAAGAA TTTAAAATGG CAAGATTATA GAGAAAACGC CCTTAAAAGA     840
CTGAACGCTT TTAAAATCGG CTCGCATAAA ATGGAAGAAT TTAGGGATAA ACAAGGGCGT     900
TTGTGGGTAG ATGACAGCAA AGCCACGAAT ATTGATGCCA CCTTACAAGC CCTAAAAACC     960
TTTAAAAACC AAAAAATCCA TTTGATTTTA GGGGGCGATA TTAAAGGGGT CAATTTAACC    1020
CCCCTTTTTG AAGAGTTTAA AAACTATAAA ATAAGCCTTT ATGCCATAGG ATCAAGCGCT    1080
TCTATCATAC AAGCCTTAGC GTTAGAATTT AATGTTTCTT GTCAGGTTTG TTTGAAGTTA    1140
GAAAAAGCGG TTCAAGAAAT TAAAAGCGTT TTATTACAAA ATGAAGTCGC TTTGCTTTCA    1200
CCTAGCGCGG CCAGTTTGGA TCAATTTTCT TCGTATAAAG AAAGGGGTGA AAAATTCAAA    1260
GCGTTTGTTT TAAAAGAT                                                  1278
```

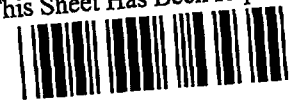
(2) INFORMATION FOR SEQ ID NO:1348:

(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

This Sheet Has Been Replaced



(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:1348

GATATGGGTA ATCATTTTTC TAAATTAGGA TTTGTTTTAG CGGCTTTAGG GAGCGCGATA 60
GGTTTAGGGC ATATCTGGCG CTTCCCCTAT ATGACTGGGG TGAGTGGTGG GGGTGCTTTT 120
GTTTTATTGT TTTTATTTTT ATCCTTAAGC GTTGGTGCGG CGATGTTTAT CGCTGAAATG 180
CTATTAGGAC AAAGCACGCA AAAAAATGTA ACAGAAGCTT TTAAAGAGCT TGACATTAAC 240
CCTAAAAAAC GCTGGAAATA CGCAGGGATC ATGCTTATTT CTGGACCTTT AATACTGACT 300
TTTTATGGCA CTATTTTAGG TTGGGTGCTT TATTATTTGG TGAGTATTAG TTTTAATTTG 360
CCTAGCAGTA TCCAAGAATC TGAACAAATT TTTACTCAAA CTTTGCAGTC TATAGGGTTA 420
CAATCCATAG GGCTTTTTAG CGTTTTATTC ATAACCGGAT GGATTGTTTC TAGGGGGATT 480
AAAGAAGGCA TTGAAAAACT CAATTTGGTT TTAATGCCCT TACTCTTTGC CACTTTTTTT 540
GGTTTGCTTT TTTATGCGAT GAGCATGGAT TCTTTTTCTA AAGCTTTCCA TTTCATGTTT 600
GATTTCAAGC CAAAAGATTT GACCTCTCAA GTGTTCACTT ATTCCTTGGG GCAGGTTTTC 660
TTTTCTCTAA GTATCGGTTT AGGGATCAAT ATCACTTATG CTGCCGTTAC GGATAAAACG 720
CAGAATTTGC TTAAAAGCAC GATTTGGGTG GTTTTATCAG GGATTTTAAT TTCTCTTGTG 780
GGCAGGGCTT ATGATTTTCA CTTTTGTGTT 810

(2) INFORMATION FOR SEQ ID NO:1349:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349

TGTCTCACAA GGCACAGGGT TAATCTTCAC TTCTTTACCG GTGGTTTTTG GCCAAATGGG 60
AGCGATAGGC GTTCTTGTTT CAATTCTTTT CTTGCTCGCG CTCGCTTTTG CTGGCATCAC 120
TTCTACGGTG GCTTTATTAG AGCCAAGCGT GATGTATCTT ACCGAAAAGT ATCAATACTC 180
TCGTTT 186

(2) INFORMATION FOR SEQ ID NO:1350:

(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:1350

```
TTTCTCTTGT GGGCAGGGCT TATGATTTTC ACTTTTGTGT TTGAATATGG GGCTAATGTC    60
TCACAAGGCA CAGGGTTAAT CTTCACTTCT TTACCGGTGG TTTTTGGCCA AATGGGAGCG   120
ATAGGCGTTC TTGTTTCAAT TCTTTTCTTG CTCGCGCTCG CTTTTGCTGG CATCACTTCT   180
ACGGTGGCTT TATTAGAGCC AAGCGTGATG TATCTTACCG AAAAGTATCA ATACTCTCGT   240
TTTAAGGTTA CTTGGGGTCT TGTAGCGTTA ATCTTTGTGG TAGGCGTGGT GTTGATTTTC   300
TCGCTCCATA AGGATTATAA AGACTATCTC ACTTTCTTTG AAAAAAGTCT TTTTGATTGG   360
TTGGATTTTG CATCAAGCAC CATTATCATG CCTTTAGGCG GGATGGCAAC CTTTATTTTT   420
ATGGGCTGGG TTTTGAAAAA AGAAAAATTG CGTCTTTTGA GCGCGCACTT TTTAGGCCCT   480
AAATTGTTTG CAACTTGGTA TTTCTTGCTT AAATACATCA CCCCTTTAAT TGTGTTTTCC   540
ATTTGGTTGA GCAAGATTTA T                                             561
```

(2) INFORMATION FOR SEQ ID NO:1351:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351

```
GAGTCTTTTA TGGGGTGTTC GTTTATCTTT AAAAAAGTTA GGGTTTATTC TAAAATGTTG    60
GTTGCTTTGG GGCTTTCAAG CGTGTTGATC GGTTGCGCGA TGAATCCAAG CGCTGAGACA   120
AAAAAACCAA ATGACGCCAA AAACCAACAA CCAGTTCAAA CTCATGAAAG AATGACAACA   180
AGTTCTGAAC ATGTTACGCC ACTAGATTTT AATTACCCGG TGCATATTGT TCAAGCCCCA   240
CAAAACCATC ATGTTGTAGG TATTTTAATG CCACGCATTC AAGTGAGCGA TAATCTAAAA   300
CCCTATATTG ATAAGTTTCA AGACGCTTTA ATTAATCAAA TCCAAACTAT TTTTGAAAAA   360
AGAGGCTATC AAGTGTTGCG TTTTCAAGAT GAAAAAGCTT TGAATGTGCA AGATAAGAAA   420
AAGATTTTTT CCGTTTTGGA TTTGAAAGGG TGGGTAGGAA TCTTAGAAGA TTTGAAAATG   480
AATTTAAAAG ATCCCAATAG TCCCAATTTA GACACGCTAG TGGATCAAAG CTCAGGCTCT   540
GTATGGTTTA ATTTTTATGA ACCAGAAAGC AATCGTGTCG TCCATGATTT TGCTGTAGAA   600
GTAGGAACTT TTCAGGCAAT AACATACACA TACACCTCTA CTAATAACGC TTCAGGAGGG   660
TTTAATTCTT CAAAAAGCGT TATCCATGAA AATTTGGATA AGAATAGAGA AGACGCGATA   720
CACAAGATTT TAAACAGAAT GTATGCGGTT GTCATGAAAA AAGCTGTAAC AGAACTTACA   780
AAAGAAAATA TCGCCAAATA CAGAGACGCT ATTGATAGAA TGAAAGGCTT TAAAAGTTCT   840
ATGCCTCAAA AAAAG                                                    855
```

(2) INFORMATION FOR SEQ ID NO:1352:

(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:1352

```
GAATTGGTTT TGTTTGAAAA GTTGAAATTT TTTAAAATCA AAAAAGACGA TGAAAATCAG      60
CCAGAAGTCA ATTTAAATTC TGAAATCTAT GAGCAATTTA AGGTCTTTAG ACTCCCGCTT     120
ATTTTAATCC AATTGCTCGT GCTTTTAGGC ACTCTGGGAT ACTTCGCCCT AGAAAATTAT     180
AGCCTTATGC AAGCTTTCTT TCAAACGACT TACACCATGA CAGCTACAGG GTTTGGCGCT     240
TTAAATGAAA GCCAGTTTGG GCCTATAAGT ATTTTTTTAA CTTCCATTTT AATGTTTTGT     300
GGGACGGGAA TTATTGCTTT TAGCGTGGCT ATTTTAGTTA GCGTGGTCAA TAAAGGCACG     360
CTTACCAGAT TGATTAAGGA GAAAGGTATG ATTTATAAAA TCGCGCGCCT TAAGGATCAT     420
TATGTGATTT GTTACCATAA TGAATACACC ATTGAGTTGA GCAAGCAGTT TCGCTCCGCT     480
CAAATCCCCT TTGTGGTCGT GGATAATGAT CCTAATTTTG AAGAAGAAGC CATTAAGCAC     540
AAATACCCCT ACTATATCAT AGGCGATCCG CACACCAATT TAGCCATGCT AAAAACCCAC     600
TTAAGCAGCG CTAGGGGCGT TGTGGCGTTG TCTAAGATTT TACCGGTGAA CGTGGCGTTA     660
ATGGTGAGCG TGCGCTTGTT TGAAAAGGAA TTAAAACGCA AACCTTACTA CATCATTGCG     720
AGCGCACACA GCGATGAAGG TTTAGAAAAA TTAAAAAAAT TAGGGGCTGA TATGGTGGTT     780
TCCCCTACAA AACTCATGGC GCAGAGAGTG AGCGCGATGG CGGTGCGTCC GGATATGGAA     840
AATATCTTAG AGCGTTTTAT CAACAAAAAA GACACGCTTT TAGACTTAGA GGAAGTGATT     900
GTCCCCAAAA CCAGCTGGCT TGTGTTAAGG AAATTAAAAG AAGCCCATTT TAGAGAGATC     960
GCTAAAGCCT TTGTGATTGG TATCACTCAA AAAGATGGCA AATACATCCC CATGCCTGAC    1020
GGGAAACGAT TATTGCAAGC GAATCCAAGC TAT                                 1053
```

(2) INFORMATION FOR SEQ ID NO:1353:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1353

ACCAAAAAGT TAAACAATAC TCTATTCAAT AAAGGATTAA TTATTTTTAA AATGTTTAAA 60
AAAATCATTT TTTTGTGCGT TTTTTTGATA GGGGGATTTG TCATTCCACC CCTTGAAGCC 120
ATGCCTATTT TGCGCAATAA AACCCCCAAA AAAAATTACC AAGAAGCCCA TGAAAAGCTC 180
TATAGAAGCA TCATTAACCG CCAAAAGCTC ACGCGTAAAA AAAGCGGGTG GTATTTTTTA 240
GGGGGGGTTG GCGCTGTAGA AGCCATTAAG GACTATCAAG GCAAGGAAAT GAAAGATTGG 300
ATGCCACGCT CAATT 315

(2) INFORMATION FOR SEQ ID NO:1354:

(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:1354

ATCATGGCGT GTAAATTTTG CCCTAAGATC AGAAAAACAG ATTGGATTTT TATTTTAATC 60
GCCGCTTTAG GCTTTTATTC AGTTAATAAG CTAGGGTATG CGCCCAAATT CAATACCCCC 120
ACTCCAAAAT CTTCACGCCC TCTTTCACGC CCTATTGAAA AGCCTAACAA TATGACTGAA 180
GAAGAAAGGA AAAAGCGTTT TATAGAGTTG CAAAAAGCAT GCTTACTTCA TAAAGACAAA 240
AAGGCATGCG AAGAGGTTTT T 261

(2) INFORMATION FOR SEQ ID NO:1355:

(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:1355

CGAGCTATCA CAACAAATCA ATTCGTAGGA ACAAACATGT TTTTTAAAAC TTATCAAAAA 60
TTACTGGGCG CGAGCTGTTT GGCGCTGTAT TTAGTGGGCT GTGGGAATGG TGGTGGCGGT 120

This Sheet Has Been Replaced



```
GAATCGCCGG TTGAGATGAT TGCAAATAGC GAGGGTACGT TTCAAATCGA CTCCAAAGCA     180
GATAGCATTA CTATTCAAGG CGTGAAGCTT AATAGAGGTA ATTGTGCTGT CAATTTTGTT     240
CCAGTAAGTG AGACGTTTCA AATGGGTGTT TTAAGTCAAG TTACTCCAAT CTCTATACAG     300
GATTTTAAAG ATATGGCAAG CACTTATAAG ATATTTGATC AAAAGAAAGG GTTGGCAAAC     360
ATAGCAAATA AAATTTCTCA ATTAGAGCAA AAGGGTGTGA TGATGGAACC TCAAACCCTT     420
AATTTTGGAG AAAGTTTAAA AGGCATTTCT CAAGGGTGCA ATATTATAGA GGCAGAAATA     480
CAAACCGACA AAGGCGCTTG GACTTTTAAC TTTGATAAA                            519
```

(2) INFORMATION FOR SEQ ID NO:1356:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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

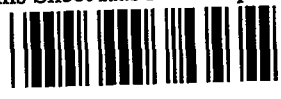
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356

```
ATATCAAACA TGGAAAATAC CCCGAAAGAC AGAGCAAGAA TCCTTATAGA AGAGCTTAAA      60
ATCTTGCAAG GCGTTATCAA CAGAATGGCA CAAAATTCTT TAGAATGCAA AAAATGGACT     120
CTCGCTCTCG CTGTGGGTGT CTTATCCCTC AAAATAGAGG CAATTTCTAA TTTTTATGGG     180
TTATGCGTTT TAGGGGTGTT GTTAGCATGT TTTTATCTTT TAGACGCTTA TTATCTCATG     240
CAAGAAAGGC TGTTTAGGGA GCAATACCAA TGGCTAATAA AAAACCGACT TAAAACCGAT     300
GAAAGGCTGT TTGAAGTCTT CCCTATTCAT CAAACTTGCC AATCAACGCA ATTCTTATCC     360
GCCATGCGTT CGTTTAGTCT TTTCCCCTAT TGGGCGTTAG GTTTGTGTTT GGTGGGCTAT     420
GGTTTTTGTT GT                                                        432
```

(2) INFORMATION FOR SEQ ID NO:1357:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 966 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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

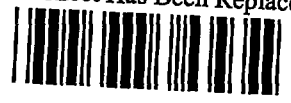
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357

```
CCCCTTAAAT CAAAGGCAAG CAAACTTTTA GGCGCTAACA TCGTGTATAA AATCCATTGT      60
TTGGTTAAAG GGGTAACTTT AGAGCAGCAA AACAAGCTTT TAAAAACCAT TGAGCCTTTT     120
AAAAAATTCG CTTCATTAGA GTTTATAGAC ATCAATTCGC TAGATTATTC CATAGAAAGC     180
TATCTTAATG AGTCTTGCTC CAAGCGTTAT GGCGGGCTTC TTGTTTTGTG CCGGCTCTTG     240
CTCGCTTCGC TCTTCCCTAA TTATTCTAAA ATCATTTCCA TAGATGTGGA TACGGTGTTT     300
TTAGGCGATG TTGCAAGCGC TTATTTTGCG CTGGATAATG AACCCACTAA ATTGCTTGGC     360
ATGGTGAGAG ACACTTTTTC CCACCTTCCT TTTGAAGCCT TTTGTGATTT TTGCGAACGC     420
ACATGCAAGA ATTTTAAAAT TGATCTTTTG CGCTTTAGCC AAAACGAATT AAAACGCATC     480
CATCAGGGCT TTAACATGGG CTTTTTGGTG GCGAATTTAG ATTTATGGCG CGAAAATGGG     540
TTTGAAAAAA TCGCTTTAGA GTTTTTGAAA ACTAGGGGAA AGGATCTTTT CTACCCTGAG     600
CAGTGTTTAA TCAATATGGT GTTTTTAGAG CGTATTTTAG AATTGCCTAT TCATTATAAT     660
TGCTATTCTG ATTTTTTCAA AGAGCACTAC CCTAAAAGTA TCATCATGCT CCATTTCATC     720
AAATACAAGC CGTGGCGTTC TGTCAGTTCT TTGAACGGGC GTTTGATTTG CTATGAAGCT     780
GAAGCGAGTT TTTGGCTCGC CAACCTTTTT TGCACCCCTT TTAAAAACGA TTTTTTTAAA     840
GAACGCCTTG AAATGGCTAA AGACCAACAA ATGCAATCTT TTAAAACCCA CATCCGATCA     900
AAAACGATTA GGGATTATTT TTATTTTAGG ATAAAAAATA TTTTGAAAAA AGTTTTCGAA     960
CTCTCT                                                               966
```

(2) INFORMATION FOR SEQ ID NO:1358:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1698 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358

```
AAAAAGTTTT CGAACTCTCT TAAAGGACAA AAAAAAACGA TGAAATTTTT AAAATTCTTT      60
GCCAGTAGCG TAACTCTAGA TGAAAAATTT TTAATGTTCC TTCTTTGCAA CGCTCTTTCT     120
AACGCTTACA AAAATAGCGA TTTGTTTTCT TTCTCTAAAG GCTTTTTAGG CGCTTTTTTA     180
ATCGGGTTTG TGGTGTATTA TGGTTGCGCG CTAATCCCTA AAAAACGCTT GAAATATTCA     240
TTAGAATGGC TGTTTATAGG AAGCGGTATT ATTTTTAGCG TGGCAGAAAT TTTTACGCTG     300
TTTATGTTTA AAATGCCTTT TTCCAAAGGC TTGATTGACA CGCTTTTAGC CACAAACAGC     360
TCTGAAACGA TGGCGTTTAT AAAAAGCTAT AAAAATTATT TGCTTTACTA CGCTTTGATT     420
TTGATCGCTT TGTTGATCGC CATTAAAATC ATTCGCTTTA GAGCGCTTGT GCCTGGTGTG     480
ATAGCGAGCG TTTTAGGGCT TTCTATCCTT ACAATAGGGA GCGTTCGTAA CATTAAACAC     540
CTTACAAAGA ACGATGCGAT TTTAAAAAGA TCACTCTTTT CTCTTTCTTT AGCTAGGGGG     600
TTTTATTCCG CTTATTTGAG TTTGTTTGAT CGCCAACAAG CCATAAAATT TTATAGCTTT     660
TTAAATAATC TTTATTTACC AAGCGATTAT CTTTCTAGCA CGGGCGATAT TTCAAATGTC     720
GTCTTAGTCA TCGGCGAAAG CGCGAGCAGA AATTTCATGC AACTCTATGG CTATAGCGTT     780
CCTAATAATC CCTTATGCGA GCGAACTCGC CAAGCGAGAG AGAGAGAGAG AGAGAGTAAC     840
AACCTGTTCG TGTTTTCTGA CACGATAAGC AAAGAAGCCC ACACCTCTGA TGTCTTTGAA     900
AGCCTGCTCA ATTATAGCGA TGCTGAAACG ACTAAACCTT GGTATCATTA CCACAACATG     960
ATAGATATTT TCAAGCGATC CCATTATGAA ACTTTTTGGT TAGAAAAACA AATCGTCGAT    1020
GAATGGGGGA TCACACAAAA TCTAGTCTCT AATCGTTCTA AAAACCGCTA CTATATTTTG    1080
GGAAACTATG GTGCATACGA TGAAGAGCTA GTGAAATTTT ATTCTAAAAA TGTCCAACCC    1140
CAATTAAAAA GCAAGAATTT TATCGTGTTC CATTTGCTTG GCTCTCATTC TTGGTATGCC    1200
GATCGTTTCC CTAAAAGCTT TGCCAAATTC AAACCAAGCG ATTTGTCTTT TTCTAATTTG    1260
CATGCAAGCA GCGATAGAGA CAAGCAAATC GTCGCTGATT ATGTCAATTC GCTTTATTAT    1320
AACGACTTTG TTTTGAATGG AATTTTTAAC CTCTTTAAAG ATAAAGACGC TATTGTGTTT    1380
```

```
TATTTGAGCG ACCATGCGCA AGATATTTTT GAAAGCGGCC CTACTTATGG GCATAGCTGT    1440
TCTAAAGCGG GATTAGAAAT CCCTTTTATG ATTTATGTGA GCGATATTTT TAAAGAAAAA    1500
CACCCCGAGA AAGTGAAGTT GATTAAAAAC GCTTTAAACA AACCTTTCAT GAGCGATGAT    1560
TTAATCCATT CTCTTTTGCC TTTGGTGGGC ATTCACACTA AAGATGAAAT AGAGAGTAAA    1620
AACCTTTTTA GCCCCCAATT TGACGCCCAA AGAAAAAGGG CTGTTTGTTA TGGCAGCATG    1680
AATTATGATA GGACTAAA                                                  1698
```

(2) INFORMATION FOR SEQ ID NO:1359:

(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

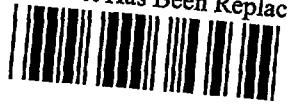
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359

```
AAATCTTTTA TGCCACCCAC ACGCCCCCAA GCGAGTATTT TAAGGCTAAC CCTAAAAAAC      60
CCTTTGAGCA TGCTATCTCG TTATTCGCTC TGTCTGTTGA AAAAAACGCG CTTGCAAACA     120
ACATCAAACA GCGCACCAAA AGCATGCTTG ATTGCGGGCT TATTGAAGAA ATCAAAGCCC     180
TTTATATTAA ATACCCTAAA GATTCGCAGC CTTTTAAAGC CA                        222
```

(2) INFORMATION FOR SEQ ID NO:1360:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1360

```
ACTTCCGCAT CAAGGGTGGC TAAAGACATC ATCAGCGAGT CTCAAAACCT TTGCGCAAGA      60
AAATTCCGCC GTTTGTATGC GTTATTGAAA GAAAATGAAA TGCTCATTCG CATCGGATCT     120
TATCAAATGG GGAACGATAA AGAGCTTGAT GAAGCGATTA AGAAAAAGGC TCTAATGGAG     180
CAATTTTTAG TGCAAGATGA AAACGCTTTA CAGCCTTTTG AACAAAGCTT TCAGCAATTA     240
GAAGAAATCT TAAGA                                                     255
```

(2) INFORMATION FOR SEQ ID NO:1361:

(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:1361

```
GATAAAAGGA ATATCATGGA ATCACAACTC ATGAAACTCG CCATTGAAAC TTATAAAATC      60
ACTTTGATGA TTTCTTTACC GGTATTATTA GCGGGCTTAG TGGTGGGGCT GTTAGTCAGT     120
ATTTTTCAAG CGACCACCCA AATCAATGAA ATGACTTTGT CTTTTGTGCC TAAGATTTTA     180
GCCGTGATTG GGGTGCTGAT TTTAACCATG CCGTGGATGA CGAACATGCT TTTAGATTAC     240
ACCAAAACCT TAATCAAGCT CATTCCTAAA ATCATAGGC                            279
```

(2) INFORMATION FOR SEQ ID NO:1362:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 783 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1362

```
AAAATGCTAG AAACCACTAT TGATTTTTCT CGTTACAGCA GCGTGAAAAT CGGTGCGCCT      60
TTAAAAGTGA GCGTTTTAGA AAACGATAAT GAAATCTCTC AAGAACACCA GATCATAGGA     120
TTAGCGAACA ACCTTTTTAAT CGCTCCTGAC GTGAAAAATC TCGCTTTATT AGGAAAAAAC    180
TACGATTATA TTTGCGATAA GGGTGAGTGG GTGGAGGTAG GGGGAGCGGC CAATGCGTCT     240
AAAATTTTTA ATTATTTTAG GGCGAATGAT TTAGAGGGTT TAGAGTTTTT AGGGCAATTC     300
CCTGGCACTT TAGGGGCGTT AGTTAAAATG AATGCTGGCA TGAAAGAATT TGAAATAAAA     360
AATGTTTTAG AAAGCGCTTG CGTTAATGGC GAATGGCTAG AAAAAGAAGC TTTGGGGCTA     420
GATTATCGCA GCAGCGGGTT TAATGGCGTT GTTTTGAGGG CTAGGTTTAA AAAGACGCAT     480
GGTTTTAGAG AAGGGGTTTT AAAAGCGTGT AAAAGCATGC GCAAAAGCCA CCCCAAATTC     540
CCTAATTTTG GGAGCTGTTT CAAAAACCCG CCTAACGATT ATGCGGGGCA GGCTTTTAGA     600
```

```
GGGCGTGGGC TTAAGGGGTT ATTGTCTAAA AAGAGTGGGG CTTTGCCAAA GCAACATGCG     660
AATTTTTTGG TGAATTTGGG GGGCGCAGAA TTTGAAGAAG CCCTAGATCT GATAGAACTC     720
GCCAAAACCA GAGTGCTACA AGAATATGGC ATTCATTTAG AAGAAGAAGT GAAAATTTTA     780
AGG                                                                   783
```

(2) INFORMATION FOR SEQ ID NO:1363:

(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

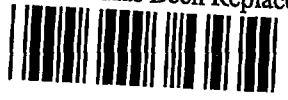
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363

```
CTCAATAGCG AACATCCCTT GTTTGATTGG GCTAGCAAGC AGACTTATAT CCAAATGGCG      60
AACATGATGA TGGCAGCGGC CATGTTAGGG ATTGATTCTT GCCCGATTGA AGGGTATGAT     120
CAAGAAAAAG TGGCGGCTTA TTTAGAGGAA AAAGGCTATC TAAACACGGC AGAATTTGGC     180
GTGTCGGTAA TGGCTAGTTT TGGTTATCGT AACCAAGAGA TTACCCCTAA AACCCGCTGG     240
AAGACAGAAG TTATTTATGA AGTGATTGAA                                      270
```

(2) INFORMATION FOR SEQ ID NO:1364:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1364

```
AAAGAGATAA CCATGAGAAA ACTATTCATC CCACTTTTAT TATTCAGCGC TTTAGAAGCG      60
AACGAGAAAA ACGGCTTTTT CATAGAAGCC GGCTTTGAAA CTGGGCTATT AGAAGGCACA     120
CAAACGCAAG AAAAAAGACA CACCACCACA AAAAACACTT ACGCAACTTA CAATTATTTA     180
CCCACAGACA CGATTTTAAA AAGAGCGGCT AATTTATTCA CCAATGCCGA AGCGATTTCA     240
AAATTAAAAT TCTCATCTTT ATCCCCTGTT AGAGTGTTGT ATATGTATAA TGGTCAATTA     300
ACTATAGAAA ACTTCTTGCC TTATAATTTA AATAATGTTA AGCTTAGTTT TACAGACGCT     360
```

```
CAAGGCAATG TGATTGATCT AGGCGTGATA GAGACTATCC CCAAACACTC TAAGATTGTT     420
TTGCCCGGAG AGGCATTTGA TAGTCTAAAA ATTGACCCAT ATACTTTATT TCTTCCAAAA     480
ATTGAAGCCA CTAGCACTTC TATTTCTGAC GCTAACACGC AGAGGGTGTT TGAAACGCTC     540
AATAAGATTA AGACAAATTT GGTCGTAAAT TATAGGAATG AAAACAAATT TAAAGATCAC     600
GAAAATCATT GGGAAGCCTT TACCCCACAA ACCGCAGAAG AATTCACCAA TTTAATGTTG     660
AACATGATCG CTGTTTTAGA CTCCCAATCT TGGGGCGATG CGATCTTAAA CGCTCCTTTT     720
GAGTTCACTA ACAGCCCAAC AGATTGCGAT AATGATCCTT CAAAATGCGT AAATCCTGGG     780
ACAAACGGGC TTGTCAATTC TAAAGTCGAT CAAAAATATG TGTTAAACAA ACAAGACATT     840
GTCAATAAAT TTAAAAACAA AGCGGATCTT GATGTAATTG TTTTAAAGGA TTCAGGGGTT     900
GTAGGGCTTG GGAGTGATAT TACCCCTAGC AACAATGATG ATGGCAAGCA TTATGGCCAG     960
TTAGGGGTAG TAGCTTCTGC TTTAGATCCT AAAAAACTCT TTGGCAACGA CCTTAAGACT    1020
ATCAATTTAG AGGATTTAAG AACCATCTTG CATGAATTCA GCCACACTAA AGGCTATGGG    1080
CATAACGGGA ATATGACCTA TCAAAGAGTG CCGGTAACGA AAGATGTCAA G             1131
```

(2) INFORMATION FOR SEQ ID NO:1365:

(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:1365

```
ATAATGGGCG TTGGAGAGAA AGAAGAGAAA AAAGAAAGCC AAAAGGTGGC GGTTATCACT      60
GGGGCGAGTT CTGGGATTGG GTTAGAGTGC GTGTTAATGC TGTTAAATCA AGGCTATAAG     120
GTCTATGCGC TCTCTAGGCA CGCGACTTTG TGCGTAGCGT TAAACCATGC GTTATGCGAG     180
TGCGTTGATA TTGATGTGAG CGATTCTAAC GCTTTAAAGG AAGTGTTTTT AAACATCAGC     240
GCTAAAGAAG ATCATTGCGA CGTTTTGATC AATTCCGCCG GTTATGGGGT GTTTGGGAGC     300
GTGGAAGACA CGCCCATTGA AGAGGTTAAA AAGCAATTTA GCGTGAATTT TTTCGCCCTT     360
TGTGAAGTGG TGCAACTTTG TTTGCCCTTA TTAAAAAACA AGCCTTATTC TAAGATTTTC     420
AATCTTTCTT CCATAGCGGG GCGTGTGAGC ATGCTCTTTT TAGGCCATTA CAGCGCGAGT     480
AAGCATGCCT TAGAGGCTTA TAGCGATGCC TTGCGTTTAG AGCTTAAGCC CTTTAACGTT     540
CAAGTGTGTT TGATTGAGCC AGGCCCGGTG AAAAGCAATT GGGAAAAAAC CGCTTTTGAA     600
AATGATGAGC GGAAAGATAG CGTTTATGCT TTGGAAGTGA ATGCGGCT                  648
```

(2) INFORMATION FOR SEQ ID NO:1366:

(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

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366

```
GACTCAAATA GAAGCGCTTT TATATGCCAC AATCTAGCGA TGGTTTTGAT GATTTTCACA      60
AGCATCTTGA AGATAGCGTT AAAAGTTTTA TCAGAGCGAA AAAAAAATCG TTATGGTTTT     120
CCTAGAATCT TTGATGTTGC AGACATAGAA CAAGAAGAGA GGGAAGTCAT TGAATGGCGA     180
GAAAAAAAGA AAGCGTCAAA ACAAAGCTAT AAACAAAACC TTCAAATCAA TAAAATCGCT     240
AACGATTTAA AGCGTGATAA GATAGTGGAT AAAAGAACGA TTTTAAGCGT GATAGACGCT     300
GATATAGAGC GTGGTTTTAT CCCGCCTAAA GATTTGTTAA AACAATTAGA AAAAATTAGC     360
GCTTCTCTTT CTAAAGACAT CGTAATAACG ATAAAGCAAG TAGAAAAATT AGAGCTTAAC     420
TATGCGCTAA TAGACAATAT CCAACATAAC ACGCTTGATG ACACGCTTGA TTTTACCTTT     480
ATTGTTGGGG ATTCTTTGAG CGTTCAGTCG CTTTATGTTA CCTTTAATCT TGTGATTGAT     540
ATTGATAGAC CCATGAGCGA GCAGTTTCTC AACCATATTG GGAAATTGGG GAGTTTTGAA     600
TCTAGAGAGC AAGCGTTAGA GTGGGTGCGA TTATCGCAAA CTAAACTGAT CATTGAAACG     660
CCTAAAGAAG CGTTAAAAAA TGCGGAATTA TCACAAATTG AAGAAATATT GACCGGCTGT     720
ATTTTTAATG GCGCTTACCG CCTTCAAAAC GATCTTAAGA AAGGGCGA                  768
```

(2) INFORMATION FOR SEQ ID NO:1367:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 588 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

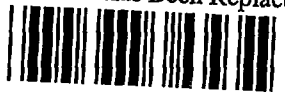
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367

```
GGCAATGCTA GGACTTGTAT TGTTATATGT TGGGATTGTC TTAATCAGCA ATGGGATTGC      60
GGATTAACCA AAGTCGATCC TAAAAGCACC GCGGTGATGA ACTTTTTTGT GGGCGGACTT     120
TCCATTGTTT GTAATGTGGT GGTCATCACT TACTCCGCGC TCCACCCTAC AGCCCCTGTA     180
GAAGGTGCAG AAGATATTGT TCAAGTATCG CACCATTTGA CCAGTTTCTA TGGGCCAGCG     240
ACTGGGTTAT TGTTTGGTTT TACCTACTTG TATGCCGCTA TCAACCACAC TTTTGGTTTG     300
GATTGGAGAC CCTATTCTTG GTATAGCTTA TTCGTAGCGA TCAACACTGT TCCTGCTGCG     360
ATTTTATCCC ACTATAGCGA TATGCTTGAT GACCACAAAG TGTTAGGCAT CACTGAAGGC     420
GATTGGTGGG CAATCATATG GTTGGCTTGG GGTGTTTTGT GGCTTACCGC TTTCATTGAA     480
AACATCTTGA AAATCCCTTT AGGGAAATTC ACTCCATGGC TTGCTATCAT TGAGGGTATT     540
TTAACCGCTT GGATCCCTGC TTGGTTACTC TTTATCCAAC ACTGGGTG                  588
```

(2) INFORMATION FOR SEQ ID NO:1368:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1920 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368

```
AGCATTTGCC ATGAATATTT AAAGGTTAAT TTGCAAGAAA AATTAGCCGG TTTTAGAGAT     60
TTTGTGCATT ATAATGAAAA CGCCAAAGAC TCCTTGCCTT TAAAAGCGCT TTTTTTAAGC    120
GGGGTGGATG CTTTGAGTAA AGACGCGCTT TATTATCTAG AAAAGATCAT GCGTTTTGGC    180
TCTAAAAATG GGGTTTTGAG CTTTGTCAAT TTGGAGAGCG AAAAAAACAA TCAATCCGCA    240
GAAGATTTGA AACGCTATGC GGAGTTTTTT AAAGACAGGA CAAGTTTTGA GGGGTTAAAA    300
TACCTTAATG TAGAAATCAT CAGCGATCAA GGTATTAAAT CCCAACACAT GCAAGACTTC    360
GCTGATAAAA TTAAAGCGTA TTACAAGCAA AAAAAAGAAG TTAAAAGGGA GTTGAAGGAC    420
TTACAAAGAG ACAAAGAATT TTGGACTAAA AGCTCTCAGC ATGAAGTAAG CGTGCCGGTG    480
GGGTGGGATA TTAACCATAA GGAAGTGTGT TTTAAAATCG GTAACGAACA AAACCACACG    540
CTCATTTGCG ACCACAGCGG GAGTGGGAAA TCCAATTTCT TGCATGTGTT GATTCAAAAT    600
CTAGCTTTCT ACTACGATCC CGATGAAGTC CAACTCTTTT TGTTAGACTA TAAAGAGGGG    660
GTGGAATTTA ACGCGTATGT AGCAGATCCC GCTTTAGAGC ATGCGAGGTT GGTGAGCGTG    720
GCGAGTTCAA TCTCTTATGG CATCACTTTC TTGAAATGGC TTTGTGATGA AATGCAAAAA    780
AGAGCCGATC GGTTCAAGCA GTTTAATGTG AAAGATTTAA GCGATTACCG CAAACATGAA    840
AAAATGCCCA GACTGATCGT GGTGATTGAT GAATTTCAGG TGCTTTTTAG CGATAATAAA    900
TCCACTAAAG CGGTGGAGGG GCATTTAAAC ACCCTGCTTA AAAAGGGCCG TAGCTATGGG    960
GTGCATTTGG TTTTGGCCAC TCAAACCATG CGCGGCACTG ACATTAATCC AAGCTTTAAG   1020
GCTCAAATCG CCAACCGCAT CGCTTTGCCT ATGGATGCAG AAGACAGCAG TAGTGTTTTG   1080
GGCGATGATG CGGCTTGTGA GATTCAAAAC CCAGAAGGCA TTTTCAACAA CAACGGAGGG   1140
AATAGAAAAT ACCACACCAA GATGAGTGTC CCTAAAGCCC CTGATGATTT CAAATCTTTT   1200
CTCACAAAAA TACACGCTGA ATTTAACCAA AGAAATCTCG CACCCATAGA TCGTAAAATC   1260
TATAATGGCG AGACACCTTT AAAAATGCCC GACACCCTTA AGGCTAATGA AATGCGTTTG   1320
CATCTGGGCA AAAAAGTGGA TTATGAGCAA AAGGACCTGA TAGTGGAGTT TGAAAGTAAC   1380
GAATCGCATT TGTTGGTGGT GATCCAAGAT TTAAACGCTC GCATCGCTTT AATGAAACTC   1440
TTATTCCAAA ACGTTAAGAG CGCGAACAAA GAATTGGTTT TTTGCAATAA AGAAAAACGC   1500
TTGATAAGGT CTTTTGATGC ACAAAAAGAA TACGGCATCA CGCCTGTAGA AAATATTTTA   1560
AGCGTTTTAG ACACCGCTAT GAATCCTAAC AGCGCGCTTG TGATAGACAA TCTCAACGAA   1620
GCGAAAGAAT TGCACGACAA AGTAGGGGCG GAAAAGTTAA AATCGTTTTT AGAAAAAGCC   1680
ATAGACAACG AGCAGTATTG CGTCATTTTT GCGCATGACT TTAGGCAAAT TAAAACTAAT   1740
TACCATTTTG ACAAGTTAAA AGAATTGTTA AACAACCACT TCAAGCAATG CCTAGCCTTT   1800
AGGTGCAATG GGGAAAACTT GAACGCTATC AAAAGCGATT TGCCTCCACC AAGCAAACTT   1860
AACGTGCTAT TGATAGAGCT TTCCAAAGAC AGCGTTACTG AATTCAGGCC TTTCAGCTTA   1920
```

(2) INFORMATION FOR SEQ ID NO:1369:

(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:1369

```
AGGCCCAATC TCTCTAGCCA GTTCCTTTAC ACGGAAATGC TGAGCTTAAA ACTAACCTAT      60
GAAAGCACCC TCCAACAGGA TTTAAAAAAA ATCTTAGGGA TTGAAGAAGT CATAATGCTA     120
TCCACAAGCC CCATGGAATT ACGATTGGCC AATCAAAAGC TAGGCAATCG TTTCATTAAA     180
ACCTTACAAG CCATGAACGA ATTAGACATG GGTGCATTTT TTAACGCTTA CGCTCAAACA     240
ACCCAAAGAT CCCACCCATG CCAC                                            264
```

(2) INFORMATION FOR SEQ ID NO:1370:

(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:1370

```
GAAAAATCAA CGAGCAACTT GAAGAAGCCA AGCGTTTGGA GAAGCAAGTT GATATGCAAG      60
ATCGCCACTC ACAAAGCGAG ATCGATAGGC TTATGCGTGA AGCCAAAGAG CATGAAAGAG     120
AAGCTAAGAG GCGCTATGGT GAATATCTTA AGGATAAAAA TGATTGAAAT AAGCGAATGG     180
TTGCAAAAAC TAGACGATGC CTTAGATAAA GTTGTTGCTA AAAAAGAGCC AGAGAGTTTT     240
CTCAAGCCGA TCATTTCACC AATAGAGGAC TACCAAAAGA GTGTCAGGCA AATTCAAGCG     300
CAATTCACAG ACGCGCCGAA GTTCAATGAA GAGGGTGCTT ACCCTCAATT TTTAAGCTGT     360
GGTTTATTGC AAGTTAGGGG CAAAAATGGT GCTAACATGG AATTTTTATT GCCTAAAGTT     420
TATCCTTTCC CCCCTAAAAG CTTGTATATA GAGCATGAAA AAGACGGGCA GTTTTTGAGA     480
GAAATGCTCA TGCGCTTACT CTCCAGCGCG CCTTTAGTGC AATTGGAAGT GATCTTAATT     540
GATGCGTTGA GCTTGGGGGG CATTTTCAAT CTGGCCAGAA GGCTTTTAGA TAAAAACAAT     600
GACTTTATTT ACCAGCAAAG GATTTTGACC GAAAGCAAGG AAATAGAAGA AGCCCTAAAG     660
CATTTGCCA                                                            669
```

(2) INFORMATION FOR SEQ ID NO:1371:

(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

This Sheet Has Been Replaced



(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:1371

```
ACATGGGTGC ATTTTTTAAC GCTTACGCTC AAACAACCCA AAGATCCCAC CCATGCCACT      60
AGCTATGGCG TTTTTGCGGC GAGTTTGAAT ATGGAATTGA AAAAGGCTTT AAGGCATTAT     120
CTTTATGCGC AAACTTCTAA CATGGTGATC AACTGCGTTA AAAGCGTCCC CTTATCCCAA     180
AACGACGGGC AAAAAATCTT ATTGAGCTTG CAAAGCCCTT TTAACCAGCT CATAGAAAAA     240
ACCCTAGAAC TAGACGAAAG CCACTTGTGC GCAGCAAGCG TTCAAAACGA CATTAAGGCG     300
ATGCAGCATG AGAGTTTATA CTCGCGCCTT TATATGTCT                            339
```

(2) INFORMATION FOR SEQ ID NO:1372:

(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
(B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372

```
CGAGCTTCAA TGAAAAACTT TTCCCCACTC TATTGTCTTA AAAAGCTCAA AAAACGCCAT      60
TTAATCGCTC TGAGTCTGCC CTTGCTTTCT TATGCGAATG GCTTTAAAAT CCAAGAGCAA     120
AGCTTGAATG GCACGGCTTT AGGCTCGGCG TATGTCGCTG GGGCTAGGGG TGCTGACGCT     180
TCTTTTTACA ACCCGGCTAA CATGGGCTTT ACTAACGATT GGGGCGAAAA CAGAAGCGAA     240
TTTGAAATGA CCACCACCGT GATCAATATC CCGGCCTTTA GCTTTAAAGT CCCTACGACC     300
AATCAAGGCT TATATTCGGT AACAAGTTTA GAAATTGATA AAAGCCAACA AAATATTTTA     360
GGCATCATCA ACACTATAGG GTTAGGCAAT ATCCTTAAAG CGCTTGGCAA TACGGCCGCT     420
ACCAATGGCT TATCACAAGG TATCAATCGT GTTCAAGGGG TTATGAAC                  468
```

(2) INFORMATION FOR SEQ ID NO:1373:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 651 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1373

```
GCGGATCGAG AGGATAAACT CTCTCACTCT ATAATCATGC GGTATTTTAG AAGCGCTTTT      60
TTATTATTTT TCATGACGCT TTTTTTTGTT TCTTGCTCTA AGCACCCTTT TTCTAAGCAA     120
ACCCCTAAGA CTAAGGAGCG GATCCGACAA GAAGAAGCCA ATAAAAAAAG AGAAGAGACT     180
TTGAATGCCT TGCGCCAATT CAGACTCATT TACATTAACA CGCCGGTTTT TCGCTTTTAT     240
GATTACGGCA CGATCAAAAC CGATAAAGAC CACAATACTG AAGTAACCCT TTATAAGCTC     300
AGCCAAAAAG TGGGCGATAT TTACATGACT AAACGGAGCA TTTGTTTTAG CCAAAAATGT     360
TCGGCCAAAT GGATTGCTGC AAGGGATTTG TTTGGCAAGG TGAGCTATGG GGATTTGTTT     420
GATGATATTG TTTTAGGGAG GGATATTTTT AAAGGTTTAG GGAAACGCCA CCTAACCCCT     480
GAATATGTGA TCCAAAGGTT TCAAAAAAGC GGGGAAATTA TCCTTTATGA AAGAAAAAAT     540
GGCCTGATTT CTTTCCAAAA CTTGACTCAA AAAATTGCTA TTAGGATTGA ACCCTATGAG     600
CCTTCTTTGC AAGATTTAGA AGACAATGAA AACGCTGATA GCGAGCTTCA A               651
```

(2) INFORMATION FOR SEQ ID NO:1374:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374

```
GAAATCGCTG AGATCGTGAG CCAATGGACG CACATCCCGT TCCAAAAAAT GTTCCAAAGC      60
GAAAAAAATA GGGTTTTAAA CATTGAAAGC GAATTGCAAA AAAGGGTGGT GGGGCAAGAA     120
AAAGCGCTCA AAGCGATCGC TAAAGCGATT AAAAGGAATA AGGCTGGGCT TAGCGATAGC     180
AACAAGCCCA TAGGGAGTTT CCTCTTTTTA GGGCCAACAG GCGTGGGTAA AACCGAGAGC     240
GCTAAAGCTT TGGCGCAATT CTTGTTTGAT AGCGATAAAA ATCTTATACG AATTGACATG     300
AGCGAATACA TGGAAAAGCA CGCTATCAGC CGTCTTATTG GGGCCGCTCC TGGGTATGTG     360
GGCTATGAAG AAGGCGGGCA ATTGACCGAA GCGGTGCGCA GAAAACCTTA TAGCGTAGTG     420
TTATTAGATG AAGTGGAAAA AGCCCATCCG GATGTGTTTA ACTTCTTGTT ACAGGTTTTT     480
GATGAGGGGC ATTTAACCGA TAGTAAGGGC GTGAGGGTGG ATTTCAAAAA CACGATTTTG     540
ATTTTAACCA GCAATGTGGC TAGCGGCGCG CTTTTAGAAG AGGATTTGAG TGAAGCCGAT     600
AAACAAAAAG CGATCAAAGA GAGCCTGAGA CAATTCTTCA AGCCGGAATT TTTAAACCGC     660
TTAGATGAAA TCATCTCCTT TAACGCCCTA GATAGTCATG CTATCATC                   708
```

(2) INFORMATION FOR SEQ ID NO:1375:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 777 base pairs
(B) TYPE: nucleic acid

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

(ii) MOLECULE TYPE: DNA (genomic)

(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:1375

```
GTGAGGTTTT GTTATTCTAA AAAATATAAA AAAACGATTA TTTTAAAAAA GGATTGGATG      60
ATGTTTGATA ACACGCTTAT CAATTTATTT GAGACAGCGC CTCTTTTAAC TTCGCTTTTA     120
GCTGGGATTT TAACTTTTTT AAGCCCTTGC GTGTTGCCTT TGATCCCGGC GTATATGTCT     180
TATATTTCGC AAATTTCTTT AGAGGATATT AAAGATGGTA AGGCTAAAAG GGTTTCGGTT     240
TTTTTAAAAT CCTTGATGTT TGTGGTGGGG TTTTCGCTCG TGTTTTTGGG CGTGGGCATG     300
TCTATGGCCA AGCTTATCCA TAGCTTTTCG TTTTCCTGGG TGAATTATAT CGCTGGGGGG     360
ATTGTGATCC TTTTTGGTTT GCATTTTTTA GGCGTGTTTC GTTTTGCGCT TTTGTATAAA     420
ACCCAAAGCG CTGGTTTAGC GAGCAAATCT AACAGCATGC AGCGCTTTTA CCCCTTTCTT     480
TTGGGCATGA GTTTCGCTTT GGGTTGGACG CCATGCATCG GGCCGATATT CACTTCTATA     540
GTGATCATGA GTGCGAGTAA GGACGCTTAT GGCTTAATGC TTATGGTGGT GTTTGTAATG     600
GGCTTGGCGA TCCCTTTTGT ATTGGTGGCT TTAATGCTAG AAAGAGCGCT TTTGTTTTTA     660
AAATCCTTAA GAAAATACAA CCGCGCGATT GAAATTGTTT CAGGGTTGGT GCTTATTTTA     720
ATGGGAATAT TGATCATGAC AAATTCTTTA GAAAGCCTAA CTAACTTTTT ACAAAAT        777
```

(2) INFORMATION FOR SEQ ID NO:1376:

This Sheet Has Been Replaced



(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:1376

```
ATAGGAGGTG CGCATGCGTT TTTATATTAT CTTACATTTT TGTTTATTGT GGGTTTTGGC      60
GTGTTTGTTT ATAGTATTGA TCCGCAAGCT TACGCTTTCA ATTTAGGGAG CTATAGCTTT     120
AACCTCCCCA TTGCCGTATG GCTTATGGGC GTTTTGGGCA TGTTCGCTTT TTTTTCATGG     180
GTTTTTTTTAT TCAAGCACAA TCTCAGCCAT AAAATCCGCT TATACCATGA AAAAAAGGAT     240
TTTGACAAAT TGCTCAAACA AATCCTATCC CAAGACACCC AAAAGACTTT TTTAAAAACA     300
AAATTTAAAA GCGATCTCGC TAAAAACCTC TCTCAAATCT TAGCCCGCTA TGATTTAAAA     360
GCTGATTTAA ACACGCCAAA TAGCGGGTGC GAAAAAGTGG ATAACCTTTT TAAACATTAC     420
CACAATATAG AAAATAACAC CCTTGAGCCT AAAGATCACG CTAAACATTC CCTAGCTTAT     480
GAGCATGCTT ATTTTTCTAA ACGCTTGAAG GCTTTCATTC ATAACGATTT GAAAAACGCC     540
```

TTTGAAGTTT TAACAAACGC GCAAATCCCT TTGGAATTAC GCCGCTACGC CTTA 594

(2) INFORMATION FOR SEQ ID NO:1377:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(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:1377

CAAGATAAGG GGTTATTATT GAGTGTAGCA CTACCTAACT CAAACAACGC CTCTCAAAAC 60
AACATTTTAA GCCTTTCTGT CCTTCACAAC CAGATTAAAA TGTCTTATGG TAATAAAGTG 120
ATGGACTTTA CCCCTCCCAC CTTACAGGAT TACATTGTGG GCATTCAAGG ACAAAGCGCA 180
CTCAATCAAA TTGAAGCTGT TGGGGGGAAT AACGCTATCA AGTGGCTTTC AACATTGATG 240
ATGGAGACTA AAGAAAACCC GCTTTTTGCG CCGATTTATT TAGAAAACCA CTCTTTAAAT 300
GAAATCTTAG GCGTAACAAA AGATCTTCAA AACACCGCAA GCTTGATTTC TAACCCTAAT 360
TTTAGAAATA ACGCTACCAG CCTTTTAGAA ATGGCGAGTT ACACCCAACA AACCAGCCGT 420
TTGACAAAAC TCTCTGATTT TAGGGCTAGA GAGGGAGAGT CCAATTTTTC AGAGCGCTTG 480
TTAGAGCTTA AAAACAAGCG TTTTAGCGAT CCTAACCCTA 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
GAATTCACTT TGAGCGCGAA TGAAACTTAT GGAGGCAATG CGAGTCATAT CAATTCTTCT 840
AATTCCTTGC TCTCTGTGTT GAACCAACGC TACAACTACA ACACCTGGAC AACGAGCGTG 900
AATGGGAATT ACGGCTATGA TTTCATGTTC 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 TGGTGCGTTT 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:1378:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

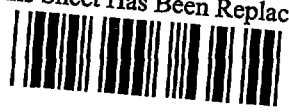
(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378

```
ACGATACTAT GCCCAGGGGC TAAAAGCTAT AAGTATTGGG AAGGCATGGG CATGTCTCAT     60
ATTATTAAGA GCATTGAAGC TTTAGATGAC TATACCATTA GATTCACGCT TAATGGGCCA    120
GAAGCCCCGT TTTTAGCGAA TTTGGGCATG GACTTTTTAA GCATTTTGAG TAAGGATTAC    180
GCTGATTACT TGGCTCAAAA TAATAAAAAA GACGAGTTGG CTAAAAAACC TGTTGGGACA    240
GGGCCTTTCA AATTCTTTTT GTGGAATAAA GATGAGAAAA TCATTCTGGT TAAAAACCAG    300
GATTATTGGG GCCTTAAAGC GTATTTGGAT AAGGTGGTGG TGCGCACCAT TCATAATTTT    360
TCCACTCGCG CCTTAGCGTT AAGAACCGGT GAAATCATGC TCATGACCGG GCATAATCTC    420
AATGAAGTGG AGCAATTAGA AAAACTTCAT AATATCGTGG TGGATAGAAG CCCTGGGTTG    480
ATCGCCAACT GGCTTTCATT GAACACGCAA AAAAAGTATT TTAATAACCC TTTGGTGCGT    540
TTGGCTATCA ATCATGCCAT CAATGTTGAT GATTACATCA AGGTGATTTA TGAAGGTTTT    600
GCTCAAAAAA TGGTCAATCC CTTCCCGCCC ACCATATGGG GTTATAACTA TAATATCAAA    660
CCCTACGAAT ACGATTTGAA AAAGGCTAAG GAGTTGTTGA AACAAGCGGG CTATCCTAAC    720
GGCTTTAAAA CCAATATTTG TACATCTTTA CTC                                 753
```

(2) INFORMATION FOR SEQ ID NO:1379:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2637 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2637

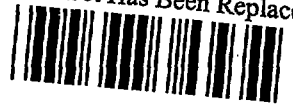
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379

```
ATTCATATTA AACGAATTTT TTTACTTAAA AACACCCCAT TTAACCCGCC ATTATTCCTC     60
CACATTGCCC CACTCAAACC ATTCATGATT ATTATTAACT TGTTTTGGAA TACTTTTAGC    120
TTGTTTGTTA AAAAAACCAA TAAGGATTTG ATCATGCGCG TTACCTTTGG CTCCAAATAC    180
AACCAAATGA ATCACTACCA AAACGCTTTA CAAAATAAAA TCAACGACGC TAACACGCAG    240
ATCGCTTCAG GGCTAAAAAT CCGTTATGGT TATCAAAACA GCGACATTAA CAACCAGAAT    300
TTAAAATTCC AATACGAAGA AAACACCTTA GATCAAGGCA TTGATGTGGC TCAAAACGCT    360
TACACTTCAA CGCTCAATAC CGACAAAGCC TTGCAAGAAT TTTCTAAAAC GATGGAGGCG    420
TTTAAAACCA AACTCATCCA ATCCGCTAAC GATGTGCATT CAGAGACTTC TCGCGCCGCT    480
ATCGCTAACG ATTTAGAACG CTTAAAAGAG CATATGATAA ATGTCGCTAA TACCTCCATA    540
GGGGGGGAAT TTTTATTTGG AGGCAGTAAG GTGGATAGAC CCCCCATTGA TAGTAATGGG    600
AAATACCATG GCAATGGCGA AGATTTAAAC GCGCTTATTA GCTCTGATAA CCTTGTGCCT    660
TATAATATCA GCGGGCAAGA TTTGTTTTTA GGCACCGATA AAGACAAACA CAAACTCATT    720
ACCACCAACA TTAAATTACT CAATCAAAAC AAGCTCCACC CTGATGTGAT GGACGCTTTA    780
GAGCATTCTT CATTGCCTGA AGAAGTTTTC ATTAAACCCA GCGATACCTT GCGAGAACTC    840
ATCGGCGATA ACGATAAAAA CCCCACCAAT GACCCTAAAG AGTTTTTTTA TTTGCAAGGC    900
ATTAGGCCTG ATGGCTCTAG TTTTAAAGAA AAATTCGCGT TGGATAAAGC CTATCAAAAC    960
CAAGAAAGCG CGACTAAAGT GAGCGATTTG TTGGATAAAA TCGGGCATGC TTACGGGAAC   1020
ACTTCGCAAA ATAAAGTCGT GGATGTGAGT TTGAACAATT GGGGGCAAAT TGAGATTAAA   1080
```

```
AACCTAACCC CCGGCAGTGA AAATTTGGAT TTTCATTTGA TTTCTAGCGA TGGGGATTTT    1140
GACGATTTAG ACGCCTTGCG TTCGAGCGGT AAAAGGGTTA CTGAATATGT CAAAAGCGCG    1200
TTTGTAACGG ATAGGAGTTT GAGCCAAGTT AAAGCGGTGC CTAACATGTA TAACCCTAAA    1260
GTGCTTGAAA TCCCTAGCGT GTTTGTGACT AAAGACAATG TTTTAGCTAA CAAAAACACC    1320
AAGTTGAGCG AGATTTTTGG CGATAAGGTG GAAACTTTAA AAATCAACGC CAGCCGTTTG    1380
GGCGATGAAA GCGCTATTAA AATCCCAAAC CTCCCTATTA ATTTGGATAT TCCCATTCTT    1440
TTAGATGTGA AAAACTCTAC GATTAAAGAT TTGAAAGACG CGATTAAAGA ACGCTTCAAT    1500
AATGAAGTGG ATGTGGAAAT TGAAACGAAC GGGCGTTTGA GGATCATTGA CAATTCTTCT    1560
AAAGAATCGC CTATTTCTTT TGCCTTAAGC ACCCTGGATC AAAAAGGGCT AGAAGTGGCC    1620
GGTATCCCCA CTAATAACGC GAGCGAATAC CAAAAAACCT ATTTCAATAA AGAAGGGGCC    1680
AAATTAGAAA GCAATGTTGC CCAAACCGCT CAAAATGATG CGGCTAATGG CTCTACTAAA    1740
CTGAGTGAAG TCTCTAAGGG GAGTTTGGAA AATAGCGTTT TTAACATGAA ATTAAACGAT    1800
GTGAATGGTT CGTTTTTAGA AGCGCAAATA AACTTGGATA ATAATGGGGC TTTTTTGAGT    1860
TTGCCTAATG GCGTTAAAAT CCCGCTTTAT GACCCCACAA CCGCTGATAT TCAAGCGTCT    1920
AAACCCAATG AAGTCACTTA CAGGCAGCTC ATGGATGCGA TGAGTATCGC GCTCAATTAC    1980
AGCAACACTG ATCCTGCAAT CTACCAACAA ATCAGCGATA ACCCTACTTC AAAAGAAAGC    2040
AAGGAGCGAT TCATTGAATT GTTAAAACAA GCTAAAGACA ACCTTTCTAT TAATTTGAAT    2100
GAAGAGGGTA AAGTCATTAT CCAAGACAAC ATGCATTCAA ACACCAAAAT GCAGTTCATG    2160
CTTTTTGATA AAGACGCGAA TGATTTTTCT CAAAACGCCT TACACAGCGA CAAACCAAGC    2220
CTTAAATTAA ACGCTAATAA CGCCCTAATT ATTGACAAGC CAAGCGTGAA TTTTTTTGAT    2280
CAATTAGAAA ATATTATCAC TTCTGTAAGA AAAGGGATTT ATCGCCCAGA CGCTTTAGGG    2340
GATACTTATT CTAGCGACAT GCGTAATTTA GGCATTCAAA ACGGCATCAC CCTTATAGAT    2400
CACTTGAGCG ATCACATAGA AAAAATGATC GCTAAAAACG GCGCTCATGG TAAGGCATTT    2460
GAAAACATCA TCAGGCGTAA TGAAGTTTTA AAAACACAAG TTCAAAGCAT TCGTGGGGAA    2520
ACGACCGGCA CGGATATGGC AGAAACTTAT AACAAGTTTT CCAATCTCAC TAACAACTAT    2580
AACGCCGTTT TGGCTTCCAC GAACAAAATC AATAATCTGT CTTTAACGAA GTATTTA       2637
```

(2) INFORMATION FOR SEQ ID NO:1380:

This Sheet Has Been Replaced



(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

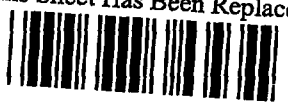
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380

```
AGGATTGATC AAATTAAAAT TATGAAATTG GTGAGTCTTA TTGTAGCGTT AGTTTTTTGT      60
TGTTTTTTAG GGGCTGTAGA GTTGCCTGGA GTTTATCAAA CTCAAGAATT TTTATACATG     120
AAAAGCTCTT TTGTGGAGTT TTTTGAGCAT AACGGGAAGT TCTATGCCTA TGGTATTTCT     180
GATGTGGATG GCTCTAAAGC CAAAAAAGAC AAACTCAATC CTAACCCAAA GCTAAGGAAT     240
CGCAGCGATA AAGGCGTGGT GTTTTTAAGC GATTTGATTA AGGTTGGGGA ACAATCTTAT     300
AAAGGCGGTA AGGCGTATAA TTTTTATGAC GGCAAGACCT ACCATGTGAG AGTCACTCAA     360
AATTCAAACG GGGATTTGGA ATTCACTTCA AGCTATGACA AATGGGGGTA TGTGGGCAAT     420
ACCTTCACTT TGAAACGCGT GAGGGGTGCC GAAATCAGTA TTTTAAAGCT CAAGCGTTTT     480
AATCTCATGC GCTCTTTTTA CAGGCAGACC CACCTTTTTT CTATTGGTAA GGCCTACGCG     540
ACA                                                                   543
```

(2) INFORMATION FOR SEQ ID NO:1381:

This Sheet Has Been Replaced



(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:1381

```
AAGGATTTAA GCAAGATGTT TGTGGTTTTT ATAGAAGGTT TTGGTTTAGC GATTTCTTTG      60
TGCGCGGCGG TGGGGGCGCA ATCCTTGTTT ATTGTGGAAA GGGGGATGGC TAGGAATTAT     120
GTGTTTTTGA TTTGCGCCTT GTGTTTTATG TGCGATATTG TCTTAATGAG CATGGGCGTG     180
TTTGGCGTGG GGGCTTATTT CGCTAAAAAC CTTTATTTGA GCTTGTTTTT GAATTTATTT     240
GGGGCAGTTT TTACCGGATT TTACGCTTTT TTGGCTTTAA AAACCCTTTT TCAAACCTTT     300
AAAAAAAAGC AAGTCCAAAC CCCTAAAAAA TTATCCTTAA AAAAGACCTT ATTATTCACT     360
TTAGGCGTTA CCTTACTCAA TCCTCAAGTG TATTTGGAAA TGGTGTTTTT AATTGGCGCG     420
AGCGCTATGT CTTTTAACCT AGTGCAAAAA TTCGTCTTTC TAGCTGGCAC TTTATCGGCT     480
GCCTTTTCTT GGCTTTTATT GTTATGCACC ATGTCCTTAC GCTATGGCTC TAAACTTTTG     540
AACAACCAAA AAATCTTTAT GGGCGTGAAT CTCTTTGTAA CCGCTATCAT GGGAACGCTC     600
AGCGTTACTT TATTCAGGGA TTTTTTAGCG TTATTGAGCA AAACC                     645
```

(2) INFORMATION FOR SEQ ID NO:1382:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 720 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382

```
ATGGATATTT TAAAAGCAGA GCATTTAAAC AAACAGATTA AAAAAACCAA AATCGTTTCA      60
GATGTTTCTT TAGAAGTGAA AAGCGGCGAA GTGGTGGGGC TTTTAGGGCC TAATGGGGCG     120
GGTAAAACCA CCACCTTTTA CATGATATGC GGGCTTTTAG AGCCTAGTGG GGGGAGCGTT     180
TATTTAAACG ATGTGGATTT AGCTAAATAC CCCTTACACA AGCGTTCTAA CTTGGGCATA     240
GGCTACTTGC CCCAAGAATC CAGTATTTTT AAAGAATTGA GCGTGGAAGA GAATTTGGCC     300
CTAGCAGGGG AGAGCACTTT TAAAAACTCT AAAGAGAGCG AAGAAAAAAT GGAAAGCTTG     360
CTTGATGCTT TTAATATCCA AGCCATAAGA GAGCGCAAGG GCATGAGCTT GAGTGGGGGA     420
GAAAGAAGGC GCGTAGAAAT CGCTAGGGCT TTAATGAAAA ACCCTAAATT CGTGCTGTTA     480
```

GATGAGCCTT TTGCGGGCGT GGATCCGATT GCGGTGATTG ACATTCAAAG AATCATTGAA 540
AGCTTGATTG GATTAAACAT TGGCGTGTTG ATTACTGATC ACAATGTGCG AGAGACCTTG 600
AGCGTGTGCC ATAGGGCGTA TGTGATCAAA AGCGGCACGC TTTTAGCGAG CGGGAACGCT 660
AATGAAATTT ATGAAAACGC TTTGGTGCGT AAGTATTATT TAGGGGAAAA TTTTAAGGTA 720

(2) INFORMATION FOR SEQ ID NO:1383:

(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

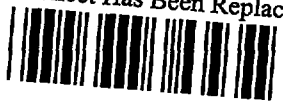
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383

AACACTGGTT TGTGGCACTC TTGGGGTTTG GCTCCAGCGC TTTTGGAAAC GCAACTGCCC 60
AAACATGCTC ACCAATTTTT TCAAATCTTC TTTTTCCCCA AAAAGCCCTT CAAACAAATG 120
ATCGTTATTG TGGAGTTGCT TGTCAATTTT ATCTTTAATC TCTTTCACGC CATACATGTT 180
GGGGTTAAAA TGATAGATAA TATCAAACTC CCACTTAGAC GCATAAAAAT GCGCGCTCTC 240

(2) INFORMATION FOR SEQ ID NO:1384:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1644 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384

ATTGATCTAG GCGTGATAGA GACCATCCCC AAACACTCTA AGATTGTTTT ACCCGGGGAG 60
GCGTTTGATA GTTTAAAAGA GGCGTTTGAT AAAATTGACC CCTATACTTT CTTTTTTCCA 120
AAATTTGAAG CCACTAGCAC TTCTATTTCT GATACTAACA CGCAGAGGGT GTTTGAAACG 180
CTCAATAACA TTAAAACAAA TCTTATAATG AAATATAGTA ATGAAAATCC AAACAATTTC 240
AACACTTGTC CTTACAATAA TAATGGTAAT ACAAAAAATG ATTGTTGGCA AAATTTCACC 300
CCACAAACCG CAGAAGAATT CACCAATTTA ATGTTGAACA TGATCGCTGT TTTAGACTCC 360
CAATCTTGGG GCGATGCGAT CTTAAACGCT CCTTTTGAAT TCACTAACAG CTCAACAGAT 420

```
TGCGATAGCG ATCCTTCAAA ATGCGTAAAT CCCGGAGTAA ATGGGCGTGT TGATACTAAA     480
GTCGATCAAC AATATATACT CAACAAACAA GGTATTATTA ATAATTTTAG AAAAAAAATA     540
GAAATTGATG CGGTTGTTTT AAAAAATTCA GGGGTTGTAG GGTTAGCCAA TGGATATGGC     600
AATGATGGTG AATATGGCAC ATTAGGGGTA GAAGCCTATG CTTTAGATCC TAAAAAACTC     660
TTTGGCAACG ACCTTAAGAC TATCAATTTA GAAGATTTAA GAACCATCTT GCATGAATTC     720
AGCCACACTA AAGGCTATGG GCATAACGGG AATATGACCT ATCAAAGAGT GCCGGTAACG     780
AAAGATGGTC AAGTGGAAAA GGATAGTAAT GGCAAGCCAA AAGATTCTGA TGGCCTTCCC     840
TATAATGTGT GTTCGCTTTA TGGGGGATTC AATCAGCCCG CTTTCCCTAG CAACTACCCT     900
AATTCCATCT ATCACAATTG TGCGGATGTC CCGGCTGGCT TTTTAGGGGT AACAGCAGCG     960
GTTTGGCAGC AGCTCATCAA TCAAAACGCC TTGCCGATCA ACTACGCTAA CTTGGGGAGT    1020
CAAACAAACT ACAACCTAAA CGCTAGTTTA AACACGCAAG ATTTAGCCAA TTCCATGCTC    1080
AGCACCATCC AAAAAACCTT TGTAACTTCT AGCGTTACCA ACCACCATTT TTCAAACGCA    1140
TCGCAAAGTT TTAGAAGCCC TATTTTAGGG GTTAACGCTA AAATAGGCTA TCAAAACTAC    1200
TTTAATGATT TCATAGGGTT GGCTTATTAT GGCATCATCA AATACAATTA CGCTAAAGCT    1260
GTTAATCAAA AAGTCCAGCA ATTGAGCTAT GGTGGGGGGA TAGATTTGTT ATTGGATTTC    1320
ATCACCACTT ACTCCAATAA AAATAGCCCT ACAGGCATTC AAACCAAAAG GAATTTTTCT    1380
TCATCTTTTG GTATCTTTGG GGGGTTAAGG GGCTTGTATA ACAGCTATTA TGTGTTGAAC    1440
AAAGTCAAAG GAAGCGGCAA TTTAGATGTG GCTACCGGGT TGAACTACCG CTATAAGCAT    1500
TCTAAATATT CTGTAGGGAT TAGCATCCCT TTAATCCAAA GAAAAGCTAG CGTCGTTTCT    1560
AGCGGTGGCG ATTATACGAA CTCTTTTGTT TTCAATGAAG GGGCTAGCCA CTTTAAGGTG    1620
TTTTTCAATT ACGGGTGGGT GTTT                                           1644
```

(2) INFORMATION FOR SEQ ID NO:1385:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

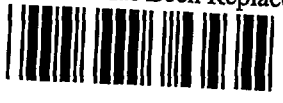
(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1260

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385

```
GATCATAGCT TTAATATTCA AAATAGTATA AAAAGGAAAG TCATGTATGC GGCTCATCCT      60
ATTAAACCCA TAAAAGCCCC TAAACTCAAA TCTCAATTTT TAAGGCGTGT GTTTGTGGGC     120
GCGTCCATTA GGCGCTGGAA TGACCAAGCA TGCCCTTTGG AATTTGTGGA ATTAGACAAG     180
CAAGCCCATA AAGCGATGAT TGCGTATCTG CTCGCTAAAG ATTTAAAAGA TAGGGGTAAA     240
GATTTAGATT TAGATCTTTT AATCAAATAT TTTTGCTTTG AGTTTTTGGA GCGCTTGGTT     300
TTAACCGATA TTAAACCCCC TATTTTTTAC GCCCTCCAAC AAACGCATAG TAAAGAGTTA     360
GCTTCCTATG TTGCGCAAAG TTTGCAAGAT GAAATCAGTG CGTATTTTTC TTTAGAGGAA     420
CTCAAAGAGT ATTTAAGCCA CAGGCCTCAA ATTTTAGAAA CTCAAATTTT AGAGAGCGCG     480
CATTTTTATG CGTCTAAGTG GGAGTTTGAT ATTATCTATC ATTTTAACCC CAACATGTAT     540
GGCGTGAAAG AGATTAAAGA TAAAATTGAC AAGCAACTCC ACAATAACGA TCATTTGTTT     600
GAAGGGCTTT TTGGGGAAAA AGAAGATTTG AAAAAATTGG TGAGCATGTT TGGGCAGTTG     660
CGTTTCCAAA AGCGCTGGAG CCAAACCCCA AGAGTGCCAC AAACCAGTGT TCTAGGGCAT     720
ACTTTATGCG TGGCGATTAT GGGGTATTTA TTGAGTTTTG ACTTGAAAGC TTGTAAAAGC     780
ATGCGGATCA ATCATTTTTT GGGCGGGCTT TTCCATGATT TACCCGAAAT TTTAACCCGA     840
GACATTATCA CGCCCATCAA ACAAAGCGTT GCAGGGCTTG ATCATTGCAT TAAAGAGATT     900
GAAAAAAAGG AAATGCAAAA CAAAGTCTAT TCCTTTGTGT CTTTGGGCGT TCAAGAAGAT     960
TTGAAATATT TCACCGAAAA CGAGTTTAAA AACCGCTACA AAGACAAGTC TCATCAAATC    1020
GTTTTCACTA AAGACGCTGA AGAATTATTC ACGCTTTATA ATAGCGATGA ATATCTTGGG    1080
GTTTGCGGGG AGCTTTTGAA GGTGTGCGAT CATTTGAGCG CGTTTTTAGA AGCCCAAATC    1140
```

TCTCTTTCTC ATGGCATTTC TAGCTACGAT TTAATCCAAG GAGCTAAAAA CCTTTTAGAA 1200
TTGCGATCCC AAACGGAACT GCTTGATTTG GATTTAGGGA AATTGTTTAG AGATTTTAAG 1260

(2) INFORMATION FOR SEQ ID NO:1386:

(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:1386

AATATTACAA TCAAGGATAG AACGATGAAA ACAAATGGTC ATTTTAAGGA TTTTGCATGG 60
AAAAAATGCT TTTTAGGCGC GAGCGTGGTG GCTTTATTAG TGGGGTGTAG CCCGCATATT 120
ATTGAAACCA ATGAAGTTGC TTTGAAATTG AATTACCATC CAGCTAGCGA GAAAGTTCAA 180
GCGTTAGATG AAAAGATTTT ACTTTTAAGG CCAGCTTTCC AATACAGCGA TAATATTGCT 240
AAAGAGTATG AAAACAAATT CAAGAATCAA ACCACGCTTA AAGTTGAAGA GATCTTGCAA 300
AATCAGGGCT ATAAGGTTAT TAATGTGGAT AGCAGCGATA AAGACGATTT TTCTTTTGCG 360
CAAAAAAAAG AAGGGTATTT GGCTGTCGCT ATGAATGGCG AAATTGTTTT ACGCCCCGAT 420
CCTAAAAGGA CCATACAGAA AAAATCAGAA CCCGGGTTAT TATTCTCCAC TGGTTTGGAT 480
AAAATGGAAA GGGTTTTAAT CCCGGCTGGG TTTGTCAAGG TTACCATACT AAAGCCTATG 540
AGTGGGGAAT CTTTGGATTC TTTTACGATG GATTTGAGCG AGTTGGACAT CCAAGAAAAA 600
TTCTTAAAAA CCACCCATTC AAGCCATAGC GGAGGGTTAG TTAGCACTAT GGTTAAGGGG 660
ACGGATAATT CTAATGACGC AATTAAGAGC GCTTTGAATA AGATTTTTGC AAGTATCATG 720
CAAGAAATGG ATAAGAAACT CACTCAAAGG AATTTAGAAT CTTATCAAAA AGACGCCAAG 780
GAATTAAAAA ACAAGAGAAA CCGA 804

(2) INFORMATION FOR SEQ ID NO:1387:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced

(ii) MOLECULE TYPE: DNA (genomic)

(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:1387

TCAAATTTTA AAAAAGGATT TTTTATGTTT AAAAGCAGAT TAAATTCATG GATTTTATTA 60
GGGATTTTAG GGGTTTTAGT GGTGGTTTTT TGGGATGTCA TAAAATACAA AATAGAAGAT 120
TTGCAACATG ATCATTATCT ATCACAAGTG AAAGAAAGGG AAGAATATTA TAAAAACCAC 180
ATAGAAGAAG CTTTGAAAAA GGATAGCGAA TGCTTTGAAA AAGGAGGCGA TAAAGTGGAT 240
TGCTCGGCTG CTATGAGAAT AGCTGCTGGT GAAAGAAATA GAAGAATGTT AGAGATTAAA 300

(2) INFORMATION FOR SEQ ID NO:1388:

(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:1388

AAATTATTTT TAGTTATAAT TTTTCAAAAA ACCTTAAGAG AAATCATGCA AGATTTACAA 60
CATTTCAAAA ATGATATTAC GCTCATTCTA TCTAAAGACA GATTAGATAC TTATGACAGC 120
CTAGAGCAAT ACAAAGAAAA TTTAAAACTC ATTGCTTTCA TCACGCCTAA AATTTCTAAC 180
TTAGAAATTT ATTTACGCAA CGCTTTAGAC TATTGCCTGA CTCAAATGAA AGGGAGTGAA 240
TGGGTGTTTA ACGAAAGCGT TTTAACCCCT TTAATCAAAG AATTAAAAGA AAAGAAAAAA 300
GAAATCACGC ATTCTTTAAT CTTATCTAAA ATGTCTTTAG GGGCAGTGAT CAGGCTTATT 360
TTTTGTTATA AGTTAGAGGG GGTAATATTA GATTTAAAGC GCATCAATTT CAAATCCTAT 420
TACCCCAATA ATAAAAATGC ATTATTTATC AACAATAAGA AAAATCCATT ATCTAGTGCT 480
TCAAAGGTTC ATATTGCTTT AAACTTGCTA TGGACAATTA GAAATCGTGC GTATCATTGG 540
GAAAATTTAC TCAAAATCCA ACCGAACAAG CGCCCACGCA TTACGACTTA TTTCATTGGG 600
TTAAAAGACA ATGATAGGGC AAGAATTCCT ATGAATATCA GTGTAGAACC AAGTAAAATC 660
GTCTTGTTTT TAGATGATTT AATTAAAAGC ATCGGAAATA AAGACTTGGA AGATTTAAGT 720
AGTTTG 726

(2) INFORMATION FOR SEQ ID NO:1389:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1401 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature

(B) LOCATION 1...1401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389

```
GGCATGAAAG CGTTGAAGAC TTTTTTAAAA AAATCCCTTA TTCTGTTACT AGCAATTGCC      60
TTAAACCACT TAAACGCTGT GGCTATGATT GTGGATAATC CTACGCAGAA CGCTTGGAAT     120
GGTGCTAAAA GAGCATGGGA TGAAAGCAAG TGGGCTAAAC ATTTAGCCAC TATTACTGAA     180
AGGATCAAGC TCGCTCAAGA CACATTAGAT AGGGCTAATC AGACGCTTAA TTCCATCAAC     240
AAAGTGAATG ATGTTTTGAA CAAAACCAAT CAATTTCTAA CAGGCAGTAT TTTAAGCATC     300
CCCAATCCCA TGCAGTATGT AGAAAAAATC CAAAGTTTTG CCAAGCAAGT TCAAGCCAAT     360
ACTGAAAGGA TCAAAGAAAA TGCACAAAAC TATGATATAC GCAATCAAAT TGCAGCCAAA     420
CGCATCTCTG AAAAATGCCC TGAACTCAAT TGGGATGTCA GTCAAGACGC GAGCCCTACA     480
GAGAAAAACT TACACCAATT TTTCACGAGC AAGGGGAAAG AAAGCGCTAA CACAAAGGCT     540
CTAAAGGATT TTGCTAACGC CATAGGTAAC ACTCAAATCA GCACGGCGAA CGATTTAGGA     600
GCTGGACTTA GAGGCAGAGC CTTATTAGAA TACATTTGCA TTCAAAAAGG CAATTTAGAA     660
GCGGCTAAAA AAATCCAATT ATTAGACAGC CAAATGACTT TAGCTCTACT CAATAACGAC     720
TATACGGCTT ATGAAAAACT TAGAGCTGAA AAAGAAGAAT TAAAAAGACA AATCGCTTCA     780
AATGTGTATG CGAAAGTCAA ACAGCTTGTT GTAGCTTCCC AAGATAGAGC GTTTAGTCAA     840
ATGGATAATG AGTTGGGCGT TAAAACTTTT GGGTTCAACG ATGAGAATGT TAAAAAAGGT     900
TATTGCAAGA AAGAAAACAG AAATGGCAAA AGCGAGTGCA TCCCTAACAT GCTCAATGTT     960
AATCGCTTAA AAGCGCAATT TGATGAGCTT AATTTAGATT ATAGTAGGGA TATTGCTGGT    1020
AAAAAAGGTG AAGCAGCCGC TAAAGTGTTC AATGACTACA AACACCGATT CCAACAATTA    1080
AGCGTAGAAA CTGCTTTAGA AATCGCTCAA AATTTAAGTT TTATGAATAA GACGCTAGGT    1140
TTAATGGTGC AAATGCAAAG CTATGCATTC AAGCAACAAA TGGGCTATTT TGAAGATATT    1200
ATTCCTGCTG ACGCCCTAAA AGATGACAAA GAGCATCAAG AAAATCTTGA ACAAAAACAA    1260
CAAGAAATAG AGAAAGTCTA TAGGGCTAAA TTAGACGCTT ATGGTTTCCC TAATGGTAGT    1320
GTAGGAAAGG CAAGTGGCGT GAATTCAAAT AGTAATAATG AAGCCCCAAG CTCTGATAAT    1380
ATCCAGTCGT TTAATCCGTA T                                              1401
```

(2) INFORMATION FOR SEQ ID NO:1390:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390

```
AGATTAAATA ACATGGCCGC TCCACTACTT GCTCTGCCCT TTCTTTCTAA CCCTTTAGTG      60
CTTGGTGCTT TAGCTGTCAT AGGAGTGGGT GCTTACTTGT ATCCCAATAA GCAAGATTCT     120
TTAGTTGTGC AAGCAGATGG GCTTTATAGT GAAATTCTTG GGTTTTTCAT TTCGTTTTCT     180
AGCAAGATCT TGAAAGGAAT TGGTGAGCCT TTAGCCAATG TTATCCAACC TTTTGGTATG     240
GTTTTAGGAA TGCTTTTAAT CCTTTTGTAT TCCTTTAAAC GCTATCAAAA CAATGATTTA     300
TTTGAAATCA AAACCTTTTT AATGCTTTTT GTGTTTGTAG GATACCTTTC TTTGTACCAT     360
TATGCTTTTA AATCTGATGG TTCTAGTAGC GGTAATGGTC GCTCCAGTTT TGCCTTTCAA     420
AATCATGTAA CAGAAATTTT TGACACGCCT GCTAACTTGC TAAATGCTGG GATTTCTAAT     480
GTGGTTAAGG AATATCAAAC AAATAGTGCA AGAGAACACA AGAATATAGA CACGCACCAT     540
AGTATCACTA ACGCTAATAT TTCATTCCAT GTCAGACAAA TTTTAACGAG TTTGAATAAA     600
CTATATGAAG ACTTCAAAAT TAATAATGGA CTATCGCTAA AAACCCTTAT TGCAGCTGTT     660
TTGTTATTAG TTATTTTAGG ATTAGAATTG TTTTTATTGT TCAAAGTTTT CTGTTATGTT     720
```

This Sheet Has Been Replaced



```
TTTATGACTT ATTTAGAAAA AATTATTTAC TTGTCTTTGG TTATTTTCAT GCTACTGCTA     780
GGGTTTTTTC AGCAGACTAG AGGTTTTTTA GTGTCTTATG TGAAAAAAAT TATTTCATTG     840
ACTTTTTACA TGCCTTTGTT GTTGCTATTA GTGTTATTCA ACTCTTTTGC ATTACAATAC     900
GCAATCAAAG TGGGAGGGAG CAATGAAATA GTGGCTAAAT TTGGCATTAT TGTAGCAATA     960
GGAATTTCAC TGACATTTAT TCAAAAAGTC CCCGAAATGA TTAACGCTAT CTTTGGCACA    1020
CAAGGTGGTC TAACGGATGC TAAAAGCTTC ATATATCAAG GTGTGCAAAT GGCTAGTGCT    1080
GGAGCTGGAG CCATAGCTGG AAGTCTTAAG AGTGTGGGTC GTTCAGCATT TGGTAGAACG    1140
CTAGAAGCTT ATAAAGACGC AAAATCTACG ATAAACAGCA CTACGGCTAA CATGAGAGAC    1200
ATGCCAGGAC ATCCTGGTGT TAGAGTGGGT GTGGAGACGA TTGAACTTCC CAAGTCTCAT    1260
AGAGCTAGCA AA                                                        1272
```

(2) INFORMATION FOR SEQ ID NO:1391:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391

```
AAAAATCGCT ATCTTAAGAG GGGGCGAAAC GCTATCTTGG AACCTTCAAG AAATCGCCTA      60
AAACATGCCG CCTTTTTTGT GGGGCTTTTT ATCGTTTTGT TTTTAATTAT AATGAAGCAC     120
CAAACCTCCC CCTATGCTTT CACGCATAAT CAAGCCCTTG TCACTCAAAC CCCCCCCTAT     180
TTCACGCAAC TCACTATCCC TAAACCAAAT GACGCTTTAA GCGCGCATGC GAGCTCTTTA     240
ATCAGCTTGC CTAACGACAA TCTTTTGAGC GCTTATTTTA GCGGCACTAA AGAAGGGGCA     300
AGGGATGTGA AAATCAGCGC GAATCTTTTT GACAGCAAGA CTAATCGCTG GAGCGAAGCC     360
TTCATTCTTT TAACCAAAGA AGAGCTTTCT CATCATTCGC ATGAATACAT CAAAAAATTA     420
GGTAACCCCT TGCTTTTTTT GCATGATAAT AAAATTTTGT TGTTTGTCGT AGGGGTGAGC     480
ATGGGCGGGT GGGCCACTTC TAAAATCTAT CAATTTGAAA GCGCTTTAGA GCCGATTCAT     540
TTTAAGTTTG CGCGAAAACT CTCTTTAAGC CCTTTTTTAA ATTTGAGCCA TTTAGTAAGG     600
AATAAGCCTT TAAACACCAC TGATGGCGGG TTTATGCTAC CACTCTATCA CGAATTAGCC     660
ACCCAATACC CCTTGTTGTT GAAATTTGAC CAACAAAATA ACCCAAGAGA GCTTTTAAGG     720
CCTAATACCT TAAACCACCA GCTCCAACCA AGCTTAACCC CCTTTAAAGA CTGCGCTGTC     780
ATGGCGTTTA GAAACCATTC TTTTAAAGAT AGCCTCATGC TAGAAACCTG TAAAACCCCC     840
ACTGATTGGC AAAAACCCAT TTCTACAAAT CTTAAAAACT TAGATGATTC TTTAAATTTA     900
CTCAATTTAA ATGGAATATT GTATTTGATC CACAACCCTA GCGATTTATC ACTGCGTCGT     960
AAAGAACTTT GGCTTTCTAA ATTAGAAAAC TCCAACTCGT TTAAAACCTT AAAAGTTTTG    1020
GATAAAGCGA ATGAAGTGAG TTACCCAAGC TATAGCCTTA ATCCGCATTT TATAGATATT    1080
GTCTATACTT ACAACCGCTC TCATATCAAA CACATCCGTT TCAATATGGC TTATTTAAAT    1140
TCCCTTCTCA AG                                                        1152
```

(2) INFORMATION FOR SEQ ID NO:1392:

(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:1392

```
TTAGTCATGT TTATATCTTC TTCTTACACG CTGAGTTTTG TATGGCTTTT TTTAATTTTC      60
TTTTTTTTCA AAAATAAGCC ATTGGGTTTG AGGTTTTCGC TCTCTTTGAT AAGCGTGATT     120
TTAAGCAATA TCGCTTTGAA AGACTCCCTA TCGCTCAATG AATTTTTAAG CAGTTTTACA     180
GCCCCCTTAA GCCCCTTTAG CTGTCTTTTG ATCCTTGCTT ATGCAAGCTT TTCTTGCCAT     240
ATACTCAAAA AGCCCCCTTT AGAAACCTTG CAATCTTATA GCGTCATGCT GTTTTTCAAT     300
CTGTTGCTTT TGACAGATAT TTTAGGGTTT TTGCCTTTTT CAATCTACCA TCATTTCATG     360
GCTTCTCTGA TTTTTAGCGC GCTTTTTTGC AGCAGTTTGT TTTTGAGTAG CCCCTTATTA     420
GGCGTGATCG CTTTAGTGGC TTTATCCAGT TCGCTTTTGA TGCGTTCTAA TTTTCAAATC     480
TTAGATTCTT TATTGGATTT CCCATTATTT CTTTTTGTCT TTTTTAAGAC TTTATATCTT     540
GCTAAAAAAA GGTTA                                                     555
```

(2) INFORMATION FOR SEQ ID NO:1393:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2946 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393

```
AAAAGAATAC TGATGAAGAA AAGAAAACAT GTATCCAAGA AAGTGTTTAA TGTCATTATC      60
TTGTTTGTGG CAGTATTCAC TCTTTTAGTC GTCATTCACA AAACCCTTTC AAACGGCATT     120
CACATACAAA ATTTAAAAAT TGGAAAACTT GGCATTTCTG AATTATACTT AAAACTCAAT     180
AACAAGCTTT CTTTGGAAGT TGAGCGGGTT GATCTCTCTT CTTTCTTCCA TCAAAAACCC     240
ACTAAAAAGC GTTTAGAAGT TTCTGATTTG ATTAAAAATA TCCGTTATGG CATTTGGGCG     300
GTGTCTTATT TTGAAAAACT TAAAGTCAAA GAAATCATTT TAGACGATAA AAATAAAGCC     360
AATATCTTTT TTGATGGGAA TAAATACGAG TTAGAATTTC CAGGAATCAA AGGGGAATTT     420
TCCCTAGAAG ACGATAAAAA TATCAAGCTT AAAATCATCA ATTTGCTTTT TAAAGATGTT     480
AAAGTCCAAG TGGATGGCAA CGCCCACTAT TCACCCAAAG CCAGGAAAAT GGCGTTCAAT     540
TTGATTGTCA AGCCCTTAGT TGAACCCAGC GCTGCAATTT ATTTGCAAGG GCTAACCGAT     600
TTAAAAACCA TAGAATTAAA AATTAACACT TCTCCAATGA AAAGCCTAGC GTTTTTAAAG     660
CCTCTTTTCC AACGCCAATC GCAAAAAAAT TTAAAAACGT GGATTTTTGA CAAGATCCAA     720
TTTGCCAGCT TTAAGATTGA TAACGCTTTA ATCAAGGCTA ATTTCACTCC TAGCGAGTTT     780
ATCCCATCGC TTTTGGAAAA TTCTGTAGTT AAAGCCACTT TGATTAAGCC TTCAGTCGTT     840
TTTAATGATG GCTTATCGCC CATTAAAATG GATAAAACCG AATTGATTTT CAAAAACAAA     900
```

CAGCTCCTCA TACAGCCCCA AAAAATCACT TATGAAACCA TGGAATTAAC CGGCTCTTAC 960
GCCACTTTTT CCAATTTGTT AGAAGCCCCT AAGTTGGAGG TTTTTTTAAA AACGACCCCT 1020
AATTATTATG GCGATAGCAT TAAGGATTTA TTGAGCGCTT ATAAAGTCGT TTTACCTTTG 1080
GATAAAATCA GCATGCCATC TAGCGCGGAT TTGAAGCTCA CTTTGCAATT CTTAAAAAAC 1140
ACCGCCCCCT TATTTAGCGT TCAAGGCAGC GTTAATTTGC AAGAAGGCAC TTTCTCGCTC 1200
TATAATATCC CCCTTTACAC GCAAAGCGCT CAAATCAATT TGGACATCGC CCAAGAATAC 1260
CAATACATCT ACATAGACAC GATCCACACG CGCTATGCAA ACATGCTGGA TTTAGACGCT 1320
AAAATCGCTT TAGATTTAGG TCAAAAAAAC CTTTCTTTGG ATTCTTTAGT CCATAAAATC 1380
CAAGTCAATA CCAATAACAA TATCAACATG CGCTCTTATG ATCCCAATAA CACTCAAGAA 1440
GATCCGCAAA CTAACTTTAC TTTGGATCTA AAAAGCTTGC ATTCTATCAT TCAAGAGGGT 1500
GAAAATTCAG AAGTTTTTAG AAGAAAAATC ATAGACACCA TTAAAGCCCA AAGCGAAGAT 1560
AAATTCACTA AAGATGTTTT TTACGCCACA GGAGACACTC TCAAAAGCCT GTCGTTGAGT 1620
TTTGATTTTT CCAACCCCGA TCACATACAA TGGAGCGTGC CACAACTCTT ATTAGAAGGC 1680
GAATTTAAAG ATAACGCCTA TACTTTTAAG ATCAAAGATT TGAAAAAGAT CAAGCCCTAT 1740
TCCCCCATTA TGGACTATAT TGCCCTAAAA GACGGCTCTT TAGAGGTTTC TACGAGCGAT 1800
TTTGTCAATA TTGATTTTTT TGCTAAAGAT TTGAAAATCA ACCTCCCCAT TTATAGGAGC 1860
GATGGATCGC ATTTTGATTC TTTTTCTTTA TTTGGCTCTA TCAATAAAGA TGAAATTTCT 1920
GTCTATACTC CAAGCAAAAG CATATCCATA AAAGTTAAGG GGGATCAAAA GGATATTACC 1980
CTTAATAACA TTGATTTGAG TATTGATGAT TTCTTGGATA GTAAAATGCC AGCTATTGCG 2040
GGATTATTCT CAAAAGAACG AAAAGAAAAG CCTAGCTCTA AAGAAATCCA AGATGAAGAT 2100
GTTTTCATTA GCGCCAAACA ACGCTATGAA AAAGCCCACA AAATTATCCC CATCTCTACA 2160
CGCATCCATG CTAAAGATGT CGTGCTGATC TATAAAAAAA TGCCTTTTCC TTTAGAAAAT 2220
CTTGATATTG TCGCTCAAGA CGATAGGGTG AAAATTGATG GCAATTATAA AAACGCCATG 2280
ATCATGGCGG ATTTAGTGCA TGGGGCTTTG TATCTTAAGG CTCATAATTT TAGCGGGGAT 2340
TATATCAACA CCATTCTTCA AAAAGATTTC GTAGAAGGAG GCTTATTCAC GCTTATTGGG 2400
GCTCTTGAAG ATCAGGTTTT CAATGGCGAA TTGAAATTCC AAAACACAAG CTTAAAGAAT 2460
TTCGCCCTCA TGCAAAACAT GGTCAATCTC ATCAACACCA TTCCCTCCCT TATTGTCTTT 2520
AGAAACCCTC ATTTAGGGGC TAATGGCTAT CAAATCAAAA CCGGCTCCGT TGTGTTTGGG 2580
ATCACTAAAG AATATTTAGG GTTAGAAAAA ATTGATCTTG TCGGCAAAAC GCTTGATATT 2640
GCTGGCAATG GAATCATTGA ATTAGACAAA AACAAATTAG ATTTAAACTT AGAAGTTTCC 2700
ACTATCAAGG CTTTGAGTAA TGTCTTAAAT AAAATCCCTA TCGTGGGCTA TCTCGTTTTA 2760
GGAAAAGGAG GTAAAATCAC CACTAACGTG AATGTCAAAG GCACGTTGGA TAAGCCTAAA 2820
ACCCAAGTAA CTTTAGCGTC AGATATTATC CAAGCGCCTT TTAAAATCTT ACGCCGTATT 2880
TTCACGCCTA TTGACATCAT CGTGGATGAA GTCAAGAAAA ACATTGATTC AAAAAGGAAA 2940
TTAAAA 2946

(2) INFORMATION FOR SEQ ID NO:1394:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394

AGACCATTCA GATCGCTTAT AAGGATTACC CACGCCCCAA AACTAAAACC CTCATTCGCA 60
TTAGAGTGCG TTATTACTTG GGAGGCAATT AACAGCATGG AAATCACGCT TTTTGACGCT 120
ATAGACGCCC ACTTGCATGT GCGAGAAAAC GCGCTTTTAA AAGCGGTGTT GGAATATTCT 180
AGCGAACCTT TTAGCGCCGC AGTGATCATG CCCAATCTCA GTAAGCCTTT GATTGACACT 240
CCAATCACCC TAGAATATGA AGAAGAAATT TTAAAAAATT CTTCAAACTT CAAGCCTTTA 300

This Sheet Has Been Replaced



```
ATGAGTTTGT ATTTTAACGA TGGTTTGACT TTAGAAGAAT TGCAACGAGC TAAAAACAAA     360
GGCATTAAAT TTTTAAAACT CTACCCCAAA GGCATGACCA CAAACGCGCA AAATGGCACT     420
TCGGATTTGT TGGGTGAAAA GACTTTGGAG GTTTTAGAAA ACGCCCAAAA ATTAGGCTTT     480
ATTTTATGCG TCCATGCAGA ACAAGCTGGG TTTTGTTTGG ATAAAGAATT TTTATGCCAT     540
AGCGTTTTAG AAACTTTCGC CCTTTCATTC CCTAAACTCA AAATCATTAT AGAGCATTTG     600
AGCGATTGGC GCAGTATCGC TTTGATTGAA AAGCATGACA ACCTCTATGC GACTTTGACC     660
TTACACCATA TCAGCATGAC TTTAGATGAC TTATTAGGGG GGAGTTTGGA CCCGCATTGT     720
TTTTGCAAAC CCTTAATCAA AACCAAAAAA GACCAAGAAA GGCTCTTATC CCTTGCTTTA     780
AAAGCCCACC CTAAAATCTC TTTTGGATCG GACAGTGCCC CGCATTTCAT TTCTAAAAAG     840
CATAGCGCTA ACATCCCGGC GGGCATCTTT TCTGCCCCTA TTTTGTTGCC TGCGTTGTGC     900
GAACTTTTTG AAAAACACAA CGCTTTAGAA AATTTGCAAG CCTTTATCAG TGATAACGCT     960
AAAAAAATCT ACGCGCTAGA CAATTTACCC AGTAAAAAAG CGCATTTGTC TAAAAAACCC    1020
TTTATAGTCC CTACGCACAC GCTTTGCTTG AATGAAAAAA TCGCTATCTT AAGAGGGGGC    1080
GAAACGCTAT CTTGGAACCT TCAAGAAATC GCC                                 1113
```

(2) INFORMATION FOR SEQ ID NO:1395:

This Sheet Has Been Replaced



(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:1395

```
GAAATTTATA TGCCGGAAAA TTCTAAACTA CAACCTGCTA AGTTAGGGAA AAATTTTGAC      60
CCTGTGGATC ATTCTAACAG GAATTTTTTC TTTTCTCTCA TTCTGTCTGT ATTGTTACAC     120
TGGTTGATTT ATTTTTTATT TGAACACAGA GAAGATTTTT TTCCTTCAAA ACCCAAGCTC     180
GTTAAATTAA ATCCTGAAAA TTTATTGGTT TTAAAAAGAG GCCATTCACA AGATCCCAGT     240
AAAAACAACC CAGGCGCTCC TAAACCCACG CTAGCTGGCC CTCAAAAACC CCCCACACCC     300
CCCACACCCC CCACTCCGCC AACCCCACCA AAACCTATAG AAAAGCCAAA GCCTGAGCCT     360
AAACCAAAGC CCAAACCAGA ACCCAAAAAG CCCAACCACA AACATAAGGC GCTCAAAAAA     420
GTGGAAAAAG TGGAAGAGAA AAAAGTAGTA GAGGAGAAAA AAGAAGAGAA AAAAGTAGTA     480
GAACAAAAAG TAGAGCAGAA AAAAATAGAA GAGAAAAAAC CTGTCAAAAA AGAATTTGAC     540
CCTAACCAGC TTTCTTTCTT GCCTAAAGAA GTTGCGCCAC CCAGACAGGA AAACAATAAA     600
GGCTTGGATA ACCAGACTAG AAGGGATATT GATGAATTGT ATGGCGAAGA ATTTGGAGAT     660
TTAGGCACAG CCCGAAAAAG ATTTCATCAG GAA                                  693
```

(2) INFORMATION FOR SEQ ID NO:1396:

(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

This Sheet Has Been Replaced



(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:1396

```
AGTCGTTATC ACCCAAGAGG TTTTAGCCAA TTGCCTAAAC TCAAACTCAT TTGCATCACC      60
GCTACAGGCA CGGATAATGT GGATATAAAA AGCGCGAAAG CTTTAGGCAT AGAAGTCAAA     120
AACGTGAGCG CTTATTCTAC CGAATCTGTA GCCCAGCACA CTTTAGCGTG CGCGTTGTCT     180
TTGTTGGGGA GGATCAATGA TTACGATCGT TATTGCAAAA GCGGGGAATA TAGTCAAAGC     240
GATATTTTTA CGCACATTAG CGATATTAAA ATGGGGCTTA TTAAAGGAGG TCAATGGGGG     300
GTTATTGGTT TAGGCAATAT CGGTAAAAGA GTCGCCAAGC TCGCTCAAGC TTTCGGGGCA     360
AAGGTGGTGT ATTTTTCCCC TAAAGATAAA AAAGAAGAAT ACGAGCGCTT GAGTTTAGAG     420
GAATTGCTTA AAACAAGCGG TATTATCAGC ATTCATGCCC CCTTAAATGA AAGCACGCGC     480
GATTTAATCG CTCTGAAAGA ATTGCAAAGC TTAAAAGATG GGGCGATTTT AATCAATGTG     540
GGGCGTGGGG GCATTGTGAA TGAAAAGGAT TTGGCTTTAA TTTTAGAAAC CAAAGATTTG     600
TATTACGCGA GCGATGTG                                                   618
```

(2) INFORMATION FOR SEQ ID NO:1397:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397

```
ATATTAGAGA ATTTGAGGAT TTACGCCAGG CTTTTGGAAA TGATACTAAA AAATTTGATT      60
TTGTTATTTT TAGCAAAGAG AAAACTTATT TTCATAGAAG CTAATTTTTA TACCATTAGT     120
GGGAGCAAGC TTAATGAAGT CGCAAGATCC TATCAAGACT TAGCTTTAAA ATTTGAAGCA     180
TTTCCTAATT ACGAATTTAT TTGGATAACT GATGGCATAG GTTGGCTAGA CGCTAAAAGC     240
AAGCTCCAAG AAGCTTACAA ATCTGTAGAA ATCTATAACT TAAGCTATGT GAATGATTTT     300
ATATCAAAGG TGCAAAAA                                                   318
```

(2) INFORMATION FOR SEQ ID NO:1398:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398

```
TGCGTGATGC TAATGGCAAT TTTTACCCCT TATATTCTTA TTTTGAAAAT GATGAAAAAG      60
TCTATGAGTT TATTCGCCAA TATGGGGTTG GAGCAAATTT TTTGCAACAG AGACATTAAA     120
GATTTAAATG ATTTTGTTTT TGGTATAGAA GTGGGGCTTG ATAGCAATGC GAGAAAAAAT     180
CGTAGCAGAA AGGCTATGGA AAATCATCTT ATCGGTCTTT TTGTCCAAGC TCAATTAAAT     240
TTTAAAGAAC AAGTAGATAT TAGAGAATTT GAGGATTTAC GCCAGGCTTT TGGAAATGAT     300
ACTAAAAAAT TTGATTTTGT TATTTTTAGC AAAGAGAAAA CTTATTTTCA TAGAAGC        357
```

(2) INFORMATION FOR SEQ ID NO:1399:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 912 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399

```
CTTGTGATCA ATTCTAAAAC CGGACTGCTC ACCATTAAGG GCGAGGACGC TTTAGGCAAG      60
GCTAGTTTGA AGGATTTGGG TTTGAGCGCT GGCATGGTGC AATCTTATGA AGCTTCGCAA     120
GACACGCTTT TTATGTCTAA GAATTTGCAA AAAGCGAGCG ATTCGCAATT CACTTACAAT     180
GGGGTGAGCA TCACGCGCCC CACTAATGAG GTCAATGATG TGATCAGCGG GGTTAATATC     240
ACTTTAGAGC AAACCACAGA GCCTAATAAG CCTGCCATTA TCAGCGTGAG CAGAGACAAT     300
CAAGCCATTA TAGACAGCCT TAAAGAATTT GTCAAAGCCT ATAATGAGCT TATCCCTAAA     360
CTAGACGAAG ACACGCGCTA TGACGCTGAC ACTAAAATCG CCGGGATTTT TAACGGCGTG     420
GGCGATATTC GTGCCATTAG ATCCTCTCTT AATAATGTGT TTTCTTATAG CGTGCATACG     480
GATAATGGGG TAGAAAGCTT GATGAAATAC GGGCTTAGTT TAGACGATAA GGGCGTGATG     540
AGTTTGGATG AAGCTAAATT ATCAAGTGCA TTAAATTCTA ACCCTAAAGC GACTCAAGAT     600
TTTTTCTATG GGAGCGATAG CAAGGATATG GGGGGCAGAG AAATCCACCA AGAGGGCATT     660
TTTTCTAAAT TCAATCAAGT CATCGCTAAC CTCATAGATG GAGGGAACGC TAAATTAAAG     720
ATTTATGAAG ATTCCCTAGA CAGAGACGCT AAAAGCCTGA CCAAAGACAA AGAAAACGCT     780
CAAGAGCTTT TAAAAACCCG CTATAACATC ATGGCGGAGC GCTTTGCCGC TTATGATAGT     840
CAAATCTCTA AAGCCAATCA AAAATTCAAT TCCGTGCAAA TGATGATCGA TCAAGCAGCG     900
GCTAAAAAGA AT                                                        912
```

(2) INFORMATION FOR SEQ ID NO:1400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400

AGGAACATTA TGCAATACGC TAACGCTTAT CAAGCCTACC AGCATAACCG AGTGAGTGTG 60
GAATCCCCGG CAAAACTCAT TGAAATGCTT TATGAAGGGA TTTTAAGATT TTCTTCGCAA 120
GCCAAACGCT GTATTGAGAA TGAAGACATT GAAAAGAAGA TCTATTATAT TAATAGGGTT 180
ACGGATATTT TCACGGAGTT GTTGAATATT TTAGACTATG AAAAAGGGGG GAAAGTGGCG 240
GTGTATCTTA CAGGCTTATA CACCCATCAA ATCAAAGTTT TAACGCAAGC CAATGTGGAA 300
AATGACGCGA GTAAGATTGA TTTGGTGTTG AATGTGGCTA GGGGGTTGTT AGAGGCATGG 360
AGGGAAATCC ATTCAGATGA ACTCGCC 387

(2) INFORMATION FOR SEQ ID NO:1401:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401

TTTGATGATC TTTATGGATC AAACTCACTT CCATTTTATC CACGGGTAAC CCCGGTAAAA 60
TTCCCCACTT TCAAATGGGC GTTACTCAAA GCGTTGATTA AGGACGATTT CCCCACATTA 120
GGCTGGCCCA CAAGGGCGAC AATGATTTCT TTCATTGGGT TTGAATGCTC CGCATTAAAA 180
GTTTTTTTAA TTTTTGGTTA TATAGTTTTT AAAAGTTGGC ACTATAGCGC TATAAGACTA 240
ATTGTTATA 249

(2) INFORMATION FOR SEQ ID NO:1402:

(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:1402

```
AAGCGAGACA AGAATGTTAA AATGCGAAAG GGGCGTGTGA TGTTATGCGT GTTTGATATA      60
GAAACCATTC CTAATATAAG CTTGTGTAAA GAGCATTTTC AATTAAAAGA AGACGATGCG     120
CTAAAAATCT GTGAATGGAG TTTTGAAAAG CAAAAAGAAA AAAGCGGGAG CGAGTTTTTG     180
CCCCTTTATT TGCATGAAAT CATCTCTATT GCAGCAGTCA TTGGCGATGA TTACGGGCAA     240
TTTATCAAAG TAGGGAATTT TGGTCAAAAA CACGAGAATA AAGAGGATTT TGCGAGCGAA     300
AAAGAGCTTT TAGAGGACTT TTTCAAATAC TTTAACGAAA AGCAACCGCG CCTAATAAGC     360
TTTAATGGCA GAGGTTTTGA TATTCCCCTA CTCACGCTCA AAGCCCTTAA ATACAATTTA     420
ACCTTAGACG CTTTTTTACAG CCAAGAAAAC AAATGGGAAA ATTACCGCGC GCGTTATAGC     480
GAGCAGTTTC ATTTGGATTT GATGGATAGC TTGAGCCATT ATGGATCCGT TAGGGGGTTG     540
AATCTAAATG GCGTTTGCTC TATGACGAAT ATTCCTGGTA AATTTGATGT GAGCGGGGAC     600
TTAGTGCATG CGATTTATTA CAACCCCCAT TTAAGGCCAA AAGGAGGAAA AAGGCATTAT     660
```

(2) INFORMATION FOR SEQ ID NO:1403:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 762 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

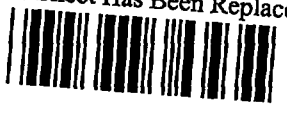
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403

```
AGATTTAAGG CTAGAATTGT GCGTTTTTTC ATTTTTTTAA TTCTCATTTG CCCTTTAATA      60
TGCCCCTTAA TGAGCGCGGA TAGCGCTTTA CCTAGCGTCA ATCTCTCTTT AAACGCTCCT     120
AGTGATCCTA AACAACTCGT AACCACCCTT AATGTCATCG CCTTACTCAC GCTTTTGGTT     180
TTAGCCCCAT CGTTGATTTT AGTGATGACG AGTTTCACCC GTTTGATCGT GGTGTTTTCT     240
TTTTTAAGGA CCGCTTTAGG CACGCAACAA ACCCCACCCA CTCAAATTCT AGTCTCGCTC     300
TCTTTGATAT TGACTTTTTT TATCATGGAA CCTAGCTTGA AAAAGGCTTA TGATACAGGG     360
ATTAAGCCTT ATATGGATAA AAAGATTTCT TACACCGAAG CGTTTGAAAA AAGCACTCTG     420
CCTTTCAAGG AATTCATGCT TAAAAACACA CGAGAAAAAG ATCTAGCCCT TTTTTTTAGG     480
ATTAGGAATT TGCCTAACCC TAAAACCCCT GATGATGTGA GCTTGAGCGT TTTAATCCCG     540
GCATTTATGA TAAGCGAGTT GAAAACAGCG TTTCAAATCG GCTTTTTACT CTACTTGCCT     600
TTTTTGGTGA TTGATATGGT TATCAGCTCT ATTTTAATGG CGATGGGTAT GATGATGCTC     660
CCGCCTGTAA TGATTTCTCT GCCTTTTAAA ATTTTGGTGT TTATTCTGGT GGATGGGTTT     720
```

AATTTATTGA CCGAAAATTT AGTGGCGAGT TTTAAAATGG TT 762

(2) INFORMATION FOR SEQ ID NO:1404:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1842 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404

AAGTGGGGAA TTTTACCGGG GTTACCCGTG GATAAAATGG AAGTGAGTTT GATCCATAAA 60
GATCATCAAA TCACTATCAT TGATTTACCG GGCACTTACG CGCTCAATGA CTTCACCACT 120
GAAGAAAAGG TGACTAAAGA TTTTTTAGAA AAAGGGCAAT ACAATCTCAT TCTCAATGTG 180
GTGGATTCCA CCAATTTAGA GCGTAATTTA GCCTTAAGCG CGCAGTTATT AGACACAAAT 240
AAAAAAATGC TGCTTGCGCT CAACATGTGG GATGAAGCCA AGAAAGAAGG GATCAACATC 300
AATACAGAAA AGCTCTCTCA AGAATTGGGG GTTGTGTGCG TGCCAACAAG CGCGAGATCC 360
AAAGAAGATC GCTTGAACAC AGAGCTTTTA TTAGACGAAA TTGTCAGGCT TTATTCTCAA 420
AACACTACAA ACAACGAAAA CATCAAAGTC CCATCTCAAA GTTTTAAAGA GTCTTTAAAA 480
TACAGCCAGA GCGCCCAAAG AATCGCTAAA TCAGTGATCA GTGAAAACAA ACAAAATGCG 540
AGTTTTGAAC ACACTTATAA GATTGATAAG ATTTTAATGC ACCAGCGTTA TGGGATTTTC 600
ATTTTTTTAG GGTTTATGTT TATCATCTTT TCTTTGAGCT TTTTAATAGG AGGGGGAGTG 660
CAAAAAGCCC TTGAAGAAGG GTTTAAAATT TTGAGCGATA GTATTAAAGA AAATGTGGCT 720
AATGAAGATT TAGCGTCTTT GGTGGGCGAT GGCATTATTG GGGGAGTGGG AGCGACGGTT 780
TCATTCTTGC CTTTAATTGT GGTGTTGTAT TTTGGGATTT CTTTACTAGA GACGACAGGC 840
TATATGAGTA GGGTAGCGTT TTTACTAGAC GGGATCTTGC ATAAATTTGG TTTGCATGGG 900
AAGAGTTTTA TCCCTTTAAT CACCGGTTTT GGTTGCTCAG TGCCTGCTTA CATGGCGACA 960
AGAACCTTAC AAAACTATAA CGAACGATTG ATCACGCTTT TTGTGATCGG CTTTATGAGT 1020
TGCTCGGCAA GACTGCCTAT TTATGTGCTG TTTGTAGGCT CGTTTTTCCC CTCTTCAAGT 1080
GCTGGGTTTG TGCTGTTTTG CATTTATATT TTGGGGGCGG TTGTGGCGTT AGTGATGGCC 1140
AAATTACTCA AATTAAGCGT GTTTAAAGGA CAGACTGAAT CCTTTATCAT GGAAATGCCC 1200
AAATACCGCT TTCCCAGTTG GAGAATGGTC TATTTCAGTA TTTACACCAA ATCGCTTTCT 1260
TACCTCAAAA AAGCCGGGAC TTATATTTTA GTGGGAGCGA TTTTGATCTG GTTTATGTCC 1320
CAATACCCTA AAAATGATGC GGCTATGAAG ACTTATAAAC AAGAAAGCTT GTTAGTCCAA 1380
AAAAACGCTA ATCTTTCAAG CGAAGCTAAA GAAGAAAAAT TAAAAGAATT AAAAACCGAA 1440
TTGGATAAAA AGAATTTAAA AAATAGCGTT GTAGGAAGAG GCGGGGCGTA TTTAGAAAAA 1500
GTCTTTAACC CTATGGATTT TGATTGGCGT TTGAGCGTCT CGCTTGTAAC CGGTTTTATG 1560
GCTAAAGAGG TGGTGGTTTC TACTTTGGGG GTGTTGTTTT CTTTAGGGGA TCAAAACGAA 1620
AAATCTGATG CTTTTAGAGA GATAATCAGA AAAGAAGTCA GCGTGCCTAG CGGGATCGCT 1680
TTTATCGTGT TTGTGATGTT TTATATCCCT TGTTTTGCAG CGACCATTAC TTTTGGTAGG 1740
GAAGCTGGGG GGATCAAGTT TGTAGCGTAT TTATTCATCT TCACAACCGT TGTAGCGTAT 1800
GCGTTTTCCT TGATAGCTTT TTATGCGACT CAAATTTTGG TT 1842

(2) INFORMATION FOR SEQ ID NO:1405:

(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

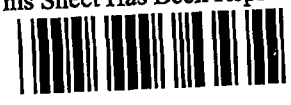
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405

```
ATGAAAAGAA TTTTAGTTTC TTTGGCTGTT TTGAGTCATA GCGCGCATGC TGTCAAAACT      60
CATAATTTGG AAAGGGTGGA AGCTTCAGGG GTGGCTAACG ATAAAGAAGC GCCTTTAAGC     120
TGGAGGAGCA AGGAAGTTAG AAATTATATG GGTTCTCGCA CGGTGATTTC TAACAAGCAA     180
CTCACTAAAA GCGCCAATCA AAGCATTGAA GAAGCTTTGC AAAATGTGCC AGGCGTGCAT     240
ATTAGAAACT CTACCGGTAT TGGAGCTGTG CCTAGCATTT CCATTAGGGG GTTTGGTGCT     300
GGAGGCCCAG GGCATTCTAA TACGGGAATG ATTCTAGTCA ATGGGATTCC TATTTATGTC     360
GCGCCCTATG TTGAAATTGG CACGGTTATT TTTCCTGTAA CCTTTCAGTC TGTGGATAGA     420
ATCAGCGTAA CTAAGGGTGG GGAGAGCGTG CGTTATGGCC CTAACGCTTT TGGCGGTGTG     480
ATCAACATCA TCACCAAAGG CATTCCTACC AATTGGGAAA GTCAGGTGAG CGAGAGGACC     540
ACTTTTTGGG GCAAGTCTGA AAACGGGGGC TTTTTCAATC AAAATTCTAA AAACATTGAT     600
AAAAGCTTAG TTAATAACAT GCTTTTTAAC ACCTATTTAA GAACGGGGGG TATGATGAAT     660
AAGCATTTTG GAATCCAAGC TCAAGTCAAT TGGCTCAAAG GGCAAGGGTT TAGATACAAC     720
AGCCCTACGG ATATTCAAAA TTACATGTTA GATTCATTGT ATCAAATCAA TGATAGCAAT     780
AAAATCACCG CTTTTTTTCA ATATTATAGT TATTTCTTGA CAGACCCTGG ATCTTTAGGC     840
ATAGCCGCTT ACAATCAAAA TCGTTTTCAA AACAACCGCC CCAATAACGA TAAAAGCGGG     900
AGAGCGAAGC GATGGGGAGC TGTGTATCAA AACTTTTTTG GGGACACGGA TAGGGTAGGG     960
GGGGGATTTC ACTTT                                                     975
```

(2) INFORMATION FOR SEQ ID NO:1406:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2391 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406

```
AGACTAAAAC CAAATGTTAT AGAGCGTAGG ATGTTAGAAA AGCTTTTAAG CGCTATCAAA      60
CAAAAAGTTT CAAACTATTT TTTAGGGGTT TTGCCTAAAA GCTATTCTAT GAGCGAAGAA     120
AACAACATTT TAGGCTTGTA TGATGAGCAT TTTTTGCTCA CTAAAAACGA AAACTTAGTG     180
GGCATCCTCC GTTTAGAGGG GGTTAGCTAC ACCCATTTAA GCACAGAGCA ATTGCAAGAT     240
CTTTTCACTG AGCGCCAAAT GGCGTTAGAT TCTTTAGAAA AAGTCGTGGC GCGTCTTGTG     300
GTTAAAAGGC GTAAAATTGA TTATAAACAA AGCATTCAAT CTGACTCTCA ATACTTGCAA     360
```

```
GCGATCTTGA ATCAGTTTGA AAATAAAGAA GTGTATGAGA ATCAGTATTT TTTAGTTTTA    420
GAAAGCACTC ACTCTTTGCA TGGCGTTTTG GAGCATAAGA AAAAATCTTT CATGCACGCT    480
AATAGAGAAA ATTTTAAGGA TATTCTCTCT TATAAAGCGC ATTTTTTGCA AGAAACTTTA    540
AAAAGCTTAG AAATCCAGCT CAAAAACTAT GCCCCCAAAC TCTTAAACTC TAAAGAGGTT    600
TTGAATTTTT ATGCAGAATA TATTAATGGG TTTGAACTCC CTTTAAAACC CCTAGTAGGG    660
GGGTATTTGA GCGATAGCTA TATCGCTAGT TCTATCACTT TTGAAAAAGA TTATTTCATT    720
CAAGAAAGCT TTAATCAAAA AACCTATAAC CGCTTGATTG GCATTAAAGC TTATGAGAGC    780
GAAAGGATCA CTTCTATAGC GGTGGGAGCG CTTTTATACC AAGAGACGCC TTTGGATATT    840
ATCTTTTCCA TAGAGCCTAT GAGCGTCAAT AAAACGCTGA GTTTTTTAAA AGAGAGGGCC    900
AAGTTTAGCA TGTCTAATCT TGTTAAAAAC GAGCTATTAG AATACCAAGA ATTAGTCAAA    960
ACCAAACGAT TATCCATGCA AAAATTCGCC CTAAACGTTC TTATCAAAGC CCCCAGTTTG   1020
GAGGATTTAG ACGCTCAAAC CAGCTTAATT TTAGGGCTTT TATTTAAAGA AAACTTAGTG   1080
GGCGTTATAG AAACTTTTGG CTTGAAAGGG GGGTATTTTT CCTTTTTCCC TGAACGCATC   1140
CATTTAAACC ACCGCTTGCG TTTTTTAACC TCTAAAGCCC TAGCGTGTTT GATGGTGTTT   1200
GAAAGGCAAA ATTTAGGTTT TAAGGCTAAT TCATGGGGGA ATAGCCCTTT GAGCGTGTTT   1260
AAAAATTTGG ATTATTCCCC TTTTTTATTC AATTTCCACA ACCAAGAAGT GAGCCATAAT   1320
AACGCTAAAG AAATTGCCAG AGTGAATGGG CATACTTTAG TTATAGGGGC AACCGGAAGC   1380
GGTAAAAGCA CGCTGATTAG CTATTTAATG ATGAGCGCTT TAAAATACCA AAACATGCGC   1440
CTTTTAGCTT TTGACAGGAT GCAAGGGTTG TATTCTTTCA CCGAATTTTT TAAAGGGCAT   1500
TACCATGACG GCCAATCTTT TAGTATCAAC CCCTTTTGTT TAGAGCCTAA TTTGCAGAAT   1560
TTAGAATTTT TGCAATCCTT TTTTTTGAGC ATGTTGGATC TTGCCCCTTC AAGGGATAAA   1620
GAAGCCTTAG AAGACATGAA TGCGATTTCT GGCGCGATTA AGAGCCTTTA TGAGACCTTA   1680
TACCCCAAAG ATTTTAGTTT GCTGGATTTT AAAGAAACGC TTAAAAGAAC CTCATCTAAC   1740
CAATTGGGCT TGAGTTTAGA GCCGTATTTG AATAACCCCC TTTTTAACGC TTTGAATGAC   1800
GCGTTCAACT CCAACGCTTT TTTAAATGTG ATAAACCTAG ATGCGATCAC CCAAAACCCT   1860
AAAGACTTAG GGCTTTTAGC CTATTACTTG TTTTATAAGA TCTTAGAAGA GTCTAGGAAA   1920
AACGACAGCG GCTTTTTGGT TTTTTTAGAC GAATTTAAAT CCTATGTGGA AAACGATTTG   1980
TTAAACACTA AAATCAACGC TTTAATCACG CAAGCCAGGA AAGCTAATGG CGTGGTGGTG   2040
TTGGCCTTGC AAGACATTTA CCAACTTAGC GGGGTTAAAA ACGCCCATAG TTTTTTAAGC   2100
AACATGGGGA CTCTCATTTT GTATCCGCAA AAAAACGCTA GGGAATTGAA ACACAATTTC   2160
AATGTGCCTT TGAGCGAAAC TGAAATTTCT TTTTTAGAAA ACACCCCTCT GTATGCCAGG   2220
CAGGTTTTAG TCAAAAATCT GGGTAACGGG AGTTCCAACA TGATTGATGT GAGTTTGGAG   2280
GGCTTGGGGT GTTATTTGAA AATCTTTAAT TCAGATTCCA GTCATGTCAA TAAAGTGAAA   2340
GCGTTACAAA AAGACTACCC TACAGAGTGG CGTGAGAAAC TTTTGAAGAG T            2391
```

(2) INFORMATION FOR SEQ ID NO:1407:

(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

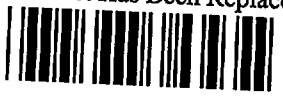
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407

```
AAAATGATTC TTAAAAGTTC CATTGATCGC CTTTTACAAA CGATAGATAT TGTAGAAGTC     60
ATTAGCTCTT ATGTGGATTT GAGGAAATCA GGTTCGAATT ACATGGCTTG TTGCCCTTTT    120
CATGAAGAAA GGAGCGCGAG TTTTAGCGTC AATCAAGTTA AAGGGTTTTA CTATTGCTTT    180
GGGTGTGGGG CGAGCGGGGA TAGCATTAAA TTTGTGATGG CGTTTGAAAA ACTTTCGTTT    240
GTGGAAGCGC TTGAGAAATT AGCCCACCGA TTCAATATAG CTTTAGAGTA TGACAAAGGC    300
GTTTATTACG ATCATAAAGA AGATTACCAC CTTTTAGAAA TGGTGAGTTC GTTGTATCAA    360
```

This Sheet Has Been Replaced



```
GAAGAGCTTT TTAACGCCCC GTTTTTTTTG AATTATTTGC AAAAAAGAGG GCTTAGCATG     420
GAGAGCATCA AAGCGTTTAA GTTAGGCTTA TGCACGAATA AAATTGATTA CGGCATTGAA     480
AATAAAGGCT TGAATAAGGA CAAATTGATT GAATTGGGCG TGCTAGGCAA GAGCGATAAA     540
GAGGATAAAA CCTATTTGCG CTTTTTGGAT CGCATCATGT TCCCTATTTA TAGCCCTAGT     600
GCTCAAGTGG TGGGTTTTGG AGGGCGCACC TTAAAAGAAA AAGCGGCCAA GTATATCAAT     660
TCGCCCCAAA ATAAGCTTTT TGATAAATCC AGCTTGCTCT ATGGCTATCA TTTGGCTAAA     720
GAACACATTT ATAAACAAAA GCAGGTCATT GTAACAGAAG GGTATTTGGA TGTGATTTTA     780
TTGCACCAGG CGGGTTTTAA AAACGCCATA GCCACGCTTG GGACAGCTTT AACGCCATCG     840
CATTTGCCCT TGCTTAAAAA AGGCGATCCA GAAATCCTTT TGAGCTATGA TGGGGATAAG     900
GCAGGGCGGA ATGCGGCTTA TAAAGCGAGC TTGATGTTAG CTAAAGAGCA AAGGAAAGGG     960
GGGGTGATTT TGTTTGAAAA CAACCTAGAC CCAGCGGATA TGATCGCTAA TCATCAGATT    1020
GAAACTTTAA AAAATTGGCT ATCGCGCCCC ATAGCTTTCA TTGAATTTGT TTTAAGGCAC    1080
ATGGCGGGTT CTTATCTTTT AGACGATCCT TTAGAAAAAG ATAAGGCCCT TAAAGAAATG    1140
TTAGGGTTTT TGAAAAACTT TTCCTTGCTT TTACAAAATG AATACAAGCC CTTAATCGCT    1200
ACGCTTTTGC AAGCGCCTTT GCATGTTTTA GGGATTAGAG AGCCAGTTTC TTTTCAGCCT    1260
TTTTACCCCA AAACAGAAAA GCCTAATCGC CCTCAAAAGT TCGCGCATGT TTCTAGCATG    1320
CCCAGTTTGG AATTTTTAGA AAAATTGGTG ATCCGCTACC TTTTAGAAGA CAGAAGCCTA    1380
TTGGATTTAG CGGTGGGTTA TATCCATAGT GGGGTATTCT TGCATAAAAA ACAAGAATTT    1440
GACGCTTTAT GTCAAGAAAA ATTGGACGAC CCTAAATTAG TTGCGTTATT ATTAGATGCG    1500
AATTTACCCC TAAAAAAAGG GGGTTTTGAA AAGGAATTGC GTTTGTTGAT TTTGCGCTAC    1560
TTTGAGCCGC CAACTCAAAG AAATCCC                                        1587
```

(2) INFORMATION FOR SEQ ID NO:1408:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1290

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408

```
CTAAGAGGGC ACAGGCGTAC TTATATAGGC TCCATGCCCG GGCGTATTGT CCAAGGGCTT      60
ATTGAAGCTA AAAAGATGAA TCCGGTCATG GTTTTAGATG AAATTGATAA GGTGGATCGA     120
AGCGTTAGGG GCGATCCAGC GAGTGCTTTA TTAGAGATCT TAGACCCTGA GCAAAATATC     180
GCCTTTAGGG ATCATTACGC GAATTTCAGC ATTGATTTGT CGCAAGTGAT TTTTATCGCT     240
ACCGCTAATA ATATTGACAG GATCGCAGCT CCTTTAAGAG ACAGAATGGA ATTTATCAGC     300
GTGTCCAGCT ACACGCCTAG CGAAAAAGAA GAGATCGCTA AAAACTACCT CATCCCCCAA     360
GAATTAGAAA AGCACGCCTT AAAGCCTAGC GAAGTGGATA TTAGCCATGA ATGTTTGAAA     420
CTCATTATTG AAAAATACAC CAGAGAAGCG GGCGTTAGGG ATTTACGAAG ACAGATCGCA     480
ACGATTATGC GTAAAGCGGC TTTAAAATAC CTAGAAGATA ACCCGCACAA AAAAGGGCGG     540
ACCAAAAAAA GCGAAGACAA AGATAAAAAA GGCGGAAATG AAGAAAACGA AAAAAGAGGT     600
GAGAGTAAAG ATTTTTGCGT CTCTATCACG CCTGATAACC TTAAAGAGTA TTTAGAACGC     660
ATGGTGTTTG AAATTGACCC CATAGATGAA GAAAATAAAA TCGGTATCGT CAATGGCTTG     720
GCATGGACTC CAGTGGGCGG TGATGTGCTT AAAATTGAAG CGGTTAAGAT TAGAGGCAAG     780
GGGGAATTGA AACTCACCGG GAGTTTGGGC GACGTGATGA AAGAATCCGC CATTATTGCC     840
TTTTCTGTTG TCAAAGTCTT GTTGGATAAC GAAACCTTAA AAGTGCCTAA AATCCCTAGC     900
GAGACCGATG CAGAGAATAA GAAAAAGAAA AAAGTGCTGA AAGTTTATAA CGCTTACGAT     960
TTGCACTTGC ATGTCCCTGA GGGGGCTACG CCTAAAGACG GCCCGAGCGC TGGGATCGCT    1020
ATGGCGAGCG TGATGGCGAG CATTTTGTGC GATAGGGCTA TAAGAAGCGA AGTGGCGATG    1080
ACGGGCGAAT TGACTTTGAG CGGGGAAGTT TTACCCATAG GGGGGTTGAA AGAAAAATTG    1140
```

ATCGCTGCTT TTAAAGCCGG CATCAAAACC GCTCTCATTC CTGTCAAAAA TTACGAAAGG 1200
GATTTAGACG AGATCCCTAC TGAAGTGCGA GAGAATTTAA ACATCGTTGC GGTGAAAAAC 1260
ATCGCTGAAG TGTTAGAAAA AACCTTGCTT 1290

(2) INFORMATION FOR SEQ ID NO:1409:

(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:1409

AAAAGATATA GAAAAACTGC TCTCTTACGG CTTGACAATG GCGACAAGCT GTCATTAATG 60
AGGGAATTTT TTAAAAGCGT TAGAGGGTTT TTGAACCTTC TTAGAATGAT TTTCCCCGAG 120
CGCTTTCAAA ACGCCTTTTT AGGGTTAAGC GAATTGTTTT ACTACGCTTC CAGCTTGAGT 180
TTTTATACGA TTTTGTCTTT ATCGCCTATT TTGTTGTTCG TGTTCAGTCT TTTTGTGTCT 240
CATTACTTGC AAGCGCACAG CGGTGAAATG GAAGCCTTGA TTTTCCCTAA CGCTCCTAAA 300
CTCATTGGCG CGATTAAGGA TTTTTTAGAA AATTTTAAAA AAACAGACAT GACCTTAGGC 360
ACGCTTGAAG AGGTGTCTAT TGTGGTGGCG TTGGTGCTTT TTTGTGAAAA CTACCGCTCC 420
ATCGCGTCAA AAATTTTTGA CGCAAAGCCC AGAGATTATG CGCATTTTAA GGGTAAAGAA 480
ATCTTTTTAT TTTGGGGGTT TGGCACGACT TTAGTGTTTT TATTCGCTTT GCCTTTGGTG 540
GTGTTTTTTG ATATTAAGAT CCAAGTGTTT TTTGAAGATA AAGATTCAAG CTTGTTGCAT 600
GTTTTAAGAT GGATAGGCAC TTACGCGTTT TTTTTGATCC TTTTTACCAT TCCCACGAAT 660
AAGGTGTTTA AACATTATTT TTGGGTGTTT TTATGGGTGT TTTTTACGAG CGTTTCTTGG 720
CATGTGCTGA AATGGGCTTC CACCTTATTT ATGTGTTATA CCAATCCGCA CTTACTCATG 780
AGCCTGTATG GGAGCCGTTT CCCATTTTGT GGTTTT 816

(2) INFORMATION FOR SEQ ID NO:1410:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 747 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...747

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410

GTAGGTGTTG TTATGATAAA AAAGACCCTT GCATCGGTTT TATTAGGATT GAGTTTGATG 60
AGTGTGTTAA ATGCCAAAGA ATGCGTTTCG CCCATAACAA GAAGCGTTAA GTATCATCAG 120
CAAAGTGCTG AGATCAGAGC CTTGCAATTA CAAAGTTACA AAATGGCGAA AATGGCGCTA 180
GACAATAACC TTAAGCTCGT TAAAGACAAA AAGCCAGCCG TCATCTTGGA TTTAGATGAA 240
ACCGTTTTGA ACACTTTTGA TTATGCGGGC TATTTAGTCA AAAACTGCAT TAAATACACC 300
CCAGAAACTT GGGATAAATT TGAAAAAGAA GGCTCTCTTA CGCTCATTCC TGGAGCGCTA 360
GACTTTTTAG AATACGCTAA TTCTAAGGGC GTTAAGATTT TTTACATTTC TAACCGCACC 420
CAAAAAAATA AGGCATTCAC TTTAAAAACG CTCAAAAGCT TTAAGCTCCC CCAAGTGAGT 480
GAAGAATCCG TTTTGTTAAA GGAAAAAGGC AAGCCTAAAG CCGTTAGGCG GGAGTTAGTC 540
GCTAAGGATT ATGCGATTGT TTTACAAGTG GGCGACACTT TGCATGATTT TGACGCCATT 600
TTTGCTAAAG ACGCTAAAAA CAGCCAAGAA CAACAAGCCA AAGTCTTGCA AAACGCTCAA 660
AAATTCGGCA CAGAATGGAT TATTTTACCC AACTCTCTTT ATGGCACATG GGAAGATGGG 720
CCTATAAAAG CATGGCAAAA TAAAAAA 747

(2) INFORMATION FOR SEQ ID NO:1411:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1089 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1089

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411

CATGACAAAA AATTTGATCT CTTAGGCGGA GTCATGGATT TCGTAGGGTT TGAAGATTTA 60
AAATGCAAAG ACAAAGAAAA CTCTCAAAAA GTTTTTGTGA TCCGTAACGA TAAGTTAGGC 120
GATTTTATTT TAGTGATTCC CGCTTTAATC GCTCTCAAGC ATGCTTTTTT AGAAAAAGGC 180
GTAGAAGTGT ATTTGGGCGT GGTTGTGCCT AGCTATACCA CCCCAATCGC TTTAGAATTC 240
CCTTTCATTG ATGAAGTTAT CATAGAAGAC AACCATTTAG CCACCACCCC CAAAAACCGC 300
TCCACCGACG CCCTTATCTT TTTATTTTCT AATTTTAAAA ACGCCAAACT TGCTTTCAGT 360
TTGAGAAAAT CCATCCCTTA TATCCTAGCC CCAAAGACCA AAATCTATTC TTGGCTTTAT 420
CAAAAGAGAG TGCGCCAAAA CCGCTCTTTA TGCTTAAAAA CCGAATACGA ATACAATTTG 480
GACTTAATCC ATGCGTTTTG TAAAGACTAC GATCTCCCTA ACGCTCAACT TAAAAAAATC 540
GCATGGAAGC TTAAAGACAA ATCCAAAGAG CGATCCATCA TCGCTTCAAA ACTCAACGCT 600
AATGTTGATC TATTGTGGAT TGGCGTGCAT ATGCATAGCG GAGGCAGTTC GCCCGTATTG 660
CCCGCTTCGC ATTTCATTGA GTTGATTGCA ATCTTGCATG AAAAATTAAG TTGTGAGATC 720
ATTCTTATTT GCGGGCCAGG CGAGAGAAAA GCCACAGAAG AACTCCTTAA AGAAGTCCCT 780
TTCGCTCACC TCTATGATAC GAGCCATAGT TTAGTGGATT TAGCCAAATT GTGCGCGAAT 840
TTAAGCGTCT GTATCGGGAA CGCTTCAGGC CCTTTGCATG TGAACGCTTT ATTTGACAAC 900
CAATCTATCG GGTTTTACCC TAACGAACTC ACCGCCTCTA TTGCCAGATG GCGGCCTTTC 960
AACGAACAAT TTTTAGGCAT CACCCCGCCT AATGGCTCAA ACGATATGGG TTTGATTGAC 1020
ATTCAAAAAG AAAGCGAAAA GATTATGGGA TTTATCACAA AAAATCTTTC TCATCACATG 1080
CAAGAAAGA 1089

(2) INFORMATION FOR SEQ ID NO:1412:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1986 base pairs

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

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412

```
GGTAACACGA TTATAAAGAT GCAAAAATCA CTGATCACAA CCCCCATTTA TTATGTGAAT      60
GACATCCCTC ATATTGGCCA TGCTTATACG ACTTTGATTG CGGACACTTT AAAGAAGTAT     120
TACACGCTTC AAGGCGAAGA AGTCTTTTTT TTAACCGGCA CCGACGAGCA TGGGCAAAAG     180
ATCGAACAAA GTGCGAGACT GAGGAATCAA AGCCCCAAAG CTTACGCCGA TAGCATTAGC     240
GCGATTTTTA AAAACCAGTG GGATTTTTTC AATTTAGATT ATGATGGTTT TATCCGCACC     300
ACAGACAGCG AGCATCAAAA ATGCGTGCAA AACGCCTTTG AAATCATGTT TGAAAAAGGG     360
GATATTTATA AAGGCACTTA TAGCGGGTAT TATTGCGTGA GCTGTGAGAG TTATTGCGCG     420
GTCTCTAAAG TGGATAATAC AGATAGTAAA GTCCTATGCC CTGATTGCTT GAGAGAGACC     480
ACGCTTTTAG AAGAAGAGAG TTATTTTTTC AAATTGAGTG CGTATGAAAA GCCTTTATTG     540
GAGTTTTACG CTAAAAACCC TGAAGCGATT TTGCCCATTT ATCGTAAAAA CGAGGTAACT     600
TCTTTTATTG AGCAGGGTTT ATTGGATCTG TCTATCACGC GCACGAGCTT TGAATGGGGT     660
ATTCCTTTGC CTAAAAAGAT GAACGATCCT AAGCATGTGG TGTATGTTTG GCTGGACGCT     720
TTATTGAATT ATGCGAGCGC GTTAGGGTAT TTGAACGGTT TAGACAATAA AATGGCGCAT     780
TTTGAACGCG CTAGGCATAT TGTGGGTAAG GATATTTTAC GCTTCCATGC CATTTATTGG     840
CCAGCCTTTT TGATGAGTTT GAATTTGCCC TTATTCAAAC AGCTCTGTGT GCATGGGTGG     900
TGGACGATAG AGGGCGTGAA AATGAGTAAG AGCTTGGGTA ATGTTTTAGA CGCTCAAAAG     960
CTCGCCATGG AGTATGGGAT TGAAGAATTA CGCTATTTTT TATTGCGTGA GGTGCCTTTT    1020
GGGCAAGATG GGGATTTTTC TAAAAAAGCG TTAGTAGAAC GGATTAATGC GAATTTGAAT    1080
AACGATTTGG GGAATTTGTT GAATCGTTTG CTAGGCATGG CTAAAAAGTA TTTCAATTAT    1140
TCTCTAAAAA GCACCAAAAT CACTGCGTAT TATCCTAAAG AGCTAGAAAA AGCACATCAA    1200
ATTTTAGATA ACGCTAATTC TTTTGTGCCT AAAATGCAAT TGCATAAGGC TTTAGAGGAA    1260
TTGTTTAATA TTTATGATTT TTTGAATAAA CTCATCGCTA AAGAAGAGCC GTGGGTCTTG    1320
CACAAAAACA ACGAATCAGA AAAATTAGAA GCCTTATTGA GTTTGATCGC AAACACGCTA    1380
CTACAATCAA GCTTCTTGCT CTATGCGTTC ATGCCAAAGA GCGCTATGAA ATTAGCGAGC    1440
GCTTTTCGTG TAGAAATCAC GCCCAATAAT TACGAACGCT TTTTTAAGGC TAAAAAATTA    1500
CAAGATATGG TTTTACAAGA CACCGAGCCT TTATTTTCCA AAATTGAGAA AATTGAAAAG    1560
ATTGAAAAGA TTGAAAAGAT TGAAAAGATT GAAAAAGGGG AGGAAGCCCT AGCAGAAAAA    1620
GCAGAAAAAA AAGAAAAAGA AAAAGCCCCA CCAACACAAG AAAATTATAT TAGTATTGAG    1680
GATTTCAAGA AAGTAGAGAT TAAAGTGGGG CTTATCAAAG AAGCTCAAAG GATTGAAAAA    1740
TCCAATAAAT TACTGCGCTT AAAAGTGGAT TTAGGCGAAA ATCGTTTGAG GCAGATCATC    1800
TCAGGGATCG CTTTGGATTA TGAGCCTGAA AGCTTGGTGG GTCAAATGGT GTGCGTGGTG    1860
GCTAATTTAA AACCCGCAAA GCTTATGGGT GAAATGAGTG AGGGCATGAT TTTAGCGGTG    1920
CGAGATAATG ATAATCTGGC TTTAATCAGC CCTACCAGAG AAAAAATTGC AGGAAGTTTG    1980
ATCAGC                                                               1986
```

(2) INFORMATION FOR SEQ ID NO:1413:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1026 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413

GGACGCATGA TGAAAATTGT AATAGACTTA ATGGGGGCTG ACCATGGGGT TTTACCCATT 60
ATTGAGGGAG TCTCAAGGGC TTTAGAGAAT AAGAGTTTTA GCGTGGTTTT AGTGGGGGAT 120
AAAGACAAAG CGACCCCTTT TATTTCTAAA GAGTTAGCCA GCAAAGTGGA AATGATCCAC 180
ACGCAAGATT ACATTAAAAT GGAAGAAGCC GCCACTGAGG CGATTAAGCG TAAGGAATCT 240
TCCATTTACT TGGGCATGGA TATTTTAAAA AATGGGGCTG ACGCTTTGAT TTCAGCGGGG 300
CATAGCGGGG CGACTATGGG TTTAGCGACC TTGCGTTTAG GGCGTATCAA GGGGGTTGAA 360
AGGCCTGCTA TTTGCACTTT AATGCCTAGC GTTGGCAAAC GCCCTAGCGT GCTATTAGAC 420
GCAGGAGCGA ACACGGATTG CAAGCCTGAA TATTTGATTG ATTTTGCTCT CATGGGGTAT 480
GAATACGCTA AAAGCGTGTT GCATTATGAC AGCCCTAAAG TGGGTCTTTT GAGTAATGGT 540
GAAGAAGATA TTAAGGGGAA TACGCTCGTT AAAGAAACGC ATAAAATGTT GAAAGCTTAT 600
GACTTTTTTT ATGGCAATGT GGAGGGGAGC GATATTTTCA AAGGGGTTGT GGATGTAGTG 660
GTTTGCGATG GCTTTATGGG GAATGTGGTC TTAAAGACAA CTGAAGGGGT CGCTAGTGCG 720
ATAGGCTCTA TTTTTAAAGA TGAAATTAAA AGCTCTTTTA AATCTAAAAT GGGGGCTTTG 780
ATGCTTAAGA ACGCGTTTGG TATTTTAAAA CAAAAAACCG ATTACGCTGA ATATGGGGGA 840
GCACCGCTTT TGGGCGTGAA TAAAAGCGTG ATCATTAGCC ATGGCAAGAG CAACGCTAGA 900
GCGGTTGAAT GCGCGATTTA TCAGGCTATT AGCGCTGTTG AAAGTCAGGT TTGTTTGAGG 960
ATTACTCAAG CGTTTGAGAG TTTGAAATCT CAATCTTTTG AGAGCCAAAG CGATCAACAA 1020
GACGCT 1026

(2) INFORMATION FOR SEQ ID NO:1414:

(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:1414

AACGCTCATG CCTTTACCCA TTCATTTAGC GCACCAGCTC GCTTTCGCCT AGCTCAAAAA 60
AGAAAAGACA ACACCTTGCC [illegible]TTTTAAGG CCTGATGGCA AGTCTCAAGT GAGCGTGCGT 120
TATGAAAACA ACAAGCCTGT AAGCGTTGAT ACGATTGTCA TTTCCACCCA ACATTCCCCA 180
GAAGTTTCAC AAAAGCATTT AAAAGAAGCG GTGATTGAAG AGATCGTGTA TAAGGTTTTA 240
CCCAAAGAAT ATTTGCATGA CAATATCAAG TTTTTTATAA ACCCTACAGG AAAATTCGTC 300
ATCGGTGGGC CTCAAGGCGA TGCGGGTTTG 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:1415:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 435 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1415

TCAACAATTC ACAAGGAGTT TAAATTGAAA CAAAGAACGC TGTCTATTAT TAAACCGGAT 60
GCACTTAAGA AAAAAGTGGT AGGCAAAACC ATTGATCGCT TTGAGAGTAA CGGCTTGGAA 120
GTGGTGGCCA TGAAACGCTT GCATTTGAGC GTGAAAGACG CTGAAAACTT TTATGCGATC 180
CTCAGAGAGA GACCCTTTTT TAAAGATTTG ATAGAGTTTA TGGTGAGTGG TCCGGTGGTG 240
GTTATGGTTT TAGAAGGCAA AGATGCGGTG GCTAAAAACA GAGAGCTTAT GGGAGCGACT 300
GATCCCAAAC TCGCCCAAAA AGGTACTATC AGAGCGGATT TTGCTGAGAG CATTGACGCT 360
AATGCGGTGC ATGGGAGCGA TAGCTTGGAA AACGCGCACA ATGAAATCGC TTTCTTTTTT 420
GCCGCTAGAG AGTTT 435

(2) INFORMATION FOR SEQ ID NO:1416:

(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:1416

GGGCGAGGTG GAATTTATAT TGAACATGGC AGGGTTAAAA TGGTAGCTTT AAGCAACGCT 60
CTTTCAAGGG TTTTTGGTTC TGTGGCTGGC TATAAATTCC CTTCTTTTAT CCAAAAAAGC 120
ATCAACGCTC TTTATGTTAA GATCTTTAAA ATTGATTTGA GCGAGTTTGA GCCTTTAGAA 180

AATTATAAGA GTTTGAACGC TCTTTTCATG CGCTCTTTAA AAAAAGAACG CCCCTTTGAC 240
AAAGCCCCTA ATATTTGCAT TGCGCCTTGC GATGCTTTAA TCACTGAATG CGCTTTTTTA 300
GACAACGATA GCGCTTTACA AATTAAAGGC ATGCCCTATA AAGCGCATGA ATTAGTGGGC 360
GAAATCAACC CCTTAAGCCC TTCTTTTTTC TATGTGAATT TTTACCTTTC GCCCAAAGAT 420
TACCACCACT ACCACGCCCC TTGCGATTTA GAAATTTTAG AGGCTCGTTA TTTTGCGGGG 480
AAATTACTAC CAGTCAATAA GCCCTCATTA CACAAAAACA AAAATCTGTT TGTGGGCAAT 540
GAAAGGGTCG CGCTTGTTGC AAAAGACGAT TCAAGGCAA 579

(2) INFORMATION FOR SEQ ID NO:1417:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 720 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417

AACCATAATA AAGGGGCGGA AATTTCGCTA TGGGGTTTAA CCCGCTTGGT GGATAGAGAC 60
ATTGATAAGG ATAACCCAAG GACGAAAAAC CGCCCGAGCG TGGATGGTAG GATCAGCGTT 120
AAAGGCATGG TCATTTTTAG CGTTTCAAAC GCTATTTTGT TTGTGGGATG GAGTAATTTC 180
ATCAACCCTT TAGCTTTCAA GCTTTCGTTA CCTTTTTTAA TCATTTTAGG GGGGTATTCG 240
TATTTCAAGC GCTTTTCTTC TTTGGCGCAT TTTGTCGTGG GTTTGGCTTT GGGTTTAGCC 300
CCCATTGCAG GAAGCGTGGC GGTTTTAGGG GATATTCCTT TATGGAATGT CTTTTTGGCT 360
TTAGGGGTGA TGTTGTGGGT GGCTGGGTTT GATTTGCTCT ATTCTTTACA GGATATGGAG 420
TTTGATAAAG AAAGGGGCTT GTTTTCCATT CCTAGCCAAT TAGGGGAAAA ATGGTGCTTG 480
AATCTTTCAA GGCTCTCGCA CCTTGTGGCA CTGATCTGCT GGCTTTGTTT TGTGAAATGC 540
TATCATGGGG GGCTTTTTGC GTATTTGGGC TTAGGGGTTT CAGCCTTGAT CTTACTCTAT 600
GAGCAGATTT TAGTGGCCAG AGATTATAAA AACATTCCTA AAGCCTTTTT TGTGAGTAAT 660
GGCTATTTGG GGGTGGTGTT TTTTATTTTT ATCGTCCTTG ATGTGGGGTT CAAGCATGCA 720

(2) INFORMATION FOR SEQ ID NO:1418:

(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

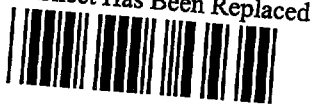
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418

```
GTAATGGCTA TTTGGGGGTG GTGTTTTTTA TTTTTATCGT CCTTGATGTG GGGTTCAAGC     60
ATGCATGAGT TGGTTTTAAG ATCCCAAGCT TTAGGGTTTG AAACGCGCTT AGTCCAGTGC    120
GATTTATCGT TTTCTTATGA AAGGTTTATT TCTAAAACCA AACGCTCTTT AGCGGTGTTA    180
GAAGAATTTG ATTGGTTAAA TTCTGGCTTT GATTTTTCAC GCTTGAACGT TGAAAATGAC    240
ACTCTGGAAT TACTCAAAGC GCTGTATTTT AAATTAGAAA AATTAGAGAG CCTGCTTTTA    300
AAAGAAAATT TACTTGAATT GGAGCAAAAG GATCGCATCA TCGCTTTAGG GCATGGGCTA    360
GTTTGCCTAA AAAAACAAAG CCTGATAGCG CCTCAAACTT ACTATGGGCG TTGCGTGTTA    420
GAGGGGAAAA TCCTAGCCTT TTTTGGCGTG GCAAGGGATA AAGATTTTTT AGAAATCACT    480
CGCATGCACG CCTTAGACAT TAAGCGTTAT GATTCCTTCA TTGTTGATAG CGAAAGAAAA    540
GGCTTGAAAT TA                                                        552
```

(2) INFORMATION FOR SEQ ID NO:1419:

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

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1419

```
ACGGGAGCAA TCATGTTATC TTCTAATGAT TTGTTTATGG TCGTTTTAGG GGCGATTTTA     60
TTGGTGTTGG TGTGCTTGGT GGGGTATTTG TATCTTAAAG AAAAAGAGTT TTACCATAAA    120
ATGAGGCGTT TAGAAAAAAC TTTAGATGAA TCCTATCAAG AAAATTATCT CTATTCTAAG    180
CGTTTGAGAG AATTAGAGGG GCGTTTGGAA GGCCTTTCTT TAGAAAAAAG CGCTAAAGAG    240
GACAGCTCAT TAAAAACGAC TCTTTCGCAC CTTTATAACC AGTTGCAAGA AATCCAAAAA    300
TCCATGGATA AAGAGCGCGA TTACTTAGAA GAAAAAATCA TTACT                    345
```

(2) INFORMATION FOR SEQ ID NO:1420:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1005 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420

```
GAGCCCATTA AAAGCGACAA AGAAGCCTTT GATCTGGTCA TGCAAAATCG ATCGCATGAA      60
ATACAAGGCG TATCACACAT TAAGAATAAT TATAAATTTT TCACCAAAGA GCTTGACAAT     120
TATATCAGCA AAGGGTATCG CATTGAAGAG ATTTATGGCG CGTTTTTGTG GCTCAAAATC     180
GTAGCCATAG GTTTAGAGTT GGGCGAAGAC GATCCGCAAG TGGTGTTTGA GAGCATCAAC     240
GCTACAGGCG TGCAATTAAA AGGGCTGGAT CTCATCCGCA ACTATTTGAT GATGGGGGAA     300
AATTCTGACA ACCAGAATCG TCTTTATAAT ACTTATTGGG TGCCTTTAGA AAATTGGCTT     360
GGTGAAAAGG ATTTGAATGA TTTCATCAAA ACCTATTTGA GAATCTATTT TGAGGATAGA     420
GTTAAAGAGG GAGAGCGCGA AGTGTATTAC GCGCTAAAAG CCCACCACAG AGACAATTTC     480
CCTAACAATA TACAAGGTCT TATGAGCGAT ATGCGAGAAT ATGGCAGAAT CTTTCAAATC     540
TTTTTAGACA GAGATCATTA TTTTTTACAT CGTGGAGACC CGCAACAGTT AGCGAATTTA     600
CGCTTGCGCG TTAAAGATCT CGTAAAAATC AAATTTGGCG TGGCAAAGCC CTTTGTTTTG     660
CGTTGCGCCA GAGATTTTGA AGAAGGCAAA TTGGATTATG AAAACTTCCA TGAAATCTTG     720
CAAATCCTTA TCAGCTACTT CGTGCGCCGA AGCGTGTGCG GGGATTCTAC CCCTACGCTT     780
ACCAGAGTTC TTTATTCTTT ATACAGACAG CTAGGGGAAG ATGTTTCAGC CGATGCATTG     840
AAGCGGTATT TGGGCAAGAG CGTTGGTCAA ATGGCGTTCC CTAATGACGA TAAAATTAAA     900
GCGGCGTTTC TTGTGCGTAA CGCTTATGCA GCAAATCAAG TGTGCAAATT CATCCTGCTT     960
GAGATTGAAA AATTAGCAAC GCTGAACCGC CAAAAGAAGA GAATT                     1005
```

(2) INFORMATION FOR SEQ ID NO:1421:

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

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1421

```
TTCTATGTCT CGATCATTAA ATGCACGCCT TTATTGGTCC AAATCGTAAT CGTGTTTTAT      60
GGTTTGCCCG CCCTTGGGGT CTATATGGAT CCAATCCCGG CAGGCATTAT TGCGTTTTCT     120
TTTAATGTGG GGGCATACGC TTCAGAGACT TTGAGGGCGA GCTTTCTTTC TGTCCCTAAA     180
GATCAATGGG ATTCAAGCTT GAGTTTGGGC TTGAATTACT TGCAAACCTT TTGGCATGTC     240
ATCTTTTTTC AAGCGCTCAA AGTCGCCACG GCCAAGCCTA AG                        282
```

(2) INFORMATION FOR SEQ ID NO:1422:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1383 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422

```
TCAATAAAAC ATTTAGGCAA AAAAGAGGTG AAAACCTTAG GATTGTCTTC GCTTGGTGGG      60
ACTTTAGAAT TTTACGATTT TATCATCTTT GTATTTTTTA CAAGTATCAT TGCCAAACAC     120
TTTTTCCCAA ACACGCTTAG CCCTATCTGG TCTGAAATCA ACACTTATGG GATCTTTGCT     180
GCAGGTTATC TGGCGCGCCC GCTTGGTGGC ATAGTGATGG CCCACTTTGG GGATAAATTC     240
GGTCGTAAAA ACATGTTCAT GCTCTCTATT TTATTAATGG TAATCCCAAC CTTTGCGCTA     300
GCTTTGATGC CAACTTTTAA TGATTTGGTG GGTTTTGGCG TGGATAGCAT GGGGCTTACC     360
CCTAAAAACG CTCATTATCT TGGTTACATA GCTCCTGTTT TTTTGGTGCT TGTTAGGATT     420
TGTCAAGGCG TCGCTGTGGG TGGTGAATTG CCTGGCGCTT GGGTTTTTGT CCATGAACAT     480
GCCCCACAAG GACAAAAAAA CACTTATATC GGTTTTTTAA CCGCTTCCGT AGTTTCTGGG     540
ATTTTGCTTG GGAGTTTGGT TTATATCGGG ATTTACATGG TTTTTGACAA GCCTGTTGTT     600
GAAGATTGGG CTTGGCGGGT TGCCTTTGGG CTTGGAGGAA TTTTTGGTAT CATTTCTGTG     660
TATTTGAGGC GCTTTTTAGA AGAAACTCCC GTTTTTCAGC AAATGAAGCA GGACGATGCC     720
TTAGTCAAAT TCCCGCTTAA AGAGGTGTTT AAAAATTCCC TCTTTGGTAT ATCAATCTCC     780
ATGCTTATCA CTTGGGTTTT AACCGCTTGT ATTTTGATTT TTATCCTTTT TGTCCCGAAT     840
TTTACCCTTA CGCATCCCAA TTTTCATTTC ACTCCGTTTG AAAAAACCTA TTTTCAAATT     900
CTAGGACTTG TTGGTATTGT AAGTTCTATT ATTTTCACCG GGTTTTTGGC TGATAAAATC     960
AAACCGCACA AAGTTTGCAT GGCTTTTAGC GCGGCCTTTG GGTTTTTTGG CTTTTTATTC    1020
TTTAAGGAAT TTTATTCTAA CGCGCCAAGT TTAGTCAATA CTATAATTTT ATACTTTTTA    1080
GCTTGCTTTT GCGCGGGCAT TATGAATTTT TGCCCCATTT TCATGAGCGA TGTGTTTAGC    1140
GCTAGAATCC GTTTTAGCGG GATTTCCTTT GCTTATAACA TAGCCTATGC TATAACCGCT    1200
GGCTTTACCC CTCAACTTTC AAGCTGGTTA AACGCAAAAG CTATAGCAGT GCCTGAAAGT    1260
TTGCAAAGTT ATGGTTTAAG CTTTTATATC CTTATAGTTT CTTTAATTGC TTTTATTACA    1320
TCGCTTTTAA TGGCGCCAAT TTATCACAAA TCTAATACCC AACACGAAGT GTCGCCCACG    1380
GCA                                                                 1383
```

(2) INFORMATION FOR SEQ ID NO:1423:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1521 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423

```
AAATCGCTCA AAAAGAAGTG CCGGAGCTTT TTGCAAGAAT ATGAGGTTTA TTCTTTGGAT      60
TTGGCTTTAA TGGTAGCTGG GGCAAAATAC AGAGGGGATT TTGAAAAGCG CCTGAAAAAA     120
ACGCTCAAAG AGATCCAGCA AAACGGCCGT ATCATTTTAT TCATTGATGA AATCCACACC     180
CTTTTAGGTG CAGGGAGCAG TAACGCTGGG AGCTTGGATG CGGCGAATAT ATTAAAACCG     240
```

```
GTTTTAACGG ATGGGAGCTT GAAATGTTTG GGGGCGACCA CTTTTGAAGA ATACCGCAGC      300
GTGTTTGAAA AAGACAAGGC TTTCAACAGG CGCTTTTCTA TAGTGAATGT TGAAGAGCCT      360
TCTAAGGAAG CGTGTTACTT GATTTTAAAG AATATTGCCC CCCTTTATGA AGAACACCAC      420
CAGGTGCGTT ATAATGAAAG CGTGTTTAAG GCATGCGTGG ATTTGACGAG CTATTACATG      480
CATGATAAAT TCTTGCCGGA TAAGGCGATT GAATTATTAG ATGAGGTGGG ATCAAGGAAA      540
AAGATCAACC CTAAAAAAGG CAAAAAAATC AGCGTTGATG ACGTGCAAGA AACGCTCGCT      600
CTCAAGCTTA AAATCCCTAA AATGCGTTTA AATAGCGATA AAAAAGCCCT TTTAAGGAAT      660
TTGGAAAAAT CGCTAAAAAA TAAGATTTTT GCCCAAACCG AAGCGATCAA CCTTGTCAGC      720
AATGCGATCA AAATCCAGCA TTGCGGGCTT TCTGCAAAAA ATAAGCCTGT GGGGAGCTTT      780
TTATTCGTGG GGCCTAGTGG GGTAGGGAAA ACAGAATTGG CTAAAGAATT GGCCTTGAAT      840
TTGAATTTGC ATTTTGAACG CTTTGACATG AGCGAATACA AAGAAGCCCA TAGCGTGGCA      900
AAGCTCATCG GAAGTCCTAG CGGTTATGTG GGGTTTGAGC AAGGGGGGTT ATTGGTGAAT      960
GCGATTAAAA AGCACCCGCA TTGTTTGCTG CTTTTAGATG AGATAGAAAA GGCCCACCCT     1020
AATGTGTATG ATTTGTTGTT GCAGGTGATG GATAACGCCA CTTTGAGCGA TAATTTAGGC     1080
AACAAGGCGA GTTTTAAGCA TGTGATACTG ATTATGACTT CAAATGTGGG GAGTAAGGAT     1140
AAGGACACGC TAGGGTTTTT TAGCACTAAA AACGCCAAGT ATGATAGAGC CGTTAAAGAG     1200
CTTTTAACCC CTGAATTGCG ATCCAGAATT GATGCGATCG TGCCGTTTAA CGCGCTCAGT     1260
TTGGAGGATT TTGAACGCAT TGTTTCTGTG GAATTGGACG GGTTAAAAGC CCTAGCAATA     1320
GAGCAAGGCG TGATCTTAAA ATTCCATAAA GAAGTTGTGA AATGCATCGC GCAAAAGAGC     1380
TACCAGAGGA GTTTTGGTGC GAGAGAAATT AAAAAAATCA TTCAGAGGGA AATCAACCCC     1440
CAATTAAGCG ATATAGTGCT TAAACAATCG CTTAAAAAAC CAACAAGATC GTTGCGCATG     1500
AAGAGCACAT TTCACAAAGT G                                               1521
```

(2) INFORMATION FOR SEQ ID NO:1424:



(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

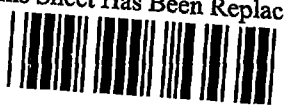
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424

```
GGAATAAAGT TGATAAAATT TGTGCGTAAT GTGGTTTTAT TCATTTTAAC AGCGATCTTT       60
TTAGCGTTCA TGCTTTTAGT GAGTTATTGC ATGCCCCATT ATAGCGTGGC TGTCATTAGC      120
GGGGTGGAAG TCAAAAGAAT GAATGAAAAT GAAAACACGC CCAATAATAA GGAAGTAAAA      180
ACCCTTGCTA GAGATGTCTA TTTTGTGCAA ACTTACGACC CTAAGGATCA AAAAAGCGTG      240
ACCGTCTATC GTAACGAAGA CACGCGCTTT GGCTTCCCTT TTTATTTTAA GTTTAATTCG      300
GCTGATATTT CAGCTCTCGC TCAAAGTTTA GTCAATCAGC AAGTGGAAGT GCAATACTAT      360
GGCTGGCGGA TCAATTTGTT TAACATGTTC CCTAATGTGA TTTTTTTAAA ACCCTTAAAA      420
GAGAGCGATG AGATGTCAAA ACCCGTTTTT AGCTGGATTT TATACGCCCT GCTACTAGTG      480
GGCTTTTTTA TCAGTGCACG TTCTGTTTGC ACTTTATTTA AGGGCAAAGC TCAT            534
```

(2) INFORMATION FOR SEQ ID NO:1425:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1914 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1425

```
GCGCGGCTTT TATTGTATAA TCTTAAAAAT TTTATTAAAG GAAAAAGTTC AATGTCTAAT      60
CAAGAATACA CCTTCCAAAC TGAAATCAAC CAGCTTTTGG ATTTGATGAT CCACTCTTTG     120
TATTCTAATA AAGAGATTTT TTTAAGGGAG TTGATTTCTA ACGCGAGCGA CGCTTTGGAT     180
AAGCTGAATT ATTTGATGCT AACCGATGAG AAATTAAAAG GGCTGAATAC CACGCCTAGC     240
ATCCATTTGA GTTTTGATAG CCAAAAAAAA ACCTTAACGA TTAAAGACAA TGGTATAGGC     300
ATGGATAAAA GCGATCTCAT CGAGCATTTA GGCACGATCG CTAAATCAGG CACGAAGAGT     360
TTTTTAAGCG CTTTGAGTGG GGATAAGAAA AAAGATAGCG CCTTAATTGG CCAATTTGGC     420
GTGGGCTTTT ATTCGGCGTT CATGGTAGCG AGTAAGATTG TCGTTCAAAC CAAAAAAGTT     480
ACCAGTCATC AAGCTTATGC ATGGGTGAGC GATGGTAAGG GCAAGTTTGA AATCAGCGAA     540
TGCGTCAAAG AGGAGCAAGG CACAGAAATC ACCCTCTTTT TAAAAGAAGA AGATTCTCAT     600
TTTGCGAGCC GTTGGGAGAT TGATAGCGTT GTTAAAAAGT ATTCTGAGCA TATCCCTTTC     660
CCTATTTTTT TAACTTACAC CGATACGAAA TTTGAGGGCG AAGGGGATAA TAAAAAAGAA     720
GTTAAAGAAG AAAAATGCGA TCAGATCAAT CAAGCGAGCG CTTTATGGAA AATGAATAAG     780
AGCGAATTGA AAGAAAAGGA TTACAAAGAC TTTTACCAAT CGTTTGCGCA TGATAACAGC     840
GAGCCTTTGA GCTATATCCA TAATAAAGTG GAAGGCTCTT TAGAATACAC GACGCTTTTT     900
TATATCCCTA GCAAAGCGCC CTTTGATTTG TTTAGGGTGG ATTATAAAAG CGGGGTCAAA     960
CTTTATGTTA AACGGGTGTT TATCACTGAT GATGACAAAG AATTGTTGCC GTCTTATTTG    1020
AGGTTTGTTA AAGGCGTGAT TGACAGCGAA GATTTGCCCT TGAACGTGAG TCGTGAAATC    1080
TTACAGCAGA ATAAGATTTT AGCCAATATC CGTTCGGCTT CAGTGAAAAA GATTTTAAGC    1140
GAGATTGAAA GGCTGAGCAA GGATAACAAG AATTACCATA AATTCTATGA GCCTTTTGGG    1200
AAAGTGTTAA AAGAAGGCTT GTATGGGGAT TTTGAAAACA AAGAAAAACT TTTAGAATTG    1260
TTGAGATTCT ATTCTAAAGA CAAAGGAGAA TGGATTTCTT TAAAAGAATA CAAAGAAAAT    1320
TTAAAAGAAA ATCAAAAAAG CATTTACTAC CTTTTAGGCG AAAATTTAGA CTTATTAAAA    1380
GCGTCCCCCC TTTTAGAAAA ATACGCTCAA AAAGGCTATG ATGTTTTGTT ATTGAGCGAT    1440
GAAATTGATG CGTTTGTGAT GCCAGGCGTG AATGAATACG ATAAAACGCC CTTTAGAGAC    1500
GCTAGCCATA GTGAGAGTTT GAAAGAGCTT GGTTTGGCAG AAATCCATGA TGAGGTAAAA    1560
GATCAGTTTA AAGATTTAAT CAAAGCGTTT GAAGAAAATC TTAAAGATGA GATTAAGGGC    1620
GTAGAGCTTT CTGGTCATCT CACTTCAGCG GTGGCTTTAA TAGGCGATGA ACCAAATGCG    1680
ATGATGGCTA ATTGGATGCG TCAAATGGGG CAAAGCGTGC CTGAAAGCAA GAAAACTTTA    1740
GAATTAAACC CTAACCATGC GATTTTGCAA AAACTCTTAA AATGCGAAGA TAAAGAGCAG    1800
TTGAGCGCTT TTATCTGGTT GCTTTATGAT GGGGCGAAGC TTTTAGAAAA AGGGGCTTTA    1860
AAAGACGCTA AAAGTTTTAA CGAACGCCTA AATAGCGTGC TATTGAAGGC GTTG          1914
```

(2) INFORMATION FOR SEQ ID NO:1426:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

This Sheet Has Been Replaced



(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426

```
AAGCAATTTG GTAGGCGAGT TTTTACCCAA ATTCCTAAAA TGGTGCAATT TCAAAACACG      60
CTTATAAAAT TCCATGCCCT ATCCTTTAAA AACGCAAATT TAATTTATAA TGCAAAATTA     120
AACAAAACAT GCTATAAAGA AAATTCAAAT ACTATCATTT TAAGGATTAA AATGCTCACC     180
CAAGAAGATG TCTTAAACGC GTTAAAAACG ATCATCTACC CTAATTTTGA AAAGGATATT     240
GTCAGCTTTG GTTTTGTTAA AAACATCACC TTGCATGACA ACCAATTAGG GCTTTTAATA     300
GAAATCCCCT CAAGCTCTGA GGAAACGAGT GCGATTTTAA GGGAAAATAT CTCCAAAGCG     360
ATGCAAGAAA AAGGCGTGAA AGCTTTGAAT TTGGATATTA AAACCCCGCC TAAACCGCAA     420
GCTCCAAAGC CCACCACTAA AAATCTGGCT AAAAACATCA AGCATGTGGT CATGATAAGC     480
TCAGGCAAGG GCGGTGTGGG TAAAAGCACC ACCAGCGTGA ATTTAAGCAT CGCTTTAGCG     540
AATTTAAACC AAAAAGTGGG GCTACTAGAC GCTGATGTGT ATGGCCCTAA TATCCCTAGA     600
ATGATGGGCT TGCAAAACGC TGATGTGATC ATGGATCCTA GCGGTAAAAA ACTCATTCCT     660
TTAAAAGCTT TTGGCGTTTC TGTGATGAGC ATGGGGCTTT TGTATGATGA GGGGCAGAGT     720
CTCATTTGGA GAGGACCCAT GCTCATGCGA GCGATTGAGC AGATGCTAAG CGATATTATT     780
TGGGGGGATT TAGACGTGCT GGTGGTGGAT ATGCCCCCAG GAACAGGCGA TGCGCAGCTC     840
ACGCTAGCCC AAGCCGTGCC ACTCAGCGCA GGAATCACCG TTACTACGCC TCAAATCGTG     900
AGTTTAGATG ACGCTAAACG GAGTTTGGAC ATGTTTAAGA AACTACACAT TCCTATTGCG     960
GGCATTGTAG AAAATATGGG GAGTTTTGTG TGCGAGCATT GCAAGAAAGA GAGCGAGATT    1020
TTTGGCTCAA ATTCCATGAG TGGATTATTA GAGGCTTATA ACACGCAGAT TTTAGCCAAG    1080
CTCCCTTTAG AGCCTAAAGT GCGTCTAGGG GGGGATAAGG GTGAACCGAT TGTGATTTCT    1140
CATCCCACTA GCGTGAGTGC TAAAATTTTT GAAAAAATGG CAAAGGATTT GAGTGCTTTT    1200
TTAGACAAGG TGGAAAGGGA AAAACTAGCC GATAATAAGG ACATCCAGCC CACACAAACG    1260
CATGCTTATT CGCAT                                                     1275
```

(2) INFORMATION FOR SEQ ID NO:1427:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427

```
CTAGGGTTTT TGGCTTTGCA TGGGTTTTTT CTCAGCGCTT TTGAGTATCA AGTGAGCGCT      60
AGAGTGGGAT CGTTTTCGCG TATCGCTTTC AACCAATCGA TCATCAATTC CAAAAAAGGG     120
ATTTACCCTA CAGGGAGTTA TGTAACCACT ACCGGGGCTT TACAAGTTGA TTCTAGTTTG     180
CTCCCTAAAG GGATTGAAAA CCACAAATTG GGTTTTGGGG TGGGGGGCGA AATAGGAGCG     240
TTAGCTTATG ATTCCACGAA ATTTTTGATT GATGAAGCCA ACCCTAAGGC AGGGTTTCAG     300
CCAGCGAACT GGTATTACAT GGGGCGATGG GAGGGCTATT TGATGCAACA CAGCCAAAAT     360
TGGACCAGAG AGCAAAAGGC TCAAAACGCC AGGCCTTATG TGTTATACAA TTTGTATTTA     420
GATTATCAAT ATAAGGACAT TTTTGGGATT AAACTAGGGC GTTACCCTTC TAAGGCTTTG     480
TTTTTGAGCG GGTTTAATCA AGGGTTTGAG ATTTTTTACC GGTGGAAAAA GTTTAAGATA     540
GTGTGGTTTA GCACCTTTGG AAGGGCTTTA GCCAATGAGC AATACATTAG GGATTTTTAC     600
```

GCTCCTGTCA ATTACAAGCA AAAAATCAAC TACGGCATGC ACAATTTCAA CCTCGTTTAC 660
GAAAATAAAT ACATTAGGAT CGCGCCTTTT ATTTGGTTTT ACCCTAAGAA TTTTAACGCT 720
CCTGGATTTG AAATCACCCA TGACACAAAA TCTTATTGGA AATCTCTTTG GCGCATCCAA 780
ACGACTTTTT ACGCATGGTT TCCTCTCTAT AGCGACTATT TGTCTAAAGA TTATTATAGG 840
GCCGCTTTAG TGGGTAAAAA AAGCGCGGCT TTGTTTGTGT TTCAAAGAGT GAATTTCCGC 900
TCTTATCGTT TTGGCTGGAG CGTGTATAAG AATTTTGGGA ACGCGAGCGT TCAGTTAGGT 960
TGGAATGGCT CACCCATTGA TCCTTTTTAC GACACGAAAG ATGATACCCC TTATGAAGAC 1020
GCTTATTCCA ATTTTTACAA CGCTAATTCC ATAACGATTA ACGCTTTTAT AGGGAAGAGC 1080
ATTAAGAATC TTTTGGTGCA ATTGTATGGG AAATTAACCT ATTCCCCAAG GGCTGATGCG 1140
CAAAGCTTAG GGGTTACTTT TAAATATAAC CTTAAAAAAC ATATCTATTT CATGCTAATG 1200
GTTAATGGCT ATCAAATCAC GATGCATAAG GGTTATAAGG TAGGGTTTTT TACAAGCGGT 1260
TACAACCCTG ATTTCGCTCA AACCATTCAA AATAGAAGCT ATTTGATGAG CTCTATGAGT 1320
TATCGTTTT 1329

(2) INFORMATION FOR SEQ ID NO:1428:

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

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1428

TACCCTACAA ATACTATTAT TGAAAGGATT TTGATGTTTA AAAAAATGTG TTTGAGCCTG 60
CTAATGATAA GCGGTGTTTG TGTGGGGGCA AAGGATTTGG ATTTCAAGCT GGATTATCGC 120
GCGACTGGGG GGAAATTCAT GGGGAAAATG ACGGACTCTA GTCTTTTAAG TATCACTTCT 180
ATGAACGATG AACCGGTGGT GATTAAAAAC CTTATTGTCA ATAGGGGAAA TTCAGTCGAA 240
GCGACTAAAA AAGTAGAACC CAAATTTGGC GATAAGTTTA AAAAAGAAAA ACTCTTTGAT 300
CATGAATTAA AATACTCGCA ACAGATATTT TACCGCCTGG ATTGCAAGCC TAACCAATTG 360
TTAGAAGTTA AAATCATCAC GGACAAGGGC GAATATTACC ATAAATTTTC CAAA 414

(2) INFORMATION FOR SEQ ID NO:1429:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429

```
AGGATTGGCA TGGACGCTTT AGAAATCACC CAAAAACTCA TCAGTTACCC TACCATTACG      60
CCCAAAGAAT GCGGTATTTT TGAATACATT AAATCGCTTT TTCCTGCTTT TAAAACCCTA     120
GAATGTGAAA AAAATGGCGT GAAAAACCTT TTTTTATACC GCATTTTTAA CCCCCTCAAA     180
AAGCATGCAG AAAAAGAACA TGCAAAAGAA AAGCATGTAA AAGAAAATGT TAAGCCCTTG     240
CATTTTTGCT TTGCAGGGCA TATTGATGTC GTGCCTCCTG GGAACAATTG GCAAAGTGAT     300
CCCTTTAAAC CCATCATTAA AGAGGGGTTT TTATACGGTC GTGGGGCGCA AGACATGAAG     360
GGGGGCGTTG GGGCGTTTTT GAGTGCGAGT TTAAATTTTA ACCCTAAAAC CCCTTTTTTG     420
CTTTCTATTT TACTCACGAG CGATGAAGAA GGGCCAGGGA TTTTTGGCAC TAGGCTTATG     480
CTAGAAAAAC TCAAAGAAAA GGATTTGCTG CCTCATATGG CGATTGTGGC TGAACCCACT     540
TGCGAAAAAG TCTTAGGCGA TAGCATCAAA ATTGGCCGAA GAGGCTCTAT TAATGGCAAA     600
CTCATTTTAA AAGGCGTTCA AGGGCATGTG GCTTACCCGC AAAAATGCCA AAACCCTATT     660
GATACGCTCG CTTCAGTTTT GCCTCTCATT TCAGGAGTTC ATTTAGACAA TGGCGATGAG     720
TGTTTTGACC CTTCAAAATT AGTCATCACC AACTTGCATG CAGGGTTAGG GGCTAATAAT     780
GTTACACCAG GGAGCGTAGA AATTGCCTTT AATGCGCGCC ATTCTTTAAA AACCACCCAA     840
GAGAGTTTGA AAGAATATTT GGAAAAGGTT TTGAAAGATT TGCCTTATAC TTTAGAATTA     900
GAATCAAGCA GTTCGCCTTT CATCACGGCT TCCCATTCAA AGCTTACTAG CGTTTTACAA     960
GAAAATATTT TAAAAACATG CCACACCACC CCCCTTTTAA ACACCAAAGG CGGCACGAGC    1020
GATGCGCGAT TTTTTAGCGC TCATGGTATA GAAGTGGTGG AGTTTGGCGC CATTAATGAC    1080
AGGATCCATG CCGTTGATGA AAGGGTGAGC TTGAAGGAAT TAGAGCTTTT GGAAAAAGTG    1140
TTTTTGGGGG TTTTAGAGGG CTTGAGCGAG AAA                                 1173
```

(2) INFORMATION FOR SEQ ID NO:1430:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2784 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430

```
ACAAGCCTTG ATCACAAAAT CACAGATTTT TCTTGCGTGG ATTTGAGGAT CCAATCTAAA      60
GAAGTCAGTC ATAATTTAAA GGAATTATCA AAAACGCTAA TCAGCTATCC TTTTGAAAAA     120
CATGTAGAAG CTTTAGGGGA ACAATGCAGT AACTTCGTTT CTATTCCCAT TAACAATGAC     180
GACTATTCAA ATATTTGCAC TTTTGTGAGT GATTTTATAA ATCTTATAGC TTCTTACAAT     240
TTATTAGAAT CATTTTTAGA TTTTTATAAA GATAAATTAA AATTGAGCGA GCTTGTAACT     300
GAATATGCCA ACGTAACCAA TAATCTGCTT TTCAAAAAAT TAATCAAACA TTTAAGCGGC     360
AACAATCAAT TGGTTAAAAA TTTTTATCAG TGTATAAGAG AAATTATAAA ATACAACGCC     420
CCTAATAAAG AATACAAACC CAATCAATTT TTTATAATAG GGAAAGGCAA ACAAAAACAA     480
TTAGCAAAAA TTTATTCTCA TTTAAAAGAA CTTAGTGCAA GTGAAATTAA ACCACAAGAT     540
ATGGAAGACA TCTTAAAAAA GCTAGAGGAA TTAGATAAAA TTTTTAAAAC TACCGACTTT     600
ACAAAATTCA CACCAAAAAC TGAAATTAAG GATATTATTA AAGAAATAGA CGAAAAATAC     660
CCTATCAATG AAAATTTTAA ACGGCAATTT AATGAGTTTG AATCAAATAT TGAAAAACAT     720
GATGAAATAA AAAAGGATTT TGAGCGAAAC AAAGAGTCGC TGATCCGAGA AATTGAAAAT     780
CACTGCAAAA ATGAATGCAA TAGCGAAGAA GAGCCGGAGT ATAAGATTAA TGATCTGCTC     840
AAAAATATCC AACAAATATG CAAAAATTAT ATAGAAAGTC ATGCCGTTAA TGATGTGTCT     900
```

This Sheet Has Been Replaced

```
AAAGATATTA AATCCATGAT GTGTCAGTTT TATTTGAAAC AGATAGATTT ATTAGTCAAT     960
TCAGAAATTG TGCGATACAG ATACAGCAAT CTTTTTGAAC CAATACAAAG ATCTTTATGG    1020
GAGAGTATAA AAATTTTAGA TAATGAAAGT GGCATTTATT TGTTCCCTAA AAATATTGGT    1080
GAAATCAAGG ATAAATTTGA AGCAAACAAG GAAAAATTCA AACAAAGCAA AAATGTTTCT    1140
GAGTTCGCAG AATATTGCCG AGAGTGTAAC CCCTATACAG CGTTTAACTT TCATCTAAAT    1200
ATAAATAATG GTTTATCTCA TCAATTTGAA AAATTCGTGC CAATCATGAA AGAATACAAA    1260
GAGCCAAAAA TCACAGATAA TGACCTTGAA GCCATATCAA CCAAAGAGAC TGGTCTTGCT    1320
AGCCAATTAT CTGGGCACTG GTTTTTTCAG CTTTCGTTAT TTAATAAAAC AAACTTTAAT    1380
CCTAATAAAA TTTGGATTCC TTTAGAGTTC AATAAAAGAT CAAAAATAAA GTTTGATAAA    1440
GATTTAGAAA TCTATTTTGA TAGTCATGAA TCGTTCAATA TCTCTAAAAA ATACTTGCAA    1500
GAAATAGATC AAGAATCACT AAAAAAGATC AAACAATCAA AAGATTTTTT TTCAATTCAA    1560
AAAATAGAGA GTAAGCATGA TAATAACGAT ATACTGCAAC TTGAATTTTT TGAGAATGAT    1620
ACAAGTTTTC TTTTTGCTAA AGGAAGTTTT GCAGAAATTT TAGAATACAA CATGCAATTA    1680
AAAATAGATT CTTTAATTAC AAAAGAATTT AATAAGCTTT TAGCGATCGT TCAAGATAGT    1740
CCCCAAGATA GTTACCAATT AAAAATTCGT GTCCGACATA ACAATAAGCT TCCTAGAGAG    1800
AAATATACGG AACATGAAAT AAAACTTGAA GTTTATGATT GCAGAAAATC CCACGATCAC    1860
AATGAGCCAA TCATCTTAAG CCAGCAAAGC ACCGGCTTCC AATGGGCGTT TAATTTCATG    1920
TTTGGCTTTC TTTATAATGT GGGATCACAT TTTAGTTTTA ACCATAATAT TATCTATGTC    1980
ATGGACGAGC CAGCCACTCA TTTGAGCGTG CCAGCCAGAA AGGAGTTTAG GAAATTTTTA    2040
AAAGAATACG CTCATAAAAA TCATGTTACT TTTGTTTTAG CCACCCATGA CCCCTTTTTA    2100
GTGGATACGG ATCATTTAGA TGAAATAAGG ATTGTGGAAA AGGAAACAGA AGGCTCTGTA    2160
ATTAAGAATC ACTTTAACTA TCCCCTAAAT AATGCAAGCA AAGACTCCGA CGCTTTGGAC    2220
AAAATCAAAC GCTCTTTAGG AGTGGGCCAG CATGTTTTTC ATAACCCCCA AAAACACCGA    2280
ATCATTTTTG TAGAAGGCAT CACGGATTAT TGTTATTTGA GCGCTTTTAA ATTGTATTTG    2340
CGTTACAAAG AATACAAGGA CAACCCCATT CCTTTCACTT TCTTACCCAT TTCAGGGCTT    2400
AAAAACGATT CAAACGATAT GAAAGAAACC ATTGAAAAAC TTTGCGAGTT AGACAATCAC    2460
CCTATTGTTT TGACAGACGA TGACAGAAAA TGCGTTTTTA ACCAACAAGC AACGAGCGAA    2520
CGATTTAAAA GAGCTAATGA AGAAATGCAT GATCCCATCA CCATCCTACA ACTCTCAGAC    2580
TGCGATAGGC ATTTCAAACA AATTGAAGAT TGTTTCAGCG CAAACGATAG AAACAAATAC    2640
GCTAAAAATA AGCAAATGGA ATTGAGCATG GCTTTTAAAA CAAGGCTTTT GTATGGCGGA    2700
GAAGATGCGA TAGAAAAACA AACAAAAAGA AATTTTTTAA AATTATTCAA ATGGATTGCA    2760
TGGGCTACAA ACTTGATCAA AAAC                                           2784
```

(2) INFORMATION FOR SEQ ID NO:1431:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 873 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1431

```
CAAGCATTGG GTATCAATAT GTGTTCTAAA AAAATAAGAA ATCTCATTTT ATGCTTTGGT      60
TTTATTTTAA GCTTGTGCGC TGAAGAAAAT ATCACCAAAG AAAACATGAC TGAAACGAAC     120
ACGACTGAAG AAAACACCCC TAAAGACGCT CCCATTCTTT TGGAAGAAAA ACGCGCCCAA     180
ACTCTAGAGC TTAAAGAAGA AAATGAAGTG GCAAAAAAGA TTGATGAAAA AAGCCTGCTT     240
GAAGAAATCC ATAAGAAAAA ACGCCAGCTT TACATGCTCA AAGGGGAATT GCATGAAAAG     300
AATGAATCCA TCTTATTCCA ACAAATGGCT AAAAATAAGA GCGGCTTTTT TATAGGCGTG     360
ATCCTTGGCG ATATAGGGAT TAACGCTAAT CCTTATGAGA AGTTTGAACT TTTAAGCAAT     420
ATTCAAGCTT CTCCCTTGCT GTATGGTTTA AGGAGCGGGT ATCAAAAGTA TTTCGCTAAC     480
```

```
GGGATTAGCG CCTTACGCTT TTATGGGGAA TATTTAGGGG GGGCGATGAA AGGGTTTAAA     540
AGCGATTCTT TAGCTTCTTA TCAAACCGCA AGCTTGAATA TTGATCTGTT GATGGATAAG     600
CCTATTGACA AAGAAAAAAG GTTTGCGTTA GGGATATTTG GAGGCGTTGG AGTGGGGTGG     660
AATGGGATGT ATCAAAATTT AAAAGAGATT AGAGGGTATT CACAGCCTAA CGCCTTTGGG     720
TTGGTGTTAA ATTTAGGGGT GAGCATGACG CTCAACCTCA AACACCGCTT TGAATTAGCC     780
CTAAAAATGC CTCCCTTAAA AGAAACTTCG CAAACCTTTT TATATTATTT TAAAAGCACT     840
AATATTTATT ATATTAGTTA CAACTATTTA TTG                                  873
```

(2) INFORMATION FOR SEQ ID NO:1432:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 678 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1432

```
AGATTTTTTA GAAAGCATAG GGTTATAAGC ATGAAAGAAA TCGTTACAAT AGAGAATGTG      60
TCTTTTAACT ACCACAATCG CGCTATTTTT AAGGATTTTA ATTTAAGCAT TCAAGAAGGG     120
GATTTTTTAT GCGTTTTAGG GGAGAGCGGG AGCGGTAAAA GCACGCTTTT AGGCTTGATT     180
TTAGGGCTTT TAAAACCCAG TCTGGGGAGC GTTAAAATCT TTAATGAGAC CCTTTCAAAC     240
AACGCTTTTT TACGCCAAAA AATAGGCTAT ATCGCTCAGG GCAATTCCTT ATTCCCTCAT     300
TTAAACGCCT TACAAAACAT GACTTTTTGC CTTAATTTAC AAGGCATAAA CAAACAAGCC     360
GCTCAAAAAG AAGCCAAAGC CTTAGCGTTA AAAATGGGGT TAGACGAGAG CCTTATGGAT     420
AAATTCCCTA ATGAATTGAG TGGGGGGCAA GCCCAAAGAG TGGGCATTAT TAGGGGGATT     480
ATCCACAGGC CAGAACTCAT TTTATTAGAT GAGCCTTTTA GCGCTTTAGA TAGTTTGAAT     540
CGTAAGAATT TACAGGATCT CATCAAAGAA ATACACCAAA ATTCTTGCGC TACTTTCATT     600
ATGGTAACGC ATGATGAAAA CGAGGCGCAA AAGTTAGCCA CAAAAACCCT AGAAATCAAA     660
GCCCTTAAAC AAGAGCAG                                                   678
```

(2) INFORMATION FOR SEQ ID NO:1433:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1782 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature

(B) LOCATION 1...1782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433

```
ATGGCTGATT TATTGTCCAG TTTGAAAAAC CTTTCTAGTA GTAGTGGGGT GTATCAATAT      60
TTTGATAAAA ACCGCCAATT ACTCTACATC GGTAAGGCGA AAAATTTAAA AAAGCGCATC     120
AAAAGCTATT TTTCTGTCCG TAATAATGAA ATCACGCCCA ATCCTCGCAC AAGCTTACGC     180
GTCCAAATGA TGGTCAAACA GATCGCTTTT TTAGAAACCA TTTTAGTGGA AAACGAGCAA     240
GACGCTTTGA TTTTGGAAAA TTCTTTGATC AAGCAGCTCA AGCCTAAATA CAACATTCTT     300
TTAAGAGACG ATAAAACTTA CCCTTATATT TACATGGATT TTTCTATTGA TTTCCCTATC     360
CCTTTAATCA CACGAAAAAT CTTAAAACAG CCTGGCGTTA AATATTTTGG CCCTTTTACG     420
AGCGGGGCTA AGGATATTTT GGACAGCTTG TATGAATTGC TCCCTTTGGT TCAAAAGAAA     480
AATTGCATCA AGGATAAAAA GGCATGCATG TTTTATCAAA TAGAGCGTTG TAAAGCCCCA     540
TGCGAGGATA AAATCACTAA AGAAGAATAT TTAAAAATCG CTAAAGAATG TTTAGAAATG     600
ATTGAAAATA AAGACAGGCT CATCAAAGAG CTTGAATTGA AAATGGAGCG CCTTTCTAGT     660
AACTTGCGTT TTGAAGAAGC CTTAATTTAT AGGGATAGGA TTGCAAAAAT CCAAAAAATC     720
GCCCCTTTCA CTTGCATGGA TTTAGCCAAA CTCTACGATT TGGATATTTT TGCTTTTTAT     780
GGTGGGAACA ACAAGGCGGT GTTAGTGAAA ATGTTCATGC GTGGGGGTAA AATCATTTCT     840
TCAGCGTTTG AAAAAATCCA CTCTCTCAAC GGGTTTGACA CTGATGAAGC GATGAAACAA     900
GCCATTATCA ATCATTACCA ATCGCATTTG CCTTTGATGC CTGAACAAAT CTTATTGAGC     960
GCTTGTTCTA ATGAAACGCT TAAAGAATTG CAAGAGTTTA TCTCTCACCA ATATTCTAAA    1020
AAAATCGCTC TTAGCATTCC TAAAAAGGGT GATAAGCTCG CTTTAATAGA AATCGCTATG    1080
AAAAACGCTC AAGAGATTTT TAGCCAAGAA AAAACCTCTA ATGAAGATCG GATCTTAGAA    1140
GAAGCGCGAT CGCTCTTCAA TTTAGAGTGC GTGCCTTATA GGGTAGAAAT CTTTGACACA    1200
AGCCACCATT CAAACAGCCA ATGCGTGGGG GGAATGGTCG TGTATGAAAA CAATGCATTT    1260
CAAAAAGACT CTTATCGGCG CTACCATCTA AAAGGCTCTA ACGAATATGA TCAAATGAGC    1320
GAATTGCTCA CCAGAAGGGC TTTAGACTTT GCTAAAGAGC CACCGCCTAA TTTGTGGGTG    1380
ATAGATGGAG GGAGGGCGCA ATTAAACATC GCTTTAGAAA TTTTAAAAAG CAGCGGGAGT    1440
TTTGTAGAAG TGATCGCTAT TTCTAAAGAA AAAAGGGATT CTAAGGCTTA TCGTTCTAAA    1500
GGGGGTGCTA AAGACATTAT CCATACGATT AGTCATACTT TTAAATTGCT CCCTAGCGAC    1560
AAACGCTTGC AGTGGGTGCA AAAATTGCGC GATGAAAGCC ACCGGTATGC GATAAACTTC    1620
CATAGATCCA CTAAACTTAA AAACATGAAA CAAATCGCTC TTTTAAAAGA AAAGGGCATA    1680
GGAGAAGCCA GCGTGAAAAA ATTGTTGGAT TATTTTGGGA GTTTTGAAGC GATAGAAAAA    1740
GCGAGCGATC AGGAAAAAAA CGCCGTTTTA AAAAAACGAA AA                        1782
```

(2) INFORMATION FOR SEQ ID NO:1434:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434

```
AGGAAAAACA TGAAAAAAAG ATTGAATATA GGGCTTGTGG GTTTAGGGTG CGTGGGGAGC      60
ACGGTCGCTA AAATCTTACA AGAAAATCAA GAAATCATTA AAGACAGAGC CGGCGTGGAA     120
ATTAAAATTA AAAAAGCGGT GGTGCGAGAC GTGAAAAAAC ACAAGGGCTA TGCTTTTGAA     180
ATCAGTGATG ATTTAGAAAG CGTGATAGAA GATAAAGGGA TTGATATTGT CGTGGAGCTT     240
ATGGGTGGGG TGGAAGCGCC TTATCTTTTA GCTAAAAAAA CTTTAGCCAA ACAAAAAGCC     300
TTCGTTACAG CCAATAAAGC CATGTTAGCG TACCACCGCT ATGAATTAGA ACAAATCGCT     360
```

```
AAAAACACCC CCATAGGCTT TGAAGCGAGC GTGTGTGGGG GTATCCCCAT TATCAAGGCT     420
TTAAAAGACG GCTTGAGCGC TAATCACATC CTTTCTTTTA AAGGGATTTT AAACGGCACG     480
AGCAATTACA TTTTAAGCCA GATGTTTAAA AATCAAGCGA GCTTTAAGGA CGCTTTGAAA     540
GACGCGCAGC ATTTAGGCTA TGCGGAATTG AACCCTGAAT TTGACATTAA GGGCATTGAT     600
GCGGCGCACA AATTATTGAT TTTAGCGTCT TTAGCGTATG GCATTGATGC GAAATTAGAA     660
GAAATCTTGA TTGAAGGCAT TGAAAAGATA GAGCCAGATG ACATGGAATT TGCAAAAGAG     720
TTTGGTTATA GCATCAAACT TTTAGGCATC GCTAAAAAAC ACCAGGATTG CATTGAATTA     780
AGGGTGCATC CAAGCATGAT TAAAAATGAA TGCATGCTCT CTAAAGTGGA TGGGGTGATG     840
AACGCTATCA GCGTCATAGG GGATAAGGTG GGCGAGACTT TGTATTATGG GGCTGGGGCT     900
GGAGGAGAGC CTACCGCAAG CGCGGTCATT AGCGATATTA TAGAAATCGC AAGGAAAAAA     960
AGCTCTCTAA TGCTGGGCTT TGAAACCCCT CAAAAACTCC CCCTAAAACC CAAAGAAGAA    1020
ATCCAATGCG CTTACTATGC GCGCTTGTTA GTGAGCGATG AAAAAGGGGT TTTTTCTCAA    1080
ATCAGCGCGA TTTTAGCCCA AAATGATATT TCGCTCAACA ATGTCTTGCA AAAAGAAATC    1140
CCGCAATCCA ACAAGGCTAA AATCTTATTT TCCACGCACA CCACCAACGA AAAATCTATG    1200
CTGAACGCCC TTAAAGAGCT TGAAAATTTA CAAAGCGTGT TGGATACCCC TAAAATGATC    1260
CGTTTGGAAA AT                                                        1272
```

(2) INFORMATION FOR SEQ ID NO:1435:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 978 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435

```
AGTCGCTTTA AAAGAGCAAT TGAACAAGCT TTTAGGCTAG TGGCCATGAT AGATTGCGCG      60
ATTATTGGAG GTGGTCCTGC AGGTTTGAGT GCGGGGCTTT ATGCCACTAG AGGCGGTGTT     120
AAAAACGCCG TTTTATTTGA AAAAGGAATG CCTGGGGGGC AAATCACTGG CAGTAGTGAG     180
ATTGAAAATT ATCCGGGCGT TAAGGAAGTG GTGAGCGGAT TGGATTTCAT GCAACCATGG     240
CAGGAGCAAT GCTTTCGCTT TGGTTTAAAG CATGAGATGA CCGCCATTCA AAGGGTTTCT     300
AAAAAAGGTT CTCATTTTGT TATTTTGGCA GAAGATGGCA AGACTTTTGA AGCTAAGAGC     360
GTGATCATCG CTACCGGTGG TAGCCCTAAA CGCACAGGTA TCAAGGGCGA GTCAGAATAT     420
TGGGGTAAAG GCGTTAGCAC TTGTGCAACA TGCGATGGCT TCTTTTACAA AAATAAGGAA     480
GTAGCGGTGC TTGGTGGAGG CGATACCGCC GTAGAAGAGG CGATTTATCT AGCCAATATC     540
TGCAAAAAAG TCTATCTCAT CCACAGAAGA GATGGTTTTA GGTGTGCGCC TATCACTTTA     600
GAGCATGCTA AAAACAATAG TAAGATTGAG TTTTTAACCC CTTATGTGGT GGAAGAAATC     660
AAGGGCGATG CTTCTGGCGT GTCTTCTTTA AGCATTAAAA ACACAGCCAC TAACGAAAAA     720
AGAGAATTAG TCGTGCCGGG GCTTTTTATT TTTGTGGGTT ATGATGTGAA TAACGCCGTG     780
TTGAAGCAAG AAGATAACTC CATGCTATGC GAATGCGATG AATACGGCTC TATTGTCGTG     840
GATTTTTCCA TGAAGACGAA TGTTCAGGGC TTGTTTGCGG CAGGAGATAT TCGCATTTTT     900
GCCCCCAAGC AAGTGGTTTG TGCGGCAAGC GATGGTGCTA CGGCAGCCTT AAGCGTGATT     960
TCTTATTTAG AACACCAT                                                  978
```

(2) INFORMATION FOR SEQ ID NO:1436:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 837 base pairs
(B) TYPE: nucleic acid

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

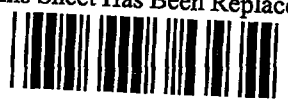
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436

```
AAATTATGGG AGTTTAGCTT GCGTGTTTTT ATCATTTCTT TAAATCAAAA AGTGTGCGAT      60
AAATTTGGTT TGGTTTTTAG AGACACCACA ACTTTACTCA ATAATATCAA CGCCACCCAC     120
CACCAAGCGC AAATTTTTGA TGCGATTTAT TCCAAGACTT TTGAAGGCGG GTTGCACCCC     180
CTAGTTAAAA AGCATTTACA CCCTTATTTC ATCACGCAAA ATATCAAAGA CATGGGGATT     240
GCAACCAGTC TCATCAGTGA GGTTTCTAAG TTTTATTACG CTTTAAAATA CCATGCGAAA     300
TTTATGAGCT TGGGGGAGCT TGGGTGCTAT GCGAGCCATT ATTCGTTGTG GCAAAAATGC     360
ATAGAGCTCA ATGAAGCGAT CTGTATTTTA GAAGACGATA TAACCTTGAA AGAGGATTTT     420
AAAGAGGGCT TGGATTTTTT AGAAAAACAC ATCCAAGAGT TAGGCTATGC GCGTTTGATG     480
CATTTATTGT ATGATGCCAG CGTGAAAAGT GAGCCTTTAA ACCATGAAAA CCAAGAGATA     540
CAAGAGCGTG TGGGGATCAT TAAAGCTTAT AGCCATGGGG TGGGGACGCA AGGCTATGTG     600
ATCACGCCCA AGATTGCCAA AGTTTTTTTG AAACACAGCC GAAAATGGGT TGTTCCTGTG     660
GATACGATAA TGGACGCTAC TTTTATCCAT GGCGTGAAAA ATCTGGTGTT ACAACCTTTT     720
GTGATCGCTG ATGATGAGCA AATCTCTACG ATAGCGCGAA AAGAAGAACC CTATAGCCCT     780
AAAATCGCTC TAATGAGAGA ACTCCATTTT AAATTTTTGA AATGGTGGCA GTTTGTA        837
```

(2) INFORMATION FOR SEQ ID NO:1437:

(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:1437

```
GGGGATTTTA TAATTTCTAA CATCAGCATA CACCCAAAAA CCATGTTTAA AAACGCTTTA      60
AATATACAAG ATTTTTCATT TAAAAATCAT ACTAGTACAG CCATTATTGG CACAAATGGT     120
GCTGGAAAAT CAACGCTTAT CAACACTATT CTAGGCATTA GATCAGACTA TAATTTTAAA     180
GCACAAAACA ATAATATTCC ATACCACGAC AATGTTATAC CACAACGCAA GCAATTGGGA     240
GTTGTCTCTA ACCTATTCAA CTACCCACCT GGATTAAACG CAAACGACCT TTTTAAATTC     300
TATCAATTTT TTCACAAAAA CTGCACTCTA GATTTGTTTG AAAAAAATCT TTTAAATAAA     360
ACCTACGAAC ACCTAAGCGA CGGACAAAAA CAGCGCTTAA AAATTGACTT AGCTCTTAGC     420
CATCACCCAC AATTAGTTAT TATGGATGAA CCAGAAACCA GTTTAGAGCA AAACGCTCTT     480
```

ATAAGACTAT CAAATCTCAT AAGCTTGCGC AACACCCAAC AACTTACAAG TATCATCGCC 540
ACTCATGATC CTATTGTCTT AGATAGTTGC GAATGGGTAT TGCTCCTTAA GAATGGCAAC 600
ATTGCTCAAT ACAAACCTTT AAATTCTATA TTAAAATCTG TAGCTAAAAC TTTTAACTTT 660
AAAGAAAAAC CAACCACAAA AGACTTATTA GCGTTACTAA AGGATATT 708

(2) INFORMATION FOR SEQ ID NO:1438:

(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:1438

ATTTATTCTC ATCTCGCTCC CATTATGCAC TATCAATTAA CAAGTTTCAA TATAATACAA 60
GATCTTTTTA TAACTTGTCA TGTGTTAAGG ATCAAAATGC GCGTGTTTGT TTGCTTTTTA 120
GGGGTTTTTG TATCTAACGG CTTGGCTCGT TTTGGCTATG TGGTTTTAAT CCCCCTACTC 180
ATTTTATCAG GGAGTTTAAC CCCACACCAA AGCTTCCAAC TGGGTATTGC GGTGCTAATG 240
GGCTATGTTT TTGGGAGCTT TTTAATCCAA TTTTTAAGCC CGTTAATGTC ATTAGAAAGC 300
ATCGCTAAAA TCAGTTTTAA ATTAATCACT TTGAGTTTT 339

(2) INFORMATION FOR SEQ ID NO:1439:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1439

AGTATGGGCG GATTCACAAG CATATGGCAT TGGGTCATTG TTTTATTAGT GATTGTGTTG 60
TTATTTGGGG CTAAAAAGAT CCCAGAATTG GCTAAAGGTT TAGGCAGTGG GATTAAGAAT 120
TTCAAAAAAG CCGTGAAAGA CGATGAAGAA GAGGCTAAAA ACGAGCTAAA AACCCTAGAC 180
GCTCAAGCAA CACAAACCAA AGTGCATGAA ACTAGCGAAA TTAAAAGCAA ACAAGAAAGT 240

(2) INFORMATION FOR SEQ ID NO:1440:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 801 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440

```
AGAAAAACCA ACCACAAAAG ACTTATTAGC GTTACTAAAG GATATTTAAT GGGTGCAATT      60
TTATCTATTT TAAAACTTGA AATCAAATCT TATCTCACCA ATACAAGCGC GCTATTTTGG     120
ACTTTTATTT ATCCTATTTT AATGCTCCTA TTACTAATTT TTGTTTTTTC AAAAAATACC     180
ACTGAAATTT TTTACTTTAA TAACATTATA GGTCTAATGG GACTTCTTAT TATTTCTAGC     240
GCGATCTTTG GTCTCACACA AGCTATAACA AGCTCTAGAT CGCATAATAT ATTCTTATTC     300
TACATGCTAT CACCAGCAAC TTTCAAACAA ATAACTCTAG CATTAATCGC TTCAAGACTA     360
ATCGTTGTAA TCCTATATGC TTTTATCTTT ATTGTTCTCT CTTTTTATGC GCTCAATATC     420
ATCACTATTC TTAATTTTAA AGCGCTTATT TTGGGGTTTA TTAGCATTTT TTCAAGCGCA     480
TTGTTTTGTT TTTGCTTGGC AATTTTTGTA GCTAGAATTT TTCAAAACGA ACAAAGCATC     540
TTAGGATTTT GTAATATCAT CAATCTCTAT GCGCTAATGT CTTGTAATGT TTTTGTTCCT     600
TTAGAATACC TACCTAATAT TGGTCAATTA TTTATCAAAA CATCTATTTT TTACTACCTT     660
AATCAACTTC TAATCAAAGC TTTTCAAGGG ATTGATACTA TACTGGTTTT AGCAACTTCA     720
ACATTTTTCA TTATTGGTGG CATTATTTTA TTTTTACTAA GCGCTAATCG CATGTTACTA     780
ACACCAAAAG AACGCATGCG T                                               801
```

(2) INFORMATION FOR SEQ ID NO:1441:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 816 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1441

```
AGAAAACAAG AAATGAAAAA ACTTCTTTTA CTCTTAGAGC ATAAGATCGT AAAAATTGGC      60
TTAATTATTG TGATTGTGTT AGTGGGTTTT TTTCTTTTTT ATGAACAAGA AATCAAAGAA     120
```

```
AAAGCTGTTA ATGTTTCTCA AGGTAAATTC CCCACTTCAT CTTATTTGTT TCAAGCTTAC    180
GAAGGCATTA AGAATAAAAT AGATACTATC AATCAAGTGA AGCCAAACGA TGAAACTAAA    240
AGCGTTAATG AGAATATAGA AAAAACACAA AAAGATTTAG ATGATTTTAA TGCGCTAGTG    300
CAAAAGTTAC CAAATTTGCC TAAGGACTTT AATAAAACAC TTATTAAACC ACAAAGTCCA    360
TTTTTCAACT ACAATACCGC TAACGAAGAT GAAAAAAACC GCCTGGTGAT TTTAGCGTCT    420
CGTATTAGCA GCCAAAAAGA AACGCAACCT CCCATTTCTA TAAAAAATAG CGTTTCTCAC    480
ATAAAATCCA AAGAAAAACG AGAACTTGAA AAAGAATGGG CAAAACCTAG TGTTTCTTTT    540
GGTTCTTTTT CCTTGCTTTC CAGTTCTTCT TCTTTTTCTT CTTTTGAAGT TTCTTTTTTA    600
TCAAGGGGAA TAGGATTGGA TTGTGAGAAG CTCAAATCCT TTTTAAAAGC TTTTTCAAGT    660
TCGCTATTTT CCTTATTATC TTCATTGTTT TGCCATCCAC TTTCTCTTTT TTGCTCTCTA    720
ATAGGATTAA TCTTTTGTTT TTCTAAGTTT TCTAGAGAGC TAGTGAATGC GTCTAACAAT    780
TCGCTTGAGT TTTCATCATT GTCAAGGCTA GGATCA                               816
```

(2) INFORMATION FOR SEQ ID NO:1442:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1014 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442

```
AAAATCTTCA AAAAGGCTTT AAGGCATAAA ATGGAAAAAG TTTGCGTGAG CGCATGGGGG     60
TTGCCTAAGA TTTTAGAAGA AAGATTAAAA GAAAAATATG GCGATGATTG GGAAAAACAT    120
GTTAAGGCTA AAGCAATAAA CGAAGAAGAG CTTGAAGAAC AAGTCAAAGC TAAAGCCAAA    180
GAGCAACAAA AGACACAAAG AGAAAAAACA CTCAATGGAT TTTTAAAAAA AGTTGGTTTA    240
AAAAAGCGTG ATATGTTACA AAGCACTATG TTATTTGATG AAGTCAAAGA AGCTGATGTG    300
CTTTTTCAAG CAGAGCGTAA AATTGGCGAT TGGATTTTTA GCAGTGCGGT GTTCTTTTTT    360
GCTCTAGCCC TTATAGAAGC CATTATTATT GTATGCTTAT TGCCGTTAAA AGAAAAAGTG    420
CCTTATTTAG TAACCTTTTC AAACGCTACA CAAAATTTTG CCATAGTCCA AAGAGCAGAC    480
AAGAGCATCC GTGCTAATCA AGCGCTTGTG AGACAATTGG TAGCGTCTTA TGTTAATAAT    540
AGAGAAAATA TTTCAAGTAT AAAAGAGCAA AACGAAATAG CCCACGAAAC CATTAGGTTG    600
CAAAGCGCAT TTGAAGTGTG GGATTTTTTT GAAAAACTGG TTTCTTATGA GCATAGCATT    660
TACACTAATA TAAATCTAAC ACGAAAAATT AGCATTATCA ATATCGCTTT AATCAGTAAA    720
ACCCAAGCCA ATATTGAAAT ATCCGCACAA CTTTTTCATA AAGAAAAGTT AGAAAGCGAA    780
AAGCGTTATA GAATAATTAT GACCTTTGAA TTTGAACCTA TTGAAATTGA TACAAAATCT    840
GTTCCCCTAA ACCCTACAGG CTTTATTGTT ACAGGTTATG ATGTAACTGA AATTGCGATT    900
TTAAAAGATT TAGATGAGAA AAATAAAGTC AAAGATGATG GTGTGAAATC TAGGATTATT    960
CATGTCGAGA AAAAAGACCC TCATATGAGC CAGTATAAAG ATGTTAAGGA GCAA         1014
```

(2) INFORMATION FOR SEQ ID NO:1443:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 930 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443

```
GTTGTGGTAA TAAGGTTAGT CCTAAACATG CTAACATGTC AAATTAGCTA TATAAGGATA     60
AGTTATCTTG TCTCTGTTAG CGATTTTGTG ATTTGCAAGG AAAGATTTAT GGATGAAATT    120
AAAACGCTGT TAGTGGATTT TTTCCCGCAG GCAAAGCATT TTGGGATAAT CTTAATCAAG    180
GCTATTGTTG TCTTTTGTAT AGGTTTTTAT TTTTCGTTTT TCTTACGGAA CAAAACCATG    240
AAACTCTTAT CCAAAAAGGA TGAGATTTTG GCGAATTTTG TCGCGCAGGT TACTTTTATC    300
TTAATCCTTA TCATTACTAC AATCATCGCG CTCAGCACGC TAGGCGTCCA AACCACCTCT    360
ATTATCACTG TTTTAGGAAC GGTGGGGATT GCGGTGGCGT TGGCTTTAAA AGATTATCTT    420
TCAAGCATTG CTGGAGGGAT AATCCTTATT ATTTTACACC CTTTCAAAAA AGGAGACATC    480
ATTGAAATCT CTGGCCTAGA GGGCAAAGTA GAAGCGCTTA ATTTTTTTAA TACTTCTTTA    540
CGCTTGCATG ACGGGCGCTT GGCGGTTTTG CCTAATAGAA GTGTCGCTAA TTCTAATATT    600
ATCAATAGCA ATAACACTGC GTGTCGGCGC ATTGAATGGG TCTGTGGGGT AGGGTATGGG    660
AGCGATATTG AACTGGTGCA TAAGACTATA AAAGATGTTA TTGACGGGAT GGAAAAAATT    720
GATAAAAACA TGCCCACTTT CATTGGAATC ACGGATTTTG GACAAAGTTC GCTGAACTTC    780
ACCATTAGGG TTTGGGCAAA GATTGAAGAC GGGATCTTTA ATGTGAGGAG CGAACTCATT    840
GAACGCATCA AAAACGCCCT GGACGCTAAT CGTATTGAAA TCCCTTTCAA CAAGCTAGAT    900
ATTTCTATCA ACAAACAAGA CTCTTCTAAG                                     930
```

(2) INFORMATION FOR SEQ ID NO:1444:

(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

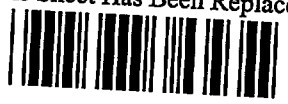
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444

```
AGCAAAAGAA CACAACAAAC CTTTTTTCTA TTCATTGATG AAACTAAAGA CTACATTATG     60
CATCCTATAA TGTTTGCCTA TATCGCTAAC GCGCTCGCTC AAGCTAGAAA GATCAACGGA    120
ACACTTTGCA TGGCGTTTCA AAAAATATCT CAAGTCAAAG AATTAGGCAT TGATAAAGCA    180
AAGAGTTTGA TAGGCAACCT TTCTCAAGTG ATTATCTACC CCACAAAAGA TACTGATGAA    240
TTAATAGAAT GTGGCGTCCC ATTAAGCGAT AGTGAAATCA ATTTCTTACA CAACACGGAC    300
ATGAGAGCCA GACAAGTGCT AGTAAAAAAT ATCGTTACAA ACGCTTCAGC TTTTATTGAA    360
ATTGATTTAA AAAAGATTTG CAAGAACTAC TTTATATTCT TGATAGCAAT GCTGGTAATA    420
GAAAAATCCT CAATGATCTT AAAAAAGCAA ACCAAGAAAC TTATAAGGAA GAGTATT       477
```

(2) INFORMATION FOR SEQ ID NO:1445:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 774 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1445

```
CTCCTTAAAA ATATTGATGA GAAAAAGCTT TCCGTAAGTA AGGTAAATGA AAAAAGGCAC      60
ATGGATTTTA AAAAATGCCC TAATTTTGAA AAAAAATGTG CGTTTCTTTG TTTCTCAAAT     120
TTGGTTTTAC TTATTGAAAT CCACTCTAAA GGACTACACA TGCAAAAAAA GAAACCCAAG     180
AACCCGCAAC CGAATTTATT TAGCATCTTA GATAAGGGCG ATGTTGCAAC AAACAATCCT     240
GTTGAAGAGT CAGACAAGGC CAATAAAATA CAAGAGCCAC TCCCTTATGT CGTGAAAACG     300
CAAATCAATA AAGCAAGCAT GATTTCTAGA GATCCTATTG AATGGGCAAA GTATTTAAGC     360
TTTGAAAAAC GAGTCTATAA GGATAATAGT AAAGAAGATG TCAATTTCTT TGCCAATGGT     420
GAGATAAAAG AAAGTTCTCG TGTTTATGAA GCGAATAAAG AAGGGTTTGA AAGGCGCATC     480
ACTAAAAGAT ACGATCTGAT TGATAGAAAT ATTGATAGAA ATAGAGAATT TTTTATAAAA     540
GAAATTGAAA TTCTAACCCA CACAAACAGC TTAAAAGAAT TGAAAGAGCA AGGGTTAGAA     600
ATCCAATTGA CCCACCATAA TGAAACGCAT AAGAAAGCCT TAGAAAATGG CAATGAAATC     660
GTTAAAGAAT ACGACCATCT TAAAGATATT TACCAAGAAG TAGAAAGAAC AAAAGATGGT     720
GGATTGGTAA GAGAAATAAT CCCCAGTATT TCTAGCGCTG AGTATTTCAC CCTT           774
```

(2) INFORMATION FOR SEQ ID NO:1446:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 274 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446

```
Asp Ala Arg Ser Phe Phe Leu Arg Leu Val Ala Met Ala Leu Cys Leu
1               5                  10                  15
Ile Leu Ile Asn Ser Arg Gly Val Ala Met Gly Tyr Ala Ser Lys Leu
            20                  25                  30
Ala Leu Lys Ile Cys Leu Val Gly Leu Cys Leu Phe Ser Thr Leu Gly
        35                  40                  45
Asp Glu His Leu Glu Gln Lys Gly Asn Tyr Ile Tyr Lys Gly Glu Glu
```

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

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1447:

(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:1447

```
Thr Met Lys Asn Thr Ser Ser Ser Thr Thr Leu Thr Met Asn Asp Thr
1               5                   10                  15
Ile Ala Ala Ile Ala Thr Pro Leu Gly Lys Gly Ala Ile Ser Ile Ile
            20                  25                  30
Lys Ile Ser Gly His Asn Ala Leu Asn Ile Leu Lys Gln Leu Thr Gln
        35                  40                  45
Lys Gln Asp Phe Thr Pro Arg Tyr Ala Tyr Val Cys Asp Ile Phe Ser
    50                  55                  60
Asp Gly Val Leu Leu Asp Lys Ala Leu Val Ile Tyr Phe Lys Ala Pro
65                  70                  75                  80
Tyr Ser Phe Thr Gly Glu Asp Val Cys Glu Ile Gln Cys His Gly Ser
                85                  90                  95
Pro Leu Leu Ala Gln Asn Ile Leu Gln Ala Cys Leu Asn Leu Gly Ala
            100                 105                 110
```

```
Arg Leu Ala Lys Ala Gly Glu Phe Ser Lys Lys Ala Phe Leu Asn His
        115                 120                 125
Lys Met Asp Leu Ser Glu Ile Glu Ala Ser Val Gln Leu Ile Leu Cys
    130                 135                 140
Glu Asp Glu Ser Val
145
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1448:

(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:1448

```
Asn Leu Ile Tyr Arg Ser Ser Gln Arg Ser Ala Ala Ala Cys Val Val
1               5                  10                  15
Arg Leu Asn Lys Glu Pro Met Ile Glu Tyr Leu Lys Ser Asn Ile Lys
            20                  25                  30
Leu Ile Asp Glu Met Ile Ala Ser Gly Tyr Glu Asp Lys Glu Thr Leu
        35                  40                  45
Lys Lys Arg Arg Asp Ala Met Gln Ala Trp Val Asp Lys Pro Val Leu
    50                  55                  60
Leu Glu Pro Asp Ser Asn Ala Gln Tyr Ala Ala Val Ile Glu Ile Asp
65                  70                  75                  80
Val Ala Glu Ile Thr Glu Pro Ile Leu Ala Cys Pro Asn Asp Pro Asp
                85                  90                  95
Asp Val Ala Thr Leu Ser Glu Val Leu Ala Asp Thr Thr Gly Lys Arg
            100                 105                 110
Pro His Ala Ile Asp Glu Val Phe Ile Gly Ser Cys Met Thr Asn Ile
        115                 120                 125
Gly His Phe Arg Ala Phe Gly Glu Ile Val Lys Asn Ala Pro Pro Ser
    130                 135                 140
Gln Ala Arg Leu Trp Val Val Pro Pro Ser Lys Met Asp Glu Gln Glu
145                 150                 155                 160
Leu Ile Asn Glu Gly Tyr Tyr Ala Ile Phe Gly Ala Ala Gly Ala Arg
                165                 170                 175
Thr Glu Val Pro Gly Cys Ser Leu Cys Met Gly Asn Gln Ala Arg Val
            180                 185                 190
Arg Asp Asn Ala Val Val Phe Ser Thr Ser Thr Arg Asn Phe Asp Asn
        195                 200                 205
Arg Met Gly Arg Gly Ala Lys Val Tyr Leu Gly Ser Ala Glu Leu Gly
    210                 215                 220
Ala Ala Cys Ala Leu Leu Gly Arg Ile Pro Thr Lys Glu Glu Tyr Met
225                 230                 235                 240
Asn Leu Val Ser Glu Lys Leu Glu Ser Gln Lys Asp Lys Ile Tyr Arg
                245                 250                 255
Tyr Met Asn Phe Asn Leu Met Glu Asn Phe Arg Leu
            260                 265
```

(2) INFORMATION FOR SEQ ID NO:1449:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 430 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449

```
Lys Met Pro Tyr Ala Leu Arg Lys Arg Phe Phe Lys Arg Leu Leu Leu
1               5                  10                  15
Phe Phe Leu Ile Val Cys Met Ile Asn Leu His Ala Lys Ser Tyr Leu
            20                  25                  30
Phe Ser Pro Leu Pro Pro Ala His Gln Gln Ile Ile Lys Thr Glu Pro
        35                  40                  45
Cys Ser Leu Glu Cys Leu Lys Asp Leu Met Leu Gln Asn Gln Ile Phe
    50                  55                  60
Ser Phe Val Ser Gln Tyr Asp Asp Asn Asn Gln Asp Glu Ser Leu Lys
65                  70                  75                  80
Thr Tyr Tyr Lys Asp Ile Leu Asn Lys Leu Asn Pro Val Phe Ile Ala
                85                  90                  95
Ser Gln Thr Pro Ala Lys Glu Ser Tyr Glu Pro Lys Ile Glu Leu Ala
            100                 105                 110
Ile Leu Leu Pro Lys Lys Val Val Gly Arg Tyr Ala Ile Leu Val Met
        115                 120                 125
Asn Thr Leu Leu Ala Tyr Leu Asn Thr Arg Asn Asn Asp Phe Asn Ile
    130                 135                 140
Gln Val Phe Asp Ser Asp Glu Glu Ser Pro Glu Lys Leu Glu Glu Thr
145                 150                 155                 160
Tyr Lys Glu Ile Glu Lys Glu Lys Phe Pro Phe Ile Ile Ala Leu Leu
                165                 170                 175
Thr Lys Glu Gly Val Glu Asn Leu Leu Gln Asn Thr Thr Ile Asn Thr
            180                 185                 190
Pro Thr Tyr Val Pro Thr Val Asn Lys Thr Gln Leu Glu Asn His Thr
        195                 200                 205
Glu Leu Ser Leu Ser Glu Arg Leu Tyr Phe Gly Gly Ile Asp Tyr Lys
    210                 215                 220
Glu Gln Leu Gly Met Leu Ala Thr Phe Ile Ser Pro Asn Ser Pro Val
225                 230                 235                 240
Ile Glu Tyr Asp Asp Asp Gly Leu Ile Gly Glu Arg Leu Arg Gln Ile
                245                 250                 255
Thr Glu Ser Leu Asn Val Glu Val Lys His Gln Glu Asn Ile Ser Tyr
            260                 265                 270
Lys Gln Ala Thr Ser Phe Ser Lys Asn Phe Arg Lys His Asp Ala Phe
        275                 280                 285
Phe Lys Asn Ser Thr Leu Ile Leu Asn Thr Pro Thr Thr Lys Ser Gly
    290                 295                 300
Leu Ile Leu Ser Gln Ile Gly Leu Leu Glu Tyr Lys Pro Leu Lys Ile
305                 310                 315                 320
Leu Ser Thr Gln Ile Asn Phe Asn Pro Ser Leu Leu Leu Leu Thr Gln
                325                 330                 335
Pro Lys Asp Arg Lys Asn Leu Phe Ile Val Asn Ala Leu Gln Asn Ser
            340                 345                 350
Asp Glu Thr Leu Ile Glu Tyr Ala Ser Leu Leu Glu Ser Asp Leu Arg
        355                 360                 365
```

```
His Asp Trp Val Asn Tyr Ser Ser Ala Ile Gly Leu Glu Met Phe Leu
    370                 375                 380
Asn Thr Leu Asp Pro His Phe Lys Lys Ser Phe Gln Glu Ser Leu Glu
385                 390                 395                 400
Asp Asn Gln Val Arg Tyr His Asn Gln Ile Tyr Gln Ala Leu Gly Tyr
                405                 410                 415
Ser Phe Glu Pro Ile Lys Asn Glu Ser Glu Thr Lys Lys Glu
            420                 425                 430
```

(2) INFORMATION FOR SEQ ID NO:1450:

This Sheet Has Been Replaced



(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

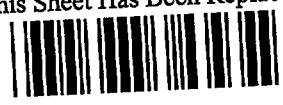
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450

```
Tyr Leu Asp Asn Tyr Leu Asn Thr Phe Ile Phe Asn Gly Phe Leu Arg
1               5                  10                  15
Lys Ile Asp Tyr Tyr Ala Ser Gly Lys Leu Lys Arg Ile Gly Ala Val
            20                  25                  30
Leu Lys Phe Gln Lys Leu Pro Leu Leu Phe Val Ser Ile Leu Tyr Asn
        35                  40                  45
Gln Ser Pro Leu Leu Ala Phe Asp Tyr Lys Phe Ser Gly Val Ala Glu
    50                  55                  60
Ser Val Ser Lys Val Gly Phe Asn His Ser Lys Leu Asn Ser Lys Glu
65                  70                  75                  80
Gly Ile Phe Pro Thr Ala Thr Phe Val Thr Ala Thr Ile Lys Leu Gln
                85                  90                  95
Val Asp Ser Asn Leu Leu Pro Lys Asn Ile Glu Lys His Ser Leu Lys
            100                 105                 110
Ile Gly Val Gly Gly Ile Leu Gly Ala Leu Ala Tyr Asp Ser Thr Lys
        115                 120                 125
Thr Leu Ile Asp Gln Ala Thr His Gln Ile Tyr Gly Ser Glu Leu Phe
    130                 135                 140
Tyr Leu Ile Gly Arg Trp Trp Gly Phe Leu Gly Asn Ala Pro Trp Lys
145                 150                 155                 160
Asp Ser Leu Ile Glu Ser Asp Ala His Thr Arg Asn Tyr Val Leu Tyr
                165                 170                 175
Asn Ser Tyr Leu Phe Tyr Ser Tyr Gly Asp Lys Phe His Leu Lys Leu
            180                 185                 190
Gly Arg Tyr Leu Ser Asn Met Asp Phe Met Ser Ser Tyr Thr Gln Gly
        195                 200                 205
Phe Glu Leu Asp Tyr Lys Ile Asn Ser Lys Ile Ala Leu Lys Trp Phe
    210                 215                 220
Ser Ser Phe Gly Arg Ala Leu Ala Phe Gly Gln Trp Ile Arg Asp Trp
225                 230                 235                 240
Tyr Ala Pro Ile Val Thr Glu Asp Gly Arg Lys Glu Val Tyr Asp Gly
                245                 250                 255
Ile His Ala Ala Gln Leu Tyr Phe Ser Ser Lys His Val Gln Val Met
            260                 265                 270
Pro Phe Ala Tyr Phe Ser Pro Lys Ile Tyr Gly Ala Pro Gly Val Lys
```

```
        275                 280                 285
Ile His Ile Asp Ser Asn Pro Lys Phe Lys Gly Leu Gly Leu Arg Ala
    290                 295                 300
Gln Thr Thr Ile Asn Val Ile Phe Pro Val Tyr Ala Lys Asp Leu Tyr
305                 310                 315                 320
Asp Val Tyr Trp Arg Asn Ser Lys Ile Gly Glu Trp Gly Ala Ser Leu
                325                 330                 335
Leu Ile His Gln Arg Phe Asp Tyr Asn Glu Phe Asn Phe Gly Phe Gly
            340                 345                 350
Tyr Tyr Gln Asn Phe Gly Asn Ala Asn Ala Arg Ile Gly Trp Tyr Gly
        355                 360                 365
Asn Pro Ile Pro Phe Asn Tyr Arg Asn Asn Ser Val Tyr Gly Gly Val
    370                 375                 380
Phe Ser Asn Ala Ile Thr Ala Asp Ala Val Ser Gly Tyr Val Phe Gly
385                 390                 395                 400
Gly Gly Val Tyr Arg Gly Phe Leu Trp Gly Ile Leu Gly Arg Tyr Thr
                405                 410                 415
Tyr Ala Thr Arg Ala Ser Glu Arg Ser Ile Asn Leu Asn Leu Gly Tyr
            420                 425                 430
Lys Trp Gly Ser Phe Ala Arg Val Asp Val Asn Leu Glu Tyr Tyr Val
        435                 440                 445
Val Ser Met His Asn Gly Tyr Arg Leu Asp Tyr Leu Thr Gly Pro Phe
    450                 455                 460
Asn Lys Ala Phe Lys Ala Asp Ala Gln Asp Arg Ser Asn Leu Met Val
465                 470                 475                 480
Ser Met Lys Phe Phe Phe
                485
```

(2) INFORMATION FOR SEQ ID NO:1451:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451

```
Val Tyr Ala Gly Leu Ala Ile Ala Ile Gly Met Leu Ile Asp Ser Ser
1               5                   10                  15
Val Val Val Val Glu Asn Ala Phe Glu Lys Leu Ser Ala Asn Thr Lys
            20                  25                  30
Thr Thr Lys Leu His Ala Ile Tyr Arg Ser Cys Lys Glu Ile Ala Val
        35                  40                  45
Ser Val Val Ser Gly Val Val Ile Ile Ile Val Phe Phe Val Pro Ile
    50                  55                  60
Leu Thr Leu Gln Gly Leu Glu Gly Lys Met Phe Arg Pro Leu Ala Gln
65                  70                  75                  80
Ser Ile Val Tyr Ala Leu Leu Gly Thr Leu Val Leu Ser Ile Thr Ile
                85                  90                  95
Ile Pro Val Val Ser Ser Leu Val Leu Lys Ala Thr Pro His Ser Glu
            100                 105                 110
Thr Phe Leu Thr Arg Phe Leu Asn Arg Ile Tyr Ala Pro Leu Leu Glu
        115                 120                 125
```

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

(2) INFORMATION FOR SEQ ID NO:1452:

This Sheet Has Been Replaced



(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:1452

```
Trp Leu Phe Leu Thr Cys Tyr Gly Ser Val Ile Lys Lys Gly Tyr Ile
1                   5                   10                  15
Arg Gly Asp Leu Met Arg Ile Val Arg Asn Leu Phe Leu Val Ser Phe
            20                  25                  30
Val Ala Tyr Ser Ser Ala Phe Ala Ala Asp Leu Glu Thr Gly Thr Lys
        35                  40                  45
Asn Asp Lys Lys Ser Gly Lys Lys Phe Tyr Lys Leu His Lys Asn His
    50                  55                  60
Gly Ser Glu Thr Glu Thr Lys Asn Asp Lys Lys Leu Tyr Asp Phe Thr
65                  70                  75                  80
Lys Asn Ser Gly Leu Glu Gly Val Asp Leu Glu Lys Ser Pro Asn Leu
                85                  90                  95
Lys Ser His Lys Lys Ser Asp Lys Lys Phe Tyr Lys Gln Leu Ala Lys
            100                 105                 110
Asn Asn Ile Ala Glu Gly Val Ser Met Pro Ile Val Asn Phe Asn Lys
        115                 120                 125
Ala Leu Ser Phe Gly Pro Tyr Phe Glu Arg Thr Lys Ser Lys Lys Thr
    130                 135                 140
Gln Tyr Met Asp Gly Gly Leu Met Met His Ile Arg Phe
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:1453:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 amino acids
(B) TYPE: amino acid

This Sheet Has Been Replaced



(D) TOPOLOGY: linear

(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:1453

```
Pro Lys Ile Ala Pro Leu Ala Met Ala Leu Asn Pro Lys Thr Phe Gln
1               5                  10                  15
Pro Leu Trp Ile Ala Leu Val Arg Ala Thr Leu Leu Gly Trp Gly His
            20                  25                  30
Arg Asn Leu Ser His Val Ala Gly Val Leu Asn Ala Ser Phe Leu Ala
        35                  40                  45
His Phe Ile Lys Asp Pro Val Lys Thr Ala Lys Leu Ser His Lys Phe
    50                  55                  60
Asn Asp Glu Arg Pro Tyr Pro Met Pro Ala Phe Ser Gln Phe Ser Asp
65                  70                  75                  80
Gln Asp Leu Ser Asp Ile Val Ala Tyr Leu Thr Ser Ile Leu Pro Lys
                85                  90                  95
Asn Leu Ser Asp Lys Glu Val Phe Ala Gln Ser Cys Gln Arg Cys His
            100                 105                 110
Ser Leu Asp Tyr Ala Lys Asp Lys Ala Phe Ser Asp Pro Lys Asp Leu
        115                 120                 125
Ala Asn Tyr Leu Gly Ser His Ala Pro Asp Leu Ser Met Met Ile Arg
    130                 135                 140
Ala Lys Gly Glu His Gly Leu Asn Val Phe Ile Asn Asp Pro Gln Lys
145                 150                 155                 160
Leu Leu Pro Gly Thr Ala Met Pro Arg Val Gly Leu Asn Glu Lys Ala
                165                 170                 175
Gln Lys Gln Val Ile Ser Tyr Leu Glu Lys Ala Gly Asp Arg Lys Lys
            180                 185                 190
His Glu Arg Asn Thr Leu Gly Ile Lys Ile Met Ile Phe Phe Ala Val
        195                 200                 205
Leu Ser Phe Leu Ala Tyr Asp Trp Lys Arg Lys Val Trp Ser Glu Val
    210                 215                 220
His
225
```

(2) INFORMATION FOR SEQ ID NO:1454:

(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:1454

```
Thr Trp Arg Tyr Gln Leu Gly Ser Leu Lys Gly Lys Ile Gln Met Ile
1               5                  10                  15
Lys Ser Val Glu Ile Glu Asn Tyr Lys Asn Phe Glu His Leu Lys Met
            20                  25                  30
Glu Asn Phe Lys Leu Ile Asn Phe Phe Thr Gly Gln Asn Asp Ala Gly
        35                  40                  45
Lys Thr Asn Leu Leu Glu Ala Leu Tyr Thr Asn Thr Gly Leu Cys Asp
    50                  55                  60
Pro Thr Ala Asn Gln Val Ser Leu Pro Pro Glu His Ala Val Asn Ile
65                  70                  75                  80
Ser Glu Phe Arg Lys Ile Lys Leu Asp Ala Asp Asn Leu Lys Thr Phe
                85                  90                  95
Phe Tyr Gln Gly Asn Thr Ala Asn Pro Ile Ser Ile Arg Thr Glu Phe
            100                 105                 110
Glu His Ala Thr Ile Pro Leu Thr Ile Gln Tyr Pro Thr Gln Thr Ser
        115                 120                 125
Tyr Ser Lys Asp Ile Asn Leu Asn Ser Asp Asp Ala His Met Thr Asn
    130                 135                 140
Leu Ile Asn Thr Thr Ile Thr Lys Pro Gln Leu Gln Phe Ser Tyr Asn
145                 150                 155                 160
Pro Ser Leu Ser Pro Met Thr Met Thr Tyr Glu Phe Glu Arg Gln Asn
                165                 170                 175
Leu Gly Leu Ile His Ser Asn Leu Asp Lys Ile Ala Gln Thr Tyr Lys
            180                 185                 190
Glu Asn Ala Met Phe Ile Pro Ile Glu Leu Ser Ile Val Asn Ser Leu
        195                 200                 205
Lys Ala Leu Glu Asn Leu Gln Leu Ala Ser Lys Glu Lys Glu Leu Ile
    210                 215                 220
Glu Ile Leu Gln Cys Phe Asn Pro Asn Ile Leu Asn Ala Asn Thr Ile
225                 230                 235                 240
Arg Lys Ser Val Tyr Ile Gln Ile Lys Asp Glu Asn Thr Pro Leu Glu
                245                 250                 255
Glu Ser Pro Lys Arg Leu Leu Asn Leu Phe Gly Trp Gly Phe Ile Lys
            260                 265                 270
Phe Phe Ile Met Val Ser Ile Leu Ile Asp Asn Arg Val Lys Tyr Leu
        275                 280                 285
Phe Ile Asp Glu Ile Glu Ser Gly Leu His His Thr Lys Met Gln Glu
    290                 295                 300
Phe Leu Lys Ala Leu Phe Lys Leu Ala Gln Lys Leu Gln Ile Gln Ile
305                 310                 315                 320
Phe Ala Thr Thr His Asn Lys Glu Phe Leu Leu Asn Ala Ile Asn Thr
                325                 330                 335
Ile Ser Asp Asn Glu Thr Gly Val Phe Lys Asp Ile Ala Leu Phe Glu
            340                 345                 350
Leu Glu Lys Glu Ser Ala Ser Gly Phe Ile Arg His Ser Tyr Ser Met
        355                 360                 365
Leu Glu Lys Ala Leu Tyr Arg Gly Met Glu Val Arg Gly
    370                 375                 380
```

(2) INFORMATION FOR SEQ ID NO:1455:

This Sheet Has Been Replaced



(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:1455

```
Thr His Cys Leu Phe Leu Gly Gly Ser Ile Lys Ile Leu Leu Ile Leu
1               5                  10                  15
Lys Glu Gly Ile Asp Leu Asn His Gly Tyr Tyr Gln Leu Gly Lys Tyr
            20                  25                  30
Thr Ile Lys Asp Asp Phe Ile Pro Ser Lys Lys Ala Val Val Glu Asp
        35                  40                  45
Val Leu Ile Gln Ser Ser Asn Val Gly Met Ile Lys Ile Ser Lys Ser
    50                  55                  60
Leu Asn Pro Glu Asp Phe Tyr Asn Gly Leu Leu Gly Tyr Gly Phe Ser
65                  70                  75                  80
Gln Lys Thr Gly Ile Asp Leu Ser Leu Glu Ala Thr Gly Lys Ile Pro
                85                  90                  95
Pro Leu Ser Ala Phe Lys Arg Glu Val Leu Lys Gly Ser Val Ser Tyr
            100                 105                 110
Gly Tyr Gly Leu Asn Ala Thr Phe Leu Gln Leu Leu Arg Ala Tyr Ala
        115                 120                 125
Val Phe Ser Asn Glu Gly Lys Leu Thr Thr Pro Tyr Leu Val Gln Arg
    130                 135                 140
Glu Thr Ala Pro Asn Gly Asp Ile Tyr Ile Pro Ser Pro Lys Pro Thr
145                 150                 155                 160
Phe Gln Val Ile Ser Pro Lys Ser Ala Arg Lys Met Lys Glu Thr Leu
                165                 170                 175
Ile Lys Val Val Arg Tyr Gly Thr Gly Lys Asn Ala Gln Phe Glu Gly
            180                 185                 190
Leu Tyr Ile Gly Gly Lys Thr Gly Thr Ala Arg Val Ala Lys Asn Gly
        195                 200                 205
Ser Tyr Ser Ala Glu Ser Tyr Asn Ser Ser Phe Phe Gly Phe Ala Glu
    210                 215                 220
Asp Glu Arg Gln Val Phe Thr Ile Gly Val Val Ile Leu Gly Ser His
225                 230                 235                 240
Gly Lys Glu Glu Tyr Tyr Ala Ser Lys Ile Ala Ala Pro Ile Phe Lys
                245                 250                 255
Glu Ile Thr Glu Ile Leu Val Arg Tyr Asn Tyr Leu Ser Pro Ser Ile
            260                 265                 270
Ala Ile Gln Asn Ala Leu Glu Lys Asn Arg Leu Lys
        275                 280
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1456:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456

```
Asp Lys Lys Ile Leu Leu Ile Ile Gln Gly Lys Phe Met Glu Phe His
1               5                  10                  15
Gln Val Tyr Asp Pro Leu Gly His Ile Trp Leu Ser Ala Leu Val Ala
            20                  25                  30
Leu Ser Pro Ile Ala Leu Phe Phe Ile Ser Leu Ile Val Phe Lys Leu
        35                  40                  45
Lys Gly Tyr Ser Ala Gly Phe Leu Ser Leu Ala Leu Ser Ile Leu Ile
    50                  55                  60
Ala Leu Phe Val Tyr Lys Met Pro Val Gln Met Val Ser Ala Ser Phe
65                  70                  75                  80
Phe Tyr Gly Phe Leu Tyr Gly Leu Trp Pro Ile Ala Trp Ile Val Ile
                85                  90                  95
Ala Ala Ile Phe Leu Tyr Asn Leu Ser Val Lys Ser Gly Tyr Phe Glu
            100                 105                 110
Ile Leu Lys Glu Ser Val Gln Ser Ile Thr Leu Asp His Arg Ile Leu
        115                 120                 125
Val Ile Leu Ile Gly Phe Cys Leu Ala His Phe
    130                 135
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1457:

(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:1457

```
Pro Lys Pro Lys Gly Val Cys Pro Lys Asn Leu Met Ser Lys Arg Ala
1               5                  10                  15
Ile Arg Phe Pro Asn Lys Leu Phe Ser Tyr Pro Lys Pro Lys Ile Lys
            20                  25                  30
Ala Thr Asn Thr Ser His Thr Val Leu Phe Ala Tyr Pro Leu Lys Pro
        35                  40                  45
His Glu Met Ala Leu Leu Ala Leu Ala Thr Ser Leu Leu Ala Pro Ile
    50                  55                  60
Phe Asn Ala Ile His Ser Thr Asn Ala Leu Asn Ala Ile Lys Pro Asp
65                  70                  75                  80
Gly Thr Gly Ser Lys Ile Asn Pro Ile Ile Met Pro Met Lys Ile Gln
                85                  90                  95
Lys
```

(2) INFORMATION FOR SEQ ID NO:1458:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 532 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458

```
Arg Asn Asp Phe Lys Gly Val Arg Lys Met Ala Leu Arg Val Leu Leu
1               5                  10                  15
Phe Phe Cys Phe Leu Phe Leu Gln Ala Glu Asp Lys Ser Gln Glu Leu
            20                  25                  30
Ser Ser Ile Gln Lys Gln Met Ala Leu Val Asp Lys Lys Leu Ala Lys
        35                  40                  45
Asp Asp Asn Val Trp Leu Lys Lys Phe Glu Asn Tyr Lys Ile Tyr Asn
    50                  55                  60
Gln Ile Tyr Thr Glu Lys Glu Ser Val Arg Gln Glu Leu Arg Arg Leu
65                  70                  75                  80
Lys Asn Lys Lys Ser Lys Asp Leu Leu Lys Ile Ser Thr Leu Glu His
                85                  90                  95
Thr Leu Lys Ala Leu Glu Ser Gln Gln Lys Met Phe Glu Ser Tyr Gly
            100                 105                 110
Val Asn Pro Phe Lys Asp Leu Ile Glu Arg Pro Asn Ile Pro Asn Ile
        115                 120                 125
Pro Asn Ile Ala Asn Pro Ile Ala Ile Ile Asp Gly Ile Ser Phe Ile
    130                 135                 140
Lys Ser Met Arg Leu Lys His Glu Asn Leu Lys Asn Asn Gln Thr Ser
145                 150                 155                 160
Leu Gly Glu Val Leu Lys Leu Leu Asp Gln Lys His Gln Leu Leu Asn
                165                 170                 175
Gln Trp His Ala Leu Asp Lys Ser Ala Lys Leu Ser Asp Glu Ile Tyr
            180                 185                 190
Gln Thr Gln Ala Lys Arg Leu Glu Leu Gln Gly Ala Gln Asn Ile Leu
        195                 200                 205
Lys Thr Thr Ile Gly Ile Phe Gln Lys Asp Ser Asp Glu Ala Ile Ser
    210                 215                 220
Ile Val Lys Ser Gln Val Lys Asn Gln Leu Phe Lys Leu Val Tyr Val
225                 230                 235                 240
Phe Leu Ala Ala Leu Leu Ser Val Val Phe Ala Trp Ile Leu Lys Ile
                245                 250                 255
Ile Ser Ser Lys Tyr Ile Glu Asn Asn Glu Arg Val Tyr Thr Val Asn
            260                 265                 270
Lys Ala Ile Asn Phe Val Asn Val Ser Val Ile Val Leu Ile Phe Leu
        275                 280                 285
Phe Ser Tyr Leu Glu Asn Val Thr Tyr Leu Val Thr Val Leu Gly Phe
    290                 295                 300
Ala Ser Ala Gly Leu Ala Ile Ala Met Lys Asp Leu Phe Met Ser Leu
305                 310                 315                 320
Leu Gly Trp Phe Ile Ile Leu Ile Gly Gly Ser Val His Val Gly Asp
                325                 330                 335
Arg Val Arg Ile Ala Lys Gly Thr Asp Ile Phe Ile Gly Asp Val Leu
            340                 345                 350
Asp Ile Ser Met Leu His Ile Thr Ile Leu Glu Asp Val Thr Phe Thr
        355                 360                 365
Thr Tyr Thr Asn Asn Arg Arg Ala Gly Arg Ile Ile Phe Val Pro Asn
    370                 375                 380
Asn Tyr Ile Phe Thr Thr Met Phe Ala Asn Tyr Ser His Phe Gly Met
385                 390                 395                 400
Lys Thr Val Trp Asp Gly Val Asp Phe Cys Val Thr Phe Asp Ser Asp
                405                 410                 415
Phe Lys Lys Ala Ser Lys Ile Ala Leu Asn Ile Ala Thr Glu Leu Ser
            420                 425                 430
```

```
Lys Glu Tyr Thr Asp Ile Thr Tyr Lys Gln Leu Asn Lys Met Arg Asp
        435                 440                 445
Arg Tyr Ser Leu Arg Ser Leu Ser Val Lys Pro Arg Cys Phe Leu Met
    450                 455                 460
Pro Glu Asn Asn Gly Ile Lys Ile Ser Val Trp Tyr Gln Thr Asn Ser
465                 470                 475                 480
Tyr Ala Thr Met Ser Leu Arg Ser Lys Ile Val Ala Glu Ile Val Glu
                485                 490                 495
Ala Phe Leu Lys Glu Glu Asn Ile His Ile Ala Tyr Thr Thr Ser Lys
            500                 505                 510
Leu Leu Lys Val Asp Ala Asp Ala Leu Gly Asp Gly Phe Gly Asn Lys
        515                 520                 525
Arg Glu Gln Lys
    530
```

(2) INFORMATION FOR SEQ ID NO:1459:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459

```
Arg Ser Glu Arg Met Gln Glu Ile Leu Ile Pro Leu Lys Glu Lys Ser
1                   5                  10                  15
Tyr Lys Val Phe Leu Gly Glu Leu Pro Glu Ile Lys Leu Lys Gln Lys
            20                  25                  30
Ala Leu Ile Ile Ser Asp Ser Ile Val Ala Gly Leu His Leu Pro Tyr
        35                  40                  45
Leu Leu Glu Arg Leu Asn Ala Leu Glu Val Arg Val Cys Val Ile Glu
    50                  55                  60
Ser Gly Glu Lys Tyr Lys Asn Phe His Ser Leu Glu Arg Ile Leu Asn
65                  70                  75                  80
Asn Ala Phe Glu Met Gln Leu Asn Arg His Ser Leu Met Ile Ala Leu
                85                  90                  95
Gly Gly Gly Val Ile Ser Asp Met Val Gly Phe Ala Ser Ser Ile Tyr
            100                 105                 110
Phe Arg Gly Ile Asp Phe Ile Asn Ile Pro Thr Thr Leu Leu Ala Gln
        115                 120                 125
Val Asp Ala Ser Val Gly Gly Lys Thr Gly Ile Asn Thr Pro Tyr Gly
    130                 135                 140
Lys Asn Leu Ile Gly Ser Phe His Gln Pro Lys Ala Val Tyr Met Asp
145                 150                 155                 160
Leu Ala Phe Leu Lys Thr Leu Glu Lys Arg Glu Phe Gln Ala Gly Val
                165                 170                 175
Ala Glu Ile Ile Lys Met Ala Val Cys Phe Asp Lys Asn Leu Val Glu
            180                 185                 190
Arg Leu Glu Thr Lys Asp Leu Lys Asp Cys Leu Glu Glu Val Ile Phe
        195                 200                 205
Gln Ser Val Asn Ile Lys Ala Gln Val Val Val Gln Asp Glu Lys Glu
    210                 215                 220
Arg Asn Ile Arg Ala Gly Leu Asn Tyr Gly His Thr Phe Gly Met Leu
```

```
225                 230                 235                 240
Ile Glu Asn Glu Thr Asn Tyr Glu Arg Phe Leu His Gly Glu Ala Ile
                245                 250                 255
Ala Ile Gly Met Arg Met Ala Asn Asp Leu Ala Leu Ser Leu Gly Met
            260                 265                 270
Leu Thr Leu Lys Glu Tyr Glu Arg Ile Glu Asn Leu Leu Lys Lys Phe
        275                 280                 285
Asp Leu Ile Phe Asn Tyr Gln Ile Thr Asp Ile Gln Lys Phe Tyr Glu
    290                 295                 300
Arg Leu Phe Leu Asp Lys Lys Ser Glu Asn Gln Thr Leu Lys Phe Ile
305                 310                 315                 320
Leu Pro Lys Gly Val Gly Ala Phe Glu Ile Ala Ser His Ile Pro Lys
                325                 330                 335
Glu Thr Ile Leu Lys Val Leu Glu Lys Trp His
            340                 345
```

(2) INFORMATION FOR SEQ ID NO:1460:

This Sheet Has Been Replaced



(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:1460

```
Lys Ser Lys Ser Met Lys Leu Arg Arg Gly Lys Ile Met Pro Phe Ser
1                   5                  10                  15
Lys Phe Leu Glu Asn Leu Thr Ala Pro Phe Lys Arg Ile Lys Asn Arg
            20                  25                  30
Ser Leu Val Leu Ala Leu Gly Phe Leu Ile Leu Thr Phe Cys Leu Leu
        35                  40                  45
Leu Phe Leu Ile Leu Ser Asp Val Ser Arg Leu Ile Ser Ser Lys Asp
    50                  55                  60
Phe Leu Tyr Val Ile Gln Ser His Pro Lys Gln Thr Leu Ile Glu Asp
65                  70                  75                  80
Glu Asn Tyr Phe Tyr Ala Asn Lys Gly Leu Tyr Lys Thr Asn Lys Glu
                85                  90                  95
Ala Phe Leu Arg Val Tyr Lys Ile Pro Glu Ser Met Pro Ile Glu Lys
            100                 105                 110
Arg Glu Ser Leu Ser Lys Val Ser Lys Ile Phe Leu Ala Leu Leu Phe
        115                 120                 125
Phe Ile Ser Ser Met Leu Phe Gly Ile Phe Trp Arg Leu Pro Lys Arg
    130                 135                 140
Leu Asp Thr Lys Met Ser Leu Glu Ser Ala His Lys Asn Glu Leu Glu
145                 150                 155                 160
Asn Ala Phe Gln Arg Tyr Asp Ala Leu Gly Val Arg Phe Glu Asp Ile
                165                 170                 175
Ala Gly Val Asn Glu Val Lys Glu Glu Leu Leu Glu Val Ile Asp Tyr
            180                 185                 190
Leu Lys Lys Pro
        195
```

This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:1461:

(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:1461

```
Met Lys Pro Leu His Phe Ser His Leu Asp Arg Glu Gln Ser Gly Asp
1               5                  10                  15
Val Gly Phe Ile Ile Lys Asn Leu Ile Phe Leu Gly Val Phe Ser Leu
            20                  25                  30
Leu Gly Trp Leu Asn Thr Glu Tyr Phe Leu Trp Pro Ser Met Leu Glu
        35                  40                  45
Leu Lys Lys Ile Leu Leu Glu Glu Asn Arg Lys Lys Ser Val Leu Glu
    50                  55                  60
Tyr Ala Gln Arg His Phe Glu Thr Ala Leu Ala Asn Tyr Arg Asn Gln
65                  70                  75                  80
Lys Glu Thr Ser Glu Ser Leu Leu Lys Ile Phe Asn Asp Glu Glu Ser
                85                  90                  95
Arg Arg Ile Leu Glu Lys Ile Leu Lys Lys Cys Phe Asp Ala Tyr Lys
            100                 105                 110
Ile Lys Pro Leu Leu Ser Gln Asn Pro Ser Gln Lys Thr Gln Phe Phe
        115                 120                 125
Ile Met Ala Arg Ala Ser Glu Leu Glu Lys Thr Tyr Leu Phe Phe Thr
    130                 135                 140
Leu Ile Asn Lys Tyr Leu Pro Ser Ala Gln Ser Gln Leu Pro Leu Lys
145                 150                 155                 160
Ile Ser Lys Asp Ser Asp Gly Leu Leu Val Gln Phe Gly Val Ser Ile
                165                 170                 175
Asp Leu Gln
```

(2) INFORMATION FOR SEQ ID NO:1462:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 452 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462

```
Phe Lys Arg Tyr Phe Ile Thr Met Lys Ile Phe Gly Thr Asp Gly Val
1               5                  10                  15
Arg Gly Lys Ala Gly Val Lys Leu Thr Pro Met Phe Val Met Arg Leu
            20                  25                  30
Gly Ile Ala Ala Gly Leu Tyr Phe Lys Lys His Ser Gln Thr Asn Lys
        35                  40                  45
Ile Leu Ile Gly Lys Asp Thr Arg Lys Ser Gly Tyr Met Val Glu Asn
    50                  55                  60
Ala Leu Val Ser Ala Leu Thr Ser Ile Gly Tyr Asn Val Ile Gln Ile
65                  70                  75                  80
Gly Pro Met Pro Thr Pro Ala Ile Ala Phe Leu Thr Glu Asp Met Arg
                85                  90                  95
Cys Asp Ala Gly Ile Met Ile Ser Ala Ser His Asn Pro Phe Glu Asp
            100                 105                 110
Asn Gly Ile Lys Phe Phe Asn Ser Tyr Gly Tyr Lys Leu Lys Glu Glu
        115                 120                 125
Glu Glu Arg Ala Ile Glu Glu Ile Phe His Asp Glu Glu Leu Leu His
    130                 135                 140
Ser Ser Tyr Lys Val Gly Glu Ser Val Gly Ser Ala Lys Arg Ile Asp
145                 150                 155                 160
Asp Val Ile Gly Arg Tyr Ile Ala His Leu Lys His Ser Phe Pro Lys
                165                 170                 175
His Leu Asn Leu Gln Lys Leu Arg Ile Val Leu Asp Thr Ala Asn Gly
            180                 185                 190
Ala Ala Tyr Lys Val Ala Pro Val Val Phe Ser Glu Leu Gly Ala Asp
        195                 200                 205
Val Leu Val Ile Asn Asp Glu Pro Asn Gly Cys Asn Ile Asn Glu Gln
    210                 215                 220
Cys Gly Ala Leu His Pro Asn Gln Leu Ser Gln Glu Val Lys Lys Tyr
225                 230                 235                 240
Arg Ala Asp Ile Gly Phe Ala Phe Asp Gly Asp Ala Asp Arg Leu Val
                245                 250                 255
Val Ala Asp Asn Leu Gly Asn Ile Val His Gly Asp Lys Leu Leu Gly
            260                 265                 270
Val Leu Gly Val Tyr Gln Lys Ser Lys Asn Ala Leu Ser Ser Gln Ala
        275                 280                 285
Val Val Ala Thr Ser Met Ser Asn Leu Ala Leu Lys Glu Tyr Leu Lys
    290                 295                 300
Ser Gln Asp Leu Glu Leu Lys His Cys Ala Ile Gly Asp Lys Phe Val
305                 310                 315                 320
Ser Glu Cys Met Arg Leu Asn Lys Ala Asn Phe Gly Gly Glu Gln Ser
                325                 330                 335
Gly His Ile Ile Phe Ser Asp Tyr Ala Lys Thr Gly Asp Gly Leu Val
            340                 345                 350
Cys Ala Leu Gln Val Ser Ala Leu Val Leu Glu Ser Lys Leu Val Ser
        355                 360                 365
Ser Ile Ala Leu Asn Pro Phe Glu Leu Tyr Pro Gln Ser Leu Val Asn
    370                 375                 380
Leu Asn Ile Gln Lys Lys Pro Pro Leu Glu Ser Leu Lys Gly Tyr Ser
385                 390                 395                 400
Ala Leu Leu Lys Glu Leu Asp Gln Leu Glu Ile Arg His Leu Ile Arg
                405                 410                 415
Tyr Ser Gly Thr Glu Asn Lys Leu Arg Ile Leu Leu Glu Ala Lys Asp
            420                 425                 430
Glu Lys Leu Leu Glu Ser Lys Met Gln Glu Leu Lys Glu Phe Phe Glu
        435                 440                 445
Gly Gln Leu Cys
    450
```

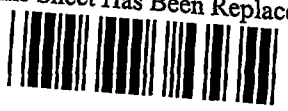
(2) INFORMATION FOR SEQ ID NO:1463:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(B) TYPE: amino acid
(D) TOPOLOGY: linear

(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:1463

```
Asn His Gln Arg Ile Arg Ser Arg Gln Gln Phe Arg Lys Pro Phe Asp
1               5                  10                  15
Pro Phe Arg Arg Ala Ser Glu Leu Lys Val Arg Ser Cys Lys Gln Ile
            20                  25                  30
Phe Asp Lys Gly Leu Lys Pro Tyr Tyr Lys His Ser Val Cys Leu Lys
        35                  40                  45
Pro Phe Phe Arg Phe Cys Phe Leu Lys Ile His Ala Tyr Gln Gln Arg
    50                  55                  60
Tyr Arg Ala Phe Ala Leu Thr Leu Phe Ser Cys Lys Phe Phe Asn Ala
65                  70                  75                  80
Cys Lys Ile Phe Ile Pro Ile Ile Asp Phe Lys Ile Val Phe Ile Pro
                85                  90                  95
Ile Leu Lys His Gln Ala Lys Leu Lys Arg Val Ser Asn Ala Tyr
            100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:1464:

(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:1464

```
Lys Arg Met Lys Glu Ser Phe Tyr Ile Glu Gly Met Thr Cys Thr Ala
1               5                  10                  15
Cys Ser Ser Gly Ile Glu Arg Ser Leu Gly Arg Lys Ser Phe Val Lys
            20                  25                  30
Lys Ile Glu Val Ser Leu Leu Asn Lys Ser Ala Asn Ile Glu Phe Asn
        35                  40                  45
Glu Asn Glu Thr Asn Leu Asp Glu Ile Phe Lys Leu Ile Glu Lys Leu
    50                  55                  60
Gly Tyr Ser Pro Lys Lys Thr Leu Ala Glu Glu Lys Lys Glu Phe Phe
65                  70                  75                  80
Ser Pro Asn Val Lys Leu Ala Leu Ala Val Ile Phe Thr Leu Phe Val
                85                  90                  95
Val Tyr Leu Ser Met Gly Ala Met Leu Ser Pro Ser Leu Leu Pro Glu
```

```
          100                 105                 110
Ser Leu Leu Thr Ile Asn His His Ser Asn Phe Leu Asn Ala Cys Leu
        115                 120                 125
Gln Leu Ile Gly Ala Leu Ile Val Met His Leu Gly Arg Asp Phe Tyr
    130                 135                 140
Ile Gln Gly Phe Lys Ala Leu Trp His Arg Gln Pro Asn Met Ser Ser
145                 150                 155                 160
Leu Ile Ala Ile Gly Thr Ser Ala Ala Leu Ile Ser Ala Cys Gly Asn
                165                 170                 175
Cys Ile Trp Phe Ile Pro Ile Ile Ile Pro Ile Ser Gly Leu Met Gly
            180                 185                 190
Ile Ile Ile Leu Lys Ala Cys Ala
        195                 200
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1465:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

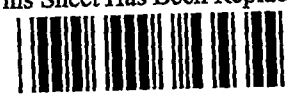
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465

```
Lys Glu Ser Leu Met Pro Ile Asn Pro Leu Tyr Leu Phe Pro Asn Leu
1               5                  10                  15
Phe Thr Ala Ser Ser Ile Phe Leu Gly Met Met Ser Ile Phe Tyr Ala
            20                  25                  30
Ser Ser Tyr Gln Phe Val Met Ala Cys Trp Leu Val Val Ala Ser Leu
        35                  40                  45
Ile Leu Asp Gly Leu Asp Gly Arg Val Ala Arg Leu Thr Asn Thr Thr
    50                  55                  60
Ser Lys Phe Gly Ile Glu Phe Asp Ser Leu Ala Asp Val Val Ala Phe
65                  70                  75                  80
Gly Val Ala Pro Ser Leu Ile Thr Tyr Phe Tyr Val Gly Tyr Asn Phe
                85                  90                  95
Gly Arg Ile Gly Met Ala Val Ser Ala Leu Phe Val Ile Phe Gly Ala
            100                 105                 110
Ile Arg Leu Ala Arg Phe Asn Ile Ser Thr Asn Thr Ser Asp Pro Tyr
        115                 120                 125
Ser Phe Ile Gly Ile Pro Ile Pro Ala Ala Ala Val Leu Val Val Leu
    130                 135                 140
Cys Val Leu Leu Asp Asn Lys Tyr His Phe Leu Glu Gly Asn Thr Glu
145                 150                 155                 160
Lys Leu Phe Leu Gly Phe Ile Val Leu Leu Gly Val Leu Met Val Ser
                165                 170                 175
Asn Ile Arg Tyr Pro Asn Phe Lys Lys Val Lys Trp Asn Leu Lys Leu
            180                 185                 190
Phe Ile Leu Val Leu Ile Phe Leu Ser Leu Val Phe Val Arg Pro Leu
        195                 200                 205
Glu Ala Leu Ser Val Phe Met Gly Leu Tyr Leu Ile Tyr Gly Ile Ile
    210                 215                 220
Arg Trp Ile Phe Leu Met Val Lys Ile Thr Phe Asn Lys Asn Lys Ser
225                 230                 235                 240
```

Ala

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1466:

(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:1466

```
Tyr Leu Pro Ala Ser Glu Asn Ala Pro Leu Pro Ser Ser Val Phe Ser
1               5                  10                  15
Ser Ile Val Ala Leu Ser Leu Lys Ile Asp Ser Leu Phe Ser Leu Phe
            20                  25                  30
Ser Val Gly Lys Ile Pro Ser Gly Ser Lys Asp Pro Phe Ala Leu Arg
        35                  40                  45
Arg Leu Ser Phe Gly Leu Leu Lys Ile Ile Ala His Tyr Gly Leu Glu
    50                  55                  60
Phe Asp Leu Lys Ala Asp Leu Lys Asn Leu Phe Glu Lys Val Gly Val
65                  70                  75                  80
Tyr Gln Ser Phe Asp Leu Glu Val Leu Glu Lys Phe Leu Leu Glu Arg
                85                  90                  95
Phe His Asn Leu Ile Asp Cys Asn Leu Ser Ile Ile Arg Ser Val Leu
            100                 105                 110
Asn Thr Asn Glu Arg Asp Ile Val Lys Ile Ile Gln Lys Val Lys Ala
        115                 120                 125
Leu Lys Arg Phe Leu Asp Asn Pro Lys Asn Ala Gln Lys Lys Glu Leu
    130                 135                 140
Leu Phe Ser Ala Phe Lys Arg Leu Ala Asn Ile Asn Lys Asp Arg Asn
145                 150                 155                 160
Pro Asn Glu Ser Ser Gly Phe Ser Thr Ser Leu Phe Lys Glu Leu Gln
                165                 170                 175
Glu His Ala Leu Phe Glu Ala Phe Asn Ala Ile Lys Thr Ser Thr Phe
            180                 185                 190
Glu Ser Leu Asp Ser Lys Ile Glu Ala Tyr Phe Gly Leu His Ala Pro
        195                 200                 205
Leu Glu Glu Tyr Phe Lys Ser Val Leu Val Met Asp Lys Asp Ile Glu
    210                 215                 220
Ile Gln Lys Asn Arg Lys Asn Phe Leu Trp Gly Val Tyr Gln Ser Phe
225                 230                 235                 240
Leu Glu Ile Gly Asp Ile Lys Glu Ile Ala Ile
                245                 250
```

(2) INFORMATION FOR SEQ ID NO:1467:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 594 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467

```
Val Val Phe Lys Ile Leu Ser Leu Trp Leu Gly Val Phe Cys Phe Leu
1               5                  10                  15
Arg Ala Thr His Leu Tyr Leu Gly Glu Glu Pro Lys Tyr Lys Asp Asn
            20                  25                  30
Phe Thr His Phe Glu Tyr Ala Asn Pro Asn Ala Arg Lys Gly Gly Val
        35                  40                  45
Leu Arg Asn Asp Ala Ile Gly Thr Phe Asp Ser Leu Asn Pro Phe Ala
    50                  55                  60
Leu Lys Gly Thr Lys Ala Glu Gly Leu Asp Leu Ile Tyr Asp Thr Leu
65                  70                  75                  80
Met Val Gln Ser Leu Asp Glu Pro Phe Ala Glu Tyr Pro Leu Ile Ala
                85                  90                  95
Lys Asp Ala Glu Val Ala Lys Asp Asn Ser Tyr Val Ile Phe Thr Leu
            100                 105                 110
Asp Lys Arg Ala Arg Phe Ser Asn Asn Ala Pro Ile Leu Ala Ser Asp
        115                 120                 125
Val Lys Phe Ser Phe Asp Thr Ile Met Lys Leu Gly Ser Pro Leu Tyr
    130                 135                 140
Arg Gln Tyr Tyr Gln Asp Val Lys Lys Ala Val Ile Leu Asp Lys His
145                 150                 155                 160
His Val Lys Phe Ile Phe Lys Thr Thr Glu Asn Lys Glu Leu Pro Leu
                165                 170                 175
Ile Leu Gly Gln Leu Gln Ile Phe Ser Lys Lys Ala Phe Gln Lys Asp
            180                 185                 190
Tyr Phe Glu Lys Asn Pro Leu Leu Ile Pro Val Ser Ser Gly Pro Tyr
        195                 200                 205
Val Ile Ala Ser Phe Asp Val Gly Lys Lys Ile Thr Tyr Gln Arg Asn
    210                 215                 220
Pro Asn Tyr Trp Ala Lys Asn Leu Pro Ser Arg Lys Gly Gln Phe Asn
225                 230                 235                 240
Phe Asp Gln Ile Lys Phe Glu Tyr Tyr Lys Asp Glu Thr Val Ala Leu
                245                 250                 255
Gln Ala Phe Leu Ser Gly Ala Tyr Asp Trp Arg Leu Glu Ser Thr Ala
            260                 265                 270
Lys Val Trp Ala Arg Gly Tyr Val Gly Lys Ala Met Asp Asn Lys Lys
        275                 280                 285
Ile Thr Lys Tyr Leu Ile Ala His Lys Met Pro Ser Gly Met Gln Gly
    290                 295                 300
Phe Phe Phe Asn Thr Arg Arg Glu Ile Phe Lys Asp Lys Arg Val Arg
305                 310                 315                 320
Glu Ala Leu Phe Tyr Ala Phe Asp Phe Glu Trp Ala Asn Lys Asn Leu
                325                 330                 335
Phe Phe Ser Gln Tyr Lys Arg Thr Thr Ser Phe Phe Ser Asn Ser Ile
            340                 345                 350
Tyr Ala Ser Pro Pro Leu Pro Ser Pro Glu Glu Lys Ala Leu Leu Ala
        355                 360                 365
Pro Tyr Glu Lys Ser Leu Asp Glu Arg Val Phe Lys Glu Pro Tyr Ile
    370                 375                 380
Val Pro Arg Thr Asp Gly Pro Asp Val Leu Gly Tyr Asn Leu Arg Glu
385                 390                 395                 400
Asn Leu Lys Tyr Ala Gln Lys Leu Leu Glu Ser Ala Gly Phe Ser Tyr
                405                 410                 415
```

```
Lys Asn Met Arg Leu Val Asp Lys Asn Asn Lys Pro Phe Ser Phe Thr
            420                 425                 430
Leu Leu Leu Asn Ser Pro Ala Phe Glu Arg Leu Ala Leu Ala Phe Ala
        435                 440                 445
Lys Asn Leu Arg Val Leu Gly Ile Glu Met Lys Ile Gln Arg Val Asp
    450                 455                 460
Leu Ser Gln Tyr Val Asn Arg Ile Lys Ser Tyr Asp Phe Asp Met Ile
465                 470                 475                 480
Val Gly Val Ile Gly Gln Ser Ser Phe Pro Gly Asn Glu Gln Arg Phe
                485                 490                 495
Tyr Phe Gly Ser Leu Ser Ala Lys Ala Lys Gly Thr Arg Asn Tyr Ala
            500                 505                 510
Arg Ile Ser Ser Lys Ala Val Asp Asp Leu Ile Glu Arg Ile Ile His
        515                 520                 525
Ala Lys Asp Tyr Lys Glu Gln Leu Ala Ala Ile Gln Ala Met Asp Arg
    530                 535                 540
Val Leu Leu Arg Gly Phe Tyr Ala Ile Pro His Phe Tyr Leu Pro Asn
545                 550                 555                 560
Tyr Arg Ile Ala Ala Tyr Asn Tyr Ile Gly Met Pro Glu Ile Ser Pro
                565                 570                 575
Ser Tyr Gly Phe Ser Pro Tyr Leu Trp Trp Ile Lys Lys Glu Arg Gly
            580                 585                 590
Pro Lys
```

This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:1468:

(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

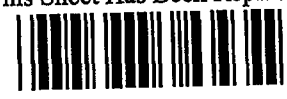
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468

```
Ser Val Ile Gly Val Tyr Ile Ile Ser Leu Lys Glu Ser Gln Arg Arg
1               5                   10                  15
Leu Asp Thr Glu Lys Leu Val Leu Glu Ser Asn Glu Lys Phe Lys Gly
            20                  25                  30
Arg Cys Val Phe Gln Ile Phe Asp Ala Ile Ser Pro Lys His Gln Asp
        35                  40                  45
Phe Glu Lys Leu Leu Gln Glu Leu Tyr Asn Ala Gln Ser Leu Leu Gln
    50                  55                  60
Ser Asp Trp Tyr His Ser Tyr Val Gly Ala Gly Leu Thr Leu Pro Glu
65                  70                  75                  80
Leu Gly Cys Tyr Leu Ser His Tyr Leu Leu Trp Lys Glu Cys Val Lys
                85                  90                  95
Leu Asp Gln Pro Val Val Ile Leu Glu Asp Asp Val Thr Leu Glu Ser
            100                 105                 110
His Phe Met Gln Ala Leu Glu Asp Cys Leu Lys Ser Pro Phe Asp Phe
        115                 120                 125
Val Arg Leu Tyr Gly Cys Tyr Trp Tyr Tyr His Glu Thr Lys Phe His
    130                 135                 140
Val Leu Pro Lys Glu Phe Val Phe Pro Pro Phe Asp His Ser Phe Lys
```

```
145                 150                 155                 160
Asn Asn Pro Ile Leu Glu Lys Phe Lys Lys Phe Phe Asp Val Ser Arg
                165                 170                 175
Phe Leu Asn Leu Ser Thr His Lys Val Ile His Leu Tyr Ser Gln Lys
            180                 185                 190
Asn Thr Lys Lys Leu Leu Arg Asn Ala
        195                 200
```

(2) INFORMATION FOR SEQ ID NO:1469:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 540 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...540

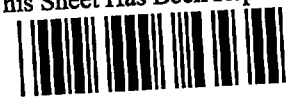
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469

```
Phe Ser Glu Arg Asp Phe Glu Leu Phe Arg Gln Lys Thr Asn Pro Tyr
1               5                  10                  15
Glu Arg Cys Ser Cys Gly Phe Gly Phe Leu Ser Asp Ala Ser Lys Arg
            20                  25                  30
Ser Leu Asn Pro Thr Leu Met Met Asn Asn Asn Asn Thr Leu Pro Lys
        35                  40                  45
Pro Leu Glu Glu Ser Leu Asp Leu Lys Glu Phe Ile Ala Leu Phe Lys
    50                  55                  60
Thr Phe Phe Ala Lys Glu Arg Gly Ser Ile Ala Leu Glu Asn Asp Leu
65                  70                  75                  80
Lys Gln Ala Phe Thr Tyr Leu Asn Glu Val Asp Ala Ile Gly Leu Pro
                85                  90                  95
Ala Pro Lys Ser Val Lys Glu Ser Asp Leu Ile Val Val Lys Leu Thr
            100                 105                 110
Lys Leu Gly Thr Leu His Leu Asp Glu Ile Tyr Glu Ile Val Lys Arg
        115                 120                 125
Leu Arg Tyr Ile Val Val Leu Gln Asn Ala Phe Lys Pro Phe Thr His
    130                 135                 140
Leu Lys Phe His Glu Arg Leu Asn Ala Ile Ile Leu Pro Pro Phe Phe
145                 150                 155                 160
Asn Asp Leu Ile Leu Leu Leu Asp Asp Glu Gly Gln Ile Lys Gln Gly
                165                 170                 175
Ala Asn Ala Thr Leu Asp Ala Leu Asn Glu Ser Leu Asn Arg Leu Lys
            180                 185                 190
Lys Glu Ser Thr Lys Ile Ile His His Tyr Ala His Ser Lys Glu Leu
        195                 200                 205
Ala Pro Tyr Leu Val Asp Thr Gln Ser His Leu Lys His Gly Tyr Glu
    210                 215                 220
Cys Leu Leu Leu Lys Ser Gly Phe Ser Ser Ala Ile Lys Gly Val Val
225                 230                 235                 240
Leu Glu Arg Ser Ala Asn Gly Tyr Phe Tyr Leu Leu Pro Glu Ser Ala
                245                 250                 255
Gln Lys Ile Ala Gln Lys Ile Ala Gln Ile Gly Asn Glu Ile Asp Cys
            260                 265                 270
Cys Ile Val Glu Met Cys Gln Thr Leu Ser Arg Ser Leu Gln Lys His
        275                 280                 285
```

```
Leu Leu Phe Leu Lys Phe Leu Phe Lys Glu Phe Asp Phe Leu Asp Ser
    290                 295                 300
Leu Gln Ala Arg Leu Asn Phe Ala Lys Ala Tyr Asn Leu Glu Phe Val
305                 310                 315                 320
Met Pro Ser Phe Thr Gln Lys Lys Met Ile Leu Glu Asn Phe Ser His
                325                 330                 335
Pro Ile Leu Lys Glu Pro Lys Pro Leu Asn Leu Lys Phe Glu Lys Ser
            340                 345                 350
Met Leu Ala Val Thr Gly Val Asn Ala Gly Gly Lys Thr Met Leu Leu
        355                 360                 365
Lys Ser Leu Leu Ser Ala Ala Phe Leu Ser Lys His Leu Ile Pro Met
    370                 375                 380
Lys Ile Asn Ala His His Ser Thr Ile Pro Tyr Phe Arg Glu Ile His
385                 390                 395                 400
Ala Ile Ile Asn Asp Pro Gln Asn Ser Ala Asn Asn Ile Ser Thr Phe
                405                 410                 415
Ala Gly Arg Met Lys Gln Phe Ser Ala Leu Leu Ser Lys Glu Asn Met
            420                 425                 430
Leu Leu Gly Val Asp Glu Ile Glu Leu Gly Thr Asp Ala Asp Glu Ala
        435                 440                 445
Ser Ser Leu Tyr Lys Thr Leu Leu Glu Lys Leu Leu Lys Gln Asn Asn
    450                 455                 460
Gln Ile Val Ile Thr Thr His His Lys Arg Leu Ser Val Leu Met Ala
465                 470                 475                 480
Glu Asn Lys Glu Val Glu Leu Leu Ala Ala Leu Tyr Asp Glu Glu Lys
                485                 490                 495
Glu Arg Pro Thr Tyr Thr Phe Leu Lys Gly Val Ile Gly Lys Ser Tyr
            500                 505                 510
Ala Phe Glu Thr Ala Leu Arg Tyr Gly Val Pro Pro Phe Leu Ile Glu
        515                 520                 525
Lys Arg Lys Pro Ser Met Ala Lys Ile Arg Lys Asn
    530                 535                 540
```

(2) INFORMATION FOR SEQ ID NO:1470:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 455 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470

```
Lys Leu Thr Glu Lys Ile Met Leu Glu Thr Pro Lys Val Leu Leu Lys
1               5                   10                  15
Asn Leu Gln Asp Cys Lys Ile His Phe Ile Gly Ile Gly Gly Ile Gly
            20                  25                  30
Ile Ser Gly Leu Ala Lys Tyr Leu Lys Ala Gln Gly Ala Lys Ile Ser
        35                  40                  45
Gly Ser Asp Ile Ala Ile Ser Pro Ser Val Lys Tyr Leu Lys Ala Leu
    50                  55                  60
Gly Val Glu Ile Asn Ile Pro His Asp Pro Lys Ala Ile Asn His Gln
65                  70                  75                  80
Asp Val Ile Ile His Ser Ala Ile Ile Lys Glu Asp Asn Thr Glu Ile
```

```
                85                  90                  95
Gln Arg Ala Lys Glu Leu Glu Ile Pro Ile Leu Ser Arg Lys Asp Ala
            100                 105                 110
Leu Tyr Ser Ile Leu Lys Asp Lys Arg Val Phe Ser Val Cys Gly Ala
        115                 120                 125
His Gly Lys Ser Ser Ile Thr Ala Met Leu Ser Ala Ile Cys Pro Ala
    130                 135                 140
Phe Gly Ala Ile Ile Gly Ala His Ser Lys Glu Phe Asp Ser Asn Val
145                 150                 155                 160
Arg Glu Ser Ala Asp Met Ser Leu Val Phe Glu Ala Asp Glu Ser Asp
                165                 170                 175
Ser Ser Phe Leu Phe Ser Asn Pro Phe Cys Ala Ile Val Pro Asn Thr
            180                 185                 190
Glu Pro Glu His Leu Glu His Tyr Asp His Asp Leu Glu Arg Phe Phe
        195                 200                 205
Phe Ala Tyr Lys Tyr Phe Leu Asp His Ala Gln Lys Arg Val Ile Tyr
    210                 215                 220
Lys Glu Asp Pro Phe Leu Lys Asn Tyr Ser Lys Asp Ala Ile Val Leu
225                 230                 235                 240
Glu Lys Lys Asp Ile Tyr Asn Ile Gln Tyr Ile Leu Lys Asp Gly Glu
                245                 250                 255
Pro Tyr Thr Ser Phe Glu Leu Lys Asn Leu Gly Ala Phe Leu Val Trp
            260                 265                 270
Gly Leu Gly Glu His Asn Ala Thr Asn Ala Ser Leu Ala Ile Leu Ser
        275                 280                 285
Ala Leu Asp Glu Leu Asn Leu Glu Glu Ile Arg Asn Asn Leu Leu Asn
    290                 295                 300
Phe Lys Gly Ile Lys Lys Arg Phe Asp Ile Leu Gln Lys Asn Asp Leu
305                 310                 315                 320
Ile Leu Ile Asp Asp Tyr Ala His His Pro Thr Glu Ile Gly Thr Thr
                325                 330                 335
Leu Lys Ser Ala Arg Ile Tyr Ala Asn Leu Leu Asn Thr Gln Glu Lys
            340                 345                 350
Ile Ile Val Ile Trp Gln Ala His Lys Tyr Ser Arg Leu Met Asp Asn
        355                 360                 365
Leu Glu Glu Phe Lys Lys Cys Phe Leu Glu His Cys Asp Arg Leu Ile
    370                 375                 380
Ile Leu Pro Val Tyr Ser Ala Ser Glu Val Lys Arg Asp Ile Asp Leu
385                 390                 395                 400
Lys Ala His Phe Lys His Tyr Asn Pro Thr Phe Ile Asp Arg Val Arg
                405                 410                 415
Lys Lys Gly Asp Phe Leu Glu Leu Leu Val Asn Asp Asn Val Val Glu
            420                 425                 430
Thr Ile Glu Lys Gly Phe Val Ile Gly Phe Gly Ala Gly Asp Ile Thr
        435                 440                 445
Tyr Gln Leu Arg Gly Glu Met
    450                 455
```

(2) INFORMATION FOR SEQ ID NO:1471:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

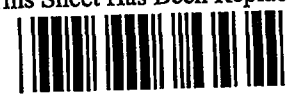
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature

This Sheet Has Been Replaced



(B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471

```
Ala Val Thr Ala Ile Leu Gly Trp Asp Glu Glu Gly Lys Leu Lys Phe
1               5                  10                  15
Gly Lys Ile Arg His Lys Tyr Leu Glu Thr Ser Asn Val Asn Ala Gly
            20                  25                  30
Asn Ala Leu Thr Asn Leu Ile Leu Met Gln Arg Gly Tyr Ser Met Asn
        35                  40                  45
Ala Arg Ala Phe Gly Ala Gly Asp Asp Met Ile Lys Glu Ala Ile Ser
    50                  55                  60
Leu Lys Lys
65
```

(2) INFORMATION FOR SEQ ID NO:1472:

(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:1472

```
Lys Leu His Arg Gly Ser Gln Lys Gln Asn Pro Ile Asn Asp Pro Thr
1               5                  10                  15
Trp Glu Ile Val Gly Phe Asp Ser Ala Thr His Lys Met Lys Ser Ala
            20                  25                  30
Pro Met Thr Leu Asp Phe Lys Gly Asn Lys Leu Thr Tyr Ser Leu Asp
        35                  40                  45
Lys Ser Glu Asn Met Ile Leu Thr Lys Leu Phe Tyr Gln Asp Ser Lys
    50                  55                  60
Leu Leu Lys Thr Ser Gln Glu Arg Lys Pro Arg Gly Ile Phe Arg Asp
65                  70                  75                  80
Met Arg Ile Glu Glu Asn Gly Val Ile Ser Leu Ala Phe Ser Asn Gly
                85                  90                  95
Val Val Glu Pro Val Ala Arg Ile Gly Ile Leu Ala Phe Thr Asn Asp
            100                 105                 110
Gln Gly Leu Arg Lys Ile Gly Gly Asn Leu Tyr Glu Met Gln Glu Gly
        115                 120                 125
Thr Ile Asn Gly Glu Asn Arg Pro Leu Ser Gly Asn Arg His Phe Arg
    130                 135                 140
Val Gly Arg Arg Gly Gln Ala Gln Val Trp Glu Asn Gln Ala Gln Ile
145                 150                 155                 160
Phe Arg Asn Glu Gln Arg Glu Cys Arg Glu Arg Pro Asn Gln Ser His
                165                 170                 175
Phe Asn Ala Lys Arg Leu Phe Tyr Glu Arg
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:1473:

(i) SEQUENCE CHARACTERISTICS:

This Sheet Has Been Replaced



(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:1473

```
Trp Met Phe Val Val Lys Met Val Leu Gly Phe Leu Ile Leu Leu Ser
1               5                  10                  15
Pro Leu Cys Ala Thr Gly Leu Asp Ile Ser Gln Thr Asp Ile Ile Glu
            20                  25                  30
Arg Ser Leu Asn Phe Leu Leu Phe Val Gly Ile Leu Trp Tyr Phe Leu
        35                  40                  45
Ala Lys Arg Leu Arg Ser Phe Leu His Ser Lys Ser Leu Glu Ile Ser
    50                  55                  60
Lys Arg Leu Glu Glu Ile Gln Ala Gln Leu Lys Val Ser Lys Glu His
65                  70                  75                  80
Lys Lys Lys Leu Leu Lys Glu Leu Glu Gln Ala Lys Glu Lys Ala Glu
                85                  90                  95
Leu Ile Ile Ser Asp Ala Asn Lys Glu Ala Tyr Thr Ile Thr Gln Lys
            100                 105                 110
Tyr Glu Leu Gln Thr Lys Met Asp Val Glu Asn Leu Ile Lys Asn Ser
        115                 120                 125
Lys Ala Leu Met Asp Leu Glu Val Lys Lys Ile Lys Arg Glu Leu Val
    130                 135                 140
Glu Ser Val Phe Lys Asp Leu Arg Glu Ser Lys Lys Val Ser Phe Asn
145                 150                 155                 160
Ala Gln Asp Cys Val Asn Ile Leu Lys Gln Arg Leu
                165                 170
```

(2) INFORMATION FOR SEQ ID NO:1474:

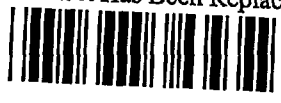
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474

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

```
Val Gln Asn Thr Pro Lys Asn Leu Pro Pro Ile Gln Leu Arg Leu Asp
        35                  40                  45
Gln Ala Tyr Glu Asp Leu Ile Lys Met Leu Asp Asn Met Gly Lys Ser
    50                  55                  60
Thr Gln Tyr Glu Phe Pro Lys Ile Lys Glu Ile Leu Glu Gln Ser Glu
65                  70                  75                  80
Glu Glu Trp Leu Gly Val Ala His Glu Glu Cys Val Ala Leu Val Met
                85                  90                  95
Leu Ile Ser Pro Lys Ala Ser Ile Glu Asn Ser Pro Ile Tyr Lys Asn
            100                 105                 110
Cys Tyr Glu Ala Tyr Val Lys Gln Arg Ile His Asp Leu Tyr Asp Phe
        115                 120                 125
Tyr Ile Glu Gly Lys Lys Val Lys Arg Lys Ile Lys Lys Ala His Glu
    130                 135                 140
His Glu Met Ala Leu Asn Lys Ser Gln Pro Leu Lys Lys Glu Pro Pro
145                 150                 155                 160
Lys Ser Glu Asn Lys Lys Gly Leu Thr Lys Pro Ser Leu Lys Asp Ala
                165                 170                 175
Lys Ile Pro Lys Gly Tyr Tyr Leu Gln Ile Gly Ala Phe Leu Asn Ser
            180                 185                 190
Pro Ser Lys Asp Phe Leu Gln Thr Leu Lys Thr Phe Pro His Gln Met
        195                 200                 205
Glu Glu Lys Asp Ser Leu Thr His Tyr Leu Ile Gly Pro Tyr Lys Thr
    210                 215                 220
Lys Glu Glu Ala Leu Lys Gln Leu Glu Asn Ala Ala Lys Ser Phe Lys
225                 230                 235                 240
Asn Lys Pro Ala Leu Val Glu Lys
                245
```

(2) INFORMATION FOR SEQ ID NO:1475:

This Sheet Has Been Replaced



(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

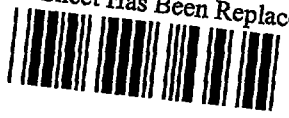
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475

```
Ser Gly Cys Tyr Phe Glu Ser Asn Ser Asp Val Tyr Val Val Ile Ile
1               5                   10                  15
Gly Leu Ala Asp Gln Lys Ile Gly Val Ile Val Asp Tyr Leu Ile Gly
            20                  25                  30
Gln Glu Glu Val Val Ile Lys Ser Leu Gly Tyr Tyr Leu Lys Asn Thr
        35                  40                  45
Arg Gly Ile Ala Gly Ala Thr Val Arg Gly Asp Gly Lys Ile Thr Leu
    50                  55                  60
Ile Val Asp Val Gly Ala Met Met Glu Met Ala Lys Ser Ile Lys Val
65                  70                  75                  80
Asn Ile Thr Thr Leu Met Asn Glu Ser Glu Asn Thr Lys Ser Lys Asn
                85                  90                  95
Ser Pro Ser Asp Tyr Val Val Leu Ala Ile Asp Asp Ser Ser Thr Asp
            100                 105                 110
Arg Ala Ile Ile Arg Lys Cys Leu Lys Pro Leu Gly Ile Thr Leu Leu
```

```
        115                 120                 125
Glu Ala Thr Asn Gly Leu Glu Gly Leu Glu Met Leu Lys Asn Gly Asp
    130                 135                 140
Lys Ile Pro Asp Ala Ile Leu Val Asp Ile Glu Met Pro Lys Met Asp
145                 150                 155                 160
Gly Tyr Thr Phe Ala Ser Glu Val Arg Lys Tyr Asn Lys Phe Lys Asn
                165                 170                 175
Leu Pro Leu Ile Ala Val Thr Ser Arg Val Thr Lys Thr Asp Arg Met
            180                 185                 190
Arg Gly Val Glu Ser Gly Met Thr Glu Tyr Ile Thr Lys Pro Tyr Ser
        195                 200                 205
Gly Glu Tyr Leu Thr Thr Val Val Lys Arg Ser Ile Lys Leu Glu Gly
    210                 215                 220
Asp Gln Ser
225
```

(2) INFORMATION FOR SEQ ID NO:1476:

This Sheet Has Been Replaced



(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:1476

```
Met Thr Leu Ser Gln Ala Leu Asn Lys Ala Lys Lys Glu Leu Ser Pro
1               5                   10                  15
Lys Gly Phe Arg Gly Gly Leu Glu Ser Glu Ile Leu Leu Gly Phe Val
            20                  25                  30
Leu Gln Lys Glu Arg Val Phe Leu His Thr His Glu His Leu Glu Leu
        35                  40                  45
Ser His Glu Glu Glu Thr Arg Phe Phe Glu Leu Val Gly Lys Arg Leu
    50                  55                  60
Asn Asp Cys Pro Ile Glu Tyr Leu Leu Gly Ser Cys Asp Phe Tyr Gly
65                  70                  75                  80
Arg Ser Phe Phe Val Asn Glu His Val Leu Ile Pro Arg Pro Glu Thr
                85                  90                  95
Glu Ile Leu Val Gln Lys Ala Leu Asn Ile Ile Ser Gln Tyr His Leu
            100                 105                 110
Lys Glu Ile Gly Glu Ile Gly Ile Gly Ser Gly Cys Val Ser Val Ser
        115                 120                 125
Leu Ala Leu Glu Asn Pro Asn Leu Ser Ile Tyr Ala Ser Asp Ile Ser
    130                 135                 140
Pro Lys Ala Leu Glu Val Ala Leu Lys Asn Ile Glu Arg Phe Cys Leu
145                 150                 155                 160
Lys Glu Arg Val Phe Leu Lys Gln Thr Arg Leu Trp Asp His Met Pro
                165                 170                 175
Thr Ile Glu Met Leu Val Ser Asn Pro Pro Tyr Ile Ala Arg Asn Tyr
            180                 185                 190
Pro Leu Glu Lys Ser Val Leu Lys Glu Pro His Glu Ala Leu Phe Gly
        195                 200                 205
Gly Val Lys Gly Asp Glu Ile Leu Lys Glu Ile Val Phe Leu Ala Ala
    210                 215                 220
```

```
Lys Leu Lys Ile Pro Phe Leu Val Cys Glu Met Gly Tyr Asp Gln Leu
225                 230                 235                 240
Lys Ser Leu Lys Glu Cys Leu Glu Phe Cys Gly Tyr Asp Ala Glu Phe
                245                 250                 255
Tyr Lys Asp Leu Ser Gly Phe Asp Arg Gly Phe Val Gly Val Leu Lys
            260                 265                 270
Ser Phe Leu Arg
        275
```

(2) INFORMATION FOR SEQ ID NO:1477:

(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:1477

```
Lys Ala Val Leu Phe Asn Pro Leu Pro Thr Lys Arg Ser Val Met Pro
1               5                   10                  15
His Ser Leu Lys Lys Arg Phe Leu Ile Val Tyr Thr Leu Ser Thr Leu
            20                  25                  30
Leu Leu Val Gly Val Leu Leu Ala Leu Phe Phe Phe Tyr Ala Lys Asn
        35                  40                  45
Asn Leu Leu Glu Asn Thr Gln Ile Arg Met Gln Tyr Thr Ala Asp Ala
    50                  55                  60
Ile Ala Lys Ser Leu Leu Glu Leu Asn Asn Ala Ser Ser Leu Glu Pro
65                  70                  75                  80
Leu Lys Ile Leu Glu Glu Arg Phe Lys Asn Thr Pro Phe Val Leu Leu
                85                  90                  95
Asp Ala Asp Asn Arg Val Lys Phe Ser Asn Ile Gly Val Phe Val Ala
            100                 105                 110
Ser Phe Lys Asn Asp Ala Leu Ile Lys Thr Pro Tyr Phe Ala Leu Lys
        115                 120                 125
Lys Gln Gly Phe Tyr Leu Thr Asp Ser Ala Pro Thr Asn Arg Leu Gly
    130                 135                 140
Val Ser Lys Ile Ile Ile Ala Glu Glu Glu Ile Gln Lys Ile Phe Ile
145                 150                 155                 160
Pro Leu Tyr Lys Met Ile Gly Tyr Val Phe Leu Gly Ala Ser Leu Phe
                165                 170                 175
Val Ala Leu Ile Ala Met Trp Leu Tyr Lys Ile Pro
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:1478:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 408 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478

```
Asn Met Leu Asp Ile Trp Ile Asp Met Ile Ile Cys Ile Phe Tyr Leu
1               5                  10                  15
Leu Phe Phe Thr Thr Pro Tyr Ile Val Gly Asp Ile Leu Gln Leu Lys
            20                  25                  30
Phe Ile Arg Gln Lys Leu Cys Glu Lys Pro Val Leu Leu Pro Gln Lys
        35                  40                  45
Asp Tyr Glu Glu Ala Gly Asn Tyr Ala Ile Arg Lys Met Gln Leu Ser
    50                  55                  60
Ile Ile Ser Gln Ile Leu Asp Gly Val Ile Phe Ala Gly Trp Val Phe
65                  70                  75                  80
Phe Gly Leu Thr His Leu Glu Asp Leu Thr His Tyr Leu Asn Leu Pro
                85                  90                  95
Glu Thr Leu Gly Tyr Leu Val Phe Ala Leu Leu Phe Leu Ala Ile Gln
            100                 105                 110
Ser Val Leu Ala Leu Pro Ile Ser Tyr Tyr Thr Thr Met His Leu Asp
        115                 120                 125
Lys Glu Phe Gly Phe Ser Lys Val Ser Leu Ser Leu Phe Phe Lys Asp
    130                 135                 140
Phe Phe Lys Gly Leu Leu Leu Thr Leu Gly Val Gly Leu Leu Leu Ile
145                 150                 155                 160
Tyr Thr Leu Ile Met Ile Ile Glu His Val Glu His Trp Glu Ile Ser
                165                 170                 175
Ser Phe Phe Val Val Phe Val Phe Met Ile Leu Ala Asn Leu Phe Tyr
            180                 185                 190
Pro Lys Ile Ala Gln Leu Phe Asn Gln Phe Thr Pro Leu Asn Asn Arg
        195                 200                 205
Asp Leu Glu Ser Gln Ile Glu Ser Met Met Asp Lys Val Gly Phe Lys
    210                 215                 220
Ser Gln Gly Ile Phe Val Met Asp Ala Ser Lys Arg Asp Gly Arg Leu
225                 230                 235                 240
Asn Ala Tyr Phe Gly Gly Leu Gly Lys Asn Lys Arg Val Val Leu Phe
                245                 250                 255
Asp Thr Leu Ile Ser Lys Val Gly Thr Glu Gly Leu Leu Ala Ile Leu
            260                 265                 270
Gly His Glu Leu Gly His Phe Lys Asn Lys Asp Leu Leu Lys Asn Leu
        275                 280                 285
Gly Ile Met Gly Gly Leu Leu Ala Leu Val Phe Ala Leu Ile Ala His
    290                 295                 300
Leu Pro Pro Leu Val Phe Glu Gly Phe Asn Val Ser Gln Thr Pro Ala
305                 310                 315                 320
Ser Leu Ile Thr Ile Leu Leu Leu Phe Leu Pro Val Phe Ser Phe Tyr
                325                 330                 335
Ala Met Pro Leu Ile Gly Phe Phe Ser Arg Lys Asn Glu Tyr Asn Ala
            340                 345                 350
Asp Lys Phe Gly Ala Ser Leu Ser Ser Lys Glu Thr Leu Ala Lys Ala
        355                 360                 365
Leu Val Ser Ile Val Asn Glu Asn Lys Ala Phe Pro Tyr Ser His Pro
    370                 375                 380
Phe Tyr Val Phe Leu His Phe Thr His Pro Pro Leu Leu Glu Arg Leu
385                 390                 395                 400
Lys Ala Leu Asp Tyr Glu Ile Glu
                405
```

(2) INFORMATION FOR SEQ ID NO:1479:

(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:1479

```
Ile Arg Arg Arg Pro Ile Val Ser Asn Gln Leu Lys Asp Leu Phe Glu
1               5                  10                  15
Arg Gln Lys Glu Ala Asn Ala Ser Ser Lys Gln Glu Asp Asn Glu Glu
            20                  25                  30
Ile Leu Gln Phe Ile Gly Phe Ile Ile Gly Asp Glu Glu Tyr Ala Ile
        35                  40                  45
Pro Ile Leu Asn Ile Leu Glu Ile Val Lys Pro Ile Gly Tyr Thr Arg
    50                  55                  60
Val Pro Glu Thr Pro Asn Tyr Val Leu Gly Val Phe Asn Leu Arg Gly
65                  70                  75                  80
Asn Val Phe Pro Leu Ile Ser Leu Arg Leu Lys Phe Gly Leu Lys Ala
                85                  90                  95
Glu Lys Gln Asn Lys Asp Thr Arg Tyr Leu Val Val Arg His Asn Asp
            100                 105                 110
Arg Ser Leu Gly Phe Ser Ser Leu Ser Gly Leu Met Pro Ser Glu Ser
        115                 120                 125
Ala Ser Thr Ile Asp Pro Ser Gln Lys Leu Cys Ala Ile Thr Ile Ile
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:1480:

(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:1480

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

This Sheet Has Been Replaced

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

(2) INFORMATION FOR SEQ ID NO:1481:

(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:1481

```
Gly Val Phe Tyr Asn Ser Ser Leu Pro Gln Pro Pro Thr Lys Asn Pro
1               5                   10                  15
Leu Thr Arg Glu Tyr Arg Phe Leu Lys Arg Leu Ser Leu Ile Tyr Ala
            20                  25                  30
Ser Ser Phe Ile Val Phe Ile Leu Lys Asn Ala Leu Lys Leu Phe Leu
        35                  40                  45
Ile Leu Leu Leu Met Leu Asn Lys Pro Lys Pro Leu Phe Leu Leu Leu
    50                  55                  60
Val Lys Pro Phe Phe Tyr Leu Phe Asp Leu Val Ala His Leu Ser Thr
65                  70                  75                  80
```

This Sheet Has Been Replaced



```
Arg Ile Asp Leu Ile Asp Lys His Val Lys Val Tyr His His Gln Lys
                85                  90                  95
His His His Lys Pro
            100
```

(2) INFORMATION FOR SEQ ID NO:1482:

(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:1482

```
Phe Ile Thr Gly Ile Glu Ile His Pro Gly Ala Lys Ile Gly Arg Gly
1               5                  10                  15
Leu Phe Ile Asp His Gly Met Gly Val Val Ile Gly Glu Thr Thr Glu
            20                  25                  30
Ile Gly Asp Asp Val Thr Ile Tyr His Gly Val Thr Leu Gly Gly Thr
        35                  40                  45
Gly Lys Phe Lys Gly Lys Arg His Pro Thr Leu Gly Asn Arg Val Val
    50                  55                  60
Val Gly Ala Gly Ala Lys Val Leu Gly Ala Ile Cys Val Gly Asp Asp
65                  70                  75                  80
Val Arg Ile Gly Ala Asn Ala Val Val Leu Ser Asp Leu Pro Thr Gly
                85                  90                  95
Ser Thr Ala Val Gly Ala Lys Ala Lys Thr Ile Thr Lys Asp Arg
            100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:1483:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483

```
Lys Gly Phe Leu Gly Val Lys Lys Val Ile Val Phe Ile Lys Lys Lys
1               5                  10                  15
Gly Glu Met Val Val Asn Ser Lys Val Gln Thr Leu Lys Val Phe Ser
```

This Sheet Has Been Replaced



```
            20                  25                  30
Lys Phe Phe Ser Asn Phe Lys Ile Thr Lys Leu Lys Asp Asn His Glu
        35                  40                  45
Glu Ala His Lys Leu Phe Gly Glu Asn Ser Arg Lys Ala His Asp Thr
    50                  55                  60
Glu Ile Ile Tyr Ser Thr Leu Gln Val Val Pro Arg Tyr Ser Ile Glu
65                  70                  75                  80
Thr Val Gly Phe Ser Leu Leu Ile Leu Ala Val Ala Tyr Ile Leu Phe
                85                  90                  95
Lys Tyr Gly Glu Ala Arg Met Val Leu Pro Thr Ile Ser Met Tyr Ala
            100                 105                 110
Leu Ala Leu Tyr Arg Ile Leu Pro Ser Val Thr Gly Val Ile Ser Tyr
        115                 120                 125
Tyr Asn Glu Ile Ala Tyr Asn Gln Leu Ala Thr Asn Val Val Phe Lys
    130                 135                 140
Ser Leu Ser Lys Thr Ile Val Glu Glu Asp Leu Val Pro Leu Asp Phe
145                 150                 155                 160
Asn Glu Lys Ile Thr Leu Gln Asn Ile Ser Phe Ala Tyr Lys Ser Lys
                165                 170                 175
His Pro Val Leu Lys Asn Phe Asn Leu Thr Ile Gln Lys Gly Gln Lys
            180                 185                 190
Ile Ala Leu Ile Gly His Ser Gly Cys Gly Lys Ser Thr Leu Ala Asp
        195                 200                 205
Ile Ile Met Gly Leu Thr Tyr Pro Lys Ser Gly Glu Ile Phe Ile Asp
    210                 215                 220
Asn Thr Leu Leu Thr Ser Glu Asn Arg Arg Ser Trp Arg Lys Lys Ile
225                 230                 235                 240
Gly Tyr Ile Pro Gln Asn Ile Tyr Leu Phe Asp Gly Thr Val Gly Asp
                245                 250                 255
Asn Ile Ala Phe Gly Ser Ala Ile Asp Glu Lys Arg Leu Ile Lys Val
            260                 265                 270
Cys Lys Met Ala His Ile Tyr Asp Phe Leu Cys Glu His Glu Gly Leu
        275                 280                 285
Lys Thr Gln Val Gly Glu Gly Gly Ala Lys Leu Ser Gly Gly Gln Lys
    290                 295                 300
Gln Arg Ile Gly Ile Ala Arg Ala Leu Tyr Asp Asn Pro Glu Ile Leu
305                 310                 315                 320
Val Leu Asp Glu Ala Thr Ser Ala Leu Asp Asn Glu Thr Glu Ser Lys
                325                 330                 335
Ile Met Asp Glu Ile Tyr Gln Ile Ala Lys Asn Lys Thr Leu Ile Val
            340                 345                 350
Ile Ala His Arg Leu Ser Thr Ile Glu Arg Cys Glu Val Ile Ile Asp
        355                 360                 365
Met Ser Gln His Lys Asp Asn Leu Gly
    370                 375
```

(2) INFORMATION FOR SEQ ID NO:1484:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484

```
Ala Tyr Lys Lys Gly Glu Ile Met Ala Leu Glu Val Val Leu Trp Asp
1               5                  10                  15
Phe Asp Gly Val Ile Phe Asp Ser Met His Leu Lys Tyr Glu Gly Phe
            20                  25                  30
Lys Ala Leu Phe Gln Lys His Gly Asn Asp Ser Lys Glu Gly Leu Lys
        35                  40                  45
Gln Phe Glu Val Tyr His Tyr Gln Ser Gly Gly Ile Ser Arg Asn Glu
    50                  55                  60
Lys Ile Gln Tyr Phe Tyr Asn Glu Ile Leu Lys Thr Pro Ile Ala Gln
65                  70                  75                  80
Glu Glu Ile Asp Ala Leu Ala Leu Glu Phe Gly Ala Ile Ile Glu Gln
                85                  90                  95
Lys Leu Phe Asp Arg Gly His Leu Asn Ser Glu Val Met Ala Phe Ile
            100                 105                 110
Asp Lys His Tyr Gln Asn Tyr Ile Phe His Ile Ala Ser Ala Ala Leu
        115                 120                 125
His Ser Glu Leu Gln Val Leu Cys Glu Phe Leu Gly Ile Thr Lys Tyr
    130                 135                 140
Phe Lys Ser Val Glu Gly Ser Pro Pro Asp Lys Pro Lys Ile Ile Ala
145                 150                 155                 160
Asn Ile Ile Gln Lys Tyr Ala Tyr Asp Pro Ser Arg Met Leu Met Ile
                165                 170                 175
Gly Asp Ser Val Asn Asp Tyr Glu Ser Ala Lys Ala Asn Lys Val Ala
            180                 185                 190
Phe Leu Gly Tyr Asn Ser Lys Val Leu Lys Asn Leu Val Gly Gln Asp
        195                 200                 205
Gly Tyr Gln Gly Lys Tyr Leu Glu Ser Phe Lys Gly Phe Asp Leu Gln
    210                 215                 220
Asn Phe Ala Lys Glu
225
```

(2) INFORMATION FOR SEQ ID NO:1485:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485

```
Asn Lys Ser Met Gln His Leu Val Leu Ile Gly Phe Met Gly Ser Gly
1               5                  10                  15
Lys Ser Ser Leu Ala Gln Glu Leu Gly Leu Ala Leu Lys Leu Glu Val
            20                  25                  30
Leu Asp Thr Asp Met Ile Ile Ser Glu Arg Val Gly Leu Ser Val Arg
        35                  40                  45
Gly Ile Phe Glu Glu Leu Gly Glu Asp Asn Phe Arg Met Phe Glu Lys
    50                  55                  60
Asn Leu Ile Asp Glu Leu Lys Thr Leu Lys Thr Pro His Ile Ile Ser
65                  70                  75                  80
Thr Gly Gly Gly Ile Val Met His Glu Asn Leu Lys Gly Leu Gly Thr
```

```
                85                  90                  95
Thr Phe Tyr Leu Lys Met Asp Phe Glu Thr Leu Ile Lys Arg Leu Asn
            100                 105                 110
Gln Lys Glu Arg Glu Lys Arg Pro Leu Leu Asn Asn Leu Thr Gln Ala
        115                 120                 125
Lys Glu Leu Phe Glu Lys Arg Gln Ala Leu Tyr Glu Lys Asn Ala Ser
    130                 135                 140
Phe Ile Ile Asp Ala Arg Gly Gly Leu Asn Asn Ser Leu Lys Gln Val
145                 150                 155                 160
Leu Gln Phe Ile Ala
                165
```

(2) INFORMATION FOR SEQ ID NO:1486:

This Sheet Has Been Replaced



(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:1486

```
Ile Phe Phe Lys Gly Leu Val Met Leu Ser Arg Asp Ile Val Gln Tyr
1               5                   10                  15
Ser Lys Ile Arg Thr Glu Leu Tyr Ala Tyr Leu Thr Tyr Leu Phe Ser
            20                  25                  30
His Asn Ile Arg Asn His Leu Pro Glu Ile Thr Leu Asp Tyr Leu Asn
        35                  40                  45
Arg Gln Ile Ser Lys Met Gln Ala Glu Ile Lys Met Ala Lys Ser Phe
    50                  55                  60
Phe Val Leu Asp Ala Lys Gly Met Leu Met Leu Lys Pro Ser Gln Phe
65                  70                  75                  80
Lys Glu Gln Gly His Lys Glu Gly Leu Leu Glu His Asp Leu Thr Glu
                85                  90                  95
Gly Ile Glu Leu Glu Ser His Val Ser Phe Ser Asp Lys Tyr Tyr Phe
            100                 105                 110
Tyr Gln Ala Val Asn Glu Lys Arg Cys Ile Leu Thr Asp Pro Tyr Pro
        115                 120                 125
Ser Lys Lys Gly Asn His Leu Val Val Ser Ala Ser Tyr Pro Val Tyr
    130                 135                 140
Asp Gln Asn Asn Asp Leu Ala Phe Val Val Cys Leu Gln Ile Pro Leu
145                 150                 155                 160
Arg Val Ala Ile Glu Ile Ser Ser Pro Ser Lys Tyr Phe Lys Thr Phe
                165                 170                 175
Ser Glu Gly Ser Met Val Met Tyr Phe Met Ile Ser Ile Met Leu Thr
            180                 185                 190
Leu Val Ser Leu Leu Leu Phe Val Lys Cys Ile Ser Ser Phe Trp Thr
        195                 200                 205
Ala Ile Val His Phe Ser Ser Phe Asp Ile Lys Glu Val Phe His Pro
    210                 215                 220
Ile Val Leu Leu Thr Leu Ala Leu Ala Thr Phe Asp Leu Val Lys Ala
225                 230                 235                 240
Ile Phe Glu Glu Glu Val Leu Gly Lys Asn Ser Gly Asp Asn His His
                245                 250                 255
```

```
Ala Ile His Arg Thr Met Ile Arg Phe Leu Gly Ser Ile Ile Ile Ala
            260                 265                 270
Leu Ala Ile Glu Ala Leu Met Leu Val Phe Lys Phe Ser Val Ser Glu
        275                 280                 285
Pro Asp Lys Ile Thr Tyr Ala Val Tyr Leu Ala Ile Gly Val Ala Val
    290                 295                 300
Leu Leu Ile Ser Leu Ala Ile Tyr Val Lys Phe Ala Tyr Ser Val Leu
305                 310                 315                 320
Pro Lys Arg Glu Arg
                325
```

(2) INFORMATION FOR SEQ ID NO:1487:

This Sheet Has Been Replaced



(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:1487

```
Glu Ser Tyr Gln Thr Val Phe Thr Arg Gln Arg Tyr Tyr Gln Arg Leu
1               5                  10                  15
Phe Arg Arg Ala Val Cys Arg Asn Leu Arg Val Cys Glu Phe Thr Asn
            20                  25                  30
Gln Asn Asn Lys Arg Gly Asp Cys Gln Arg Gln Gln Leu Phe Tyr Gly
        35                  40                  45
Ala Tyr His Gly Glu Cys Leu Ser His Phe Arg Ile Ala Lys Thr His
    50                  55                  60
Cys Gly Ala Ser Pro Phe Ile Val Ser Asp Phe Asn Phe Ile Gly Phe
65                  70                  75                  80
Ile Val Pro Pro Ser Asn His Phe Ile Cys Gly Ser Gln Leu Lys Ser
                85                  90                  95
Arg Pro Phe Arg Ala Ile Cys Leu Ala Arg Ile Ser Lys His Cys Gln
            100                 105                 110
Ser Leu Phe Thr Leu Val Cys His Arg Val Phe Tyr Gly Val Pro Tyr
        115                 120                 125
Phe Met Leu Gly Val Ile Glu Arg Tyr Tyr Phe Trp His Asp His Glu
    130                 135                 140
Asn Pro Pro Ser Ile Gln Pro Ala Arg Tyr Arg Val Ser Gly Asn Cys
145                 150                 155                 160
Asp Arg Val Cys Gly His Tyr Phe Asn Arg Phe Gly Tyr His Gly Ala
                165                 170                 175
Phe Arg Arg Asn Gln Pro Gly Leu Arg Tyr Asn Leu
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:1488:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 444 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced

(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

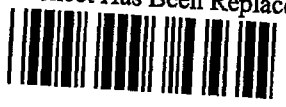
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488

```
Gly Val Leu Arg Phe Ser Ile Phe Phe Lys Val Val Ala Leu Phe Met
1               5                  10                  15
Ile Thr Leu Phe Ser Phe Gly Ala Phe Ala Tyr Tyr Phe Val Ser Ser
            20                  25                  30
Gln Ile Ser His Glu Asn Tyr Gln Asn Glu Met Arg His Tyr Gln Phe
        35                  40                  45
Val Thr Thr Ile Asn Glu Ile Leu Asn Asn Tyr Ser Asp Tyr Arg Ala
    50                  55                  60
Ile Glu Asp Tyr Leu Tyr Lys Ile Gly Phe Arg Glu Thr Thr Ile Glu
65                  70                  75                  80
Asn Leu Glu Lys Val Leu Ala Lys Arg Arg His Gln Leu His His Arg
                85                  90                  95
Asn Ile Trp Tyr Ala Glu Val Phe Lys Phe Ser Asp Met Val Phe Ile
            100                 105                 110
Leu Leu Lys Lys Asp Glu His Phe Val Leu Tyr Lys Asp Leu His Ser
        115                 120                 125
Val Ser Tyr Arg Asn Tyr Phe Leu Ala Ile Thr Val Gly Leu Leu Leu
    130                 135                 140
Ile Leu Phe Leu Phe Leu Phe Val Leu Gln Ser Leu Leu Pro Leu Arg
145                 150                 155                 160
Glu Leu Arg Ser Gln Val Lys Arg Phe Ala Gln Gly Asp Lys Ser Val
                165                 170                 175
Ser Cys Lys Ser Lys Gln Lys Asp Glu Ile Gly Asp Leu Ala Asn Glu
            180                 185                 190
Phe Asp Asn Cys Ile Gln Lys Ile Asn Ala Met Asn Glu Ser Arg Val
        195                 200                 205
Leu Phe Leu Arg Ser Ile Met His Glu Leu Arg Thr Pro Ile Thr Lys
    210                 215                 220
Gly Lys Ile Leu Ser Ser Met Leu Lys Glu Glu Leu Ser Cys Lys Arg
225                 230                 235                 240
Phe Ser Ser Ile Phe Asp His Leu Asn Met Leu Ile Glu Gln Phe Ala
                245                 250                 255
Arg Ile Glu Gln Leu Ala Ser Lys Asn Tyr Gly Ser Asn Lys Glu Lys
            260                 265                 270
Phe Leu Met Ser Asp Leu Ile Asp Lys Ile Glu Lys Met Leu Leu Ile
        275                 280                 285
Asp Glu Asp Lys Lys Ser Pro Ile His Val Ser Ser Ser Asn Tyr Ile
    290                 295                 300
Ile Glu Ala Asp Phe Glu Leu Phe Ala Ile Ala Leu Lys Asn Met Ile
305                 310                 315                 320
Asp Asn Ala Ile Lys Tyr Ser Asp Asp Lys Gln Val Phe Leu Asp Phe
                325                 330                 335
Ile Gly Asn Asn Leu Val Val Ser Asn Lys Ser Lys Pro Leu Lys Glu
            340                 345                 350
Asp Phe Glu Lys Tyr Leu Gln Pro Tyr Phe Lys Ser Ser Asn Pro Ser
        355                 360                 365
Gln Ala His Gly Phe Gly Leu Gly Met Tyr Ile Ile Lys Asn Ala Leu
    370                 375                 380
Glu Ala Met Gly Leu Asn Leu Ser Tyr His Tyr Ser Asn Gly Arg Ile
385                 390                 395                 400
Cys Phe Thr Ile His Asp Cys Val Phe Asn Ser Phe Tyr Asp Leu Glu
                405                 410                 415
```

```
Ala Asp Asn Glu Glu Leu Pro Pro Pro Arg Lys Phe Glu Arg Gly Glu
            420                 425                 430
Gly Asn Glu Gly Asn Arg Lys Ser Gln Leu Trp Gly
        435                 440
```

(2) INFORMATION FOR SEQ ID NO:1489:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489

```
Arg Lys Thr Lys Arg Glu Asn Met Phe Lys Arg Leu Arg Arg Leu Arg
1               5                  10                  15
Ser Ser Glu Asn Leu Arg Ala Met Val Arg Glu Thr Arg Leu Asn Ile
            20                  25                  30
Asn Asp Phe Ile Ala Pro Leu Phe Val Ile Glu Ser Asp Ser Gly Ile
        35                  40                  45
Lys Asn Glu Ile Ser Ser Met Pro Gly Val Tyr Gln Met Ser Ile Glu
    50                  55                  60
Pro Leu Leu Lys Glu Cys Glu Glu Leu Val Gly Leu Gly Ile Lys Ala
65                  70                  75                  80
Val Leu Leu Phe Gly Ile Pro Lys His Lys Asp Ala Thr Gly Ser His
                85                  90                  95
Ala Leu Asn Lys Asp His Ile Val Ala Lys Ala Thr Arg Glu Ile Lys
            100                 105                 110
Lys Arg Phe Lys Asp Leu Ile Val Ile Ala Asp Leu Cys Phe Cys Glu
        115                 120                 125
Tyr Thr Asp His Gly His Cys Gly Ile Leu Glu Asn Ala Ser Val Ser
    130                 135                 140
Asn Asp Lys Thr Leu Lys Ile Leu Asn Leu Gln Gly Leu Ile Leu Ala
145                 150                 155                 160
Glu Ser Gly Val Asp Ile Leu Ala Pro Ser Asn Met Met Asp Gly Asn
                165                 170                 175
Val Leu Ser Leu Arg Lys Ala Leu Asp Lys Ala Gly Tyr Phe His Thr
            180                 185                 190
Pro Ile Met Ser Tyr Ser Thr Lys Phe Ala Ser Ser Tyr Tyr Gly Pro
        195                 200                 205
Phe Arg Asp Val Ala Asn Ser Pro Pro Ser Phe Gly Asp Arg Lys Ser
    210                 215                 220
Tyr Gln Met Asp Tyr Ala Asn Gln Lys Glu Ala Leu Leu Glu Ser Leu
225                 230                 235                 240
Glu Asp Glu Lys Gln Gly Ala Asp Ile Leu Met Val Lys Pro Ala Leu
                245                 250                 255
Ala Tyr Leu Asp Ile Val Lys Glu Ile Arg Asp His Thr Leu Leu Pro
            260                 265                 270
Leu Ala Leu Tyr Asn Val Ser Gly Glu Tyr Ala Met Leu Lys Leu Ala
        275                 280                 285
Gln Lys His Asn Leu Ile Asn Tyr Glu Ser Val Leu Leu Glu Thr Met
    290                 295                 300
Thr Cys Phe Lys Arg Ala Gly Ala Asp Met Ile Ile Ser Tyr His Ala
```

305 310 315 320
Lys Glu Val Ala Asn Leu Leu Gln Arg Asn
325 330

(2) INFORMATION FOR SEQ ID NO:1490:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...362

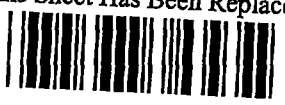
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490

Ser Ala Gly Arg Ile Leu Ala Glu Asp Ile Ile Cys Val His Ala Leu
1 5 10 15
Pro Lys Phe Asn Gln Ser Ala Met Asp Gly Tyr Gly Phe Lys Met Gln
20 25 30
Asp Leu Gly Gln Lys Thr Gln Val Ile Gln His Ile Phe Ala Gly Asp
35 40 45
Asp Val Ser Ala Leu Glu Val Lys Glu Asn Glu Cys Val Lys Ile Met
50 55 60
Thr Gly Ala Met Val Pro Lys Gly Ile Glu Thr Ile Val Pro Ile Glu
65 70 75 80
Cys Met Leu Glu Ser His Lys Asp Phe Ala Leu Ala Pro Lys Asp Phe
85 90 95
Lys Ile His Ala Asn Ile Arg Gln Lys Gly Glu Asn Ala Ser Leu Asn
100 105 110
Ser Val Leu Val Pro Lys Asn Thr Arg Leu Asn Tyr Gly His Ile Ala
115 120 125
Leu Ile Ala Ser Gln Gly Phe Lys Glu Ile Lys Ala Phe Arg Lys Leu
130 135 140
Lys Ile Ala Leu Phe Ser Ser Gly Asp Glu Leu Val Pro Leu Gly Gln
145 150 155 160
Asn Ala Leu Glu Cys Gln Val Tyr Asp Val Asn Ser Val Gly Val Phe
165 170 175
Asn Met Leu Lys Asn Tyr Asn Thr His Phe Leu Gly Val Leu Lys Asp
180 185 190
Asp Lys Asn Leu Gln Leu Lys Ile Leu Glu Leu Gln Gly Tyr Asp Val
195 200 205
Ile Leu Ser Ser Ala Gly Val Ser Val Gly Asp Lys Asp Phe Phe Lys
210 215 220
Asp Ala Leu Lys Glu Arg Asn Ala Leu Phe Tyr Tyr Glu Lys Val Asn
225 230 235 240
Leu Lys Pro Gly Lys Pro Val Thr Leu Ala Gln Leu Asn Gln Ser Ile
245 250 255
Ile Ile Gly Leu Pro Gly Asn Pro Leu Ser Cys Leu Leu Val Leu Arg
260 265 270
Val Leu Ile Leu Pro Leu Leu Glu Arg Leu Ser Leu Asn Lys Asp Phe
275 280 285
Lys Leu Lys Pro Phe Lys Ala Gln Ile Asn Ala Pro Leu Lys Leu Asn
290 295 300
Asn Lys Arg Thr His Leu Ile Leu Gly Asn Tyr Ser Asn His Gln Phe
305 310 315 320

```
Ile Pro Tyr Asn Asn Arg Tyr Glu Ser Gly Ala Ile Gln Ala Leu Ala
                325                 330                 335
Gln Val Asp Ser Ile Ala Leu Ile Asp Glu Gly Val Gly Leu Val Gln
            340                 345                 350
Gly Glu Ile Glu Ile Leu Arg Phe Glu Asn
        355                 360
```

(2) INFORMATION FOR SEQ ID NO:1491:

This Sheet Has Been Replaced



(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

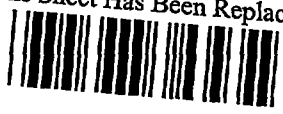
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491

```
Gly Asn Tyr Gly Leu Glu Ile Arg Phe Lys Glu Met Ala Val Leu Lys
1               5                  10                  15
Lys Met Ile Gly Leu Val Ala Val Leu Ser Val Leu Leu Ala Arg Asp
            20                  25                  30
Asn Pro Phe Glu Pro Glu Ile Asn Ser Lys Asn Leu Gln Gly Gly Phe
        35                  40                  45
Ser Gly Ile Tyr Asp Asp Tyr Leu Lys Glu Ile His Val Asp Leu Pro
    50                  55                  60
Thr Ser Ala Arg Ile Leu Lys Lys Ile Thr Leu Thr Tyr Gln Asp Ile
65                  70                  75                  80
Asp Gly Ser Ile His Ser Lys Val Val Gly Ile Asp Lys Ser Ile Asp
                85                  90                  95
Trp His Tyr Pro Leu Lys Leu Ser Gln His Thr Leu Asn Gln Asp Ala
            100                 105                 110
Phe Glu Lys Arg Tyr Gln Ile Gln Asp Phe Asp Phe Leu Met Ala Asn
        115                 120                 125
Asn Thr Met Ile Leu Arg Ser Pro Tyr Lys Ile Leu Arg Ser Phe Val
    130                 135                 140
Leu Val Asn Pro Tyr Arg Ile Val Leu Asp Thr Gln Lys Gly Pro Leu
145                 150                 155                 160
Asp Ile Tyr Gln Asn Met Asp Leu Asn Gln Lys Phe Phe Ser His Ile
                165                 170                 175
Lys Val Gly Thr His Lys Asp Tyr Tyr Arg Ile Thr Leu Ile Leu Asp
            180                 185                 190
Gly Lys Tyr Arg Tyr Leu Leu Glu Glu Lys Asn Gly Ala Tyr Glu Leu
        195                 200                 205
Lys Leu Lys
    210
```

(2) INFORMATION FOR SEQ ID NO:1492:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:1492

```
Lys Ala Val Ala Thr Pro His His Thr Pro Leu Trp Leu Ser Val Tyr
1               5                  10                  15
Glu Ser Phe Lys Glu Ala Leu Asp Phe Lys Glu Val Ile Leu Val Val
            20                  25                  30
Ser Glu Leu Asp Tyr Val Tyr Ile Gln Arg His Tyr Pro Lys Ile Lys
        35                  40                  45
Leu Val Lys Gly Gly Ala Ser Arg Gln Glu Ser Val Arg Asn Ala Leu
    50                  55                  60
Lys Val Ile Asp Ser Thr Tyr Thr Ile Thr Ser Asp Val Ala Arg Gly
65                  70                  75                  80
Leu Ala Asn Met Glu Ala Leu Lys Ser Leu Phe Leu Thr Leu Gln Gln
                85                  90                  95
Thr Ser His Tyr Cys Ile Ala Pro Tyr Leu Pro Cys Tyr Asp Thr Ala
            100                 105                 110
Ile Tyr Tyr Asn Glu Ala Leu Asp Arg Glu Ala Ile Lys Leu Ile Gln
        115                 120                 125
Thr Pro Gln Leu Ser His Thr Lys Thr Leu Gln Ser Ala Leu Asn Gln
    130                 135                 140
Gly Gly Phe Lys Asp Glu Ser Ser Ala Ile Leu Gln Ala Phe Pro Asn
145                 150                 155                 160
Ser Val Ser Tyr Ile Glu Gly Ser Lys Asp Leu His Lys Leu Thr Thr
                165                 170                 175
Ser Gly Asp Leu Lys Phe Phe Thr Pro Phe Phe Asn Pro Ala Lys Asp
            180                 185                 190
Thr Phe Ile Gly Met Gly Phe Asp Thr His Ala Phe Ile Lys Asp Lys
        195                 200                 205
Pro Met Val Leu Gly Gly Val Val Leu Asp Cys Glu Phe Gly Leu Lys
    210                 215                 220
Ala His Ser Asp Gly Asp Ala Leu Leu His Ala Val Ile Asp Ala Ile
225                 230                 235                 240
Leu Gly Ala Ile Lys Gly Gly Asp Ile Gly Glu Trp Phe Pro Asp Asn
                245                 250                 255
Asp Pro Lys Tyr Lys Asn Ala Ser Ser Lys Glu Leu Leu Lys Ile Val
            260                 265                 270
Leu Asp Phe Ser Gln Ser Ile Gly Phe Glu Leu Leu Glu Met Gly Ala
        275                 280                 285
Thr Ile Phe Ser Glu Ile Pro Lys Ile Thr Pro Tyr Lys Pro Ala Ile
    290                 295                 300
Leu Glu Asn Leu Ser Gln Leu Leu Gly Leu Glu Lys Ser Gln Ile Ser
305                 310                 315                 320
Leu Lys Val Thr Thr Met Glu Lys Met Gly Phe Ile Gly Lys Gln Glu
                325                 330                 335
Gly Leu Leu Val Gln Ala His Val Ser Met Arg Tyr Lys Gln Lys Leu
            340                 345                 350
```

(2) INFORMATION FOR SEQ ID NO:1493:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493

```
Cys Leu Gly Met Cys Phe Ile Leu Lys Pro Phe Leu Ser Cys Leu Lys
1               5                  10                  15
Trp Ala Asn Pro Ser Leu Lys Pro Leu Ser Asn Ala Val Leu Arg Leu
            20                  25                  30
Ser Arg Gly Glu Ile Glu Asp Val Phe Val Gly Glu Cys Phe Asn Ser
        35                  40                  45
Asp Lys Gln Lys Tyr Trp Arg Ile Leu Glu Asp Lys Thr Ala His Phe
    50                  55                  60
Ile Glu Ala Ser Leu Lys Ser Met Ala Ile Leu Leu Asn Lys Asp Ala
65                  70                  75                  80
Lys Met Tyr Ala Asp Phe Gly Leu His Phe Gly Met Ala Phe Gln Ile
                85                  90                  95
Ile Asp Asp Leu Leu Asp Ile Thr Gln Asp Ala Asn Thr Leu Gly Lys
            100                 105                 110
Pro Asn Phe Ser Asp Phe Lys Glu Gly Lys Thr Thr Leu Pro Tyr Leu
        115                 120                 125
Leu Leu Tyr Glu Lys Leu Asn Gln His Glu Gln Gly Leu Leu Ile Ser
    130                 135                 140
Tyr Phe Lys Gln Asp Ser His Glu Ile Ile Glu Trp Thr Lys Glu Lys
145                 150                 155                 160
Phe Lys Gln His Gly Ile Ile Glu Glu Thr Leu Lys Ile Ala Gln Val
                165                 170                 175
Tyr Ser Lys Lys Ala Leu Glu Ala Ile Lys Gly Glu Asn Asn Leu Ile
            180                 185                 190
Leu Glu Lys Leu Ala Gln Asp Val Ile Tyr Arg Thr Phe
        195                 200                 205
```

(2) INFORMATION FOR SEQ ID NO:1494:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494

```
Lys Lys Val Lys Met Asn Ile Lys Ile Leu Lys Ile Leu Val Gly Gly
1               5                  10                  15
Leu Phe Phe Leu Ser Leu Asn Ala His Leu Trp Gly Lys Gln Asp Asn
```

```
            20                  25                  30
Ser Phe Leu Gly Ile Gly Glu Arg Ala Tyr Lys Ser Gly Asn Tyr Ser
        35                  40                  45
Lys Ala Ala Ser Tyr Phe Lys Lys Ala Cys Asn Asp Gly Val Ser Glu
    50                  55                  60
Gly Cys Thr Gln Leu Gly Ile Ile Tyr Glu Asn Gly Gln Gly Thr Arg
65                  70                  75                  80
Ile Asp Tyr Lys Lys Ala Leu Glu Tyr Tyr Lys Thr Ala Cys Gln Ala
                85                  90                  95
Asp Asp Arg Glu Gly Cys Phe Gly Leu Gly Gly Leu Tyr Asp Glu Gly
            100                 105                 110
Leu Gly Thr Ala Gln Asn Tyr Gln Glu Ala Ile Asp Ala Tyr Ala Arg
        115                 120                 125
His Ala Phe
    130
```

This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:1495:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495

```
Ser Ser Lys Thr Ala Phe Arg Ala Lys Gln Ile Ile Thr Ala Thr Asp
1               5                   10                  15
Ile Ser Ala Gln Lys Arg Gln Glu Arg Leu Ala Ser Met Gly Lys Ile
            20                  25                  30
Ser Ala His Leu Ala His Glu Ile Arg Asn Pro Val Gly Ser Ile Ser
        35                  40                  45
Leu Leu Ala Ser Val Leu Leu Lys His Ala Asn Glu Lys Thr Lys Pro
    50                  55                  60
Ile Val Val Glu Leu Gln Lys Ala Leu Trp Arg Val Glu Arg Ile Ile
65                  70                  75                  80
Lys Ala Thr Leu Leu Phe Ser Lys Gly Ile Gln Ala Asn Arg Thr Lys
                85                  90                  95
Gln Ser Leu Lys Thr Leu Glu Ser Asp Leu Lys Glu Ala Leu Asn Cys
            100                 105                 110
Tyr Thr Tyr Ser Lys Asp Ile Asp Phe Leu Phe Asn Phe Ser Asp Glu
        115                 120                 125
Glu Gly Phe Phe Asp Phe Asp Leu Met Gly Ile Val Leu Gln Asn Phe
    130                 135                 140
Leu Tyr Asn Ala Ile Asp Ala Ile Glu Ala Leu Glu Glu Ser Glu Gln
145                 150                 155                 160
Gly Gln Val Lys Ile Glu Ala Phe Ile Gln Asn Glu Phe Ile Val Phe
                165                 170                 175
Thr Ile Ile Asp Asn Gly Lys Glu Val Glu Asn Lys Ser Ala Leu Phe
            180                 185                 190
Glu Pro Phe Glu Thr Thr Lys Leu Lys Gly Asn Gly Leu Gly Leu Ala
        195                 200                 205
Leu Ser Leu Gln Val Val Lys Ala His Glu Gly Ser Ile Ala Leu Leu
    210                 215                 220
```

Glu Asn Gln Glu Lys Thr Phe Glu Ile Lys Ile Leu Asn Ala Ser
225 230 235

(2) INFORMATION FOR SEQ ID NO:1496:

This Sheet Has Been Replaced

(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:1496

Lys Pro Lys Thr Ile Leu Lys Lys Gly Leu Leu Met Lys Thr Phe Glu
1 5 10 15
Ile Leu Lys His Leu Gln Ala Asp Ala Ile Val Leu Phe Met Lys Val
20 25 30
His Asn Phe His Trp Asn Val Lys Gly Thr Asp Phe Phe Asn Val His
35 40 45
Lys Ala Thr Glu Glu Ile Tyr Glu Gly Phe Ala Asp Met Phe Asp Asp
50 55 60
Leu Ala Glu Arg Ile Val Gln Leu Gly His His Pro Leu Val Thr Leu
65 70 75 80
Ser Glu Ala Ile Lys Leu Thr Arg Val Lys Glu Glu Thr Lys Thr Ser
85 90 95
Phe His Ser Lys Asp Ile Phe Lys Glu Ile Leu Glu Asp Tyr Lys His
100 105 110
Leu Glu Lys Glu Phe Lys Glu Leu Ser Asn Thr Ala Glu Lys Glu Gly
115 120 125
Asp Lys Val Thr Val Thr Tyr Ala Asp Asp Gln Leu Ala Lys Leu Gln
130 135 140
Lys Ser Ile Trp Met Leu Glu Ala His Leu Ala
145 150 155

(2) INFORMATION FOR SEQ ID NO:1497:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497

```
Gly Ile Cys Met Gln Glu Lys Arg Leu Lys Ala Ile Gln Asn Lys Ile
1               5                  10                  15
Ala Ser Trp Ile Lys Glu Ile Glu Ser Gly Phe Ile Asp Ala Leu Phe
            20                  25                  30
Ser Lys Ile Gly Pro Ser Lys Met Leu Arg Ser Lys Leu Met Leu Ala
        35                  40                  45
Leu Leu Asp Glu Lys Thr Asp Ala Ile Leu Leu Asp Lys Ala Leu Asn
    50                  55                  60
Leu Cys Ala Ile Val Glu Met Ile Gln Thr Ala Ser Leu Leu His Asp
65                  70                  75                  80
Asp Val Ile Asp Lys Ala Thr Met Arg Arg Lys Leu Pro Ser Ile Asn
                85                  90                  95
Ala Leu Phe Gly Asn Phe Asn Ala Val Met Leu Gly Asp Val Phe Tyr
            100                 105                 110
Ser Lys Ala Phe Phe Glu Leu Ser Lys Met Gly Glu Ser Ile Ala Gln
        115                 120                 125
Ala Pro Leu
    130
```

This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:1498:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 577 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498

```
Cys Met Leu Phe Ser Lys Leu Phe Ala Pro Thr Leu Lys Glu Pro Pro
1               5                  10                  15
Lys Asp Ala Val Leu Lys Ser Pro Lys His Pro Gly Asn Gly Gly His
            20                  25                  30
Pro Leu Gln Ile Gly Ser Gly Ile Tyr Asn Phe Leu Pro Leu Ala Lys
        35                  40                  45
Lys Val Leu Asp Lys Ile Glu Asn Val Thr His Lys Arg Met Gln Glu
    50                  55                  60
His Gly Ala Gln Asn Ile Leu Met Ser Phe Val Val Leu Ala Ser Leu
65                  70                  75                  80
Trp Glu Lys Ser Gly Arg Leu Asp Lys Tyr Gly Lys Glu Leu Leu Val
                85                  90                  95
Phe Lys Asp Arg Lys Asp Asn Asp Phe Val Leu Ser Pro Thr Leu Glu
            100                 105                 110
Glu Asn Ile Thr Glu Ile Ala Ala Asn Phe Ile Lys Ser Tyr Lys Gln
        115                 120                 125
Leu Pro Val His Leu Tyr Gln Ile His Thr Lys Phe Arg Asp Glu Ile
    130                 135                 140
Arg Pro Arg Phe Gly Leu Val Arg Ala Arg Glu Phe Ile Met Lys Asp
145                 150                 155                 160
Gly Tyr Ser Phe His Glu Asp Ala Glu Ser Leu Asp Lys Glu Ile Leu
                165                 170                 175
Asn Thr Gln Ser Ala Tyr Lys Glu Ile Leu Ser Asp Leu Gly Leu Asp
            180                 185                 190
```

```
Phe Arg Ile Val Glu Ala Asp Ser Gly Ala Ile Gly Gly Ser Lys Ser
        195                 200                 205
Arg Glu Phe Val Val Leu Thr Glu Cys Gly Glu Asp Thr Ile Val Val
    210                 215                 220
Cys Gln Asn Cys Asp Tyr Ala Ala Asn Ile Glu Ile Ala Lys Arg Ser
225                 230                 235                 240
Lys Arg Thr Glu Pro Leu Met Ser Pro Ser Ala Leu Ala Lys Phe Pro
                245                 250                 255
Thr Pro Asn Thr Thr Ser Ala Pro Ser Val Ala Glu Phe Phe Lys Thr
            260                 265                 270
Glu Pro Tyr Phe Val Leu Lys Ala Leu Val Asn Lys Val Ile His Lys
        275                 280                 285
Asp Lys Glu Thr Leu Ala Cys Phe Phe Val Arg Gly Asp Asp Asn Leu
    290                 295                 300
Glu Glu Thr Lys Ala Leu Asn Thr Leu Asn Leu Leu Gly Ala Asn Ala
305                 310                 315                 320
Leu Glu Leu Arg Glu Ala Asn Glu Glu Asp Leu Asn Lys Ala Gly Leu
                325                 330                 335
Ile Ala Gly Phe Ile Gly Pro Tyr Gly Leu Lys Lys His Val Cys Tyr
            340                 345                 350
Ile Ile Phe Asp Glu Asp Leu Lys Glu Gly Asp Cys Leu Ile Val Gly
        355                 360                 365
Ala Asn Glu Lys Asp Phe His Ala Val Gly Val Asp Leu Lys Gly Phe
    370                 375                 380
Glu Asn Leu Val Tyr Ala Asp Ile Val Gln Val Lys Glu Ser Asp Cys
385                 390                 395                 400
Cys Pro Asn Cys Gln Gly Ala Leu Lys Tyr His Lys Ser Leu Glu Val
                405                 410                 415
Gly His Ile Phe Lys Leu Gly Gln Ser Tyr Ala Lys Ser Leu Lys Ala
            420                 425                 430
Ser Phe Leu Asp Lys Asn Gly Lys Glu Arg Phe Phe Glu Met Gly Cys
        435                 440                 445
Tyr Gly Ile Gly Ile Ser Arg Leu Leu Ser Val Ile Leu Glu Gln Lys
    450                 455                 460
Ser Asp Asp Leu Gly Cys Val Trp Thr Lys Asn Thr Ala Pro Phe Asp
465                 470                 475                 480
Val Val Ile Val Val Ser Asn Leu Lys Asp Glu Ala Gln Lys Lys Leu
                485                 490                 495
Ala Phe Glu Val Tyr Glu Arg Leu Leu Gln Lys Gly Val Asp Ala Leu
            500                 505                 510
Leu Asp Asp Arg Asp Ala Arg Phe Gly Ala Lys Met Arg Asp Phe Glu
        515                 520                 525
Leu Ile Gly Glu Arg Leu Ala Leu Ile Val Gly Lys Gln Thr Leu Glu
    530                 535                 540
Ser Lys Glu Phe Glu Cys Ile Lys Arg Ala Asn Leu Glu Lys Gln Thr
545                 550                 555                 560
Ile Lys Asp Ile Glu Leu Glu Glu Lys Ile Leu Glu Met Leu Ala Ser
                565                 570                 575
Glu
```

(2) INFORMATION FOR SEQ ID NO:1499:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499

```
Ile Arg Glu Pro Gln Val Ala Ile Met Thr Ala Met Met Arg Tyr Phe
1               5                  10                  15
His Ile Tyr Ala Thr Thr Phe Phe Phe Pro Leu Ala Leu Leu Phe Ala
            20                  25                  30
Val Ser Gly Leu Ser Leu Leu Phe Lys Ala Arg Gln Asp Thr Gly Ala
        35                  40                  45
Lys Ile Lys Glu Trp Val Leu Glu Lys Ser Leu Lys Lys Glu Glu Arg
    50                  55                  60
Leu Asp Phe Leu Lys Gly Phe Ile Lys Glu Asn His Ile Ala Met Pro
65                  70                  75                  80
Lys Lys Ile Glu Pro Arg Glu Tyr Arg Gly Ala Leu Val Ile Gly Thr
                85                  90                  95
Pro Leu Tyr Glu Ile Asn Leu Glu Thr Lys Gly Thr Gln Thr Lys Ile
            100                 105                 110
Lys Thr Ile Glu Arg Gly Phe Leu Gly Ala Leu Ile Met Leu His Lys
        115                 120                 125
Ala Lys Val Gly Ile Val Phe Gln Ala Leu Leu Gly Ile Phe Cys Val
    130                 135                 140
Phe Leu Leu Leu Phe Tyr Leu Ser Ala Phe Leu Met Val Ala Phe Lys
145                 150                 155                 160
Asp Thr Lys Arg Met Phe Ile Ser Val Leu Ile Gly Ser Val Val Phe
                165                 170                 175
Phe Gly Ala Ile Tyr Trp Ser Leu
            180
```

(2) INFORMATION FOR SEQ ID NO:1500:

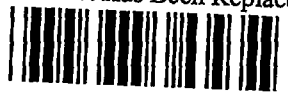
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500

```
Leu Ile Lys Ser Lys Ser Lys Lys Trp Leu Leu Val Gly Glu Gly Ala
1               5                  10                  15
Asn Ser Glu Ile Phe Glu Ala Ser Met Gln Ser Leu Leu Lys Thr Asp
            20                  25                  30
Gly Val Tyr Ser Asn His Lys Pro Ile Tyr Gln Glu Phe Tyr Glu Leu
        35                  40                  45
Asn Ser His Asn Gly Leu Tyr Tyr Gln Pro Asn Val Phe Phe Ala Tyr
    50                  55                  60
Glu Ser Cys Ala Leu Gly Phe Arg Lys Gly Gly Leu Ile Leu Asp Asn
65                  70                  75                  80
Phe Ser Lys Phe Val Ser His Arg Leu Gln
                85                  90
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1501:

(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:1501

```
Met Leu Glu Ser Val Asn Val Lys Ile Ser Ala Asp Asp Ile Lys Ser
1               5                  10                  15
Lys Asn Val Ala Ala Val Met Ile Thr Ala Ser Leu Pro Pro Phe Ala
            20                  25                  30
Arg Gln Gly Asp Lys Ile Asp Ile His Ile Ser Ser Ile Gly Asp Ala
        35                  40                  45
Lys Ser Ile Gln Gly Gly Thr Leu Val Met Thr Pro Leu Asn Ala Val
    50                  55                  60
Asp Gly Asn Ile Tyr Ala Leu Ala Gln Gly Ala Ile Ile Ser Gly Asn
65                  70                  75                  80
Ser Ser Asn Leu Leu Ser Ala Asn Ile Ile Asn Gly Ala Thr Ile Glu
                85                  90                  95
Arg Glu Val Ser Tyr Asp Leu Phe His Lys Asn Ala Met Thr Leu Ser
            100                 105                 110
Leu Lys Asn Pro Asn Phe Lys Asn Ala Ile Gln Val Gln Asn Thr Leu
        115                 120                 125
Asn Lys Val Phe Gly Asn Lys Val Ala Ile Ala Leu Asp Pro Lys Thr
    130                 135                 140
Ile Gln Ile Thr Arg Pro Glu Arg Leu Ser Met Val Glu Phe Leu Ala
145                 150                 155                 160
Leu Val Gln Glu Ile Pro Ile Tyr Tyr Arg Ala Lys Asn Lys Ile Ile
                165                 170                 175
Val Asp Glu Lys Ser Gly Thr Ile Val Ser Gly Val Asp Ile Ile Val
            180                 185                 190
His Pro Ile Val Val Thr Ser Gln Asp Ile Thr Leu Lys Ile Thr Lys
        195                 200                 205
Glu Pro Leu Asn Asp Ser Lys Asn Met Gln Asp Leu Asp Asn Asn Met
    210                 215                 220
Ser Leu Asp Thr Ala His Asn Thr Leu Ser Ser Asn Gly Lys Asn Ile
225                 230                 235                 240
Thr Ile Ala Gly Val Val Lys Ala Leu Gln Lys Ile Gly Val Ser Ala
                245                 250                 255
Lys Gly Met Val Ser Ile Leu Gln Ala Leu Lys Lys Ser Gly Ala Ile
            260                 265                 270
Ser Ala Lys Trp Arg Tyr Tyr Asp Lys Gln Gln
        275                 280
```

(2) INFORMATION FOR SEQ ID NO:1502:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 amino acids
(B) TYPE: amino acid

This Sheet Has Been Replaced

(D) TOPOLOGY: linear

(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:1502

```
Thr Gly His Gly Arg Leu Gly Trp Ile Leu Asn Pro Lys Lys Ala Lys
1               5                  10                  15
Phe Ile Ala Leu Lys Gln Ala Trp Ile Tyr Glu Arg Met Leu Ser Phe
            20                  25                  30
Ile Ser Ala Phe Asp Lys Arg Gly Val Ser Ile Arg Leu Leu Thr Ala
        35                  40                  45
Leu Leu Leu Leu Phe Ser Leu Gly Leu Ala Lys Asp Leu Glu Ile Gln
    50                  55                  60
Thr Phe Val Ala Lys Tyr Leu Ser Lys Asn Gln Lys Ile Gln Ala Leu
65                  70                  75                  80
Gln Glu Gln Ile Asp Ala Leu Asp Ser Gln Glu Lys Val Val Ser Lys
                85                  90                  95
Trp Asp Asn Pro Ile Leu Tyr Leu Gly Tyr Asn Asn Ala Asn Val Ser
            100                 105                 110
Asp Phe Phe Arg Leu Asp Ser Thr Leu Met Gln Asn Met Ser Leu Gly
        115                 120                 125
Leu Ser Gln Lys Val Asp Leu Asn Gly Lys Lys Leu Thr Gln Ser Lys
    130                 135                 140
Met Ile Asn Leu Glu Lys Gln Lys Lys Ile Leu Glu Leu Lys Lys Thr
145                 150                 155                 160
Lys Gln Gln Leu Val Ile Asn Leu Met Ile Asn Gly Ile Glu Asn Tyr
                165                 170                 175
Lys Asn Gln Gln Glu Ile Glu Leu Leu Asn Thr Ala Ile Lys Asn Leu
            180                 185                 190
Glu Asn Thr Leu Tyr Gln Ala Asn His Ser Ser Ser Pro Asp Leu Ile
        195                 200                 205
Ala Ile Ala Lys Leu Glu Ile Leu Lys Ser Gln Leu Glu Ile
    210                 215                 220
```

(2) INFORMATION FOR SEQ ID NO:1503:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

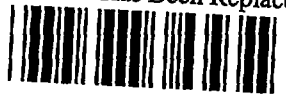
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1503

```
Ile Val Phe His Gln Gly Ser Leu Ser Val Ser Gly Leu Phe Lys Met
1               5                  10                  15
Arg Ile Leu Ser Phe Lys Lys Asn Lys Arg Ala Val Phe Ser Leu Tyr
            20                  25                  30
Leu Phe Ile Ala Leu Leu Ala Leu Ser Leu Leu Ala Pro Leu Trp Val
        35                  40                  45
Asn Asp Arg Pro Leu Phe Ile Tyr Lys Asp Asn Lys Ala Tyr Phe Pro
    50                  55                  60
Met Phe Lys Asn Tyr Ala Glu Val Glu Phe Gly Gly Asp Phe Phe Thr
65                  70                  75                  80
Pro Thr Asp Tyr Asn Asp Pro Tyr Val Gln Asn Thr Leu Leu Lys Asp
                85                  90                  95
Ala Phe Ile Ile His Ala Leu Ile Pro Tyr Ser Tyr Asp Thr Ile Ile
            100                 105                 110
Met Asp Leu Asp Ser Pro Ala Pro Thr Pro Pro Ser Phe Lys His Leu
        115                 120                 125
Leu Gly Thr Asp Asp Gln Ala Arg Asp Val Leu Ala Arg Leu Val Tyr
    130                 135                 140
Gly Tyr Arg Val Ser Leu Val Phe Gly Ile Leu Leu Thr Leu Phe Ser
145                 150                 155                 160
Val Leu Ile Gly Val Ser Leu Gly Ala Phe Gln Gly Tyr Tyr Gly Gly
                165                 170                 175
Leu Val Asp Leu Val Gly Gln Arg Leu Ser Glu Ile Trp Ser Ala Ile
            180                 185                 190
Pro Met Leu Phe Leu Leu Ile Val Ile Ser Ser Ala Phe Asn Ser Asn
        195                 200                 205
Phe Trp Ile Ile Leu Phe Leu Val Leu Leu Phe Ser Trp Met Gly Leu
    210                 215                 220
Ser Gln Val Val Arg Thr Glu Phe Leu Lys Ala Arg Asn Met Asp Tyr
225                 230                 235                 240
Thr Lys Ala Ala Arg Ala Leu Gly Val Asn Asp Leu Lys Ile Ile Phe
                245                 250                 255
Tyr His Val Leu Pro Asn Ala Leu Val Ala Thr Ile Thr Tyr Ile Pro
            260                 265                 270
Phe Leu Met Ala Ala Ser Ile Ser Thr Leu Val Ser Leu Asp Phe Leu
        275                 280                 285
Gly Phe Gly Met Pro Ile Gly Ser Ala Ser Leu Gly Glu Leu Val Asn
    290                 295                 300
Gln Gly Lys Asp Asn Leu Thr Thr Pro His Leu Ala Val Val Ala Phe
305                 310                 315                 320
Val Ala Ile Ser Leu Leu Leu Ser Val Leu Val Phe Ile Gly Glu Gly
                325                 330                 335
Val Arg Asp Ala Phe Asn Ala Asn Met Leu Lys
            340                 345
```

(2) INFORMATION FOR SEQ ID NO:1504:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 519 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1504

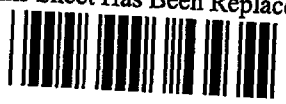
```
Arg Gly Tyr Met Leu Glu Ile Lys Asn Leu Asn Cys Val Leu Asn Ser
1               5                  10                  15
His Phe Ser Leu Gln Asn Ile Asn Ile Ser Leu Ser Tyr Ser Glu Arg
            20                  25                  30
Val Ala Ile Val Gly Glu Ser Gly Ser Gly Lys Ser Ser Ile Ala Asn
        35                  40                  45
Leu Val Met Arg Leu Asn Pro Arg Phe Lys Pro His Asn Gly Glu Ile
    50                  55                  60
Leu Phe Glu Thr Thr Asn Leu Leu Lys Glu Ser Glu Ala Phe Met Gln
65                  70                  75                  80
His Leu Arg Gly Asn Ile Ile Ala Tyr Ile Ala Gln Asp Pro Leu Ser
                85                  90                  95
Ser Leu Asn Pro Leu His Lys Ile Gly Lys Gln Met Ser Glu Ala Tyr
            100                 105                 110
Phe Leu His His Lys Asn Ala Ser Gln Val Leu Leu Lys Glu Gln Val
        115                 120                 125
Leu Asn Ala Met Lys Gln Val Gln Leu Asp Glu Lys Phe Leu Asp Arg
    130                 135                 140
Tyr Pro Tyr Glu Leu Ser Gly Gly Gln Arg Gln Arg Val Cys Ile Ala
145                 150                 155                 160
Met Gly Ile Ile Asn Ala Pro Lys Leu Leu Ile Cys Asp Glu Pro Thr
                165                 170                 175
Thr Ala Leu Asp Ala Gln Ile Gln Asn Gln Ile Leu Asp Leu Leu Lys
            180                 185                 190
Gln Leu Ser Val Glu Lys Asn Ile Ala Leu Leu Phe Ile Ser His Asp
        195                 200                 205
Leu Lys Ala Val Lys Arg Leu Ala Asp Arg Val Tyr Val Leu Lys Lys
    210                 215                 220
Gly Glu Ile Val Glu Thr Asn Leu Thr Lys Glu Leu Phe Asn Asp Pro
225                 230                 235                 240
Lys His Glu Tyr Ser Lys Leu Leu Ile Gln Ala Ser Asn Leu Pro Ala
                245                 250                 255
Lys Asn Leu Lys Ala Leu Asp Glu Thr Leu Leu Glu Val Lys Asp Phe
            260                 265                 270
Ser Val Tyr Tyr Leu Gln Lys Arg Phe Phe Arg Pro Ser Leu Lys Lys
        275                 280                 285
Pro Leu Ile Ala Ser Val Asp Phe Ser Leu Lys Ala Lys Glu Asn Ile
    290                 295                 300
Gly Ile Ile Gly Glu Ser Gly Ser Gly Lys Ser Ser Leu Ala Leu Gly
305                 310                 315                 320
Leu Leu Lys Leu Ala Leu Asn Ser Gly Glu Glu Lys Ile Leu Gly Gln
                325                 330                 335
Ser Val Gly Leu Leu Asn Ser Lys Ala Phe Lys Pro Tyr Arg Lys Ile
            340                 345                 350
Leu Gln Met Val Phe Gln Asp Pro Tyr Ala Ser Leu Asn Pro Arg Leu
        355                 360                 365
Ser Ile Gln Ser Ile Leu Ile Glu Ala Leu Arg Phe Ala Tyr Pro Lys
    370                 375                 380
Ala Ser Gln Gln Glu Trp His His Leu Ala Glu Leu Cys Leu Glu Glu
385                 390                 395                 400
Val Cys Leu Asn Pro Glu Leu Leu Asn Phe Tyr Ala Tyr Glu Leu Ser
                405                 410                 415
Gly Gly Glu Arg Gln Arg Val Ala Ile Ala Arg Ala Ile Ala Leu Lys
            420                 425                 430
Pro Arg Ile Ile Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Lys Ser
        435                 440                 445
Ile Gln Lys Ser Val Leu Glu Leu Leu Leu Asn Leu Gln Glu Lys Gln
    450                 455                 460
Asp Leu Ser Tyr Leu Phe Ile Ser His Asp Leu Asp Val Ile Lys Ala
465                 470                 475                 480
Phe Cys Asp Arg Val Leu Val Val Ser Glu Gly Lys Ile Val Glu Thr
                485                 490                 495
Gly Ala Ile Glu Glu Val Phe Asp Asn Pro Lys His Ala Tyr Thr Lys
            500                 505                 510
```

This Sheet Has Been Replaced

SUBSTITUTE SHEET (RULE 26)

Arg Leu Leu Glu Ser Arg Leu
515

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1505:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1505

```
Gly Gly Leu Met Asn Thr Ile Ile Arg Tyr Ala Ser Leu Trp Gly Leu
1               5                  10                  15
Cys Ile Thr Leu Thr Leu Ala Gln Thr Pro Ser Lys Thr Pro Asp Glu
            20                  25                  30
Ile Lys Gln Ile Leu Asn Asn Tyr Ser His Lys Asn Leu Lys Leu Ile
        35                  40                  45
Asp Pro Pro Thr Ser Ser Leu Glu Ala Thr Pro Gly Phe Leu Pro Ser
    50                  55                  60
Pro Lys Glu Thr Ala Thr Thr Ile Asn Gln Glu Ile Ala Lys Tyr His
65                  70                  75                  80
Glu Lys Ser Asp Lys Ala Ala Leu Gly Leu Tyr Glu Leu Leu Lys Gly
                85                  90                  95
Ala Thr Thr Asn Leu Ser Leu Gln Ala Gln Glu Leu Ser Val Lys Gln
            100                 105                 110
Ala Met Lys Asn His Thr Ile Ala Lys Ala Met Phe Leu Pro Thr Leu
        115                 120                 125
Asn Ala Ser Tyr Asn Phe Lys Asn Glu Ala Arg Asp Thr Pro Glu Tyr
    130                 135                 140
Lys His Tyr Asn Thr Gln Gln Leu Gln Ala Gln Val Thr Leu Asn Val
145                 150                 155                 160
Phe Asn Gly Phe Ser Asn Val Asn Asn Val Lys Glu Lys Ser Ala Thr
                165                 170                 175
Thr Asp Pro Leu Trp Leu Ile
            180
```

(2) INFORMATION FOR SEQ ID NO:1506:

(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:1506

```
Val Lys Phe Ser Val Leu Thr Leu Phe Pro Gln Leu Ile Leu Pro Tyr
1               5                  10                  15
Phe Glu Asp Ser Ile Leu Lys Arg Ala Leu Glu Lys Asn Leu Phe Glu
            20                  25                  30
Leu Glu Val Leu Asn Leu Arg Asp Phe Ser Ala Asn Lys Tyr Gln Lys
        35                  40                  45
Ala Asp His Thr Leu Ile Gly Gly Gly Ala Gly Gln Ile Leu Asp Pro
    50                  55                  60
Glu Met Ile Glu Asn Ala Leu His Ser Val Lys Asn Pro Lys His Thr
65                  70                  75                  80
Ile Phe Leu Ser Ala Val Gly Lys Pro Phe Lys Gln Ile Asp Ala Met
                85                  90                  95
Arg Leu Ala Gln Lys Lys His Val Val Leu Val Cys Gly Arg Tyr Glu
            100                 105                 110
Gly Phe Asp Glu Arg Ser Ile Glu Leu Gly Ala Asp Glu Val Phe Cys
        115                 120                 125
Ile Gly Asp Phe Ile Leu Thr Gly Gly Glu Leu Gly Ala Leu Cys Leu
    130                 135                 140
Ile Asp Ser Ile Ala Arg His Ile Gln Gly Val Leu Gly Asn Ala Gln
145                 150                 155                 160
Ser Leu Glu Asn Glu Ser Phe Glu Asn Asn Tyr Leu Glu Thr Pro Asn
                165                 170                 175
Phe Ala Asn Ala Val Phe Lys Ser Lys Glu Ile Asn Lys Ile Pro Ala
            180                 185                 190
Pro Leu Glu Tyr Ser Lys Gly Asn His Ala Lys Ile Lys Gln Leu Lys
        195                 200                 205
Leu Asp Leu Ser Lys Leu Arg Thr Lys Phe Tyr Arg Leu Asp Leu Phe
    210                 215                 220
Lys Gln His Lys Ser
225
```

(2) INFORMATION FOR SEQ ID NO:1507:

(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:1507

```
Arg Glu Gln Trp Phe His Phe Arg Ser Thr Pro Pro Thr Val Val Leu
1               5                  10                  15
Met Ala Gly Leu Gln Gly Ser Gly Lys Thr Thr Thr Thr Ala Lys Leu
            20                  25                  30
Ala His Tyr Leu Lys Thr Lys Asn Lys Lys Val Leu Leu Cys Ala Cys
        35                  40                  45
Asp Leu Gln Arg Leu Ala Ala Val Glu Gln Leu Lys Val Leu Gly Glu
    50                  55                  60
```

This Sheet Has Been Replaced



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

(2) INFORMATION FOR SEQ ID NO:1508:

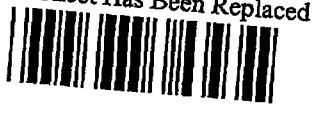
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1508

```
Arg Lys Ala Met Asn Thr His Leu Lys Gln Leu Ile Glu Ile Ser His
1               5                   10                  15
Leu Asp Lys Glu Ile Asp Ser Leu Glu Pro Leu Ile Arg Glu Lys Arg
            20                  25                  30
Lys Asp Leu Asp Lys Ala Leu Asn Asp Lys Glu Ala Lys Asn Lys Ala
```

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

(2) INFORMATION FOR SEQ ID NO:1509:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1509

```
Met Asn Glu Ile Asp Lys Ser Val Asp Ile Gly Phe Leu Arg Ile Leu
1               5                   10                  15
Asp Val Ile Lys Lys Val Lys Thr Pro Lys Gly Gly Ile Glu Val Leu
            20                  25                  30
Arg Thr Leu Ile Asp Phe Thr Pro Lys Ile Glu Asn Ala Leu Asn Leu
        35                  40                  45
Ala Thr Lys Ser His Lys Gly Gln Tyr Arg Lys Ser Gly Glu Pro Tyr
    50                  55                  60
Ile Val His Pro Ile Cys Val Ala Ser Val Val Ala Phe Cys Gly Gly
65                  70                  75                  80
Asp Glu Ala Met Val Cys Ala Ala Leu Leu His Asp Val Val Glu Asp
                85                  90                  95
Thr Pro Cys Glu Ile Glu Thr Ile Glu Arg Glu Phe Gly Gln Asp Val
            100                 105                 110
```

```
Ala Asn Leu Val Asp Ala Leu Thr Lys Ile Thr Glu Ile Arg Lys Glu
        115                 120                 125
Glu Leu Gly Val Ser Ser Gln Asp Pro Arg Met Val Val Ser Ala Leu
    130                 135                 140
Thr Phe Arg Lys Ile Leu Ile Ser Ala Ile Gln Asp Pro Arg Ala Leu
145                 150                 155                 160
Val Val Lys Ile Ser Asp Arg Leu His Asn Met Leu Thr Leu Asp Ala
                165                 170                 175
Leu Pro His Asp Lys Gln Val Arg Ile Ser Lys Glu Thr Leu Ala Val
            180                 185                 190
Tyr Ala Pro Ile Ala Ser Arg Leu Gly Met Ser Ser Ile Lys Asn Glu
        195                 200                 205
Leu Glu Asp Lys Ser Phe Tyr Tyr Ile Tyr Pro Glu Glu Tyr Lys Asn
    210                 215                 220
Ile Lys Glu Tyr Leu His Lys Asn Lys Gln Ser Leu Leu Leu Lys Leu
225                 230                 235                 240
Asn Ala Phe Ala Ser Lys Leu Glu Lys Lys Leu Phe Asp Ser Gly Phe
                245                 250                 255
Ser His Ser Asp Phe Lys Leu Val Thr Arg Val Lys Arg Pro Tyr Ser
            260                 265                 270
Ile Tyr Leu Lys Met Gln Arg Lys Gly Ala Val Asn Ile Asp Glu Ile
        275                 280                 285
Leu Asp Leu Leu Ala Ile Arg Ile Leu Leu Lys Asn Pro Ile Asp Cys
    290                 295                 300
Tyr Lys Val Leu Gly Ile Ile His Leu Asn Phe Lys Pro Ile Val Ser
305                 310                 315                 320
Arg Phe Lys Asp Tyr Ile Ala Leu Pro Lys Glu Asn Gly Tyr Lys Thr
                325                 330                 335
Ile His Thr Thr Ile Phe Asp Glu Ser Ser Val Tyr Glu Val Gln Ile
            340                 345                 350
Arg Thr Phe Asp Met His Met Gly Ala Glu Tyr Gly Asn Ser Ala His
        355                 360                 365
Trp Lys Tyr Lys Ala Gly Gly Val Asp His Glu Glu His His Glu Gly
    370                 375                 380
Met Arg Trp Leu Gln Asn Phe Lys Tyr His Asp Ser Asp Leu Lys Asn
385                 390                 395                 400
Asp Pro Lys Glu Phe Tyr Glu Leu Ala Lys Asn Asp Leu Tyr Arg Glu
                405                 410                 415
Asp Ile Val Val Phe Ser Pro His Gly Asp Thr Tyr Thr Leu Pro Val
            420                 425                 430
Gly Ala Ile Ala Leu Asp Phe Ala Tyr Met Val His Ser Asp Leu Gly
        435                 440                 445
Asp Lys Ala Thr Asp Ala Tyr Ile Asn Ser Lys Lys Ala Leu Leu Asn
    450                 455                 460
Gln Glu Leu Arg Ser Gly Asp Val Val Lys Ile Ile Lys Gly Asp Lys
465                 470                 475                 480
Val Ile Pro Arg Phe Ile Trp Met Asp Gln Leu Lys Thr Ser Lys Ala
                485                 490                 495
Lys Asn His Leu Arg Ile Gln Arg Arg Asn Arg Leu Lys Glu Ile Asp
            500                 505                 510
Thr Lys Ser Met Ile Asn Ile Leu Ser Thr Phe Phe Gly Arg Ser Val
        515                 520                 525
Phe Glu Asp Ala Asp Leu Lys Asp Tyr Lys Asn Phe Glu Glu Lys Leu
    530                 535                 540
Thr Asp Cys Gly Val Glu Thr Thr Leu Thr Glu Ala Met Lys Ser Phe
545                 550                 555                 560
Glu Asn Leu Gly Gln Thr His
                565
```

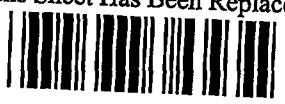
(2) INFORMATION FOR SEQ ID NO:1510:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 amino acids
(B) TYPE: amino acid

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(D) TOPOLOGY: linear

(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:1510

```
Val Thr Ile Lys Ser Phe Ile Asn Gly Leu Arg Arg Asp His Ala Gly
1               5                  10                  15
Lys Asp Lys Lys Gln Ala Gly Phe Gly Glu Ile Phe Trp Gly Ser Val
            20                  25                  30
Ser Trp Gly Gln Pro Val Trp Ile Asp Ile His Val Leu Asp His Ile
        35                  40                  45
Ala Lys Glu Ile Arg Ser Leu Val Glu Asn Asp Ile Glu Val Gly Ile
    50                  55                  60
Val Ile Gly Gly Gly Asn Ile Ile Arg Gly Val Ser Ala Ala Gln Gly
65                  70                  75                  80
Gly Ile Ile Arg Arg Thr Ser Gly Asp Tyr Met Gly Met Leu Ala Thr
                85                  90                  95
Val Ile Asn Ala Val Ala Met Gln Glu Ala Leu Glu His Ile Gly Leu
            100                 105                 110
Asp Thr Arg Val Gln Ser Ala Ile Glu Ile Lys Glu Ile Cys Glu Ser
        115                 120                 125
Tyr Ile Tyr Arg Lys Ala Ile Arg His Leu Glu Lys Gly Arg Val Val
    130                 135                 140
Ile Phe Gly Ala Gly Thr Gly Asn Pro Phe Phe Thr Thr Asp Thr Ala
145                 150                 155                 160
Ala Thr Leu Arg Ala Ile Glu Ile Gly Ser Asp Leu Ile Ile Lys Ala
                165                 170                 175
Thr Lys Val Asp Gly Ile Tyr Asp Lys Asp Pro Asn Lys Phe Lys Asp
            180                 185                 190
Ala Lys Asn Trp Thr Leu
        195
```

(2) INFORMATION FOR SEQ ID NO:1511:

(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:1511

```
Met Asn Ala Leu Lys Arg Ala Cys Leu Arg Leu Met Gly Glu Thr Asn
1               5                  10                  15
```

```
Thr Asp Asp Leu Ser Pro Ala Ser Asp Ala Phe Thr Arg Ser Asp Ile
            20                  25                  30
Pro Leu His Ala Lys Ala Met Leu Lys Asn Arg Ile Glu Asn Tyr Glu
        35                  40                  45
Gln Arg Ile Glu Ala Ile Lys Thr Lys Gly Val Pro Val Ala Tyr Val
    50                  55                  60
Gly Asp Val Val Gly Thr Gly Ser Ser Arg Lys Ser Ala Thr Asn Ser
65                  70                  75                  80
Ile Met Trp His Phe Gly Lys Asp Ile Pro Phe Val Pro Asn Lys Arg
                85                  90                  95
Ser Gly Gly Ile Val Ile Gly Gly Val Ile Ala Pro Ile Phe Phe Ala
            100                 105                 110
Thr Cys Glu Asp Ser Gly Ala Leu Pro Ile Val Ala Asp Val Lys Asp
        115                 120                 125
Leu Lys Glu Gly Asp Ile Ile Lys Ile Tyr Pro Tyr Lys Gly Glu Ile
    130                 135                 140
Thr Leu Asn Asp Lys Val Val Ser Thr Phe Lys Leu Glu Pro Glu Thr
145                 150                 155                 160
Leu Leu Asp Glu Val Arg Ala Ser Gly Arg Ile Pro Leu Ile Ile Gly
                165                 170                 175
Arg Gly Leu Thr Asn Lys Ala Arg Lys Phe Leu Gly Leu Gly Glu Ser
            180                 185                 190
Glu Ala Phe Lys Lys Pro Ser Ala Pro Lys Ser Asp Ala Lys Gly Tyr
        195                 200                 205
Thr Leu Ala Gln Lys Ile Val Gly His Ala Cys Gly Val Lys Gly Ile
    210                 215                 220
Leu Pro Gly Ala Tyr Cys Glu Pro Lys Val Thr Thr Val Gly Ser Gln
225                 230                 235                 240
Asp Thr Thr Gly Ala Met Thr Arg Asp Glu Val Lys Glu Leu Ala Ser
                245                 250                 255
Leu Lys Phe Asp Ala Pro Phe Val Leu Gln Ser Phe Cys His Thr Ala
            260                 265                 270
Ala Tyr Pro Lys Pro Ser Asp Val Ser Leu His Ala Thr Leu Pro Gly
        275                 280                 285
Phe Ile Thr Gln Arg Gly Gly Val Ala Leu His Pro Gly Asp Gly Val
    290                 295                 300
Ile His Thr Trp Leu Asn Arg Met Gly Leu Pro Asp Thr Leu Gly Thr
305                 310                 315                 320
Gly Gly Asp Ser His Thr Arg Phe Pro Leu Gly Ile Ser Phe Arg Gln
                325                 330                 335
Gly Ala Gly
```

(2) INFORMATION FOR SEQ ID NO:1512:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

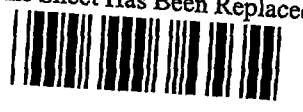
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1512

```
Thr Phe Thr Ile Lys Arg Phe Val Leu Met Lys Ile Lys Ile Gln Lys
```

This Sheet Has Been Replaced



```
1               5                  10                  15
Ile His Pro Asn Ala Leu Ile Pro Lys Tyr Gln Thr Glu Gly Ser Ser
            20                  25                  30
Gly Phe Asp Leu His Ala Val Glu Glu Val Val Ile Lys Pro His Ser
        35                  40                  45
Val Gly Leu Val Arg Ile Gly Ile Cys Leu Ser Leu Glu Val Gly Tyr
    50                  55                  60
Glu Leu Gln Val Arg Thr Arg Ser Gly Leu Ala Leu Asn His Gln Val
65                  70                  75                  80
Met Val Leu Asn Ser Pro Gly Thr Val Asp Asn Asp Tyr Arg Gly Glu
                85                  90                  95
Ile Lys Val Ile Leu Ala Asn Leu Ser Asp Lys Asp Phe Lys Val Gln
            100                 105                 110
Val Gly Asp Arg Ile Ala Gln Gly Val Val Gln Lys Thr Tyr Lys Ala
        115                 120                 125
Glu Phe Ile Glu Cys Glu Gln Leu Asp Glu Thr Ser Arg Gly Ser Gly
    130                 135                 140
Gly Phe Gly Ser Thr Gly Val Ser Lys Ala
145                 150
```

This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:1513:

(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:1513

```
Arg Lys Lys Pro Phe Lys Glu Arg Ile Asp Leu Met Asn Lys Pro Phe
1               5                  10                  15
Leu Ile Leu Leu Ile Ala Leu Ile Ala Phe Ser Gly Cys Asn Met Arg
            20                  25                  30
Lys Tyr Phe Lys Pro Ala Lys His Gln Ile Lys Gly Glu Ala Tyr Phe
        35                  40                  45
Pro Asn His Leu Gln Glu Ser Ile Val Ser Ser Asn Arg Tyr Gly Ala
    50                  55                  60
Ile Leu Lys Asn Gly Ala Val Ile Gly Asp Lys Gly Leu Thr Gln Leu
65                  70                  75                  80
Arg Ile Gly Lys Asn Phe Asn Tyr Glu Ser Ser Phe Leu Asn Glu Ser
                85                  90                  95
Gln Gly Phe Phe Ile Leu Ala Gln Asp Cys Leu Asn Lys Ile Asp Lys
            100                 105                 110
Lys Thr Ser Lys Ser Arg Ala Ala Lys Thr Glu Glu Thr Glu Leu Lys
        115                 120                 125
Leu Lys Gly Val Glu Ala Glu Val Gln Asp Lys Val Cys His Gln Val
    130                 135                 140
Glu Leu Ile Ser Asn Asn Pro Asn Ala Ser Gln Gln Ser Ile Val Ile
145                 150                 155                 160
Pro Leu Glu Thr Phe Ala Leu Ala Arg Ala Leu Lys Gly Ile Phe
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:1514:

(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:1514

```
Gly Met Ser Ile Lys Glu Asn Leu Glu Gln Val Arg Asn Glu Phe Lys
1               5                  10                  15
Ser Asp Glu Lys Leu Leu Glu Gly Ala Phe Arg Leu Glu Lys Phe Phe
            20                  25                  30
Lys Arg Tyr Lys Trp Val Leu Leu Phe Ile Val Val Ala Phe Ile Ala
        35                  40                  45
Tyr Leu Gly Asp Thr Lys Leu Gln Asp Tyr Lys His Glu Gln Thr Arg
    50                  55                  60
Glu Arg Ile Thr Gln Ile Tyr Asn Glu Val Leu Glu Ser Pro Asn Asn
65                  70                  75                  80
Ile Ala Leu Gln Lys Arg Leu Lys Glu Val Ala Pro Glu Leu Tyr Asp
                85                  90                  95
Leu Tyr Gln Phe Ala Arg Ala Ser Glu Arg Asn Asp Ala Asn Glu Phe
            100                 105                 110
Lys Arg Leu Ser Gln Ser Ser Asn Glu Ile Val Lys Ala Phe Ala Lys
        115                 120                 125
Tyr Ser Tyr Ala Ser Leu Ser Arg Asp Lys Asn Leu Leu Glu Lys Ser
    130                 135                 140
Pro Ile Leu Lys Glu Met Ser Ala Leu Gln Glu Val Asn Leu Leu Tyr
145                 150                 155                 160
Glu Glu Asn Ser Lys Asp Ala Ile Lys Lys Ala His Gln Ser Leu Ser
                165                 170                 175
Thr Ile Pro Leu Ser Ser Ser Leu Tyr Ala Ile Ile Ser Val Leu Lys
            180                 185                 190
His Tyr Gly Met Leu Glu Asp Ile Gln Gln Asn Pro Ser Lys Pro Thr
        195                 200                 205
Asn Leu Lys Lys Glu Thr Ile Gln Gly Thr His
    210                 215
```

(2) INFORMATION FOR SEQ ID NO:1515:

(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:

This Sheet Has Been Replaced



(A) NAME/KEY: misc_feature
(B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1515

```
Lys Arg Tyr Lys Arg Leu Glu Gln Glu Ile Lys Lys Arg Asp Lys Met
1               5                  10                  15
Ile Val Gly Leu Ile Gly Val Val Glu Lys Ile Ser Ala Leu Glu Ala
            20                  25                  30
His Ile Glu Val Gln Gly Val Val Tyr Gly Val Gln Val Ser Met Arg
        35                  40                  45
Thr Ala Ala Leu Leu Gln Thr Gly Gln Lys Ala Arg Leu Lys Ile Leu
    50                  55                  60
Gln Val Ile Lys Glu Asp Ala His Leu Leu Tyr Gly Phe Leu Glu Glu
65                  70                  75                  80
Ser Glu Lys Ile Leu Phe Glu Arg Leu Leu Lys Ile Asn Gly Val Gly
                85                  90                  95
Gly Arg Ile Ala Leu Ala Ile Leu Ser Ser Phe Ser Pro Asn Glu Phe
            100                 105                 110
Glu Asn Ile Ile Ala Thr Lys Glu Val Lys Arg Leu Gln Gln Val Pro
        115                 120                 125
Gly Ile Gly Lys Lys Leu Ala Asp Lys Ile Met Val Asp Leu Ile Gly
    130                 135                 140
Phe Phe Ile Gln Asp Glu Asn Arg Pro Ala Arg Asn Glu Val Phe Leu
145                 150                 155                 160
Ala Leu Glu Ser Leu Gly Phe Lys Ser Ala Glu Ile Asn Pro Val Leu
                165                 170                 175
Lys Thr Leu Lys Pro His Leu Ser Ile Glu Ala Ala Ile Lys Glu Ala
            180                 185                 190
Leu Gln Gln Leu Arg Ser
        195
```

(2) INFORMATION FOR SEQ ID NO:1516:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1516

```
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
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:1517:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1517

```
Val Ile Asn Thr Thr Ser Met Leu Lys Lys Ile Phe Leu Thr Asn Ser
1               5                   10                  15
Leu Gly Ile Leu Cys Ser Arg Ile Phe Gly Phe Leu Arg Asp Leu Met
```

```
            20                  25                  30
Met Ala Asn Ile Leu Gly Ala Gly Val Tyr Ser Asp Ile Phe Phe Val
        35                  40                  45
Ala Phe Lys Leu Pro Asn Leu Phe Arg Arg Ile Phe Ala Glu Gly Ser
    50                  55                  60
Phe Ser Gln Ser Phe Leu Pro Ser Phe Ile Arg Ser Ser Ile Lys Gly
65                  70                  75                  80
Gly Phe Ala Ser Leu Val Gly Leu Ile Phe Cys Gly Val Leu Phe Met
                85                  90                  95
Trp Cys Leu Leu Val Ala Leu Asn Pro Leu Trp Leu Thr Lys Leu Leu
            100                 105                 110
Ala Tyr Gly Phe Asp Glu Glu Thr Leu Lys Leu Cys Thr Pro Ile Val
        115                 120                 125
Ala Ile Asn Phe Trp Tyr Leu Leu Leu Val Phe Ile Thr Thr Phe Leu
    130                 135                 140
Gly Ala Leu Leu Gln Tyr Lys His Ser Phe Phe Ala Ser Ala Tyr Ser
145                 150                 155                 160
Ala Ser Leu Leu Asn Leu Cys Met Ile Leu Ala Leu Leu Ile Ser Lys
                165                 170                 175
Glu Lys Thr His Leu Glu Ala Leu Tyr Tyr Leu Ser Tyr Gly Val Leu
            180                 185                 190
Leu Gly Gly Val Ala Gln Ile Leu Leu His Phe Tyr Pro Leu Val Lys
        195                 200                 205
Leu Gly Leu Trp Asp Leu Leu Phe Lys Gly Leu Leu Gly Phe Lys Thr
    210                 215                 220
Lys Asn Thr Asn Lys Lys Glu Tyr Arg Leu Asn Arg Ala Lys Lys Asp
225                 230                 235                 240
Leu Lys Ala Phe Phe Lys Gln Phe Phe Pro Ser Val Leu Gly Asn Ser
                245                 250                 255
Ser Ala Gln Ile Ala Ser Phe Leu Asp Thr Thr Ile Ala Ser Phe Leu
            260                 265                 270
Ala Ser Gly Ser Val Ser Tyr Leu Tyr Tyr Ala Asn Arg Val Phe Gln
        275                 280                 285
Leu Pro Leu Ala Leu Phe Ala Ile Ala Ile Ser Thr Ala Leu Phe Pro
    290                 295                 300
Ser Ile Ala Ile Ala Leu Lys Asn Asn Gln Gln Asp Leu Ile Leu Gln
305                 310                 315                 320
Arg Leu Gln Lys Ala Trp Phe Phe Leu Val Gly Val Leu Leu Leu Cys
                325                 330                 335
Ser Ile Gly Gly Ile Met Leu Ser Lys Glu Ile Thr Glu Leu Leu Phe
            340                 345                 350
Glu Arg Gly Gln Phe Ser Pro Lys Asp Thr Leu Ile Thr Ser Gln Val
        355                 360                 365
Phe Ser Leu Tyr Leu Leu Gly Leu Leu Pro Phe Gly Leu Thr Lys Leu
    370                 375                 380
Phe Ser Leu Trp Leu Tyr Ala Lys Leu Glu Gln Lys Lys Ala Ala Lys
385                 390                 395                 400
Ile Ser Leu Ile Ser Leu Phe Leu Gly Leu Ala Ala Ser Leu Ser Leu
                405                 410                 415
Met Pro Leu Leu Gly Val Leu Gly Leu Arg
            420                 425
```

(2) INFORMATION FOR SEQ ID NO:1518:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

This Sheet Has Been Replaced



(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1518

```
Phe Arg Leu Pro Ser Pro Leu Thr Ser Ile Leu Met Arg Leu Asp Tyr
1               5                  10                  15
Ala Leu Phe Asn Gln His Leu Ala Asn Ser Arg Glu Lys Ala Lys Ala
            20                  25                  30
Leu Val Leu Lys Lys Gln Val Leu Val Asn Lys Met Val Val Ser Lys
        35                  40                  45
Pro Ser Phe Ile Val Lys Glu Gly Asp Gln Ile Glu Leu Ile Ala Pro
    50                  55                  60
Asn Leu Phe Val Ser Arg Ala Gly Glu Lys Leu Gly Ala Phe Leu Glu
65                  70                  75                  80
Asp His Phe Ile Asp Phe Lys Glu Lys Val Val Leu Asp Val Gly Ala
                85                  90                  95
Ser Lys Gly Gly Phe Ser Gln Val Ala Leu Leu Lys Gly Ala Lys Lys
            100                 105                 110
Val Leu Cys Val Asp Val Gly Lys Met Gln Leu Asp Glu Ser Leu Lys
        115                 120                 125
Asn Asp Gln Arg Ile Glu Cys Tyr Glu Glu Cys Asp Ile Arg Gly Phe
    130                 135                 140
Lys Thr Pro Glu Lys Ile Asp Leu Ala Leu Cys Asp Val Ser Phe Ile
145                 150                 155                 160
Ser Leu Tyr Cys Ile Leu Glu Ala Ile Leu Pro Leu Ser Gly Glu Phe
                165                 170                 175
Leu Thr Leu Phe Lys Pro Gln Phe Glu Val Gly Arg Thr Ile Lys Arg
            180                 185                 190
Asn Lys Lys Gly Val Val Met Asp Lys Glu Ala Ile Leu Asn Ala Leu
        195                 200                 205
Glu Asn Phe Lys Asn His Leu Lys Thr Lys Asp Phe Gln Ile Leu Thr
    210                 215                 220
Ile Gln Glu Ser Leu Val Lys Gly Lys Asn Gly Asn Val Glu Phe Phe
225                 230                 235                 240
Ile His Phe Lys Arg Ala
                245
```

(2) INFORMATION FOR SEQ ID NO:1519:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 849 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

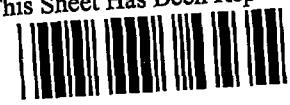
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1519

```
Arg His Val Gln Pro Met Lys Ser Lys Lys Leu Tyr Leu Ala Leu Ile
1               5                  10                  15
Ile Gly Val Leu Leu Ala Phe Leu Thr Leu Ser Ser Trp Leu Gly Asn
```

This Sheet Has Been Replaced



```
            20                  25                  30
Ser Gly Leu Val Gly Arg Phe Gly Val Trp Phe Ala Ala Ile Asn Lys
        35                  40                  45
Lys Tyr Phe Gly Tyr Leu Ser Leu Ile Asn Leu Pro Tyr Leu Ala Trp
    50                  55                  60
Val Leu Phe Leu Leu Tyr Arg Ala Lys Asn Pro Phe Thr Glu Ile Val
65                  70                  75                  80
Leu Glu Lys Thr Leu Gly His Leu Leu Gly Ile Leu Ser Leu Leu Phe
                85                  90                  95
Leu Gln Ser Ser Leu Leu Asn Gln Gly Glu Ile Gly Asn Ser Ala Arg
            100                 105                 110
Leu Phe Leu His Pro Phe Ile Gly Asp Phe Gly Leu Tyr Val Leu Ile
        115                 120                 125
Met Leu Met Val Val Ile Ser Tyr Leu Ile Leu Phe Lys Leu Pro Pro
    130                 135                 140
Lys Ser Val Phe Tyr Pro Tyr Met Asn Lys Thr Gln Ser Leu Leu Lys
145                 150                 155                 160
Glu Ile Tyr Lys Gln Cys Leu Gln Ala Phe Ser Pro Asn Phe Ser Leu
                165                 170                 175
Lys Lys Glu Gly Phe Glu Asn Thr Pro Ser Asp Ser Gln Lys Lys Glu
            180                 185                 190
Thr Asn Asn Asp Lys Glu Lys Glu Asn Leu Lys Glu Asn Pro Ile Asp
        195                 200                 205
Glu Asn His Asn Thr Pro Asn Glu Glu Ser Phe Leu Ala Ile Pro Thr
    210                 215                 220
Pro Tyr Asn Thr Thr Leu Asn Asn Ser Glu Pro Gln Glu Gly Leu Val
225                 230                 235                 240
Gln Ile Ser Pro His Pro Pro Thr His Tyr Thr Ile Tyr Pro Lys Arg
                245                 250                 255
Asn Arg Phe Asp Asp Leu Thr Asn Pro Thr Leu Lys Glu Pro Lys Gln
            260                 265                 270
Glu Thr Lys Glu Arg Glu Pro Thr Leu Lys Lys Glu Thr Pro Thr Thr
        275                 280                 285
Leu Lys Pro Ile Met Pro Ile Ser Ala Ser Asn Thr Glu Asn His Asp
    290                 295                 300
Lys Thr Glu Asn His Lys Thr Pro Asn His Pro Ile Lys Glu Asp Asp
305                 310                 315                 320
Leu Gln Glu Ser Pro Gln Glu Asn Pro Gln Lys Glu Asn Ile Glu Glu
                325                 330                 335
Asn Ile Glu Glu Lys Glu Thr Gln Asn Ala Pro Ser Phe Ser Pro Leu
            340                 345                 350
Thr Leu Thr Ser Ala Lys Lys Pro Val Met Val Lys Glu Leu Ser Glu
        355                 360                 365
Asn Lys Glu Ile Leu Asp Gly Leu Asp Tyr Gly Glu Val Gln Lys Pro
    370                 375                 380
Lys Asp Tyr Glu Leu Pro Thr Thr Gln Leu Leu Asn Ala Val Cys Leu
385                 390                 395                 400
Lys Glu Thr Ser Leu Asp Glu Asn Glu Ile Asp Gln Lys Ile Gln Asp
                405                 410                 415
Leu Leu Ser Lys Leu Arg Thr Phe Lys Ile Asp Gly Asp Ile Ile Arg
            420                 425                 430
Thr Tyr Ser Gly Pro Ile Val Thr Thr Phe Glu Phe Arg Pro Ala Pro
        435                 440                 445
Ser Val Lys Val Ser Arg Ile Leu Gly Leu Ser Asp Asp Leu Ala Met
    450                 455                 460
Thr Leu Cys Ala Glu Ser Ile Arg Ile Gln Ala Pro Ile Lys Gly Lys
465                 470                 475                 480
Asp Val Val Gly Ile Glu Ile Pro Asn Ser Gln Ser Gln Ile Ile Tyr
                485                 490                 495
Leu Arg Glu Ile Leu Glu Ser Glu Leu Phe Gln Lys Ser Ser Ser Pro
            500                 505                 510
Leu Thr Leu Ala Leu Gly Lys Asp Ile Val Gly Asn Pro Phe Ile Thr
        515                 520                 525
Asp Leu Lys Lys Leu Pro His Leu Leu Ile Ala Gly Thr Thr Gly Ser
    530                 535                 540
```

```
Gly Lys Ser Val Gly Val Asn Ala Met Ile Leu Ser Leu Leu Tyr Lys
545                 550                 555                 560
Asn Pro Pro Asp Gln Leu Lys Leu Val Met Ile Asp Pro Lys Met Val
                565                 570                 575
Glu Phe Ser Ile Tyr Ala Asp Ile Pro His Leu Leu Thr Pro Ile Ile
            580                 585                 590
Thr Asp Pro Lys Lys Ala Ile Gly Ala Leu Gln Ser Val Ala Lys Glu
        595                 600                 605
Met Glu Arg Arg Tyr Ser Leu Met Ser Glu Tyr Lys Val Lys Thr Ile
    610                 615                 620
Asp Ser Tyr Asn Glu Gln Ala Gln Ser Asn Gly Val Glu Ala Phe Pro
625                 630                 635                 640
Tyr Leu Ile Val Val Ile Asp Glu Leu Ala Asp Leu Met Met Thr Gly
                645                 650                 655
Gly Lys Glu Ala Glu Phe Pro Ile Ala Arg Ile Ala Gln Met Gly Arg
            660                 665                 670
Ala Ser Gly Leu His Leu Ile Val Ala Thr Gln Arg Pro Ser Val Asp
        675                 680                 685
Val Val Thr Gly Leu Ile Lys Thr Asn Leu Pro Ser Arg Val Ser Phe
    690                 695                 700
Arg Val Gly Thr Lys Ile Asp Ser Lys Val Ile Leu Asp Thr Asp Gly
705                 710                 715                 720
Ala Gln Ser Leu Leu Gly Arg Gly Asp Met Leu Phe Thr Pro Pro Gly
                725                 730                 735
Thr Asn Gly Leu Val Arg Leu His Ala Pro Phe Ala Thr Glu Asp Glu
            740                 745                 750
Ile Lys Lys Ile Val Asp Phe Ile Lys Ala Gln Lys Glu Val Glu Tyr
        755                 760                 765
Asp Lys Asp Phe Leu Leu Glu Glu Ser Arg Met Pro Leu Asp Thr Pro
    770                 775                 780
Asn Tyr Gln Gly Asp Asp Ile Leu Glu Arg Ala Lys Ala Val Ile Leu
785                 790                 795                 800
Glu Lys Lys Ile Thr Ser Thr Ser Phe Leu Gln Arg Gln Leu Lys Ile
                805                 810                 815
Gly Tyr Asn Gln Ala Ala Thr Ile Thr Asp Glu Leu Glu Ala Gln Gly
            820                 825                 830
Phe Leu Ser Pro Arg Asn Ala Lys Gly Asn Arg Glu Ile Leu Gln Asn
        835                 840                 845
Phe
```

(2) INFORMATION FOR SEQ ID NO:1520:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 448 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

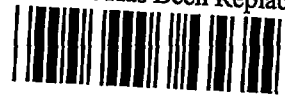
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1520

```
Asn Tyr Leu Lys Ile Ser Cys Ser Arg Ile Ala Met Asn Pro Gln Ile
1               5                   10                  15
Gln Pro Ala Thr Lys Lys Pro Leu Lys Ser Leu Leu Ala Ala Ser Ser
```

This Sheet Has Been Replaced



```
            20                  25                  30
Gly Asn Leu Val Glu Trp Tyr Asp Phe Tyr Ala Tyr Ala Phe Leu Ala
        35                  40                  45
Pro Tyr Phe Ala Lys Glu Phe Thr His Thr Asn Asp Pro Thr Leu Ala
    50                  55                  60
Leu Ile Ser Ala Phe Leu Val Phe Met Leu Gly Phe Phe Met Arg Pro
65                  70                  75                  80
Leu Gly Ser Leu Phe Phe Gly Lys Leu Gly Asp Lys Lys Gly Arg Lys
                85                  90                  95
Thr Ser Met Val Tyr Ser Ile Ile Leu Met Ala Leu Gly Ser Phe Met
            100                 105                 110
Leu Ala Leu Leu Pro Thr Lys Glu Ile Val Gly Glu Trp Ala Phe Leu
        115                 120                 125
Phe Leu Leu Leu Ala Arg Leu Leu Gln Gly Phe Ser Val Gly Gly Glu
    130                 135                 140
Tyr Gly Val Val Ala Thr Tyr Leu Ser Glu Leu Gly Lys Asn Gly Lys
145                 150                 155                 160
Lys Gly Phe Tyr Gly Ser Phe Gln Tyr Val Thr Leu Val Gly Gly Gln
                165                 170                 175
Leu Leu Ala Ile Phe Ser Leu Phe Ile Val Glu Asn Val Tyr Thr His
            180                 185                 190
Glu Gln Ile Ser Ala Phe Ala Trp Arg Tyr Leu Phe Ala Leu Glu Gly
        195                 200                 205
Ile Leu Ala Leu Leu Ser Leu Phe Leu Arg Asn Ile Met Glu Glu Thr
    210                 215                 220
Met Asp Asn Glu Ala Thr Pro Gln Lys Lys Thr Asn Val Asn Asn Thr
225                 230                 235                 240
Lys Glu Thr His Ile Lys Glu Thr Gln Arg Gly Ser Leu Lys Glu Leu
                245                 250                 255
Leu Asn His Lys Lys Ala Leu Met Ile Val Phe Gly Leu Thr Met Gly
            260                 265                 270
Gly Ser Leu Cys Phe Tyr Thr Phe Thr Val Tyr Leu Lys Ile Phe Leu
        275                 280                 285
Thr Asn Ser Ser Ser Phe Ser Pro Lys Glu Ser Ser Phe Ile Met Leu
    290                 295                 300
Leu Ala Leu Ser Tyr Phe Ile Phe Leu Gln Pro Leu Cys Gly Met Leu
305                 310                 315                 320
Ala Asp Lys Ile Lys Arg Thr Gln Met Leu Met Val Phe Ala Ile Thr
                325                 330                 335
Gly Leu Ile Val Thr Pro Ile Val Phe Tyr Gly Ile Lys His Ala Thr
            340                 345                 350
Ser Val Tyr Glu Ala Leu Phe Tyr Glu Ile Leu Ala Leu Ser Ser Met
        355                 360                 365
Ser Phe Tyr Thr Cys Ile Ala Gly Val Ile Lys Ala Glu Leu Phe Pro
    370                 375                 380
Glu His Val Arg Ala Leu Gly Val Gly Leu Ala Tyr Ala Ile Ala Asn
385                 390                 395                 400
Ala Leu Phe Gly Gly Ser Ala Ser Tyr Ile Ala Leu Glu Phe Lys Gln
                405                 410                 415
His Gly Phe Glu Glu Gly Phe Val Gly Tyr Val Met Leu Ser Ile Val
            420                 425                 430
Ile Phe Met Val Met Val Ile Ile Phe Pro Lys Lys Thr Tyr Leu Glu
        435                 440                 445
```

(2) INFORMATION FOR SEQ ID NO:1521:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 646 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

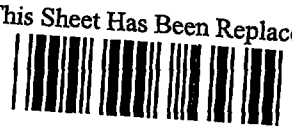
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1521

```
Lys Trp Lys Asn Leu Met Gln Leu Ser Asn Ala Asp Leu Glu Arg Leu
1               5                  10                  15
Lys Ser Met Ala Asn Thr Leu Arg Phe Leu Cys Ala Asp Met Ile Asp
            20                  25                  30
Lys Ala Asn Ser Gly His Pro Gly Val Cys Leu Gly Leu Ala Asp Val
        35                  40                  45
Met Val Val Leu Ser Leu His Leu Asn Leu Asn Pro Thr Asn Pro Lys
    50                  55                  60
Trp Leu Asn Arg Asp Arg Leu Val Phe Ser Gly Gly His Ala Ser Ala
65                  70                  75                  80
Leu Val Tyr Ser Leu Leu His Leu Trp Gly Phe Asp Leu Ser Leu Asp
                85                  90                  95
Asp Leu Lys Arg Phe Arg Gln Leu His Ser Lys Thr Pro Gly His Pro
            100                 105                 110
Glu Leu His His Thr Glu Gly Ile Glu Ile Thr Thr Ala Pro Leu Gly
        115                 120                 125
Gln Gly Phe Ala Asn Ala Val Gly Phe Ser Met Ala Ser Gln Tyr Ala
    130                 135                 140
Gln Thr Leu Leu Asp Lys Glu Ala Ile Ser His Lys Val Tyr Cys Leu
145                 150                 155                 160
Cys Gly Asp Gly Asp Leu Gln Glu Gly Ile Ser Tyr Glu Ser Thr Ser
                165                 170                 175
Leu Ala Gly His Leu Arg Leu Asp Asn Leu Ile Val Ile Tyr Asp Ser
            180                 185                 190
Asn Gln Ile Ser Ile Glu Gly Ala Ile Asn Ile Ser Phe Ser Glu Gln
        195                 200                 205
Val Lys Thr Arg Phe Leu Ala Gln Asn Trp Glu Val Leu Glu Cys Asp
    210                 215                 220
Gly His Asp Tyr Gln Ala Ile His Asn Ala Leu Glu Glu Ala Lys Lys
225                 230                 235                 240
Ser His Lys Pro Thr Leu Leu Ile Ala His Thr Ile Ile Gly Lys Gly
                245                 250                 255
Ala Ile Gly Leu Glu Gly Ser Glu Lys Thr His Gly Ser Pro Leu Ser
            260                 265                 270
Lys Glu Val Leu Lys Gln Ser Lys Glu Asn Ala Gln Ile Asn Pro Asn
        275                 280                 285
Glu Ser Phe Ile Ile Ser Pro Lys Asn Lys Met His Phe Glu Glu Val
    290                 295                 300
Lys Val Arg Gly Ile Ser Leu Glu Ala Leu Trp Glu Lys Ser Leu Ser
305                 310                 315                 320
Pro Lys Thr Lys Glu Lys Ile His Ala Leu Lys Asn Phe Asp Phe Asn
                325                 330                 335
Ala Ile Asn Tyr Pro Ala Phe Lys Lys Gly Glu Ser Leu Ala Thr Arg
            340                 345                 350
Val Ser Asn Gly Met Ile Leu Asn Ala Ile Ala Lys Glu Cys Glu Gly
        355                 360                 365
Phe Leu Gly Gly Ser Ala Asp Leu Ala Pro Ser Asn Asn Thr His Leu
    370                 375                 380
Lys His Ser Gly Asp Phe Pro Leu Gly Gln Asn Leu His Phe Gly Ile
385                 390                 395                 400
Arg Glu His Ala Met Gly Ala Ile Thr Asn Ala Leu Ala Ala Tyr Gly
                405                 410                 415
Leu Phe Val Pro Phe Cys Ala Thr Phe Phe Val Phe Ser Asp Tyr Leu
            420                 425                 430
Met Pro Ser Ile Arg Leu Ser Ala Leu Met Lys Leu Lys Ala Leu Phe
```

```
        435                 440                 445
Ile Phe Thr His Asp Ser Ile Gly Val Gly Glu Asp Gly Ala Thr His
    450                 455                 460
Gln Pro Ile Glu Gln Leu Ser His Leu Arg Ala Leu Pro His Phe Tyr
465                 470                 475                 480
Ala Phe Arg Pro Ser Asp Ala Phe Glu Asn Lys Ala Cys Met Gln Val
                485                 490                 495
Ala Leu Ser Leu Asn Ala Pro Ser Ala Leu Ile Leu Ser Arg Gln Asn
            500                 505                 510
Leu Ser Val Leu Asp Glu Val Ser Lys Glu Gln Val Leu Lys Gly Ala
        515                 520                 525
Tyr Val Lys His His Ser Lys Asp Pro Ile Ile Thr Leu Val Ala Ser
    530                 535                 540
Gly Ser Glu Val Ser Leu Ala Leu Glu Ser Ala Lys Ile Leu Glu Arg
545                 550                 555                 560
Glu Asn Ile Pro Thr Gln Val Val Ser Ala Pro Cys Phe Asp Leu Leu
                565                 570                 575
Val Glu Gln Asp Glu Ser Tyr Phe Lys Glu Leu Phe Lys Gly Lys Val
            580                 585                 590
Leu Val Ile Glu Ala Ser Arg Ala Ile Glu Trp Tyr Arg Phe Ala Asp
        595                 600                 605
Lys Ile Ile Gly Met Asp Ser Phe Gly Ser Ser Ala Lys Gly Asp Lys
    610                 615                 620
Leu Phe Glu Lys Phe Gly Phe Ser Val Glu Asn Ile Thr Ala Gln Ala
625                 630                 635                 640
Lys Arg Leu Leu Asn Ala
                645
```

(2) INFORMATION FOR SEQ ID NO:1522:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...273

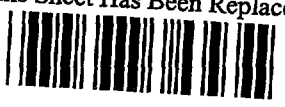
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1522

```
Lys Asp Tyr Cys Met Gln Asn Gly Tyr Tyr Ala Ala Thr Gly Ala Met
1               5                  10                  15
Ala Thr Gln Phe Asn Arg Leu Asp Leu Thr Ser Asn Asn Leu Ala Asn
            20                  25                  30
Leu Asn Thr Asn Gly Phe Lys Arg Asp Asp Ala Ile Thr Gly Asp Phe
        35                  40                  45
Leu Arg Leu Tyr Gln Glu Tyr Arg Glu Gln Leu Pro Leu Glu Asp Gln
    50                  55                  60
Thr Lys Ala Ser Ala Lys Tyr Leu Asn Arg Asn Leu Asn Arg Val Pro
65                  70                  75                  80
Ile Leu Ser Glu Ile Tyr Thr Asp Arg Ser Leu Gly Ala Phe Glu Gly
                85                  90                  95
Thr Asn Asn Pro Leu Asp Phe Ala Leu Thr Ser Pro Asn Leu Tyr Phe
            100                 105                 110
Ala Ile Gln Thr Asn Glu Gly Val Ala Tyr Thr Lys Asp Gly His Phe
        115                 120                 125
```

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

(2) INFORMATION FOR SEQ ID NO:1523:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 592 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1523

```
Gly Met Ile Ala Leu Asn Phe Asn Leu Leu Asp Lys Glu Thr Asn Thr
1               5                  10                  15
Pro Leu Phe Glu Lys Ser Pro Leu Asp Ser Ser Leu Glu Leu Tyr Lys
            20                  25                  30
Asn Ser Glu Ile His Met Leu Tyr Pro Tyr Leu Tyr Tyr Phe Gly Leu
        35                  40                  45
Gly Asn Gly Val Phe Tyr Arg Leu Leu Leu Gly Asn Glu Asn Leu Lys
    50                  55                  60
Arg Leu Val Val Ile Glu Pro Glu Ile Glu Val Ile Phe Ile Val Leu
65                  70                  75                  80
Asn Leu Leu Asp Phe Ser Thr Glu Ile Leu Glu Asn Arg Leu Ile Leu
                85                  90                  95
Leu His Ala Ser Phe Cys Asn Tyr Asn Met Ile Ala Ser Leu Phe Asp
            100                 105                 110
Met Asp Lys Lys Ser Arg Leu Tyr Ala Arg Met Tyr Asp Leu Lys Leu
        115                 120                 125
Phe Asn Ala Tyr Tyr Glu Arg Tyr Ser His Gln Met Ile Glu Ile Asn
    130                 135                 140
Gln His Phe Thr Arg Ala Leu Glu His Gly Ala Ile Ser Val Gly Asn
145                 150                 155                 160
Asp Ala Lys Asp Ala Leu Ile Gly Ile Lys Gln His Val Ala Asn Leu
                165                 170                 175
Pro Glu Val Ile Lys Ser Pro Ser Leu Val Asp Phe Val Asn Ala Leu
```

```
            180                 185                 190
Lys Asn Arg Asp Thr Ala Ile Ile Val Ser Thr Gly Pro Ser Leu Asn
        195                 200                 205
Lys Gln Leu Pro Leu Leu Lys Glu Ile Ala Pro Tyr Ala Thr Leu Phe
    210                 215                 220
Cys Ile Asp Ala Ser Phe Pro Ile Leu Ala Arg Ala Gly Ile Lys Pro
225                 230                 235                 240
Asp Ile Val Leu Ser Leu Glu Arg Val Asp Leu Thr Ala Lys Phe Tyr
                245                 250                 255
Glu Glu Thr Pro Leu Asp Phe Gln Glu Gly Val Ile Phe Ala Leu Thr
            260                 265                 270
Ser Ile Val His Lys Arg Leu Ile Gln Ala Ile Gln Lys Gly Val Lys
        275                 280                 285
Gln Phe Ser Phe Arg Pro Phe Gly Tyr Thr Asn Leu Phe Asp Leu His
    290                 295                 300
Gln Tyr Gly Tyr Val Gly Ile Gly Met Ser Ala Ala Asn Met Ala Tyr
305                 310                 315                 320
Glu Leu Val Val His Ser Arg Phe Lys Arg Cys Val Phe Ile Gly Gln
                325                 330                 335
Asp Leu Ser Phe Ser Gln Ser Gly Asn Ser His Ala Ser Gly Ala Ile
            340                 345                 350
Tyr Gly Asp Arg Glu Ile Lys Pro Lys Lys Asp Lys Asp Lys Ile Phe
        355                 360                 365
Ile Glu Lys Tyr Gly Gly Asn Gly Lys Val Glu Thr Thr Leu Val Trp
    370                 375                 380
Lys Leu Phe Leu Glu Phe Phe Glu Lys Asp Ile Phe Asn Thr Pro Tyr
385                 390                 395                 400
Lys Leu Glu Val Ile Asn Ala Thr Glu Gly Gly Ala Arg Ile Lys Gly
                405                 410                 415
Thr Lys Glu Met Pro Phe Lys Glu Val Cys Glu Lys Ile Asp Lys Ser
            420                 425                 430
Lys Pro Lys Pro Pro Ile Asn Leu Ile Tyr Pro Thr Gln Ser Glu Gln
        435                 440                 445
Ala Lys Asn Leu Lys Ile Ala Lys Lys Lys Cys Glu Glu Ile Ile Lys
    450                 455                 460
Tyr Ala Asn Glu Lys Lys Thr Gln Val Glu Glu Ala Phe Leu Lys Val
465                 470                 475                 480
Ala Glu Phe Leu Glu Lys Val Glu Lys Leu His Glu Lys Asn Lys Leu
                485                 490                 495
Glu Glu Leu Asp Phe Glu Glu Leu Glu Asn Leu Ser Ala Glu Ile Asp
            500                 505                 510
Asn Val Lys Glu Leu Phe Asp Asp Lys Arg Phe Asn Ser Tyr Phe Met
        515                 520                 525
Asp Ala Ile Gln Ser Tyr Ile Phe His Gln Glu Leu His Ile Ala Glu
    530                 535                 540
Ile Val Cys Lys Lys Thr Ser Asn Glu Asp Gly Leu Arg Ala Lys Gln
545                 550                 555                 560
Leu Glu Tyr Ile Tyr Ala His Lys Tyr Trp Leu Phe Ser Leu Ala Gly
                565                 570                 575
Gly Met Asp Cys Val Ile Glu Ala Ile Lys Met Ala Leu Lys Glu Trp
            580                 585                 590
```

(2) INFORMATION FOR SEQ ID NO:1524:

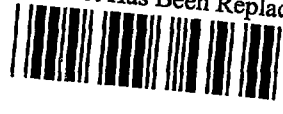
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

This Sheet Has Been Replaced



(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1524

```
Val His Phe Thr Cys Ile Phe Leu Thr Leu Leu Lys Trp Ile Leu Pro
1               5                  10                  15
Ala Lys Asn Lys Gln Ala Cys Lys Lys Pro Pro Thr Arg Ser Ile Gln
            20                  25                  30
Gly Leu Gln Asn Ile Gln Gln Asn Ile Pro Pro Gln Val Leu Thr Pro
        35                  40                  45
Gln Ile Gln Ala Gly Ile Gln Gly Val Met Gln Gly Phe Gly Ala Leu
    50                  55                  60
Ser Ser Thr Leu Glu Ala Pro Leu Leu Phe Ser Lys Gln Asn Val Val
65                  70                  75                  80
Ile Gly Gly Phe Glu His Tyr Leu Ser Pro Leu Tyr Gly Trp Gly Lys
                85                  90                  95
Ile His Asp Gly Ala His Cys Arg Ile Glu Cys Lys Lys Thr Pro Met
            100                 105                 110
Lys Cys Ile Ala
        115
```

(2) INFORMATION FOR SEQ ID NO:1525:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1525

```
Arg Met Asn Phe Phe Lys Ile Leu Leu Met Glu Leu Arg Ala Ile Val
1               5                  10                  15
Ser His Lys Gly Val Leu Leu Ile Leu Ile Gly Ala Pro Leu Ile Tyr
            20                  25                  30
Gly Leu Leu Tyr Pro Leu Pro Tyr Leu Lys Asp Ile Val Thr Gln Gln
        35                  40                  45
Lys Ile Ala Leu Val Asp Glu Asp Asn Ser Phe Leu Ser Arg Gln Leu
    50                  55                  60
Ala Phe Met Val Gln Ser Ser Asn Glu Leu Glu Ile Ala Phe Phe Ser
65                  70                  75                  80
Pro Ser Met Leu Glu Ala Lys Lys Leu Leu Lys Glu Glu Lys Ile Tyr
                85                  90                  95
Gly Ile Leu His Ile Pro Ser His Phe Glu Ala Asn Ile Tyr Lys Gln
            100                 105                 110
Val Pro Val Thr Ile Asp Phe Tyr Ala Asn Ala Asn Tyr Phe Leu Ile
        115                 120                 125
Tyr Gly Ala Leu Ala Asn Ala Val Val Gly Ser Ile Asn Ala Leu Asn
    130                 135                 140
Asp Glu Ile Arg Phe Lys Arg Asn Ala Gln Ile Glu Glu Ala Glu Leu
```

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

This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:1526:

(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:1526

```
Thr Leu Lys Gly Ile Val Leu Phe Arg Leu Ile Ser Ala Trp Val Leu
1               5                   10                  15
Gln Asp Lys Phe Leu Phe Val Val Cys Phe Ile Leu Pro Phe Cys Leu
            20                  25                  30
Gly Val Leu Gly Thr Gln Ile Phe Lys Gln Glu Thr Pro Arg Gln Leu
        35                  40                  45
Pro Ile Val Val Val Asp Leu Asp Lys Thr Thr Thr Ser His Gln Val
    50                  55                  60
Ala Phe Glu Leu Gly Ala Thr Ser Ala Val Glu Ile Lys Tyr Gln Val
65                  70                  75                  80
Thr Ser Leu Ser Glu Ala Lys Arg Phe
                85
```

(2) INFORMATION FOR SEQ ID NO:1527:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...77

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1527

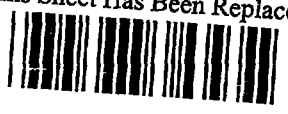
```
Ser Met Lys Lys Thr Thr Leu Phe Val Leu Gly Leu Leu Phe Asn Ser
1               5                  10                  15
Ser Leu Ser Ala Val Asp Gly Ile Ser Gln Thr Glu Pro Ser Ser Leu
            20                  25                  30
Asn Leu Ala Glu Asp Ser Leu Pro Leu Asn His Ser Asn Ala Gln Lys
        35                  40                  45
Leu Ser Leu Lys Asn Ala Trp Asn Arg Val Leu Ser Asn His Glu Gly
    50                  55                  60
Leu His Ala Gln Asn Thr Pro Leu Ser Glu Arg Val Lys
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:1528:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(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:1528

```
Val Arg Arg Gln Thr Met Lys Lys Val Ile Val Ala Leu Gly Val Leu
1               5                  10                  15
Ala Phe Ala Asn Val Leu Met Ala Thr Asp Val Lys Ala Leu Val Lys
            20                  25                  30
Gly Cys Ala Ala Cys His Gly Val Lys Phe Glu Lys Lys Ala Leu Gly
        35                  40                  45
Lys Ser Lys Ile Val Asn Met Met Ser Glu Lys Glu Ile Glu Glu Asp
    50                  55                  60
Leu Met Ala Phe Lys Ser Gly Ala Asn Lys Asn Pro Val Met Thr Ala
65                  70                  75                  80
Gln Ala Lys Lys Leu Ser Asp Glu Asp Ile Lys Ala Leu Ala Ile Tyr
                85                  90                  95
Ile Pro Thr Leu Lys
```

This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:1529:

(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:1529

```
Arg Pro Met Leu His Lys Lys Tyr Arg Pro Asn Val Ala Ala Ile Ile
1               5                  10                  15
Met Ser Pro Asp Tyr Pro Asn Thr Cys Glu Val Phe Ile Ala Glu Arg
            20                  25                  30
Ile Asp Ile Glu Gly Ala Trp Gln Phe Pro Gln Gly Gly Ile Asp Glu
        35                  40                  45
Gly Glu Thr Pro Leu Glu Ala Leu Tyr Arg Glu Leu Leu Glu Glu Ile
    50                  55                  60
Gly Thr Asn Glu Ile Glu Ile Leu Ala Gln Tyr Pro Arg Trp Ile Ala
65                  70                  75                  80
Tyr Asp Phe Pro Ser Asn Met Glu His Lys Phe Tyr Ser Phe Asp Gly
                85                  90                  95
Gln Lys Gln Arg Tyr Phe Leu Val Arg Leu Lys His Val Asn Asn Ile
            100                 105                 110
Asp Leu Asn Lys His Thr Pro Glu Phe Arg Ser Tyr Gln Phe Ile Gln
        115                 120                 125
Leu Lys Asp Leu Leu Lys Lys Ile Val Pro Phe Lys Arg Gln Val Tyr
    130                 135                 140
Arg Gln Val Ile Ala Tyr Phe Arg Lys Glu Gly Tyr Leu Gly Cys
143                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:1530:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1530

```
Cys Met Asn Leu Val Phe Leu Trp Ala Ala Leu Gly Gly Ala Ile Gly
1               5                  10                  15
Ser Ser Leu Arg Tyr Phe Val Gly Lys Met Met Pro Ser Lys Phe Leu
            20                  25                  30
Met Phe Glu Ser Phe Pro Leu Gly Thr Phe Ser Val Asn Leu Ile Gly
        35                  40                  45
Cys Phe Ile Ile Gly Phe Met Gly His Leu Ala Ala Lys Lys Val Phe
    50                  55                  60
Gly Asp Asp Phe Gly Ile Phe Phe Val Thr Gly Val Leu Gly Gly Phe
65                  70                  75                  80
Thr Thr Phe Ser Ser Tyr Gly Leu Asp Thr Leu Lys Leu Leu Gln Lys
                85                  90                  95
Ser Gln Tyr Leu Glu Ala Ile Ser Tyr Val Leu Gly Thr Asn Leu Leu
            100                 105                 110
Gly Leu Ile Gly Val Ala Ile Gly Trp Phe Leu Ala Lys Asn Phe Val
        115                 120                 125
Gly Val Asn
    130
```

(2) INFORMATION FOR SEQ ID NO:1531:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

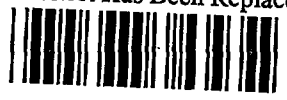
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1531

```
Tyr Leu Ser Ile Val Val Glu Asp Gln Lys Gly Ile Phe Pro Ile Ala
1               5                  10                  15
Ala Ser Lys Arg Lys Ser Gln Ser Ser Val Ile Ile Glu Asp Val Cys
            20                  25                  30
Phe Ser Lys Glu Asp Phe Val Glu Gly Ala Lys Ala Ile Glu Gly Leu
        35                  40                  45
Leu Lys Lys His Gly Phe Lys Asp Asn Gly Ile Ile Phe Gly His Ala
    50                  55                  60
Leu Ser Gly Asn Leu His Phe Val Val Thr Pro Ile Leu Glu Asn Glu
65                  70                  75                  80
Ala Glu Arg Lys Ala Phe Glu Asn Leu Val Ser Glu Met Phe Leu Met
                85                  90                  95
Val Ser Lys Ser Ser Gly Ser Ile Lys Ala Glu His Gly Thr Gly Arg
            100                 105                 110
Met Val Ala Pro Phe Val Glu Met Glu Trp Gly Glu Lys Ala Tyr Lys
        115                 120                 125
Ile His Lys Gln Ile Lys Glu Leu Phe Asp Pro Asn Gly Leu Leu Asn
    130                 135                 140
Pro Asp Val Ile Ile Thr Asn Asp Lys Glu Ile His Thr Lys Asn Leu
145                 150                 155                 160
Lys Ser Ile Tyr Pro Ile Glu Glu His Leu Asp Met Cys Met Glu Cys
                165                 170                 175
Gly Phe Cys Glu Arg Ile Cys Pro Ser Lys Asp Leu Ser Leu Thr Pro
            180                 185                 190
Arg Gln Arg Ile Val Ile His Arg Glu Val Glu Arg Leu Lys Glu Arg
```

```
        195                 200                 205
Val Ser His Gly His Asp Glu Asp Gln Val Leu Leu Asp Glu Leu Leu
    210                 215                 220
Lys Glu Ser Glu Tyr Leu Ala His Ala Thr Cys Ala Val Cys His Met
225                 230                 235                 240
Cys Ser Thr Leu Cys Pro Leu Gly Ile Asp Thr Gly Ser Ile Ala Leu
                245                 250                 255
Asn His Tyr Gln Lys Asn Pro Lys Gly Glu Lys Ile Cys Phe Lys Asp
            260                 265                 270
Ser
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1532:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1532

```
Arg Phe Leu Gln Lys Ser Ala Gln Ile Trp Gly Ile Lys Met Leu Val
1               5                  10                  15
Glu Ile Glu Asn Leu Thr Lys Thr Tyr Gly Ser Leu Lys Ala Leu Asp
            20                  25                  30
Asn Ile Ser Leu Lys Leu Pro Lys Gln Gln Phe Ile Gly Leu Leu Gly
        35                  40                  45
Pro Asn Gly Ala Gly Lys Thr Thr Leu Leu Lys Ile Leu Ala Gly Leu
    50                  55                  60
Asn Leu Asn Tyr Gln Gly Glu Val Lys Ile Leu Asn Gln Lys Ile Gly
65                  70                  75                  80
Ile Glu Thr Lys Lys Ser Val Ala Phe Leu Ser Asp Gly Asp Phe Leu
                85                  90                  95
Asp Pro Lys Leu Thr Pro Leu Lys Ala Ile Ala Phe Tyr Lys Asp Phe
            100                 105                 110
Phe Ser Asp Phe Asp Glu Ser Lys Ala Leu Asn Leu Leu Lys Arg Phe
        115                 120                 125
Ser Val Pro Leu Lys Arg Glu Phe Lys Ala Leu Ser Lys Gly Met Arg
    130                 135                 140
Glu Lys Leu Gln Leu Ile Leu Thr Leu Ser Arg Asn Ala Ser Leu Tyr
145                 150                 155                 160
Leu Phe Asp Glu Pro Val Ala Gly Ile Asp Pro Ile Ala Arg Glu Glu
                165                 170                 175
Ile Phe Glu Leu Ile Ala Lys Glu Phe Ser Gln Asn Ala Ser Leu Leu
            180                 185                 190
Val Ser Thr His Leu Val Val Asp Val Glu Lys Tyr Leu Asp Ser Ala
        195                 200                 205
Ile Phe Leu Lys Glu Ala Lys Val Val Ala Phe Gly Asp Val Gly Glu
    210                 215                 220
Leu Lys Lys Gly Tyr Ser Ser Leu Glu Ala Ala Tyr Lys Glu Arg Leu
225                 230                 235                 240
Lys
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1533:

(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

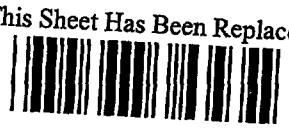
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1533

```
Lys Ser Trp Phe Phe Tyr Ala Pro Phe Tyr Gly Leu Trp Cys Leu Lys
1               5                  10                  15
Thr Pro Ile Ile Gly His Gly Met Lys Lys Lys Ala Lys Val Phe Trp
            20                  25                  30
Cys Cys Phe Lys Met Ile Arg Trp Leu Tyr Leu Ala Val Phe Phe Leu
        35                  40                  45
Leu Ser Val Ser Asp Ala Lys Glu Ile Ala Met Gln Arg Phe Asp Lys
    50                  55                  60
Gln Asn His Lys Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys
65                  70                  75                  80
Asp Asn Val Ile Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp
                85                  90                  95
Val Tyr Ile Leu Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu
            100                 105                 110
Ala Leu Leu Glu Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu
        115                 120                 125
Val Lys Thr Asp Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile
    130                 135                 140
Ile Phe Pro Phe Tyr Val Gln Asp Ser Val Ser Gly Ile Trp Val Ser
145                 150                 155                 160
Ala Asp Ile Ala Ser Gly Lys Asp Gln Lys Tyr Lys Ile Lys Asn Met
                165                 170                 175
Ser Ala Ser Gly Cys Ser Ile Asp Asn Pro Ile Trp His Val Asn Ala
            180                 185                 190
Thr Ser Gly Ser Phe Asn Met Gln Lys Ser His Leu Ser Met Trp Asn
        195                 200                 205
Pro Lys Ile Tyr Val Gly Asp Ile Pro Val Leu Tyr Leu Pro Tyr Ile
    210                 215                 220
Phe Met Ser Thr Ser Asn Lys Arg Thr Thr Gly Phe Leu Tyr Pro Glu
225                 230                 235                 240
Phe Gly Thr Ser His Leu Asp Gly Phe Ile Tyr Leu Gln Pro Phe Tyr
                245                 250                 255
Leu Ala Pro Lys Asn Ser Trp Asp Met Thr Phe Thr Pro Gln Ile Arg
            260                 265                 270
Tyr Lys Arg Gly Phe Gly Leu Asn Phe Glu Ala Arg Tyr Ile Asn Pro
        275                 280                 285
```

(2) INFORMATION FOR SEQ ID NO:1534:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid

This Sheet Has Been Replaced



(D) TOPOLOGY: linear

(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:1534

```
Ile Val Arg Lys Lys Leu Met Leu Glu Met Ser Leu Gln Ala Leu Asn
1               5                  10                  15
Thr Gln Asp Ser Ser Val Met Ala Gln Ser Leu Leu Val His Ala Phe
            20                  25                  30
Phe Ala Ala Leu Leu Ala Leu Ala Phe Met Ile Asn Leu Tyr Thr Leu
        35                  40                  45
Phe Lys Glu Lys Asn Phe Ile Gln Leu Asn Arg Lys Ile Tyr Leu Val
    50                  55                  60
Met Pro Ala Ile Tyr Ile Leu Leu Ser Ile Ala Leu Leu Ser Gly Val
65                  70                  75                  80
Phe Ile Trp Ala Met Gln Gln Phe Glu Phe Ser Phe Ser Ala Val Val
                85                  90                  95
Met Leu Leu Gly Leu Leu Leu Met Leu Ile Ala Glu Ile Lys Arg His
            100                 105                 110
Lys Ser Val Lys Phe Ala Ile Thr Lys Lys Glu Arg Met Lys Ala Tyr
        115                 120                 125
Ile Lys Lys Ala Lys Ile Leu Tyr Phe Leu Glu Thr Ile Leu Ile Ile
    130                 135                 140
Val Leu Met Gly Ile
145
```

(2) INFORMATION FOR SEQ ID NO:1535:

(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

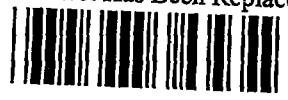
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1535

```
Pro Glu Gly Gly Asn Glu Leu Asn Val Phe Glu Pro Val Ile Ala Tyr
1               5                  10                  15
Lys Leu Phe His Ser Phe Val Ile Leu Gly Cys Ala Ile Glu Thr Leu
            20                  25                  30
Thr Thr Lys Cys Val Glu Gly Ile Thr Ala Asn Glu Lys Ile Cys His
        35                  40                  45
Asp Tyr Val Phe Asn Ser Ile Gly Ile Val Thr Ala Leu Asn Pro His
    50                  55                  60
```

```
Ile Gly Tyr Glu Lys Ser Ala Met Ile Ala Lys Glu Ala Leu Lys Ser
65                  70                  75                  80
Asp Arg Ser Ile Tyr Asp Ile Ala Leu Glu Lys Lys Ile Leu Thr Lys
                85                  90                  95
Glu Gln Leu Asp Asp Ile Phe Lys Pro Glu Asn Met Leu Ser Pro His
            100                 105                 110
Ala Phe Lys Lys His Lys Asp
        115
```

(2) INFORMATION FOR SEQ ID NO:1536:

This Sheet Has Been Replaced



(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:1536

```
Lys Arg Leu Met Val Leu Phe Leu Ser Ile Phe Lys Lys Ser Phe Asn
1               5                  10                  15
Asp Phe Leu Ser Ala Arg Met Leu Leu Ile Asn Leu Gly Pro Ile Leu
            20                  25                  30
Leu Ser Leu Ala Phe Phe Gly Ala Ile Phe Tyr Tyr Asn Gly Gly Ser
        35                  40                  45
Ile Val Asn Tyr Cys Gln Thr Leu Leu Pro Gln Ser Leu Asn Asp Tyr
    50                  55                  60
Ala His Ser Gln Gly Phe Phe Ala Gly Val Phe Ala Trp Val Phe Lys
65                  70                  75                  80
Ala Leu Val Tyr Phe Leu Ile Phe Trp Ile Val Ile Leu Leu Ser Leu
                85                  90                  95
Val Ile Asn Ile Phe Ala Ser Ile Phe Tyr Thr Pro Leu Val Val Ser
            100                 105                 110
Tyr Leu His Gln Lys Tyr Tyr Pro His Val Val Leu Glu Glu Phe Gly
        115                 120                 125
Ser Ile Leu Phe Ser Ile Lys Tyr Phe Leu Lys Ser Leu Thr Phe Met
    130                 135                 140
Leu Leu Phe Leu Ala Val Leu Thr Pro Leu Tyr Phe Ile Pro Phe Ile
145                 150                 155                 160
Gly Val Phe Gly Val Phe Phe Ser Ile Val Pro His Phe Leu Phe Phe
                165                 170                 175
Lys Asn Thr Met Ser Leu Asp Ile Ala Ser Met Ile Phe Asn His Gln
            180                 185                 190
Ser Tyr Gln Asn Leu Leu Lys Gln His Arg Leu Lys His Tyr Arg Phe
        195                 200                 205
Ser Phe Phe Cys Tyr Leu Phe Ser Leu Ile Pro Phe Phe Asn Phe Phe
    210                 215                 220
Ala Thr Leu Leu Gln Thr Leu Met Leu Thr His
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:1537:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 277 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:1537

```
Glu Cys Lys Gly Met Glu Phe Met Lys Lys Phe Val Ala Leu Gly Leu
1               5                  10                  15
Leu Ser Ala Val Leu Ser Ser Ser Leu Leu Ala Glu Gly Asp Gly Val
            20                  25                  30
Tyr Ile Gly Thr Asn Tyr Gln Leu Gly Gln Ala Arg Leu Asn Ser Asn
        35                  40                  45
Ile Tyr Asn Thr Gly Asp Cys Thr Gly Ser Val Val Gly Cys Pro Pro
    50                  55                  60
Gly Leu Thr Ala Asn Lys His Asn Pro Gly Gly Thr Asn Ile Asn Trp
65                  70                  75                  80
His Ser Lys Tyr Ala Asn Gly Ala Leu Asn Gly Phe Gly Leu Asn Val
                85                  90                  95
Gly Tyr Lys Lys Phe Phe Gln Phe Lys Ser Leu Asp Met Thr Ser Lys
            100                 105                 110
Trp Phe Gly Phe Arg Val Tyr Gly Leu Phe Asp Tyr Gly His Ala Asp
        115                 120                 125
Leu Gly Lys Gln Val Tyr Ala Pro Asn Lys Ile Gln Leu Asp Met Val
    130                 135                 140
Ser Trp Gly Val Gly Ser Asp Leu Leu Ala Asp Ile Ile Asp Lys Asp
145                 150                 155                 160
Asn Ala Ser Phe Gly Ile Phe Gly Gly Val Ala Ile Gly Gly Asn Thr
                165                 170                 175
Trp Lys Ser Ser Ala Ala Asn Tyr Trp Lys Glu Gln Ile Ile Glu Ala
            180                 185                 190
Lys Gly Pro Asp Val Cys Thr Pro Thr Tyr Cys Asn Pro Asn Ala Pro
        195                 200                 205
Tyr Ser Thr Asn Thr Ser Thr Val Ala Phe Gln Val Trp Leu Asn Phe
    210                 215                 220
Gly Val Arg Ala Asn Ile Tyr Lys His Asn Gly Val Glu Phe Gly Val
225                 230                 235                 240
Arg Val Pro Leu Leu Ile Asn Lys Phe Leu Ser Ala Gly Pro Asn Ala
                245                 250                 255
Thr Asn Leu Tyr Tyr His Leu Lys Arg Asp Tyr Ser Leu Tyr Leu Gly
            260                 265                 270
Tyr Asn Tyr Thr Phe
        275
```

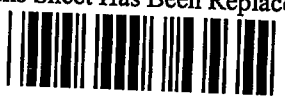
(2) INFORMATION FOR SEQ ID NO:1538:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 676 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1538

```
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
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1539:

(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:1539

```
Ala Arg Phe Val Lys Ile Thr Ala Asp Tyr Phe Ser Pro Met Glu Asn
1               5                  10                  15
Val Phe Tyr Arg Ser Ile Thr Met Thr Leu Leu Leu Leu Leu Ile Tyr
            20                  25                  30
Pro Phe Lys Pro Tyr Arg Leu Lys Ser Tyr Lys Gln Gly Gly Phe Lys
        35                  40                  45
Lys Leu Ala Phe Arg Val Val Val Gly Gly Leu Ala Met Leu Ala Phe
    50                  55                  60
Phe Tyr Asn Ile Glu Lys Ile Ser Leu Ala Thr Ala Asn Ala Phe Ser
65                  70                  75                  80
Gln Cys Ala Pro Ile Tyr Thr Val Leu Leu Ser Pro Leu Leu Leu Lys
                85                  90                  95
```

```
Glu Lys Leu Lys Arg Ser Ala Leu Ile Ser Ala Cys Ile Gly Leu Val
            100                 105                 110
Gly Val Val Leu Ile Ser Asp Pro Ser Val Glu Asn Val Gly Leu Val
        115                 120                 125
Glu Ile Ile Met Gly Ile Leu Ser Gly Ile Phe Val Ser Leu Ala Tyr
    130                 135                 140
Ile Thr Leu Arg Asp Leu Arg Glu Tyr Tyr Asp Lys Gln Ala Val Ile
145                 150                 155                 160
Leu Ala Phe Ala Phe Gly Met Ser Leu Leu Gly Leu Ala Gly Met Phe
                165                 170                 175
Ile Asp Ile Pro Phe Leu Ser Thr Gly Val His Ile Pro Arg Lys Glu
            180                 185                 190
Asp Ile Leu Trp Ile Ser Leu Ile Gly Ile Ser Gly Thr Leu Gly Gln
        195                 200                 205
Tyr Phe Leu Thr Tyr Ala Tyr Met Asn Ala Pro Ala Gly Ile Ile Ala
    210                 215                 220
Pro Ile Glu Tyr Thr Arg Ile Val Trp Gly Leu Leu Phe Gly Leu Tyr
225                 230                 235                 240
Leu Gly Asp Thr Phe Leu Asp Leu Lys Ser Ser Leu Gly Val Ala Leu
                245                 250                 255
Ile Leu Cys Ser Gly Leu Leu Ile Ala Leu Pro Ala Leu Leu Lys Glu
            260                 265                 270
Leu Lys Lys Ile
        275
```

(2) INFORMATION FOR SEQ ID NO:1540:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 269 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

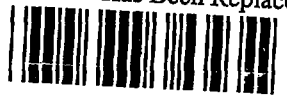
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1540

```
Val Met Gln Leu Ser Pro Leu Gln Ser Ala Leu Leu Tyr Phe Arg Tyr
1               5                   10                  15
Phe Ile Tyr Pro Glu Lys Lys Thr Arg Ser Phe Asp Leu Ser Asp Leu
            20                  25                  30
Ile Phe Ile Val Met Val Phe Leu Val Leu Ala Leu Gly Leu Leu Met
        35                  40                  45
Ser Glu Glu Ile Ser Ile Ser Tyr Asn Glu Ala Lys Asp Phe Phe Tyr
    50                  55                  60
Ser Asp Ala Trp Phe Val Lys Ile Ala Gln Lys Ser Val Ala Ile Leu
65                  70                  75                  80
Gly Gln Asn Asp Leu Ala Leu Arg Leu Pro Phe Leu Ile Ala His Val
                85                  90                  95
Ile Asn Met Phe Leu Phe Tyr Leu Ile Gly Arg Lys Ile Leu Lys Lys
            100                 105                 110
Pro Lys Asp Ala Leu Tyr Val Val Leu Thr Tyr Ala Leu Leu Pro Gly
        115                 120                 125
Val Asn Leu Phe Ala Ile Leu Leu Ala Lys Ser Val Leu Val Leu Ser
    130                 135                 140
Leu Gly Leu Leu Ile Ser Tyr Leu Tyr Ile Lys Thr Gln Lys Ile Pro
```

This Sheet Has Been Replaced



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

(2) INFORMATION FOR SEQ ID NO:1541:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1541

```
Ser Pro Phe Met Asp Arg Lys Leu Leu Arg Leu Tyr Gln Pro Leu Asn
1               5                   10                  15
Ala Tyr Ser Tyr Asn Ser Asp Ser Leu Phe Leu Tyr Asp Phe Ser Arg
            20                  25                  30
Pro Phe Ile Lys Asn Ser Gly Ala Ile Leu Asp Ile Gly Ser Gly Cys
        35                  40                  45
Gly Val Leu Gly Leu Leu Cys Ala Arg Asp Asn Pro Leu Ala Ser Val
    50                  55                  60
His Leu Val Glu Lys Asp Ser Lys Met Ala Phe Cys Ser Gln Lys Asn
65                  70                  75                  80
Ala Leu Lys Phe Pro Asn Ala Gln Val Phe Glu Ser Asp Phe Leu Asp
                85                  90                  95
Phe Asn Pro Pro Ile Leu Tyr Asp Ala Ile Val Cys Asn Pro Pro Phe
            100                 105                 110
Tyr Ala Leu Gly Ser Ile Lys Ser Gln Ile Lys Gly His Ala Arg His
        115                 120                 125
Gln Ser Glu Leu Asp Phe Ala Ser Leu Val Ala Lys Val Lys Lys Cys
    130                 135                 140
Leu Lys Pro Lys Gly Tyr Phe Ile Phe Cys Tyr Glu Ala Leu Ser Leu
145                 150                 155                 160
Cys Leu Val Ile Glu Ser Leu Lys Ser Val Lys Leu Thr Leu Glu Thr
                165                 170                 175
Leu Arg Phe Val Gln Ser Phe Lys Asp Lys Asn Ala His Leu Met Leu
            180                 185                 190
Gly Ala Ala Arg Asn Asn Ser Lys Ser Ala Leu Lys Val Leu Pro Pro
        195                 200                 205
Leu Ile Thr His Asn Ser Lys Asn Gln Ser Asp Asn Thr Lys Glu Val
    210                 215                 220
```

This Sheet Has Been Replaced



Leu Asn Ile Tyr Gln Ile Cys Asn Thr Tyr Ser Ile Lys Ala Pro Leu
225 230 235 240
Asp

(2) INFORMATION FOR SEQ ID NO:1542:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 429 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...429

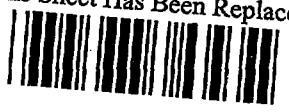
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1542

Ser Arg Ser Phe Arg Gly Leu Leu Tyr Tyr Asn Lys Ile Asn Leu Ile
1 5 10 15
Asn Lys Asp Thr Gly Leu Gln Glu Ile Lys Leu Asp Ile Tyr Ala Thr
20 25 30
Leu Val Cys Met Val Leu Val Leu Leu Leu Gly Arg Tyr Val Ile Ser
35 40 45
Lys Val Lys Phe Leu Arg Asp Tyr Asp Ile Pro Glu Pro Val Val Gly
50 55 60
Gly Val Leu Val Ala Phe Phe Ile Met Leu Ala Arg Gln Phe Tyr His
65 70 75 80
Phe Gly Leu Gln Phe Asp Ser Ser Leu Lys Asp Pro Leu Met Leu Thr
85 90 95
Phe Phe Ile Thr Ile Gly Leu Ser Ala Asp Phe Lys Ser Leu Gln Lys
100 105 110
Gly Gly Lys Met Leu Ala Val Phe Leu Leu Ala Val Ala Gly Phe Val
115 120 125
Val Cys Gln Asn Ala Val Gly Ile Ser Ile Ala Ser Leu Leu Gly Val
130 135 140
Asn Pro Leu Met Gly Leu Leu Gly Gly Ser Ile Ala Leu Val Gly Gly
145 150 155 160
His Gly Thr Ser Ala Ala Trp Ala Asn Phe Phe Thr Gln Pro Pro Tyr
165 170 175
His Phe Ser Ser Ser Leu Glu Val Gly Met Ala Cys Ala Thr Phe Gly
180 185 190
Leu Val Ser Gly Gly Ile Ile Gly Gly Pro Val Ala Lys Tyr Leu Ile
195 200 205
Ser Lys Tyr Lys Leu Glu Pro Lys Asp Thr Lys Glu Lys Asp Thr Leu
210 215 220
Glu Gly Val Val Ser Lys Gly Phe Glu Thr Pro Lys Glu Gln Arg Leu
225 230 235 240
Ile Thr Ala Ser Ser Phe Val Glu Thr Leu Ala Leu Ile Ala Ile Ala
245 250 255
Leu Leu Val Gly Thr Phe Leu Ser His Leu Met Pro Lys Ser Phe Thr
260 265 270
Leu Pro Thr Phe Val Trp Cys Leu Phe Val Gly Val Ile Leu Arg Asn
275 280 285
Ala Leu Ser Phe Phe Lys Ile His Ser Val Phe Asp Arg Glu Val Ser
290 295 300
Val Ile Gly Asn Val Ser Leu Ser Leu Phe Leu Ala Tyr Ala Leu Met

```
305                 310                 315                 320
Ser Val Asn Leu Leu Glu Leu Leu Lys Leu Ala Val Pro Leu Ala Val
                325                 330                 335
Ile Leu Ser Val Gln Val Ala Val Met Ile Leu Tyr Val Val Leu Val
            340                 345                 350
Thr Phe Arg Val Cys Gly Lys Asp Tyr Asp Ala Ala Val Leu Cys Ala
        355                 360                 365
Gly His Cys Gly Phe Gly Leu Gly Ala Thr Pro Thr Ala Met Val Asn
    370                 375                 380
Met Gln Thr Ile Thr Asn His Tyr Gly Pro Ser His Val Ala Phe Ile
385                 390                 395                 400
Val Val Pro Leu Val Gly Ala Phe Phe Val Asp Ile Ile Asn Ala Leu
                405                 410                 415
Ala Ile Lys Gly Phe Leu Leu Leu Pro Phe Phe Pro Ser
            420                 425
```

(2) INFORMATION FOR SEQ ID NO:1543:

This Sheet Has Been Replaced



(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

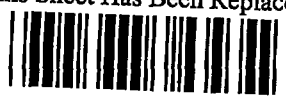
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1543

```
Lys Phe Val Leu Arg Ser Ile Ser Arg Ile Lys Met Leu Ser Val Tyr
1               5                   10                  15
Glu Lys Gly Asn Ala Leu Asp Lys Arg Val Leu Glu Glu Trp Leu Leu
            20                  25                  30
Ser Glu Asp Ile Leu Met Glu Asn Ala Ala Met Ala Leu Glu Arg Ala
        35                  40                  45
Val Leu Gln Asn Ala Ser Leu Gly Ala Lys Val Ile Ile Leu Cys Gly
    50                  55                  60
Ser Gly Asp Asn Gly Gly Asp Gly Tyr Thr Leu Ala Arg Arg Leu Val
65                  70                  75                  80
Gly Arg Phe Lys Thr Leu Val Phe Glu Met Lys Leu Ala Lys Ser Pro
                85                  90                  95
Met Cys Gln Leu Gln Lys Glu Arg Ala Lys Lys Val Gly Val Val Ile
            100                 105                 110
Lys Ala Trp Glu Glu Lys Asn Glu Asp Leu Glu Cys Asp Val Leu Val
        115                 120                 125
Asp Cys Val Val Gly Ser Ala Phe Lys Gly Gly Leu Glu Pro Phe Leu
    130                 135                 140
Asp Phe Glu Ser Leu Ser Gln Lys Ala Arg Phe Lys Ile Ala Cys Asp
145                 150                 155                 160
Ile Pro Ser Gly Ile Asp Ser Lys Gly Arg Val Asp Lys Arg Arg Leu
                165                 170                 175
Arg Arg Ile Arg Leu Ser Ala Trp Ala Leu Ser Ser His Ala Tyr
            180                 185                 190
```

(2) INFORMATION FOR SEQ ID NO:1544:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 441 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1544

```
Asn Ala His Asn Leu Lys Asp Lys Thr Phe Gln Gly Gly Phe Glu Leu
1               5                  10                  15
Leu Thr Thr Pro Lys Glu Tyr Ser Trp Cys Gly Val Val Leu Ser Leu
            20                  25                  30
Leu Leu Ala Ile Asn Leu Tyr Leu Glu Tyr Leu Asn His Gln Lys Leu
        35                  40                  45
Asp Phe Ser Lys Pro Thr Ser Leu Asn Ala Gln Ile Leu Leu Gln Tyr
    50                  55                  60
Pro Lys Thr Lys Asp Gln Lys Thr Tyr Phe Val Leu Lys Leu Gln Ser
65                  70                  75                  80
Lys Gly Met Ile Phe Tyr Thr Thr Ile Lys Glu Pro Leu Lys Asn Leu
                85                  90                  95
Gln Tyr Arg Tyr Ala Gln Phe Phe Gly Lys Ile Lys Pro Cys Ser Phe
            100                 105                 110
Leu Glu Ser Leu Lys Ser Cys Phe Phe Gln Thr Tyr Ser Phe Ser Leu
        115                 120                 125
Thr Arg Lys Gln Asp Phe Lys Ser His Leu Arg His Phe Ile Asp Ser
    130                 135                 140
Ala His Ser Asn Ala Leu Val Gly Asn Leu Tyr Arg Ala Leu Phe Ile
145                 150                 155                 160
Gly Asp Ser Leu Asn Lys Asp Leu Arg Asp Arg Ala Asn Ala Leu Gly
                165                 170                 175
Ile Asn His Leu Leu Ala Ile Ser Gly Phe His Leu Gly Ile Leu Ser
            180                 185                 190
Ala Ser Val Tyr Phe Leu Phe Ser Leu Phe Tyr Thr Pro Leu Gln Lys
        195                 200                 205
Arg Tyr Phe Pro Tyr Arg Asn Ala Phe Tyr Asp Ile Gly Val Leu Val
    210                 215                 220
Trp Val Phe Leu Leu Gly Tyr Leu Leu Leu Leu Asp Phe Leu Pro Ser
225                 230                 235                 240
Phe Phe Arg Ala Phe Leu Met Gly Leu Leu Gly Phe Leu Ala Cys Phe
                245                 250                 255
Phe Gly Val Arg Ile Leu Ser Phe Lys Leu Leu Val Leu Ala Cys Cys
            260                 265                 270
Ile Ala Ile Ala Leu Leu Pro Lys Leu Leu Phe Ser Val Gly Phe Leu
        275                 280                 285
Leu Ser Val Cys Gly Val Trp Tyr Ile Phe Leu Phe Leu Lys His Thr
    290                 295                 300
Gln Ile Phe Phe Lys Asp Ser Ser Phe Phe Lys Arg Ser Phe Gln Ala
305                 310                 315                 320
Ile Ala Leu Ser Val Leu Val Phe Leu Asn Met Leu Ile Val Ala His
                325                 330                 335
Ala Phe Phe Pro Met Phe Ser Pro Tyr Gln Leu Phe Ser Ile Pro Leu
            340                 345                 350
Gly Leu Ile Phe Thr Val Phe Phe Pro Leu Ser Leu Phe Leu His Ala
        355                 360                 365
Val Gly Leu Gly Ser Leu Leu Asp Asn Ile Leu Ser Met Pro Leu Thr
```

```
    370                 375                 380
Ile Pro Thr Ile Ser Val Ser Ser Pro Leu Trp Leu Leu Gly Ala His
385                 390                 395                 400
Leu Phe Leu Thr Ile Leu Ser Val Arg Phe Phe Lys Val Tyr Leu Ser
                405                 410                 415
Met Asn Val Leu Ser Met Gly Phe Phe Leu Tyr Cys Cys Tyr Gln Tyr
            420                 425                 430
Ile Ile Met Pro Ser Leu Ile Val Gly
        435                 440
```

(2) INFORMATION FOR SEQ ID NO:1545:

This Sheet Has Been Replaced



(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:1545

```
Glu Ala Phe Lys Ala Asp Thr Thr Ile Ser Met Gly Ala Ile Lys Ser
1               5                   10                  15
Cys Leu Leu Ser Asp Lys Ala Lys Asp Tyr Ile Gly Glu Leu Lys Val
            20                  25                  30
Gly His Leu Gly Val Phe Asn Gln Ile Tyr Glu Ile Pro Thr Asp Thr
        35                  40                  45
Phe Leu Leu Glu Lys Ser Asp Leu Lys Leu Pro Leu Arg Asp Arg Lys
    50                  55                  60
Asn Ala His Lys Gly Asp Tyr Gly His Ala His Val Leu Leu Gly Lys
65                  70                  75                  80
His Ser Gly Ala Gly Leu Leu Ser Ala Leu Ser Ala Leu Ser Phe Gly
                85                  90                  95
Ser Gly Val Val Ser Ile Gln Ala Leu Glu Cys Glu Ile Thr Ser Asn
            100                 105                 110
Asn Lys Pro Leu Glu Leu Val Phe Cys Glu Asn Phe Pro Lys Lys Leu
        115                 120                 125
Ser Ala Phe Ala Leu Gly Met Gly Leu Glu Asn Ile Pro Lys Asp Phe
    130                 135                 140
Lys Lys Trp Leu Glu Leu Ala Pro Cys Val Leu Asp Ala Gly Val Phe
145                 150                 155                 160
Tyr His Lys Glu Val Leu Gln Ala Leu Glu Lys Glu Val Ile Leu Thr
                165                 170                 175
Pro His Pro Lys Glu Phe Leu Ser Leu Leu Lys Ser Val Gly Ile Asn
            180                 185                 190
Ile Ser Met Leu Glu Leu Leu Asp Asn Lys Leu Glu Ile Ala Arg Asp
        195                 200                 205
Phe Ser Gln Lys Tyr Pro Lys Val Val Leu Leu Leu Lys Gly Ala Asn
    210                 215                 220
Thr Leu Ile Ala His Gln Gly Arg Val Phe Ile Asn Asn Leu Gly Ser
225                 230                 235                 240
Val Ala Leu Ala Lys Ala Gly Ser Gly Asp Val Leu Ala Gly Leu Ile
                245                 250                 255
Val Ser Leu Leu Ser Gln Asn Tyr Thr Pro Leu Asp Ala Ala Ile Asn
            260                 265                 270
```

```
Ala Ser Leu Ala His Ala Leu Ala Gly Leu Glu Phe Lys Asn His Tyr
        275                 280                 285
Ala Leu Thr Pro Leu Asp Leu Ile Glu Lys Ile Lys Arg Leu
    290                 295                 300
```

(2) INFORMATION FOR SEQ ID NO:1546:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 375 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

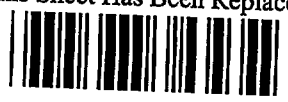
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1546

```
Leu Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala Lys Val Ala
1               5                  10                  15
Thr Met Leu Ala Val Gly Phe Ser Leu Asp Glu Ile Lys Asn Asp Ile
            20                  25                  30
Thr Asn Thr Pro Ala Ser Phe Glu Pro Ser Leu Asp Tyr Ile Val Val
        35                  40                  45
Lys Ile Pro Arg Phe Ala Phe Glu Lys Phe Ala Gly Val Ser Ser Thr
    50                  55                  60
Leu Gly Thr Ser Met Lys Ser Ile Gly Glu Val Met Ala Ile Gly Gly
65                  70                  75                  80
Asn Phe Leu Glu Ala Leu Gln Lys Ala Leu Cys Ser Leu Glu Asn Asn
                85                  90                  95
Trp Leu Gly Phe Glu Ser Leu Ser Lys Asp Leu Glu Ala Ile Lys Lys
            100                 105                 110
Glu Ile Arg Arg Pro Asn Pro Lys Arg Leu Leu Tyr Ile Ala Asp Ala
        115                 120                 125
Phe Arg Leu Gly Val Ser Val Asp Glu Val Phe Glu Leu Cys Gln Ile
    130                 135                 140
Asp Arg Trp Phe Leu Ser Gln Ile Gln Lys Leu Val Lys Ala Glu Glu
145                 150                 155                 160
Gly Ile Asn Ser Ser Val Leu Thr Asp Ala Lys Lys Leu Arg Gly Leu
                165                 170                 175
Lys Asn Leu Gly Phe Ser Asp Ala Arg Ile Ala Thr Lys Ile Lys Glu
            180                 185                 190
Asn Glu Asn Leu Glu Val Ser Pro Phe Glu Val Glu Leu Ala Arg Ser
        195                 200                 205
Asn Leu Gln Ile Ala Pro His Phe Glu Glu Val Asp Thr Cys Ala Ala
    210                 215                 220
Glu Phe Leu Ser Leu Thr Pro Tyr Leu Tyr Ser Thr Tyr Ala Pro Asn
225                 230                 235                 240
Pro Leu Pro Pro Ile Gly Asn Lys Gln Glu Lys Gln Glu Lys Lys Ile
                245                 250                 255
Leu Ile Ile Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe
            260                 265                 270
Asp Tyr Cys Cys Val His Ala Ser Phe Ala Leu Lys Asp Leu Asn Ile
        275                 280                 285
Lys Ser Val Met Leu Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr
    290                 295                 300
Asp Thr Ser Asp Thr Leu Tyr Phe Glu Pro Ile His Phe Glu Cys Val
```

This Sheet Has Been Replaced



```
305                 310                 315                 320
Lys Ser Ile Ile Gln Arg Glu Arg Val Asp Gly Ile Ile Val His Phe
                325                 330                 335
Gly Gly Gln Thr Pro Leu Lys Leu Ala Lys Asp Leu Ala Lys Met Gln
            340                 345                 350
Ala Pro Ile Ile Gly Thr Pro Phe Lys Val Ile Asp Ile Ala Glu Asp
        355                 360                 365
Arg Glu Lys Phe Pro Ser Phe
    370                 375
```

(2) INFORMATION FOR SEQ ID NO:1547:

This Sheet Has Been Replaced



(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:1547

```
Arg Pro Val Ile Ser Ala Lys Glu Gly Ser Asp Pro Ser Ser Leu Ala
1               5                   10                  15
Tyr Asn Thr Ile Glu Ser Ala Ile Ala Lys Asn Ile Asp Glu Val Phe
            20                  25                  30
Ile Asp Thr Ala Gly Arg Leu His Asn Gln Thr Asn Leu Lys Asn Glu
        35                  40                  45
Leu Ser Lys Ile Ala His Thr Cys Ser Lys Val Leu Lys Asp Ala Pro
    50                  55                  60
Phe Tyr Lys Phe Leu Ile Leu Asp Gly Thr Gln Gly Ser Ser Gly Leu
65                  70                  75                  80
Thr Gln Ala Lys Ile Phe His Glu Thr Leu Ala Leu Asp Gly Val Ile
                85                  90                  95
Met Thr Lys Leu Asp Gly Thr Ser Lys Gly Gly Ala Ile Leu Ser Val
            100                 105                 110
Leu Tyr Glu Leu Lys Leu Pro Ile Leu Tyr Leu Gly Met Gly Glu Lys
        115                 120                 125
Glu Asp Asp Leu Ile Ala Phe Asp Glu Glu Arg Phe Ile Glu Asp Leu
    130                 135                 140
Val Asp Ala Val Phe Val Glu Gln
145                 150
```

(2) INFORMATION FOR SEQ ID NO:1548:

(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:

This Sheet Has Been Replaced



(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1548

```
Asn Leu Arg Ile Ile Thr Ile Lys Thr Ile Phe Arg Asp Phe Cys Lys
1               5                  10                  15
Glu Arg Leu Lys Arg Ala Lys Ser Lys Asn Lys Val Arg Asp Lys Leu
            20                  25                  30
Ala Cys Lys Leu Leu Phe Trp Lys Leu Lys Asp Tyr Gln Asn Ile Leu
        35                  40                  45
Leu Tyr Ser Pro Leu Gly His Glu Leu Asp Ile Arg Pro Leu Ile Leu
    50                  55                  60
Lys Leu Arg Gln Lys Asn Lys Arg Val Trp Leu Pro Lys Ser Ile Lys
65                  70                  75                  80
Lys Gly Ala His Phe Ser Lys Glu Gly Phe Thr Ile Ala Pro Phe Arg
                85                  90                  95
Leu Pro Leu Arg Arg Leu Gly Trp Phe Asp Glu Pro Ser Leu Ser Arg
            100                 105                 110
Tyr Tyr Lys Arg Glu Leu Asp Cys Ile Val Val Pro Ile Leu Gly Met
        115                 120                 125
Asp Thr Ser Phe Arg Arg Val Gly Phe Gly Leu Gly Met Tyr Asp Arg
    130                 135                 140
Ser Leu Pro Gln Leu Phe Lys Lys Gln Leu Lys Arg Pro Leu Val Ile
145                 150                 155                 160
Phe Val Ser Arg Glu Leu Ala Leu Ala Asn Gly Ile Leu Thr Asp Ala
                165                 170                 175
Tyr Asp Ile Glu Ala Asn Leu Tyr Met Asn Ala Arg Ile Val Met Lys
            180                 185                 190
Asn Asn Lys Arg Lys His Tyr Glu Gln Arg Val Asn Leu His Phe Ile
        195                 200                 205
Arg Ser Leu Gly Ser Val Phe Asp His Arg Ser Asn His Val Leu Cys
    210                 215                 220
Asp Glu Lys Asp Leu Leu Arg
225                 230
```

(2) INFORMATION FOR SEQ ID NO:1549:

(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:1549

```
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:1550:

This Sheet Has Been Replaced



(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:1550

```
Ile Arg Ser Ser Asn Asp Thr Gln Thr Thr Gln Thr Pro Trp His Ser
1               5                   10                  15
Asn Thr Arg Arg Pro Lys Pro Thr Pro Lys Pro Ile Lys Lys Glu Ala
            20                  25                  30
Lys Lys Ala Lys Glu Lys Thr Thr Lys His Ala His Ser Lys His Ala
        35                  40                  45
His Ser Pro Leu Asn Glu Arg Ser Ala Lys Lys Glu Ile Pro Lys Lys
    50                  55                  60
Glu Ile Pro Lys Lys Glu Ile Pro Lys Lys Glu Ile Pro Lys Lys Glu
65                  70                  75                  80
Ile Pro Lys Lys Glu Ile Pro Lys Lys Glu Ile Pro Lys Lys Glu Ile
                85                  90                  95
Pro Lys Lys Glu Ala Glu Asn Glu Ser Lys Asn Gln Ile Phe Ile Ala
            100                 105                 110
Glu Lys Asn Asp Thr Trp Ile Lys Thr Lys Arg Lys Lys His Lys Lys
        115                 120                 125
Ile Val Leu Asp Ala Gly His Gly Gly Lys Asp Cys Gly Ala Met Ser
    130                 135                 140
Ala Asn Leu Val Cys Glu Lys Asp Ile Val Leu Glu Val Val Lys Phe
145                 150                 155                 160
Leu His Lys Glu Leu Lys Lys Arg Gly Tyr Ser Val Leu Leu Thr Arg
                165                 170                 175
```

```
Asp Lys Asp Ile Tyr Ile Asp Leu Val Ala Arg Thr Glu Leu Ala Asn
            180                 185                 190
Lys Lys Gly Ala Asp Leu Phe Ile Ser Val His Ala Asn Ser Ile Pro
        195                 200                 205
Lys Arg Ser Thr Ser Asn Ala His Gly Ile Glu Thr Tyr Phe Leu Ser
    210                 215                 220
Thr Ala Arg Ser Glu Arg Ala Arg Lys Val Ala Glu Gln Glu Asn Lys
225                 230                 235                 240
Asp Asp Val Asn Leu Met Asp Tyr Phe Ser Lys Ser Leu Phe Leu Asn
                245                 250                 255
Ser Leu Asn Thr Gln Arg Leu Ile Val Ser Asn Lys Leu Ala Ile Asp
            260                 265                 270
Val Gln Tyr Gly Met Leu Gln Ser Val Arg Lys Asn Tyr Pro Asp Val
        275                 280                 285
Val Asp Gly Gly Val Arg Glu Gly Pro Phe Trp Val Leu Ala Gly Ala
    290                 295                 300
Leu Met Pro Ser Ile Leu Ile Glu Ile Gly Tyr Asn Ser His Ala Ile
305                 310                 315                 320
Glu Ser Lys Arg Ile Gln Ser Lys Pro Tyr Gln Lys Ile Leu Ala Lys
                325                 330                 335
Gly Ile Ala Asp Gly Ile Asp Ser Phe Phe Ser Lys Asn Asp
            340                 345                 350
```

(2) INFORMATION FOR SEQ ID NO:1551:

(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:1551

```
Arg Val Ser Met Asn Val Lys Lys Lys Gly Lys Pro Gln Ser Gly Lys
1               5                  10                  15
Ile Asp Arg Val Asp Cys Leu Glu Lys Leu Gly Lys Glu Asn Thr Thr
            20                  25                  30
Phe Leu Ser Ser Ile Ala Met Gly Ser Ile Gly Gln Leu Ala Ile Pro
        35                  40                  45
Ile Pro Gly Val Gly Val Leu Ile Gly Gly Phe Val Gly Gly Val Met
    50                  55                  60
Ser Lys Thr Phe Tyr Asp Val Ser Leu Thr Ile Phe Lys Glu Ala Lys
65                  70                  75                  80
Leu Ala Arg Gln Arg Arg Ile Glu Ile Glu Lys Glu Cys Arg Glu Ser
                85                  90                  95
Ile Arg Gln Leu Glu Met Tyr Gln Asn Gln Phe Asn Glu Val Phe Glu
            100                 105                 110
Arg Tyr Phe His Gly Thr Ile Lys Phe Phe Asn Glu Ser Phe Asp Glu
        115                 120                 125
Leu Glu Arg Ala Leu Cys Ala Gly Asp Ala Asp Leu Ala Ile Ala Val
    130                 135                 140
Asn Asn Lys Ile Gln Glu Gly Met Gly Gln Glu Leu Leu Phe Asp Asn
145                 150                 155                 160
Lys Gln Glu Cys Trp Glu Phe Ile Thr Ser Arg Lys Glu Gly Trp Asn
```

This Sheet Has Been Replaced



```
                165                 170                 175
Phe Val Thr Ser Arg Gly Lys Thr Glu Ile
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:1552:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1552

```
Lys Arg Asp Gln Met Ala Glu Glu Glu Lys Thr Glu Leu Pro Ser Ala
1               5                  10                  15
Lys Lys Ile Gln Lys Ala Arg Glu Glu Gly Asn Val Pro Lys Ser Met
            20                  25                  30
Glu Val Val Gly Phe Leu Gly Leu Leu Ala Gly Leu Met Ser Ile Phe
        35                  40                  45
Val Phe Phe Ile Trp Trp Val Asp Gly Phe Ser Glu Met Tyr Arg His
    50                  55                  60
Val Leu Lys Asp Phe Ser Leu Asp Phe Ser Lys Glu Ser Val Gln Glu
65                  70                  75                  80
Leu Phe Asn Gln Leu Ala Lys Asp Thr Phe Leu Leu Leu Leu Pro Val
                85                  90                  95
Leu Ile Ile Leu Met Val Val Ala Phe Leu Ser Asn Val Leu Gln Phe
            100                 105                 110
Gly Trp Leu Phe Ala Pro Lys Val Ile Glu Pro Lys Phe Ser Lys Ile
        115                 120                 125
Asn Pro Ile Asn Gly Val Lys Asn Leu Phe Ser Leu Lys Lys Ile Leu
    130                 135                 140
Asp Gly Ser Leu Ile Thr Leu Lys Val Phe Leu Ala Phe Phe Leu Gly
145                 150                 155                 160
Phe Phe Ile Phe Ser Leu Phe Leu Gly Glu Leu Asn His Ala Ala Leu
                165                 170                 175
Leu Asn Leu Gln Gly Gln Leu Leu Trp Phe Lys Ser Lys Ala Leu Trp
            180                 185                 190
Leu Ile Ser Ser Leu Leu Phe Leu Phe Phe Val Leu Ala Phe Val Asp
        195                 200                 205
Leu Ile Ile Lys Arg Arg Gln Tyr Thr Asn Ser Leu Lys Met Thr Lys
    210                 215                 220
Gln Glu Val Lys Asp Glu Tyr Lys Gln Gln Glu Gly Asn Pro Glu Ile
225                 230                 235                 240
Lys Ala Lys Ile Arg Gln Met Met Val Lys Asn Ala Thr Asn Lys Met
                245                 250                 255
Met Gln Glu Ile Pro Lys Ser Asn Val Val Val Thr Asn Pro Thr His
            260                 265                 270
Tyr Ala Val Ala Leu Lys Phe Asp Glu Glu His Pro Val Pro Val Val
        275                 280                 285
Val Ala Lys Gly Thr Asp Tyr Leu Ala Ile Arg Ile Lys Gly Ile Ala
    290                 295                 300
Arg Glu His Asp Ile Glu Ile Ile Glu Asn Lys Thr Leu Ala Arg Glu
305                 310                 315                 320
```

This Sheet Has Been Replaced



```
Leu Tyr Arg Asp Val Lys Leu Asn Ala Thr Ile Pro Glu Glu Leu Phe
                325                 330                 335
Glu Ala Val Ala Ile Val Phe Ala Gln Val Ala Lys Leu Glu Gln Glu
            340                 345                 350
Arg Gln Lys Gln Lys Ile Ile Lys Pro Leu
        355                 360
```

(2) INFORMATION FOR SEQ ID NO:1553:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 181 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1553

```
Glu Asn Thr Met Gln Asp Leu Gln His Phe Lys Asn Asp Ile Thr Leu
1               5                   10                  15
Ile Leu Ser Lys Asp Arg Leu Asp Thr Tyr Asp Ser Leu Glu Gln Tyr
            20                  25                  30
Lys Glu Asn Leu Lys Leu Ile Ser Phe Ile Thr Pro Lys Ile Ser Asn
        35                  40                  45
Leu Glu Ile Tyr Leu Arg Asn Ala Leu Asp Tyr Cys Leu Thr Gln Ile
    50                  55                  60
Lys Gly Ser Glu Trp Val Phe Asn Glu Asn Ser Leu Thr Asp Leu Ile
65                  70                  75                  80
Asn Glu Gln Lys Glu Lys Lys Lys Glu Ile Thr His Ser Leu Ile Leu
                85                  90                  95
Ser Lys Met Ser Leu Gly Ala Val Val Arg Leu Ile Phe Cys Tyr Lys
            100                 105                 110
Leu Glu Gly Val Ile Leu Asp Leu Arg Ala Tyr Arg Leu Arg Ala Tyr
        115                 120                 125
Tyr His Glu Asn Lys Asp Thr Leu Leu Ile Lys Gly Lys Lys Arg Leu
    130                 135                 140
Leu Tyr Asn Tyr Ile Lys Ala His Ile Ala Leu Asn Leu Leu Trp Thr
145                 150                 155                 160
Ile Arg Asn Arg Thr Tyr His Trp Glu Asn Leu Leu Lys Ile Gln Pro
                165                 170                 175
Asn Asn Arg Pro Gln
            180
```

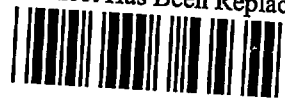
(2) INFORMATION FOR SEQ ID NO:1554:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1554

```
Ala Asn Gly Cys Glu Lys Arg Ile Phe Met Leu Leu Cys Ala Gly Arg
1               5                  10                  15
Asn Glu Thr Leu Lys Lys Ala Val Pro Ile Gly Val Gly Leu Ile Glu
            20                  25                  30
Ser Ala Ile Asn Leu Thr Arg Met Cys Leu Lys Asn Pro Asp Thr Glu
        35                  40                  45
Ser Leu Ile Phe Ile Gly Ser Ala Gly Ser Tyr Ser Pro Glu Thr Glu
    50                  55                  60
Ile Leu Ser Val Phe Glu Ser Ile Glu Gly Tyr Gln Ile Glu Glu Ser
65                  70                  75                  80
Phe Ser His Leu Asn Ser Tyr Thr Pro Leu Asp Asn Phe Ile His Ile
                85                  90                  95
Glu Thr Lys Glu Gln Ala Leu Phe Glu Arg Val Arg Val Asn Ser Ser
            100                 105                 110
Asn Tyr Ile His Thr Ser Glu Met Phe Ala Lys Lys Met Val Gln Lys
        115                 120                 125
Gly Val Leu Leu Glu Asn Met Glu Phe Phe Ser Val Leu Ser Val Ala
    130                 135                 140
Lys Ile Phe Ser Leu Lys Ala Lys Gly Ile Phe Cys Val Ser Asn His
145                 150                 155                 160
Val Gly Leu Asn Ala His Lys Glu Phe Lys Glu Asn His Ala Lys Val
                165                 170                 175
Lys Gln Ile Leu Glu Asn Ile Ile Asp Ser Leu Ile Val
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:1555:

(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:1555

```
Phe Val Leu Ala Cys Asn Arg Leu Leu Ala Arg Thr Leu Lys Ser Glu
1               5                  10                  15
Tyr Arg Ile Cys Gly Phe Ala Lys Asn His Pro Phe Ser Gly Pro Phe
            20                  25                  30
Glu Ser Gly Gly Val Trp Phe Cys Gly Tyr Ser Thr Phe Arg Leu Asn
        35                  40                  45
Arg Phe Ser Gly His Tyr Cys Cys Lys Trp Arg Arg Asn Gly Ile Gln
    50                  55                  60
Ser Val Val Asp Glu Thr Lys Pro Phe Thr His Ser Lys Asn Gly Arg
65                  70                  75                  80
```

```
Lys Arg Gly Phe Ser Leu Phe Gln Ala Ile Gln Pro Ser Val Phe Asp
                85                  90                  95
Arg Ser Thr Leu Ala Asn Gln Ser Asp His Arg Tyr Phe His Leu Phe
            100                 105                 110
Val Gly Tyr Phe Phe Glu Trp Val Pro Lys Asn Arg Phe Lys Glu Ser
        115                 120                 125
Val Gln Cys Leu Arg Gly Gly Asp Leu Tyr Cys Asn His Gln His Ala
    130                 135                 140
Gln Tyr Phe Lys Leu Glu Phe Asn Phe Arg Lys Lys Arg Ala Gly Tyr
145                 150                 155                 160
Lys Arg Arg Tyr Asn Phe His Ala Val Phe Phe Gly Gly His Cys Arg
                165                 170                 175
His Ala Arg Glu Thr Phe Phe Arg Gln Ser Ile Lys Leu Leu Arg Leu
            180                 185                 190
Leu Arg Phe Ser Glu Lys Arg Lys Thr Lys Arg Ser Lys Asp Lys Glu
        195                 200                 205
Arg Arg Lys Asp Cys Arg Lys Thr Arg Asn Gln Ala Arg Ser His Arg
    210                 215                 220
Ala Lys Ser Gln Ser Arg His Arg Lys Arg Ser His Phe Arg Arg Glu
225                 230                 235                 240
Lys Leu Pro Lys Ser Arg Ala Lys Ile Arg Arg Arg Lys Ala Ser Phe
                245                 250                 255
Lys Arg Lys Glu Lys Asn Ser His Gln Lys Gly Tyr Gly Ile Thr Lys
            260                 265                 270
Ser Glu Arg Thr Ser Arg Lys Arg Lys Arg Ala Arg Lys Lys Lys Ser
        275                 280                 285
Phe Arg Asn Glu Glu
    290
```

(2) INFORMATION FOR SEQ ID NO:1556:

This Sheet Has Been Replaced



(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:1556

```
Gly Glu Thr Thr Met Lys Leu Arg Ala Ser Val Leu Ile Gly Val Ala
1               5                  10                  15
Ile Leu Cys Leu Ile Leu Ser Ala Cys Ser Asn Tyr Ala Lys Lys Val
            20                  25                  30
Val Lys Gln Lys Asn His Val Tyr Thr Pro Val Tyr Asn Glu Leu Ile
        35                  40                  45
Glu Lys Tyr Ser Glu Ile Pro Leu Asn Asp Lys Leu Lys Asp Thr Pro
    50                  55                  60
Phe Met Val Gln Val Lys Leu Pro Asn Tyr Lys Asp Tyr Leu Leu Asp
65                  70                  75                  80
Asn Lys Gln Val Val Leu Thr Phe Lys Leu Val His His Ser Lys Lys
                85                  90                  95
Ile Thr Leu Ile Gly Asp Ala Asn Lys Ile Leu Gln Tyr Lys Asn Tyr
            100                 105                 110
Phe Gln Ala Asn Gly Ala Arg Ser Asp Ile Asp Phe Tyr Leu Gln Pro
```

```
        115                 120                 125
Thr Leu Asn Gln Lys Gly Val Val Met Ile Ala Ser Asn Tyr Asn Asp
    130                 135                 140
Asn Pro Asn Asn Lys Glu Lys Pro Gln Thr Phe Asp Val Leu Gln Gly
145                 150                 155                 160
Ser Gln Pro Met Leu Gly Ala Asn Thr Lys Asn Leu His Gly Tyr Asp
                165                 170                 175
Val Ser Gly Ala Asn Asn Lys Gln Val Ile Asn Glu Val Ala Arg Glu
            180                 185                 190
Lys Ala Gln Leu Glu Lys Ile Asn Gln Tyr Tyr Lys Thr Leu Leu Gln
        195                 200                 205
Asp Lys Glu Gln Glu Tyr Thr Thr Arg Lys Asn Asn Gln Arg Glu Ile
    210                 215                 220
Leu Glu Thr Leu Ser Asn Arg Ala Gly Tyr Gln Met Arg Gln Asn Val
225                 230                 235                 240
Ile Ser Ser Glu Ile Phe Lys Asn Gly Asn Leu Asn Met Gln Ala Lys
                245                 250                 255
Glu Glu Glu Val Arg Glu Lys Leu Gln Glu Glu Arg Glu Asn Glu Tyr
            260                 265                 270
Leu Arg Asn Gln Ile Arg Ser Leu Leu Ser Gly Lys
        275                 280
```

(2) INFORMATION FOR SEQ ID NO:1557:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1557

```
Ser Tyr Cys Gln Met Lys Thr Leu Val Lys Asn Thr Ile Tyr Ser Phe
1               5                   10                  15
Leu Leu Leu Ser Val Leu Met Ala Glu Asp Ile Thr Ser Gly Leu Lys
            20                  25                  30
Gln Leu Asp Asn Thr Tyr Gln Glu Thr Asn Gln Gln Val Leu Lys Asn
        35                  40                  45
Leu Asp Glu Ile Phe Ser Thr Thr Ser Pro Ser Ala Asn Asn Lys Ile
    50                  55                  60
Gly Gln Glu Asp Ala Leu Asn Ile Lys Lys Ala Ala Ile Ala Leu Arg
65                  70                  75                  80
Gly Asp Leu Ala Leu Leu Lys Ala Asn Phe Glu Ala Asn Glu Leu Phe
                85                  90                  95
Phe Ile Ser Glu Asp Val Ile Phe Lys Thr Tyr Met Ser Ser Pro Glu
            100                 105                 110
Leu Leu Leu Thr Tyr Met Lys Ile Asn Pro Leu Asp Gln Lys Thr Ala
        115                 120                 125
Glu Gln Gln Cys Gly Ile Ser Asp Lys Val Leu Val Leu Tyr Cys Glu
    130                 135                 140
Gly Lys Leu Lys Ile Glu Gln Glu Lys Gln Asn Ile Arg Glu Arg Leu
145                 150                 155                 160
Glu Thr Ser Leu Lys Ala Tyr Gln Ser Asn Ile Gly Gly Thr Ala Ser
                165                 170                 175
```

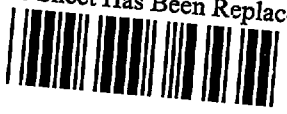
This Sheet Has Been Replaced



```
Leu Ile Thr Ala Ser Gln Thr Leu Val Glu Ser Leu Lys Asn Lys Asn
            180                 185                 190
Phe Ile Lys Gly Ile Lys Lys Leu Met Leu Ala His Asn Lys Val Phe
        195                 200                 205
Leu Asn Tyr Leu Glu Glu Leu Asp Ala Leu Glu Arg Ser Leu Glu Gln
    210                 215                 220
Ser Lys Arg Gln Tyr Leu Gln Glu Arg Gln Ser Ser Lys Ile Ile Val
225                 230                 235                 240
Lys
```

(2) INFORMATION FOR SEQ ID NO:1558:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 539 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1558

```
Ile Asn Lys Asn Met Phe Asn Ile Lys Arg Thr Phe Leu Ile Thr Ile
1               5                  10                  15
Ile Ser Phe Phe Leu Ile Val Pro Asn Trp Leu Lys Ala Ile Asp Leu
            20                  25                  30
Pro Ile Val Ser Asn Leu Lys Ile Tyr Gln Thr Val Tyr Cys Met Leu
        35                  40                  45
Ile Pro Ser Tyr Val Leu Thr Asn Lys Ser Phe Ala Asp Ile Leu Thr
    50                  55                  60
Gly Tyr Thr Ser Ile Gly Ala Ser Gly Ser Gly Lys Ser Ser Gly Gln
65                  70                  75                  80
Gly Val Ile Glu Ala Leu Ser Thr Pro Leu Ala Thr Ser Leu Ala Ala
                85                  90                  95
Ser Asn Leu Val Lys Tyr Leu Asn Thr Leu Gly Pro Leu Trp Gly Ser
            100                 105                 110
Ala Trp Ala Ser Val Ala Thr Ala Ile Gln Gly Phe Ala Leu Thr Pro
        115                 120                 125
Ser Ser Gly Cys Asn Phe Gly Trp Asn Ala Leu Ile Asn Lys Asn Ile
    130                 135                 140
Asp Val Ser Met Asp Ser Val Leu Asp Asn Leu Ser Asn Lys Ile Gln
145                 150                 155                 160
Asn Phe Thr Lys Gly Gly Val Glu Asp Asn Val Lys Gly Asn Ile Leu
                165                 170                 175
Leu Gln Ile Ile Gly Ser Ile Thr Ala Gln Ala Ser Thr Asn Ile Thr
            180                 185                 190
Ala Asp Gly Leu Ile Trp Leu Ile Gly Lys Glu Phe Thr Ala Asn Lys
        195                 200                 205
Leu Gln Asn Asn Thr Ile Ala Met Leu Ala Phe Ala Ala Leu Glu Ser
    210                 215                 220
Val Val Lys Gly Ala Asp Ala Ala Val Leu Pro Ala Tyr Gly Val Val
225                 230                 235                 240
Asn Leu Pro Asp Ile Ile Ile Gly Gln Gly Ser Tyr Leu Asp Phe Val
                245                 250                 255
Ser Tyr Leu Ile Tyr Ile Val Phe Gly Ile Phe Val Phe Ile Ser Phe
```

```
            260                 265                 270
Met Lys Leu Arg Asp Ile Ser Asn Gly Ile Gln Ile Asn Ile Gly Phe
        275                 280                 285
Glu Tyr Met Arg Phe Val Gly Gly Thr Leu Phe Lys Met Ala Met Val
    290                 295                 300
Ser Phe Ile Ala Tyr Ala Gly Phe Gly Tyr Leu Tyr Lys Ile Ser Tyr
305                 310                 315                 320
Ser Ile Tyr Phe Gly Leu Ala Gly Ala Phe Gly Leu Asn Gln Val Leu
                325                 330                 335
Phe Trp Ala Leu Asp Leu Val Leu Asn Tyr Thr Val Asn Ser Ile Leu
            340                 345                 350
Pro Ala Val Arg Ala Val Phe Ser Asn Val Gly Asn Asn Ala Pro Ser
        355                 360                 365
Leu Leu Gln Gly Leu Gln Val Ala Gly Ile Ser Leu Phe Ala Ile Phe
    370                 375                 380
Met Gln Val Thr Ile Ile Met Arg Ile Ser Thr Val Val Val Lys Pro
385                 390                 395                 400
Leu Ile Ala Gly Ala Phe Ser Gly Ile Val Phe Pro Ile Ala Val Cys
                405                 410                 415
Leu Ile Val Leu Asp Trp Phe Lys Asp Ser Met Lys Asn Ile Leu Ile
            420                 425                 430
Trp Phe Ile Asn Asn Leu Phe Ile Leu Val Leu Ala Ile Pro Ile Leu
        435                 440                 445
Leu Phe Gly Val Leu Ala Leu Leu Ala Phe Asn Leu Thr Ile Thr Pro
    450                 455                 460
Ser Val Ala Ile Gln Asn Ile Asn Gln Gly Gly Leu Gly Ile Asp Ser
465                 470                 475                 480
Thr Ile Ala Ser Leu Ile Thr Leu Phe Ile Leu Lys Gly Phe Ile Glu
                485                 490                 495
Thr Ile Ile Glu Ser Val Asn Ala Ile Val Asn Thr Ile Phe Ser Ser
            500                 505                 510
Val Ser Met Asp Gly Ser Arg Met Asp Arg Glu Arg Asp Ala Leu Met
        515                 520                 525
Val Gly Arg Val Gly Gly Ser Met Phe Lys Gly
    530                 535
```

(2) INFORMATION FOR SEQ ID NO:1559:

(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:1559

```
Leu His Arg Ile Ile Ser Cys Asp Ser Ala Trp Arg Thr Asn Leu Val
1               5                   10                  15
Val Arg Thr Asn Lys Ala Leu Tyr Gln Phe Ile Leu Arg Ile Ala Gln
            20                  25                  30
Lys Asp Asn Phe Ala Ser Ala Tyr Leu Thr Val Lys Leu Glu Tyr Pro
        35                  40                  45
Gln Arg His Glu Val Ser Ser Val Ile Glu Glu Glu Leu Lys Lys Arg
    50                  55                  60
```

This Sheet Has Been Replaced



```
Glu Glu Ala Lys Arg Gln Arg Glu Leu Ile Lys Gln Glu Asn Leu Asn
65                  70                  75                  80
Thr Thr Ala Tyr Ile Asn Arg Val Met Met Ala Ser Asn Glu Gln Ile
                85                  90                  95
Ile Asn Lys Glu Lys Ile Arg Glu Glu Lys Gln Lys Ile Ile Leu Asp
            100                 105                 110
Gln Ala Lys Ala Leu Glu Thr Gln Tyr Val His Asn Ala Leu Lys Arg
        115                 120                 125
Asn Pro Val Pro Arg Asn Tyr Asn Tyr Tyr Gln Ala Pro Glu Lys Arg
    130                 135                 140
Ser Lys His Ile Met Pro Ser Glu Ile Phe Asp Asp Gly Thr Phe Thr
145                 150                 155                 160
Tyr Phe Gly Phe Lys Asn Ile Thr Leu Gln Pro Ala Ile Phe Val Val
                165                 170                 175
Gln Pro Asp Gly Lys Leu Ser Met Thr Asp Ala Ala Ile Asp Pro Asn
            180                 185                 190
Met Thr Asn Ser Gly Leu Arg Trp Tyr Arg Val Asn Glu Ile Ala Glu
        195                 200                 205
Lys Phe Lys Leu Ile Lys Asp Lys Ala Leu Val Thr Val Ile Asn Lys
    210                 215                 220
Gly Tyr Gly Lys Asn Pro Leu Thr Lys Asn Tyr Asn Ile Lys Asn Tyr
225                 230                 235                 240
Gly Glu Leu Glu Arg Val Ile Lys Lys Leu Pro Leu Val Arg Asp Lys
                245                 250                 255
```

(2) INFORMATION FOR SEQ ID NO:1560:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1560

```
Thr Ser Ser Phe Lys Thr Lys Met Lys Arg Pro Ile Ser Lys Leu Lys
1               5                   10                  15
Gln Asn Phe Leu Gln Phe Lys His Ser Phe Asn Lys His Leu Asp Lys
            20                  25                  30
Tyr Ser Leu Tyr Tyr Arg Leu Phe Asn Ile Ser Ser Ile Val Ile Gly
        35                  40                  45
Phe Leu Ile Ala Leu Phe Ser Tyr Gly Ala Gly Val Ile Leu Val Tyr
    50                  55                  60
Pro Ile Leu Phe Leu Phe Ala Leu Ile Ile Lys Pro Ser Phe Phe Tyr
65                  70                  75                  80
Tyr Thr Thr Tyr Leu Leu Leu Leu Val Ser Leu Ser Ile Ile Ser Lys
                85                  90                  95
Tyr Tyr Leu Leu Ser His Ala Asn Phe Thr Met Lys Leu Ile Met Leu
            100                 105                 110
Met Thr Gln Trp Gln Asn Trp Phe Leu
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:1561:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1561

```
Val Cys Tyr Cys Glu Met Leu Pro Thr Lys Thr Arg Ile Arg Asp Pro
1               5                  10                  15
Asn Lys Gln Glu Leu Thr Gln Pro Lys Ile Lys Gly Leu Ser Met Gly
            20                  25                  30
Lys Ile Leu Ala Ser Leu Leu Gly Gly Gly Thr Asn Leu Phe Thr Gly
        35                  40                  45
Leu Ser Ser Asp Leu Phe Ser Met Ile Leu Asn Phe Leu Phe Phe Leu
    50                  55                  60
Met Leu Met Met Gly Leu Asn Glu Ala Leu Gly Lys Lys Phe Asn Leu
65                  70                  75                  80
Pro Met Asp Asn Ile Lys Asn Phe Met Ala Glu Val Leu Lys Asn Gly
                85                  90                  95
Phe Asp Ser Ile Lys Asn Met Gly Ser Ala Leu Val Gly Asn Gly Phe
            100                 105                 110
Gly Ser Ser Lys Ser Asp Lys Thr Thr Asn Lys Met Ser Val Pro Gln
        115                 120                 125
Val Arg Leu
    130
```

(2) INFORMATION FOR SEQ ID NO:1562:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

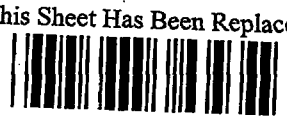
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...297

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1562

```
Glu Glu Leu Leu Met Gly Gln Ala Phe Phe Lys Lys Ile Val Gly Cys
1               5                  10                  15
Phe Cys Leu Gly Tyr Leu Phe Leu Ser Ser Ala Ile Glu Ala Val Ala
            20                  25                  30
Leu Asp Ile Lys Asn Phe Asn Arg Gly Arg Val Lys Val Val Asn Lys
        35                  40                  45
```

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

(2) INFORMATION FOR SEQ ID NO:1563:

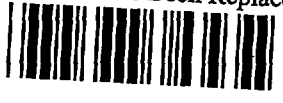
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1563

```
Ser Cys Arg Met Leu Gly Lys Lys Asn Glu Glu Val Leu Ile Asp Glu
1               5                   10                  15
Asn Leu Val Gly Gly Val Ile Ala Leu Asp Arg Leu Ala Lys Leu Asn
            20                  25                  30
Lys Ala Asn Arg Thr Phe Lys Arg Ala Phe Tyr Leu Ser Met Val Leu
        35                  40                  45
Asn Val Ala Ala Val Thr Ser Ile Val Met Met Met Pro Leu Lys Lys
    50                  55                  60
Thr Asp Ile Phe Val Tyr Gly Ile Asp Arg Tyr Thr Gly Glu Phe Lys
65                  70                  75                  80
Ile Val Lys Arg Ser Asp Ala Arg Gln Ile Val Asn Ser Glu Ala Val
```

```
                85                  90                  95
Val Asp Ser Ala Thr Ser Lys Phe Val Ser Leu Leu Phe Gly Tyr Ser
            100                 105                 110
Lys Asn Ser Leu Arg Asp Arg Lys Asp Gln Leu Met Gln Tyr Cys Asp
        115                 120                 125
Val Ser Phe Gln Thr Gln Ala Met Arg Met Phe Asn Glu Asn Ile Arg
    130                 135                 140
Gln Phe Val Asp Lys Val Arg Ala Glu Ala Ile Ile Ser Ser Asn Ile
145                 150                 155                 160
Gln Arg Glu Lys Val Lys Asn Ser Pro Leu Thr Arg Leu Thr Phe Phe
                165                 170                 175
Ile Thr Ile Lys Ile Thr Pro Asp Thr Met Glu Asn Tyr Glu Tyr Ile
            180                 185                 190
Thr Lys Lys Gln Val Thr Ile Tyr Tyr Asp Phe Ala Arg Gly Asn Ser
        195                 200                 205
Ser Gln Glu Asn Leu Ile Ile Asn Pro Phe Gly Phe Lys Val Phe Asp
    210                 215                 220
Ile Gln Ile Thr Asp Leu Gln Asn Glu Gln Thr Val Ser Glu Ile Leu
225                 230                 235                 240
Arg Lys Ile Lys Glu Val Glu Ser Lys Asn Lys Ala Leu Asn Lys
                245                 250                 255
```

(2) INFORMATION FOR SEQ ID NO:1564:

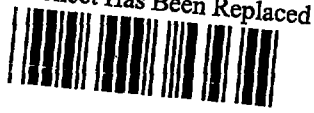
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1564

```
Lys Arg Leu Ile Gln Arg Asp Glu Thr Ile Ala Thr Gln Arg Glu Asn
1               5                  10                  15
Gly Ile Ile Ser Lys Gln Phe Leu Asn Leu Ile Leu Glu Arg Ser Phe
            20                  25                  30
Met Asn Asp Thr Thr Glu His His Gly Ser Asn Pro Leu Asn Ala Pro
        35                  40                  45
Pro Pro Ser Asn Ser Gln Ser Asn Asp Leu Leu Asn Leu Leu Asp Ser
    50                  55                  60
Leu Tyr Pro Lys Gly Ser Leu Gly Glu Gln Arg Phe His Glu Ala Leu
65                  70                  75                  80
Lys Asn Gln Glu Glu Leu Lys Asn Ile Leu Ile Glu Ile Glu Lys Leu
                85                  90                  95
Pro Gln Glu Lys Arg Tyr Glu Leu Leu Met Gln Ile Gly Gln Ala Lys
            100                 105                 110
Gln Arg Ile Met Glu Ala Tyr Ala His Ser Phe Leu Gly Tyr Ile Gly
        115                 120                 125
Gly Leu Glu His Leu Leu Gly Leu Cys Met Gly Gly Ile Phe Val Leu
    130                 135                 140
Phe Ala Ile Tyr Phe Val Phe Leu Arg Thr Ser Lys Asn Thr Glu Leu
145                 150                 155                 160
Val Glu Ser Leu Lys Thr Lys Leu Lys Leu Gln Tyr Phe Tyr Tyr Ala
                165                 170                 175
```

```
Phe Gly Val Gly Ala Val Leu Phe Phe Gly Leu Glu Thr Ile Arg Ser
            180                 185                 190
Ile Tyr Glu Leu Tyr Ile Leu Gly Ile Gly Ser Thr Asn Asp Lys Val
        195                 200                 205
Leu Phe Val Leu Lys Asn Ile Cys Phe Ile Gly Met Gly Tyr Leu Ile
    210                 215                 220
Tyr Lys Val Ile Lys Val Ile Gly Ile Lys Asn Phe Ile Asn Gly Leu
225                 230                 235                 240
Phe Ala Ser Lys Lys Gln Gly Gly Ala Glu
                245                 250
```

(2) INFORMATION FOR SEQ ID NO:1565:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1565

```
Gly Tyr Lys Asn Tyr Lys Met Leu Ala Lys Ile Val Phe Ser Ser Leu
1               5                  10                  15
Val Ala Phe Gly Val Leu Ser Ala Asn Val Glu Gln Phe Gly Ser Phe
            20                  25                  30
Phe Asn Glu Ile Lys Lys Glu Gln Glu Glu Val Ala Ala Lys Glu Asp
        35                  40                  45
Ala Leu Lys Ala Arg Lys Lys Leu Leu Asn Asn Thr His Asp Phe Leu
    50                  55                  60
Glu Asp Leu Val Phe Arg Lys Gln Lys Ile Lys Glu Leu Val Asp Tyr
65                  70                  75                  80
Arg Ala Lys Val Leu Leu Asp Leu Glu Asn Lys Tyr Lys Lys Glu Lys
                85                  90                  95
Glu Ala Leu Glu Lys Glu Thr Arg Gly Lys Ile Leu Thr Ala Lys Ser
            100                 105                 110
Lys Ala Tyr Gly Asp Leu Glu Gln Ala Leu Lys Asp Asn Pro Leu Tyr
        115                 120                 125
Lys Lys Leu Leu Pro Asn Pro Tyr Ala Tyr Val Leu Asn Gln Glu Thr
    130                 135                 140
Phe Thr Gln Glu Asp Lys Glu Arg Leu Ser Tyr Tyr Tyr Pro Gln Val
145                 150                 155                 160
Lys Thr Ser Ser Ile Phe Lys Lys Thr Thr Ala Thr Thr Lys Asp Lys
                165                 170                 175
Ala Gln Ala Leu Leu Gln Met Gly Val Phe Ser Leu Asp Glu Glu Gln
            180                 185                 190
Asn Lys Lys Ala Ser Arg Leu Ala Leu Ser Tyr Lys Gln Ala Ile Glu
        195                 200                 205
Glu Tyr Ser Asn Asn Ile Ser Asn Leu Leu Ser Arg Lys Glu Leu Asp
    210                 215                 220
Asn Ile Asp Tyr Tyr Leu Gln Leu Glu Arg Asn Lys Phe Asp Ser Lys
225                 230                 235                 240
Ala Lys Asp Ile Ala Gln Lys Ala Thr Asn Thr Leu Ile Phe Asn Ser
                245                 250                 255
Glu Arg Leu Ala Phe Ser Met Ala Ile Asp Lys Ile Asn Glu Lys Tyr
```

```
            260                 265                 270
Leu Arg Gly Tyr Glu Ala Phe Ser Asn Leu Leu Lys Asn Val Lys Asp
        275                 280                 285
Asp Val Glu Leu Asn Thr Leu Thr Lys Asn Phe Thr Asn Gln Lys Leu
    290                 295                 300
Ser Phe Ala Gln Lys Gln Lys Leu Cys Leu Leu Val Leu Asp Ser Phe
305                 310                 315                 320
Asn Phe Asp Thr Gln Ser Lys Lys Ser Ile Leu Lys Lys Thr Asn Glu
                325                 330                 335
Tyr Asn Ile Phe Val Asp Ser Asp Pro Met Met Ser Asp Lys Thr Thr
            340                 345                 350
Met Gln Lys Glu His Tyr Lys Ile Phe Asn Phe Phe Lys Thr Val Val
        355                 360                 365
Ser Ala Tyr Arg Asn Asn Val Ala Lys Asn Asn Pro Phe Glu
    370                 375                 380
```

(2) INFORMATION FOR SEQ ID NO:1566:

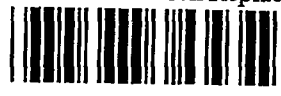
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1566

```
Lys Phe Ser Glu Val Tyr Phe Ile Met Lys Thr Lys Ala Gly Phe Val
1               5                  10                  15
Ala Leu Ile Gly Lys Pro Asn Ala Gly Lys Ser Thr Leu Leu Asn Thr
            20                  25                  30
Leu Leu Asn Ala His Leu Ala Leu Val Ser His Lys Ala Asn Ala Thr
        35                  40                  45
Arg Lys Leu Met Lys Cys Ile Val Pro Phe Lys Asp Lys Glu Gly Tyr
    50                  55                  60
Glu Ser Gln Ile Ile Phe Leu Asp Thr Pro Gly Leu His His Gln Glu
65                  70                  75                  80
Lys Leu Leu Asn Gln Cys Met Leu Ser Gln Ala Leu Lys Ala Met Gly
                85                  90                  95
Asp Ala Glu Leu Arg Val Phe Leu Ala Ser Val His Asp Asp Leu Lys
            100                 105                 110
Gly Tyr Glu Glu Phe Leu Ser Leu Cys Gln Lys Pro His Ile Leu Ala
        115                 120                 125
Leu Ser Lys Ile Asp Thr Ala Thr His Lys Gln Val Leu Gln Lys Leu
    130                 135                 140
Gln Glu Tyr Gln Lys Tyr Ser Ser Gln Phe Leu Ala Leu Val Pro Leu
145                 150                 155                 160
Ser Ala Lys Lys Ser Gln Asn Leu Asn Ala Leu Leu Glu Cys Ile Ser
                165                 170                 175
Lys His Leu Ser Pro Ser Ala Trp Leu Phe Glu Lys Asp Leu Met Ser
            180                 185                 190
Asp Glu Lys Met Arg Asp Ile Tyr Lys Glu Ile Ile Arg Glu Ser Leu
        195                 200                 205
Phe Asp Phe Leu Ser Asp Glu Ile Pro Tyr Glu Ser Asp Val Met Ile
    210                 215                 220
```

```
Asp Lys Phe Ile Glu Glu Glu Arg Ile Asp Lys Val Tyr Ala Arg Ile
225                 230                 235                 240
Ile Val Glu Lys Glu Ser Gln Lys Lys Ile Val Ile Gly Lys Asn Gly
                245                 250                 255
Val Asn Ile Lys Arg Ile Gly Thr Asn Ala Arg Leu Lys Met Gln Glu
            260                 265                 270
Val Gly Glu Lys Lys Val Phe Leu Asn Leu Gln Val Ile Ala Gln Lys
        275                 280                 285
Ser Trp Ser Lys Glu Glu Lys Ser Leu Gln Lys Leu Gly Tyr Ile Tyr
    290                 295                 300
Gln Arg Asn Arg Asp
305
```

(2) INFORMATION FOR SEQ ID NO:1567:

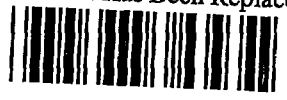
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1567

```
Phe Leu Ser Leu Ser Leu Ile Glu Arg Asp Leu Lys Thr Met Ala Lys
1               5                  10                  15
Ile Leu Lys Pro Asn Leu Asp Arg Asp Glu Leu Asn Thr Leu Tyr Lys
            20                  25                  30
Ala Asn Leu Ala Tyr Ala Lys Asn Thr His Glu His Tyr Phe Lys Phe
        35                  40                  45
Lys Lys Asp Val Asp Tyr Lys Leu Phe Asn Pro Ser Ile Met His Glu
    50                  55                  60
Gln Cys Ser Ile Ser Phe Val Gly Gly Gln Gly Ala Lys Arg Leu Leu
65                  70                  75                  80
Tyr Ile Leu Tyr Lys Leu Ala Phe Asn Ala Lys Ser Asn Lys Ile Ala
                85                  90                  95
Leu Asp Arg His Tyr Ala Lys Met Phe Leu Gln Val Val Ala Arg Thr
            100                 105                 110
Leu Ile Lys Asn Val Asn Ile Leu Glu Glu Gln Gly Phe Ile Glu Val
        115                 120                 125
Ile Lys Gly Lys Gln Arg Tyr Leu Tyr Val Tyr Leu Lys Asp Tyr Arg
    130                 135                 140
Glu Leu Glu Cys Leu Val Lys Ser Lys Met Ala Lys Tyr Val Met Tyr
145                 150                 155                 160
Leu Arg Gln Phe Phe Asp Tyr Leu Asp Arg Lys Arg Arg Tyr Gly Phe
                165                 170                 175
Asp Phe Thr Leu Lys Asn Leu Ala Phe Ala Lys Thr Lys Glu Ser Leu
            180                 185                 190
Pro Arg His Leu Asn Asp Lys Asp Leu Lys Ser Phe Leu Lys Thr Leu
        195                 200                 205
Leu Asp Tyr Lys Pro Ala Thr Ser Phe Glu Lys Arg Asn Lys Cys Ile
    210                 215                 220
Leu Leu Ile Val Ile Leu Gly Gly Leu Arg Lys Cys Glu Val Leu Asn
225                 230                 235                 240
Ile Glu Leu Lys His Ile Gln Val Glu Glu Gln Asn Tyr Ser Ile Leu
```

```
                245                 250                 255
Ile Gln Gly Lys Gly Arg Lys Glu Arg Lys Ala Tyr Ile Lys Lys Ser
            260                 265                 270
Leu Leu Glu Pro Ser Leu Asn Ala Trp Ile Ser Asp Asp Tyr Arg Leu
        275                 280                 285
Lys Tyr Phe Asn Gly Ala Tyr Leu Phe Lys Lys Asp Lys Gln Lys Ser
    290                 295                 300
Gln Asn Ser Leu Thr Leu Tyr Asn Phe Ile Pro Leu Ile Phe Lys Leu
305                 310                 315                 320
Ala Gln Ile Lys His Tyr Lys Gln Tyr Gly Thr Gly Leu His Leu Phe
                325                 330                 335
Arg His Ser Phe Ala Thr Leu Ile Tyr Gln Glu Thr Gln Asp Leu Val
            340                 345                 350
Leu Thr Ser Arg Ala Leu Gly His Ser Ser Leu Leu Ser Thr Lys Ile
        355                 360                 365
Tyr Ile His Thr Thr Gln Glu His Asn Lys Lys Val Ala Leu Val Phe
    370                 375                 380
Asp Ser Leu Ile Glu Asn Lys Lys
385                 390
```

(2) INFORMATION FOR SEQ ID NO:1568:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1568

```
Lys Arg Lys Glu His Cys Met Lys Asn Leu Arg His Phe Arg Lys Leu
1                   5                   10                  15
Ile Ala Phe Leu Gly Phe Ser Pro Leu Leu Leu Gln Ala Asp Met Thr
            20                  25                  30
Thr Phe Phe Asn Ser Ile Glu Gln Gln Leu Thr Ser Pro Thr Ala Lys
        35                  40                  45
Gly Ile Leu Met Val Ile Phe Leu Gly Leu Ala Ile Phe Ile Trp Lys
    50                  55                  60
Asn Leu Asp Arg Trp Lys Glu Ile Leu Met Thr Val Leu Ala Leu Lys
65                  70                  75                  80
Glu Val Pro Met Gln Leu Val Ala Ile Ser Val Ser Asn Leu Lys Glu
                85                  90                  95
Ile Ser Ser Lys Glu Lys Phe Leu Trp Leu Asn Ala Lys Ser Phe Leu
            100                 105                 110
Leu Ser Gly Phe Val Pro Phe Ile Met Ile Pro Trp Leu Asp Ile Leu
        115                 120                 125
Asn Ser Phe Val Leu Tyr Val Cys Phe Leu Leu Ile Phe Ser Ile Ala
    130                 135                 140
Glu Phe Phe Asp Glu Asp Ile Ser Asp Ile Leu Ile Ala His Ser Lys
145                 150                 155                 160
Ile Lys Thr Lys Ala Asn Ser Phe Tyr Ala
                165                 170
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1569:

(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:1569

```
Lys Ser Arg Asn Phe Ser Tyr Asn Gln Thr Glu Lys Ile Trp Glu Asn
1               5                  10                  15
His Phe Asn Leu Phe Ser Val Gly Ile Gly Met Ala Glu Glu Gln Glu
            20                  25                  30
Asn Thr Ala Gln Gln Pro Gln Lys Lys Ser Lys Ala Leu Leu Phe Val
        35                  40                  45
Ile Ile Gly Ser Val Leu Val Met Leu Leu Leu Val Gly Val Ile Ile
    50                  55                  60
Met Leu Leu Met Gly Asn Lys Glu Glu Ser Lys Glu Asn Ala Ser Lys
65                  70                  75                  80
Asn Thr Gln Glu Val Gln Ala Asn Pro Met Ala Asn Lys Asn Gln Glu
                85                  90                  95
Ala Lys Glu Gly Ser Asn Ile Gln Gln Tyr Leu Val Leu Gly Pro Leu
            100                 105                 110
Tyr Ala Ile Asp Ala Pro Phe Ala Val Asn Leu Val Ser Gln Asn Gly
        115                 120                 125
Arg Arg Tyr Leu Lys Ala Ser Ile Ser Leu Glu Leu Ser Asn Glu Lys
    130                 135                 140
Leu Leu Asn Glu Val Lys Val Lys Asp Thr Ala Ile Lys Asp Thr Ile
145                 150                 155                 160
Ile Glu Ile Leu Ser Ser Lys Ser Val Glu Glu Val Val Thr Asn Lys
                165                 170                 175
Gly Lys Asn Lys Leu Lys Asp Glu Ile Lys Ser His Leu Asn Ser Phe
            180                 185                 190
Leu Ile Asp Gly Phe Ile Lys Asn Val Phe Phe Thr Asp Phe Ile Ile
        195                 200                 205
Gln
```

(2) INFORMATION FOR SEQ ID NO:1570:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

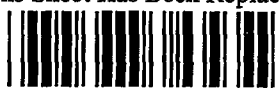
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

This Sheet Has Been Replaced



(A) NAME/KEY: misc_feature
(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1570

```
Gly Ser Met Met Thr Glu Met Glu Leu Lys Leu Ile Lys Ile Asp Thr
1               5                  10                  15
Ser His Tyr Phe Glu Lys Lys Pro Gly Leu Gly Glu Arg Met Asp Tyr
            20                  25                  30
Ala Gly Arg Cys Tyr Tyr Asn Lys Phe Gln Arg Val Asn Ala Met Leu
        35                  40                  45
Thr Ser Ser Leu Ile Gln Lys His Leu Lys Arg Glu Ile Glu Ile Ala
    50                  55                  60
His Asn Leu Ile Leu Arg Asn Asp Lys Val Glu Asn Ile Val Phe Asp
65                  70                  75                  80
Tyr Asn Gly Arg Asn Pro Glu Arg Phe Tyr His Lys Ala Gln Leu Leu
                85                  90                  95
Leu Arg Glu Glu Gly Phe Met Asn Phe Thr Ala Tyr Asn Thr Lys Thr
            100                 105                 110
Pro Gly His Leu His Leu Tyr Val His Lys Gly His Thr Glu Leu Gly
        115                 120                 125
Glu Gly Glu Arg Leu Ile Lys Thr Leu Ser Met Lys Leu Ala Gln Gly
    130                 135                 140
Leu Pro Lys Glu Trp Arg Val Phe Pro Ser Asn Glu Trp Pro Lys Glu
145                 150                 155                 160
Phe Asn Ile Leu Ala Leu Pro Tyr Glu Val Phe Ala Lys Glu Arg Gly
                165                 170                 175
Ser Ser Trp Ala Lys His Leu
            180
```

(2) INFORMATION FOR SEQ ID NO:1571:

(i) SEQUENCE CHARACTERISTICS:
(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:1571

```
Pro Phe Leu Lys Gly Phe Leu Met Ser Glu Lys Glu Arg Leu Asn Glu
1               5                  10                  15
Val Ile Leu Glu Glu Glu Asn Asn Gly Ser Gly Thr Lys Lys Val Phe
            20                  25                  30
Leu Ile Val Ala Ile Ala Ile Ile Ile Leu Ala Val Leu Leu Met Val
        35                  40                  45
Phe Trp Lys Ser Thr Arg Val Ala Pro Lys Glu Thr Phe Leu Gln Thr
    50                  55                  60
Asp Ser Gly Met Gln Lys Ile Gly Asn Thr Lys Asp Glu Lys Lys Asp
65                  70                  75                  80
Asp Glu Phe Glu Ser Leu Asn Met Asp Ser Pro Lys Gln Glu Asp Lys
                85                  90                  95
Leu Asp Lys Val Val Asp Asn Ile Lys Lys Gln Glu Ser Glu Asn Ser
            100                 105                 110
```

```
Met Pro Ile Gln Thr Asp Gln Ala Gln Met Glu Met Lys Thr Thr Glu
        115                 120                 125
Glu Lys Gln Glu Ser Gln Lys Glu Leu Lys Ala Val Glu Pro Ile Pro
    130                 135                 140
Met Ser Thr Gln Lys Glu Ser Gln Ala Val Ala Lys Lys Glu Thr Pro
145                 150                 155                 160
His Lys Lys Pro Lys Val Ala Pro Lys Asp Lys Glu Ala His Lys Asp
                165                 170                 175
Lys Ala Lys His Ala Ala Lys Glu Pro Lys Val Lys Lys Glu Ala Arg
            180                 185                 190
Lys Glu Val Ser Lys Lys Ala Asn Ser Lys Thr Asn Leu Thr Lys Gly
        195                 200                 205
His Tyr Leu Gln Val Gly Val Phe Ala His Thr Pro Asn Lys Ala Phe
    210                 215                 220
Leu Gln Glu Phe Asn Gln Phe Pro His Lys Ile Glu Asp Arg Gly Ala
225                 230                 235                 240
Thr Lys Arg Tyr Leu Ile Gly Pro Tyr Lys Ser Lys Gln Glu Ala Leu
                245                 250                 255
Met His Ala Asp Glu Val Ser Lys Lys Met Thr Lys Pro Val Val Ile
            260                 265                 270
Glu Val Arg
        275
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1572:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...189

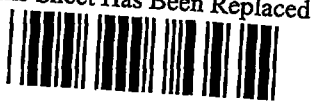
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1572

```
Ser Arg Leu Gln Lys Ala Ile Ile Lys Arg Val Glu Met Leu Glu Lys
1               5                  10                  15
Leu Ile Glu Arg Val Leu Phe Ala Thr Arg Trp Leu Leu Ala Pro Leu
            20                  25                  30
Cys Ile Ala Met Ser Leu Val Leu Val Val Leu Gly Tyr Val Phe Met
        35                  40                  45
Lys Glu Leu Trp His Met Leu Ser His Leu Asp Thr Ile Ser Glu Thr
    50                  55                  60
Asp Leu Val Leu Ser Ala Leu Gly Leu Val Asp Leu Leu Phe Met Ala
65                  70                  75                  80
Gly Leu Val Leu Met Val Leu Leu Ala Ser Tyr Glu Ser Phe Val Ser
                85                  90                  95
Lys Leu Asp Lys Val Asp Ala Ser Glu Ile Thr Trp Leu Lys His Thr
            100                 105                 110
Asp Phe Asn Ala Leu Lys Leu Lys Val Ser Leu Ser Ile Val Ala Ile
        115                 120                 125
Ser Ala Ile Phe Leu Leu Lys Arg Tyr Met Ser Leu Glu Asp Val Leu
    130                 135                 140
Ser Ser Ile Pro Lys Asp Thr Pro Leu Ser His Asn Pro Ile Phe Trp
145                 150                 155                 160
Gln Val Val Ile His Leu Val Phe Val Cys Ser Ala Leu Leu Thr Ala
```

```
                165                 170                 175
Val Thr Asn Asn Ile Ala Phe Ser Gln Lys Glu Arg His
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:1573:

This Sheet Has Been Replaced



(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:1573

```
Gly Leu Asn Tyr Ile Asp Leu Ala Leu Leu Val Val Val Val Ala Phe
1               5                  10                  15
Gly Ile Arg Gly Phe Tyr His Gly Phe Val Ser Glu Ile Ala Ala Thr
            20                  25                  30
Leu Gly Ile Val Leu Gly Val Tyr Leu Ala Ser Arg Tyr Ser Val Ala
        35                  40                  45
Val Gly Asn Leu Phe Ser Glu His Leu Tyr Asp Leu Arg Asn Glu Thr
    50                  55                  60
Met Thr Asn Leu Ile Gly Phe Leu Leu Val Leu Ala Ser Ile Trp Val
65                  70                  75                  80
Phe Phe Leu Ala Leu Gly Val Leu Leu Gly Lys Met Leu Val Phe Ser
                85                  90                  95
Gly Leu Gly Ile Ile Asp Lys Ala Leu Gly Phe Ile Phe Ser Cys Leu
            100                 105                 110
Lys Thr Phe Leu Val Leu Ser Phe Ile Leu Tyr Ala Leu Ser Lys Met
        115                 120                 125
Asp Leu Met Lys Asp Ala Asn Ala Tyr Leu Gln Glu Lys Ser Ala Ile
    130                 135                 140
Phe Pro Thr Met Lys Ser Val Ala Ser Lys Ile Met Arg Leu Asp Gly
145                 150                 155                 160
Val Lys His Val Glu Lys Asn Leu Lys Asp Asn Leu Glu Glu Met Ser
                165                 170                 175
Asp Glu Val Lys Asn Lys Gly Ser Ile Asp Asn Ala Lys Glu Ser Phe
            180                 185                 190
Asn Lys Ala Thr Asp Lys Gly Val Glu Ala Leu Lys Glu Lys Ala Lys
        195                 200                 205
Asp Leu Pro Lys Asn Met Leu Glu Pro Lys His Asn Lys Pro Asn Gln
    210                 215                 220
Thr Pro Pro Ile Pro Thr Pro Ser Asn Lys Glu Pro Leu
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:1574:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 395 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1574

```
Ser Leu Trp Val Glu Asn Pro Ile Leu Leu Ser His Ser Gln Val Tyr
1               5                  10                  15
Ser Pro Pro Arg Cys Trp Val Phe Lys Thr Pro Arg Asn Ser Ala Phe
            20                  25                  30
Ala Leu Gly Phe Phe Val Gly Ala Leu Leu Phe Tyr Trp Cys Ala Leu
        35                  40                  45
Arg Leu Ser His Ser Asp Phe Thr Tyr Leu Leu Pro Leu Ile Ile Val
    50                  55                  60
Leu Val Ala Leu Val Tyr Gly Val Leu Phe Tyr Leu Leu Leu Tyr Phe
65                  70                  75                  80
Glu Asn Pro Tyr Phe Arg Leu Leu Ser Phe Leu Gly Ser Ser Phe Ile
                85                  90                  95
His Pro Phe Gly Phe Asp Trp Leu Val Pro Asp Ser Phe Phe Ser Tyr
            100                 105                 110
Ser Val Phe Arg Val Asp Lys Leu Ser Leu Gly Leu Ile Phe Leu Ala
        115                 120                 125
Cys Ile Phe Leu Ser Ala Gln Asn Leu Lys Lys Tyr Arg Met Ile Gly
    130                 135                 140
Val Leu Leu Leu Leu Gly Ala Leu Asp Phe His Phe Phe Lys Ile Ser
145                 150                 155                 160
Asp Leu Lys Glu Val Gly Asn Ile Glu Leu Val Ser Thr Arg Thr Pro
                165                 170                 175
Gln Asp Leu Lys Phe Asp Ser Asn Tyr Leu Asn Asn Ile Glu Asn Asn
            180                 185                 190
Ile Leu Lys Glu Ile Lys Leu Ala Gln Ser Lys Gln Lys Thr Leu Ile
        195                 200                 205
Val Phe Pro Glu Thr Ala Tyr Pro Ile Ala Leu Glu Asn Ser Pro Phe
    210                 215                 220
Lys Thr Gln Leu Glu Asp Leu Ser Ala Lys Ile Ala Ile Leu Ile Gly
225                 230                 235                 240
Thr Leu Arg Ala Gln Gly Tyr Ser Leu Tyr Asn Ser Ser Phe Leu Phe
                245                 250                 255
Ser Lys Lys Ser Val Gln Ile Ala Asp Lys Val Ile Leu Ala Pro Phe
            260                 265                 270
Gly Glu Ile Met Pro Leu Pro Glu Phe Leu Gln Lys Pro Leu Glu Lys
        275                 280                 285
Leu Phe Phe Gly Glu Ser Ala Tyr Leu Tyr Arg Asn Ala Pro His Phe
    290                 295                 300
Ser Asp Phe Thr Leu Asp Asp Phe Thr Phe Arg Pro Leu Ile Cys Tyr
305                 310                 315                 320
Glu Gly Thr Ser Lys Pro Ala Tyr Ser Ser Ser Pro Ser Lys Val Phe
                325                 330                 335
Ile Leu Met Ser Asn Asn Ala Trp Phe Ser Pro Ser Ile Glu Pro Thr
            340                 345                 350
Leu Gln Arg Thr Leu Leu Lys Tyr Tyr Ala Arg Arg Tyr Asp Lys Ile
        355                 360                 365
Ile Leu His Ser Ala Asn Phe Ser Thr Ser Tyr Ile Leu Ser Pro Ser
    370                 375                 380
Leu Leu Gly Asp Ile Leu Phe Arg Lys Arg Ser
385                 390                 395
```

(2) INFORMATION FOR SEQ ID NO:1575:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1575

```
Glu Thr Ile Met Ile Lys Ala Ile Asp Ile Ser His Ala Phe Glu Lys
1               5                  10                  15
Pro Leu Tyr Asn Gly Val Asn Leu Arg Ile Lys Pro Lys Glu Ser Leu
            20                  25                  30
Ala Ile Leu Gly Val Ser Gly Ser Gly Lys Ser Thr Leu Leu Ser His
        35                  40                  45
Leu Ala Thr Met Leu Lys Pro Asp Ser Gly Thr Val Ser Leu Leu Glu
    50                  55                  60
His Gln Asp Ile Tyr Ala Leu Asn Ser Lys Lys Leu Leu Glu Leu Arg
65                  70                  75                  80
Arg Leu Lys Val Gly Ile Val Phe Gln Ser His Tyr Leu Phe Lys Gly
                85                  90                  95
Phe Ser Ala Leu Glu Asn Leu Gln Val Ala Ser Ile Leu Ala Lys Gln
            100                 105                 110
Glu Ile Asn His Ser Leu Leu Glu Gln Leu Gly Ile Ala His Thr Leu
        115                 120                 125
Lys Gln Gly Val Gly Glu Leu Ser Gly Gly Gln Gln Arg Leu Ser
    130                 135                 140
Ile Ala Arg Val Leu Ser Lys Lys Pro Gln Ile Ile Ile Ala Asp Glu
145                 150                 155                 160
Pro Thr Gly Asn Leu Asp Thr Thr Ser Ala Asn Gln Val Ile Ser Met
                165                 170                 175
Leu Gln Asn Tyr Ile Thr Glu Asn Glu Gly Ala Leu Val Leu Ala Thr
            180                 185                 190
His Asp Glu His Leu Ala Phe Thr Cys Ser Gln Val Tyr Arg Leu Glu
        195                 200                 205
Lys Glu Ser Leu Ile Lys Glu Lys
    210                 215
```

(2) INFORMATION FOR SEQ ID NO:1576:

This Sheet Has Been Replaced



(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:1576

```
Ser Leu Ala Pro Lys Leu Lys Ala Phe Phe Lys Val Ala Leu Ser Cys
1               5                  10                  15
Lys Ala Val Ile Lys Ile Thr Gly Val Glu Ile Lys Lys Ser Phe Leu
            20                  25                  30
Met Arg Leu Asn Asn Ser Lys Leu Phe Ile Ser Gly Thr Cys Thr Ser
        35                  40                  45
Lys Ser Lys Arg Leu Lys Arg Ser Thr Glu Ser Leu Ser
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:1577:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1577

```
Phe Ala Leu His Lys Lys Val Leu Leu Ala Leu Thr Ala Ser Leu Ile
1               5                  10                  15
Cys Gln Glu Ser Leu Phe Ala Lys Asp Lys Asp Tyr Thr Leu Gly Lys
            20                  25                  30
Val Ser Thr Ala Gly Lys Lys Asp Arg Ser Asp Tyr Ser Gly Gln Val
        35                  40                  45
Asn Leu Gly Tyr Ser Gly Ile Thr Ala Pro Lys Ser Trp Gln Asp Glu
    50                  55                  60
Glu Val Lys Lys Tyr Thr Gly Ser Arg Thr Val Ile Ser Asn Lys Ala
65                  70                  75                  80
Leu Thr Gln Gln Ala Asn Gln Ser Ile Glu Glu Ala Leu Gln Asn Val
                85                  90                  95
Pro Gly Leu Gln Ile Arg Asn Ala Thr Gly Val Gly Ala Met Pro Thr
            100                 105                 110
Ile Gln Ile Arg Gly Phe Gly Ala Gly Gly Ser Gly His Ser Asp Ala
        115                 120                 125
Thr Leu Met Leu Val Asn Gly Ile Pro Val Tyr Met Ala Pro Tyr Ala
    130                 135                 140
His Ile Glu Leu Asp Ile Phe Pro Val Thr Phe Gln Ala Ile Asp Arg
145                 150                 155                 160
Ile Asp Val Ile Lys Gly Gly Gly Ser Val Gln Tyr Gly Pro Asn Thr
                165                 170                 175
Tyr Gly Gly Ile Val Asn Ile Ile Thr Lys Pro Ile Pro Asn Gln Trp
            180                 185                 190
Glu Asn Gln Ala Ala Glu Arg Ile Thr Tyr Trp Ala Lys Ala Arg Asn
        195                 200                 205
Ala Gly Phe Ala Ala Pro Pro Asp Lys Thr Gly Asp Pro Ser Phe Ile
    210                 215                 220
Lys Ser Leu Gly Asn Asn Leu Leu Tyr Asn Thr Tyr Val Arg Ser Gly
225                 230                 235                 240
Gly Met Ile Asn Lys His Val Gly Ile Gln Ala Gln Ala Asn Trp Val
```

```
                245                 250                 255
Arg Gly Gln Gly Phe Arg Asp Asn Ser Pro Ser Ser Ile Ser Asn Tyr
            260                 265                 270
Trp Leu Asp Gly Val Tyr Asp Ile Asn Glu Ser Asn Gly Ile Lys Ala
        275                 280                 285
Tyr Tyr Gln Tyr Tyr Asp Phe Ala Ile Ala Gln Pro
    290                 295                 300
```

(2) INFORMATION FOR SEQ ID NO:1578:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 275 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

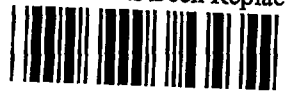
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1578

```
Val Ser Ile Leu Val Ile Ile Glu Pro Tyr Thr Phe Tyr Lys Arg Glu
1               5                  10                  15
Glu Ser Val Met Leu Gly Ser Val Lys Lys Ala Val Phe Arg Val Leu
            20                  25                  30
Cys Leu Gly Ala Leu Cys Leu Cys Gly Gly Leu Met Ala Glu Gln Asp
        35                  40                  45
Pro Lys Glu Leu Ile Phe Ser Gly Ile Thr Ile Tyr Thr Asp Lys Asn
    50                  55                  60
Phe Thr Arg Ala Lys Lys Tyr Phe Glu Lys Ala Cys Lys Ser Asn Asp
65                  70                  75                  80
Ala Asp Gly Cys Ala Ile Leu Arg Glu Val Tyr Ser Ser Gly Lys Ala
                85                  90                  95
Ile Ala Arg Glu Asn Ala Arg Glu Ser Ile Glu Lys Ala Leu Glu His
            100                 105                 110
Thr Ala Thr Ala Lys Val Cys Lys Leu Asn Asp Ala Glu Lys Cys Lys
        115                 120                 125
Asp Leu Ala Glu Phe Tyr Phe Asn Val Asn Asp Leu Lys Asn Ala Leu
    130                 135                 140
Glu Tyr Tyr Ser Lys Ser Cys Lys Leu Asn Asn Val Glu Gly Cys Met
145                 150                 155                 160
Leu Ser Ala Thr Phe Tyr Asn Asp Met Ile Lys Gly Leu Lys Lys Asp
                165                 170                 175
Lys Lys Asp Leu Glu Tyr Tyr Ser Lys Ala Cys Glu Leu Asn Asn Gly
            180                 185                 190
Gly Gly Cys Ser Lys Leu Gly Gly Asp Tyr Phe Phe Gly Glu Gly Val
        195                 200                 205
Thr Lys Asp Phe Lys Lys Ala Phe Glu Tyr Ser Ala Lys Ala Cys Glu
    210                 215                 220
Leu Asn Asp Ala Lys Gly Cys Tyr Ala Leu Ala Ala Phe Tyr Asn Glu
225                 230                 235                 240
Gly Lys Gly Val Ala Lys Asp Glu Lys Gln Thr Thr Glu Asn Leu Glu
                245                 250                 255
Lys Ser Cys Lys Leu Gly Leu Lys Glu Ala Cys Asp Ile Leu Lys Glu
            260                 265                 270
Gln Lys Gln
        275
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1579:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1579

```
Thr Arg Lys Ser Ser Ala Ser Met Ser Glu Asn Glu Lys His Pro His
1               5                  10                  15
Arg Val Leu Gln Leu Ile Lys Ser Ser Gly Ile Thr Pro Gly Ile Val
            20                  25                  30
Leu Asn Pro His Thr His Glu Glu Ser Ile Lys Tyr Leu Leu Glu Ser
        35                  40                  45
Val Gly Leu Val Leu Leu Met Ser Val Asn Pro Gly Phe Gly Gly Gln
    50                  55                  60
Lys Phe Leu Asp Leu Val Leu Glu Lys Cys Leu Lys Val Lys Glu Leu
65                  70                  75                  80
Ile Lys Arg Tyr Asn Pro Ser Cys Leu Leu Glu Val Asp Gly Gly Val
                85                  90                  95
Asn Asp Lys Asn Ile Phe Glu Leu Gln Gln Ala Gly Val Asp Val Val
            100                 105                 110
Val Ser Gly Ser Tyr Ile Phe Glu Ser Lys Asp Arg Lys Leu Ala Ile
        115                 120                 125
Glu Gly Leu Gln Asn Val Arg Gln Pro Leu Ala
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:1580:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1580

```
Lys Leu Leu Arg Val Leu His Lys Met Ile Lys Lys Ala Ala Lys Thr
1               5                  10                  15
Pro Phe Phe Lys Ile Leu Phe Gln Ala Leu Ser Tyr Asn Ile Arg Met
```

```
            20                  25                  30
Lys Asp Leu Asn Lys Thr Ile Gly Val Phe Val Arg Pro Thr His His
        35                  40                  45
Gln Asn Ala Leu Phe Lys Glu Leu Glu Gln Ala Lys Glu Trp Val Leu
    50                  55                  60
Thr Leu Leu Glu Asp Glu Gly Phe Glu Ser Phe Met Ile Asp Ser Leu
65                  70                  75                  80
Asp Gly Ala Lys Asp Ala Gln Leu Ile Lys Lys Ala Tyr Ala Phe Leu
                85                  90                  95
Cys Leu Gly Gly Asp Gly Thr Ile Leu Gly Ala Leu Arg Met Thr His
            100                 105                 110
Ala His Asn Lys Pro Cys Phe Gly Val Arg Ile Gly Asn Leu Gly Phe
        115                 120                 125
Leu Ser Ala Val Glu Leu Asn Gly Leu Lys Asp Phe Leu Gln Asp Leu
    130                 135                 140
Lys Gln Asn Arg Ile Lys Leu Glu Glu His Leu Ala Leu Glu Gly Arg
145                 150                 155                 160
Ile Gly Asn Thr Ser Phe Tyr Ala Ile Asn Glu Ile Val Ile Ala Lys
                165                 170                 175
Lys Lys Ala Leu Gly Val Leu Asp Ile Lys Ala Cys Ala Gly His Thr
            180                 185                 190
Pro Phe Asn Thr Tyr Lys Gly Asp Gly Leu Ile Ile Ala Thr Pro Leu
        195                 200                 205
Gly Ser Thr Ala Tyr Asn Leu Ser Ala His Gly Pro Ile Val His Ala
    210                 215                 220
Leu Ser Gln Ser Tyr Ile Leu Thr Pro Leu Cys Asp Phe Ser Leu Thr
225                 230                 235                 240
Gln Arg Pro Leu Val Leu Gly Ala Glu Phe Cys Leu Ser Phe Cys Ala
                245                 250                 255
His Glu Asp Ala Leu Val Val Ile Asp Gly Gln Ala Thr Tyr Asp Leu
            260                 265                 270
Lys Ala Asn Gln Pro Leu Tyr Ile Gln Lys Ser Pro Thr Thr Thr Lys
        275                 280                 285
Leu Leu Gln Lys Asn Ser Arg Asp Tyr Phe Lys Val Leu Lys Glu Lys
    290                 295                 300
Leu Leu Trp Gly Glu Ser Pro Asn Lys Lys Arg
305                 310                 315
```

(2) INFORMATION FOR SEQ ID NO:1581:

This Sheet Has Been Replaced



(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:1581

```
Arg Tyr Asn Thr Pro Met Gln Lys Lys Ile Phe Leu Leu Glu Asp Asp
1               5                   10                  15
Tyr Leu Leu Ser Glu Ser Ile Lys Glu Phe Leu Glu His Leu Gly Tyr
            20                  25                  30
Glu Val Phe Cys Ala Phe Asn Gly Lys Glu Ala His Glu Arg Leu Ser
        35                  40                  45
```

```
Val Glu Arg Phe Asn Leu Leu Leu Leu Asp Val Gln Val Pro Glu Met
    50                  55                  60
Asn Ser Leu Glu Leu Phe Lys Arg Ile Lys Asn Asp Phe Leu Ile Ser
65                  70                  75                  80
Thr Pro Val Ile Phe Ile Thr Ala Leu Gln Asp Asn Ala Thr Leu Lys
                85                  90                  95
Asn Ala Phe Asn Leu Gly Ala Ser Asp Tyr Leu Lys Lys Pro Phe Asp
            100                 105                 110
Leu Asp Glu Leu Glu Ala Arg Ile Lys Arg Phe Phe Asn Asp Asp Pro
        115                 120                 125
Ile Glu Ile Met Pro Asn Ile Phe Tyr His Gln His Ala Leu Asn Val
    130                 135                 140
Lys Gly Lys Lys Glu Ile Leu Ala Pro Lys Thr Ala Gln Leu Leu Glu
145                 150                 155                 160
Tyr Phe Leu Glu His Lys Gly Gln Ile Ile Ser Ser Gln Ala Leu Glu
                165                 170                 175
Asn Asn Leu Trp Glu Gln Ala Ile Asp Asp Ser Thr Leu Arg Thr Tyr
            180                 185                 190
Ile Lys Val Leu Arg Lys Leu Leu Gly Lys Asn Cys Ile Glu Thr His
        195                 200                 205
Lys Gly Val Gly Tyr Arg Phe Asn Pro Leu
    210                 215
```

(2) INFORMATION FOR SEQ ID NO:1582:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1582

```
Cys Gly Ala Asn Arg Ser Lys Gly Arg Gly Gly Phe Ser Ser Lys Cys
1               5                  10                  15
Ala Gly Ala Asn Ser Gly Tyr Ser Asn Glu Ala Tyr Glu Ser Val Gly
            20                  25                  30
Ala Lys Ile Val Asp Ser Lys Thr Ala Trp Gly Gln Asp Leu Val Val
        35                  40                  45
Lys Cys Lys Glu Pro Leu Glu His Glu Tyr Pro Leu Leu Lys Glu Lys
    50                  55                  60
Ala Thr Leu Phe Ser Tyr Leu Asp Leu Ala Tyr Gln Lys Ser Leu Cys
65                  70                  75                  80
Glu Met Phe Ile Asn Lys Lys Ile Thr Ser Ile Cys Thr Glu Thr Ile
                85                  90                  95
Ala Gly Pro Lys Asn Asp Tyr Pro Ile Leu Ala Pro Met Ser Val Val
            100                 105                 110
Ala Gly Arg Leu Ala Ala His Leu Val Gln His Tyr Leu Leu Ala Leu
        115                 120                 125
Glu His Val Lys Gly Phe Met Gly Lys Gly Val Met Leu Gly Gly Leu
    130                 135                 140
Ser Gly Ala Gln Arg Ala Lys Ile Val Val Ile Gly Gly Gly Val Val
145                 150                 155                 160
Gly Met Glu Ser Ala Lys Val Leu Ser Gln Met Gly Ala Lys Val Thr
```

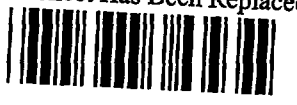
This Sheet Has Been Replaced



```
                165                 170                 175
Ile Leu Glu Leu Asp Tyr Ala Lys Leu Gln Asn His Pro Tyr Tyr His
            180                 185                 190
Leu Tyr Asp Leu Glu Val Leu Ser Val Asn Glu Ala Asn Ile Ile Gln
        195                 200                 205
Ala Leu Asn Gly Ala Val Gly Leu Val Gly Ala Val Leu Val Thr Ala
    210                 215                 220
Ser Gln Thr Pro Lys Val Ile Leu Arg Arg His Leu Lys Tyr Met Gln
225                 230                 235                 240
Thr Gln Gly Val Val Ile Asp Val Ala Cys Ser Leu Gly Gly Cys Ile
                245                 250                 255
Arg Ala Ile Arg Gln Ala Ser His Ser Asn Pro Val Tyr Val Glu Glu
            260                 265                 270
Ser Leu Leu His Tyr Gly Val Pro Asn Met Pro Gly Ile Val Ala Lys
        275                 280                 285
Thr Ser Ser Thr Ala Tyr Ser His Ala Ser Val Pro Tyr Leu Leu Tyr
    290                 295                 300
Tyr Leu Glu His Gly Leu Lys Gly Phe Leu Thr Ala Asn Thr Lys Ile
305                 310                 315                 320
Val Ala Asn Thr Leu Gly Gly Leu Ser Ala Tyr Asn Gly Tyr Ile Thr
                325                 330                 335
Gln Glu Gly Ile Ala Lys Ala Phe Asn Leu Ala Phe Lys Ser Pro Leu
            340                 345                 350
Glu Ile Leu Lys Glu Leu
        355
```

(2) INFORMATION FOR SEQ ID NO:1583:

This Sheet Has Been Replaced



(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:1583

```
Lys Gly Lys Arg Val Lys Asn Met Arg Asp Phe Asn Asn Ile Gln Ile
1               5                   10                  15
Thr Arg Leu Lys Val Arg Gln Asn Ala Val Phe Glu Lys Leu Asp Leu
            20                  25                  30
Glu Phe Lys Asp Gly Leu Ser Ala Ile Ser Gly Ala Ser Gly Val Gly
        35                  40                  45
Lys Ser Val Leu Ile Ala Ser Leu Leu Gly Ala Phe Gly Leu Lys Glu
    50                  55                  60
Ser Asn Ala Ser Asn Ile Glu Val Glu Leu Ile Ala Pro Phe Leu Asp
65                  70                  75                  80
Thr Glu Glu Tyr Gly Ile Phe Arg Glu Asp Glu His Glu Pro Leu Val
                85                  90                  95
Ile Ser Val Ile Lys Lys Glu Lys Thr Arg Tyr Phe Leu Asn Gln Thr
            100                 105                 110
Ser Leu Ser Lys Asn Thr Leu Lys Ala Leu Leu Lys Gly Leu Ile Lys
        115                 120                 125
Arg Leu Ser Asn Asp Arg Phe Ser Gln Asn Glu Leu Asn Asp Ile Leu
    130                 135                 140
```

Met Leu Ser Leu Leu Asp Gly Tyr Ile Gln Asn Lys Asn Arg Arg Leu
145 150 155 160
Ala Pro Phe

(2) INFORMATION FOR SEQ ID NO:1584:

This Sheet Has Been Replaced

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1584

Ser Asn His Lys Arg Val Phe Met Asp Tyr Lys Arg Phe Lys Gly Lys
1 5 10 15
His Ala Asn Ile Val Ile Glu Ile Ile Ser Leu Leu Glu Lys Gly Val
20 25 30
Lys Lys Ala Gln Glu Ile Leu Glu Lys Pro Asp Ala Gly Ser Tyr Thr
35 40 45
Gln Leu Glu Asn Ser Ser Gly Asp Thr Pro Ile Lys Ala Asp Leu Ala
50 55 60
Leu Asp Lys Phe Leu Glu Glu Thr Phe Leu Ser Leu Glu Asn Val Lys
65 70 75 80
Ser Val Phe Ser Glu Glu Lys Glu Thr Pro Val Thr Lys Glu Asn Gly
85 90 95
Ser Tyr Leu Ile Ala Tyr Asp Pro Leu Asp Gly Ser Ser Val Met Glu
100 105 110
Ala Asn Phe Leu Val Gly Thr Ile Ile Gly Val Tyr Glu Lys Asp Tyr
115 120 125
Lys Ala Gln Asn Leu Val Ala Ser Leu Tyr Val Val Phe Gly His Lys
130 135 140
Ile Glu Leu Val Val Ala Leu Glu Glu Val Tyr Arg Tyr Ala Phe Tyr
145 150 155 160
Gln Asn Lys Phe His Phe Ile Glu Thr Ile Val Leu Glu Asn Lys Gly
165 170 175
Lys Ile Ile Ala Ser Gly Gly Asn Gln Lys Asp Phe Ser Leu Gly Leu
180 185 190
Lys Lys Ala Leu Glu Gly Phe Phe Ala Glu Asn Tyr Arg Leu Arg Tyr
195 200 205
Ser Gly Ser Met Val Ala Asp Val His His Val Leu Val Lys Lys Gly
210 215 220
Gly Met Phe Ser Tyr Pro Gln Lys Lys Leu Arg Lys Leu Phe Glu Val
225 230 235 240
Phe Pro Leu Ala Leu Met Val Glu Lys Ala Lys Gly Glu Ala Phe Tyr
245 250 255
Phe Asp Lys Gly Val Lys Lys Arg Leu Leu Asp Gln Ser Val Glu Ser
260 265 270
Tyr His Glu Lys Ser Glu Cys Tyr Leu Ala Ser Pro His Glu Ala Gln
275 280 285
Ile Leu Glu Lys His Leu Lys Gly Glu
290 295

(2) INFORMATION FOR SEQ ID NO:1585:

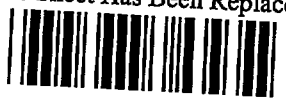
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 263 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1585

```
Thr Phe Leu Ile Ile Phe Trp Val Phe Phe Leu Arg Ile Lys His Tyr
1               5                  10                  15
Val Lys Glu Leu Ser Met Lys Lys Phe Phe Ser Gln Ser Leu Leu Ala
            20                  25                  30
Leu Ile Ile Ser Met Asn Ala Val Ser Gly Met Asp Gly Asn Gly Val
        35                  40                  45
Phe Leu Gly Ala Gly Tyr Leu Gln Gly Gln Ala Gln Met His Ala Asp
    50                  55                  60
Ile Asn Ser Gln Lys Gln Ala Thr Asn Ala Thr Ile Lys Gly Phe Asp
65                  70                  75                  80
Ala Leu Leu Gly Tyr Gln Phe Phe Phe Glu Lys His Phe Gly Leu Arg
                85                  90                  95
Leu Tyr Gly Phe Phe Asp Tyr Ala His Ala Asn Ser Ile Lys Leu Lys
            100                 105                 110
Asn Pro Asn Tyr Asn Ser Glu Ala Ala Gln Val Ala Ser Gln Ile Leu
        115                 120                 125
Gly Lys Gln Glu Ile Asn Arg Leu Thr Asn Ile Ala Asp Pro Arg Thr
    130                 135                 140
Phe Glu Pro Asn Met Leu Thr Tyr Gly Gly Ala Met Asp Val Met Val
145                 150                 155                 160
Asn Val Ile Asn Asn Gly Ile Met Ser Leu Gly Ala Phe Gly Gly Ile
                165                 170                 175
Gln Leu Ala Gly Asn Ser Trp Leu Met Ala Thr Pro Ser Phe Glu Gly
            180                 185                 190
Ile Leu Val Glu Gln Ala Leu Val Ser Lys Lys Ala Thr Ser Phe Gln
        195                 200                 205
Phe Leu Phe Asn Val Gly Ala Arg Leu Arg Ile Leu Lys His Ser Ser
    210                 215                 220
Ile Glu Ala Gly Val Lys Phe Pro Met Leu Lys Lys Asn Pro Tyr Ile
225                 230                 235                 240
Thr Ala Lys Asn Leu Asp Ile Gly Phe Arg Arg Val Tyr Ser Trp Tyr
                245                 250                 255
Val Asn Tyr Val Phe Thr Phe
            260
```

(2) INFORMATION FOR SEQ ID NO:1586:

(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:1586

```
Trp Ile Asp Ala Lys Asn Lys Glu Glu Ala Ile Ile Gln Gly Tyr Thr
1               5                  10                  15
Ile Ile Asp Pro Ser Thr Val Ile Ala Thr His Thr Ser Glu Leu Val
            20                  25                  30
Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val Lys Ser Leu
        35                  40                  45
Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu Glu Ser Lys
    50                  55                  60
Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala Leu Leu His
65                  70                  75                  80
Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu Thr Ile Thr
                85                  90                  95
Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu Thr Glu Gln
            100                 105                 110
Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe Lys Ser Glu
        115                 120                 125
Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Ser Glu Gln Phe
    130                 135                 140
Leu Leu Asn Lys Leu Arg Glu Asn Gly Thr Ser Lys Ser Leu Leu Leu
145                 150                 155                 160
Asn Val Gly Glu Leu Gln Lys Leu Ile Glu Gly Val Ser Glu Glu Ala
                165                 170                 175
Met Lys Val Leu Gln Lys Gly Ile Ala Pro Val Ile Leu Ile Val Glu
            180                 185                 190
Pro Asn Leu Arg Lys Ala Leu Ser Asn Gln Met Glu Gln Ala Arg Ile
        195                 200                 205
Asp Val Val Val Leu Ser His Ala Glu Leu Asp Pro Asn Ser Asn Phe
    210                 215                 220
Glu Ala Leu Gly Thr Ile His Ile Asn Phe
225                 230
```

(2) INFORMATION FOR SEQ ID NO:1587:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 295 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1587

```
Lys Lys Lys Thr Leu Asn Ile Ser Gln Leu Gly Lys Thr Met His Val
```

```
1               5                   10                  15
Ala Cys Leu Leu Ala Leu Gly Asp Asn Leu Ile Thr Leu Ser Leu Leu
            20                  25                  30
Lys Glu Ile Ala Ser Lys Gln Gln Gln Ser Leu Lys Ile Leu Gly Thr
        35                  40                  45
His Leu Thr Leu Lys Ile Ala Lys Leu Leu Glu Cys Glu Lys His Phe
    50                  55                  60
Glu Ile Ile Pro Val Phe Glu Asn Ile Pro Ala Phe Tyr Asp Leu Lys
65                  70                  75                  80
Lys Gln Gly Val Phe Trp Ala Met Lys Asp Phe Leu Trp Leu Leu Lys
                85                  90                  95
Ala Ile Lys Lys His Gln Ile Lys Arg Leu Ile Leu Glu Lys Gln Asp
            100                 105                 110
Phe Arg Ser Phe Leu Leu Ser Gln Phe Val Ser Ile Thr Thr Pro Asn
        115                 120                 125
Lys Glu Ile Lys Asn Val Tyr Gln Asn Arg Gln Glu Leu Phe Ser Gln
    130                 135                 140
Ile Tyr Gly His Val Phe Asp Asn Pro Pro Tyr Pro Met Ser Leu Lys
145                 150                 155                 160
Asn Pro Lys Lys Ile Leu Ile Asn Pro Phe Thr Arg Glu Asn Asp Arg
                165                 170                 175
Asn Ile Ser Leu Glu His Leu Lys Ile Val Leu Lys Leu Leu Lys Pro
            180                 185                 190
Phe Cys Val Thr Leu Leu Asp Phe Glu Glu Arg Tyr Ala Phe Leu Lys
        195                 200                 205
Asp Arg Val Ala His Tyr Arg Ala Lys Thr Ser Leu Glu Glu Val Lys
    210                 215                 220
Asn Leu Ile Leu Glu Ser Asp Leu Tyr Ile Gly Gly Asp Ser Phe Leu
225                 230                 235                 240
Ile His Leu Ala Tyr Tyr Leu Lys Lys Asn Tyr Phe Ile Phe Phe Tyr
                245                 250                 255
Arg Asp Asn Asp Asp Phe Met Pro Pro Asn Ser Gly Asn Glu Asn Phe
            260                 265                 270
Leu Lys Ala His Lys Ser His Phe Ile Glu Gln Asp Leu Ala Lys Lys
        275                 280                 285
Phe Arg His Leu Gly Leu Leu
    290                 295
```

(2) INFORMATION FOR SEQ ID NO:1588:

This Sheet Has Been Replaced



(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

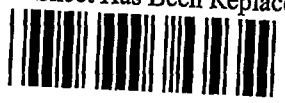
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1588

```
Asn Thr Gln Arg Gln Thr Leu Pro Leu Val Lys Ser Arg Pro His Pro
1               5                   10                  15
Leu Val Lys Ile Tyr Leu Lys Gln Met Cys Gly Met Gly Phe Ile Gly
            20                  25                  30
Phe Lys Thr Lys Leu Thr Gln Thr Lys Ala Phe Ile Ile Leu Ile Pro
        35                  40                  45
```

```
Ile Phe Gln Asp Arg Ala Val Lys Ala Ala Thr Arg Ser Ala Pro Ile
    50                  55                  60
Gln Leu Ile Cys
65
```

(2) INFORMATION FOR SEQ ID NO:1589:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1413 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1..1413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1589

```
Thr Leu Ile Ser Ile Phe Ser Ala Ser Gln Ala Asp Phe Gly Gly Asn
1               5                  10                  15
Thr Thr Ile Asp Thr Ala Ser Phe Asn Phe Asp Ser Ala Ser Ser Leu
            20                  25                  30
Asn Phe Asn Asn Leu Thr Ala Asn Gly Ala Leu Asn Phe Asn Gly Tyr
        35                  40                  45
Ala Pro Ser Leu Thr Lys Ala Leu Met Asn Val Ser Gly Gln Phe Val
    50                  55                  60
Leu Gly Asn Asn Gly Asp Ile Asn Leu Ser Asp Ile Asn Ile Phe Asp
65                  70                  75                  80
Asn Ile Thr Lys Ser Val Thr Tyr Asn Ile Leu Asn Ala Gln Lys Gly
                85                  90                  95
Ile Thr Gly Ile Ser Gly Ala Asn Gly Tyr Glu Lys Ile Leu Phe Tyr
            100                 105                 110
Gly Met Lys Ile Gln Asn Ala Thr Tyr Ser Asp Asn Asn Asn Ile Gln
        115                 120                 125
Thr Trp Ser Phe Ile Asn Pro Leu Asn Ser Ser Gln Ile Ile Gln Glu
    130                 135                 140
Ser Ile Lys Asn Gly Asp Leu Thr Ile Glu Val Leu Asn Asn Pro Asn
145                 150                 155                 160
Ser Ala Ser Asn Thr Ile Phe Asn Ile Ala Pro Glu Leu Tyr Asn Tyr
                165                 170                 175
Gln Asp Ser Lys Gln Asn Pro Thr Gly Tyr Ser Tyr Asp Tyr Ser Asp
            180                 185                 190
Asn Gln Ala Gly Thr Tyr Tyr Leu Thr Ser Asn Ile Lys Gly Leu Phe
        195                 200                 205
Thr Pro Lys Gly Ser Gln Thr Pro Gln Thr Pro Gly Thr Tyr Ser Pro
    210                 215                 220
Phe Asn Gln Pro Leu Asn Ser Leu Asn Ile Tyr Asn Lys Gly Phe Ser
225                 230                 235                 240
Ser Glu Asn Leu Lys Thr Leu Leu Gly Ile Leu Ser Gln Asn Ser Ala
                245                 250                 255
Thr Leu Lys Glu Met Ile Glu Ser Asn Gln Leu Asp Asn Ile Thr Asn
            260                 265                 270
Ile Asn Glu Val Leu Gln Leu Leu Asp Lys Ile Lys Ile Thr Gln Ala
        275                 280                 285
Gln Lys Gln Ala Leu Leu Glu Thr Ile Asn His Leu Thr Asp Asn Ile
    290                 295                 300
Asn Gln Thr Phe Asn Asn Gly Asn Leu Val Ile Gly Ala Thr Gln Asp
```

```
305                 310                 315                 320
Asn Val Thr Asn Ser Thr Ser Ser Ile Trp Phe Gly Gly Asn Gly Tyr
                325                 330                 335
Ser Ser Pro Cys Ala Leu Asp Ser Ala Thr Cys Ser Ser Phe Arg Asn
            340                 345                 350
Thr Tyr Leu Gly Gln Leu Leu Gly Ser Thr Ser Pro Tyr Leu Gly Tyr
        355                 360                 365
Ile Asn Ala Asp Phe Lys Ala Lys Ser Ile Tyr Ile Thr Gly Thr Ile
    370                 375                 380
Gly Ser Ser Asn Ala Phe Glu Ser Gly Gly Ser Ala Asp Val Thr Phe
385                 390                 395                 400
Gln Ser Ala Asn Asn Leu Val Leu Asn Lys Ala Asn Ile Glu Ala Gln
                405                 410                 415
Ala Thr Asp Asn Ile Phe Asn Leu Leu Gly Gln Glu Gly Ile Asp Lys
            420                 425                 430
Ile Phe Asn Gln Gly Asn Leu Ala Asn Val Leu Ser Gln Met Ala Met
        435                 440                 445
Glu Lys Ile Lys Gln Ala Gly Gly Leu Gly Asn Phe Ile Glu Asn Ala
    450                 455                 460
Leu Ser Pro Leu Ser Lys Glu Leu Pro Ala Ser Leu Gln Asp Glu Thr
465                 470                 475                 480
Leu Gly Gln Leu Ile Gly Gln Asn Asn Leu Asp Asp Leu Leu Asn Asn
                485                 490                 495
Ser Gly Val Met Asn Glu Ile Gln Asn Ile Ile Ser Gln Lys Leu Ser
            500                 505                 510
Ile Phe Gly Asn Phe Val Thr Pro Ser Ile Ile Glu Asn Tyr Leu Ala
        515                 520                 525
Lys Gln Ser Leu Lys Ser Met Leu Asp Asp Lys Gly Leu Leu Asn Phe
    530                 535                 540
Ile Gly Gly Tyr Ile Asp Ala Ser Glu Leu Ser Ser Ile Leu Gly Val
545                 550                 555                 560
Ile Leu Lys Asp Ile Thr Asn Pro Pro Thr Ser Leu Gln Lys Asp Ile
                565                 570                 575
Gly Val Val Ala Asn Asp Leu Leu Asn Glu Phe Leu Gly Gln Asp Val
            580                 585                 590
Val Lys Lys Leu Glu Ser Gln Gly Leu Val Ser Asn Ile Ile Asn Asn
        595                 600                 605
Val Ile Ser Gln Gly Gly Leu Ser Gly Val Tyr Asn Gln Gly Leu Gly
    610                 615                 620
Ser Val Leu Pro Pro Ser Leu Gln Asn Ala Leu Lys Glu Asn Asp Leu
625                 630                 635                 640
Gly Thr Leu Leu Ser Pro Arg Gly Leu His Asp Phe Trp Gln Lys Gly
                645                 650                 655
Tyr Phe Asn Phe Leu Ser Asn Gly Tyr Val Phe Val Asn Asn Ser Ser
            660                 665                 670
Phe Ser Asn Ala Thr Gly Gly Ser Leu Asn Phe Val Ala Asn Lys Ser
        675                 680                 685
Ile Ile Phe Asn Gly Asp Asn Thr Ile Asp Phe Ser Lys Tyr Gln Gly
    690                 695                 700
Ala Leu Ile Phe Ala Ser Asn Gly Val Ser Asn Ile Asn Ile Thr Thr
705                 710                 715                 720
Leu Asn Ala Thr Asn Gly Leu Ser Leu Asn Ala Gly Leu Asn Asn Val
                725                 730                 735
Ser Val Gln Lys Gly Glu Ile Cys Ile Asn Leu Ala Asn Cys Pro Thr
            740                 745                 750
Thr Lys Asn Ser Ser Pro Ala Asn Ser Ser Val Thr Pro Thr Asn Glu
        755                 760                 765
Ser Leu Ser Val His Ala Asn Asn Phe Thr Phe Leu Gly Thr Ile Ile
    770                 775                 780
Ser Asn Gly Ala Ile Asp Leu Ser Gln Val Thr Asn Asn Ser Val Ile
785                 790                 795                 800
Gly Thr Leu Asn Leu Asn Glu Asn Ala Thr Leu Gln Ala Asn Asn Leu
                805                 810                 815
Thr Ile Thr Asn Ala Phe Asn Asn Ala Ser Asn Ser Thr Ala Asn Ile
            820                 825                 830
```

This Sheet Has Been Replaced

SUBSTITUTE SHEET (RULE 26)

```
Asp Gly Asn Phe Thr Leu Asn Gln Gln Ala Thr Leu Ser Thr Asn Ala
        835                 840                 845
Ser Gly Leu Asn Val Met Gly Asn Phe Asn Ser Tyr Gly Asp Leu Val
    850                 855                 860
Phe Asn Leu Ser His Ser Val Ser His Ala Ile Ile Asn Thr Gln Gly
865                 870                 875                 880
Thr Ala Thr Ile Met Ala Asn Asn Asn Pro Leu Ile Gln Phe Asn Ala
                885                 890                 895
Ser Ser Pro Glu Val Gly Thr Tyr Thr Leu Ile Asp Ser Ala Lys Ala
            900                 905                 910
Ile Tyr Tyr Gly Tyr Asn Asn Gln Ile Thr Gly Gly Ser Ser Leu Asp
        915                 920                 925
Asn Tyr Leu Lys Leu Tyr Ala Leu Ile Asp Ile Asn Gly Lys His Met
    930                 935                 940
Val Met Thr Asp Asn Gly Leu Thr Tyr Asn Gly Gln Ala Val Ser Val
945                 950                 955                 960
Lys Asp Gly Gly Leu Val Val Gly Phe Lys Asp Ser Gln Asn Gln Tyr
                965                 970                 975
Ile Tyr Thr Ser Ile Leu Tyr Asn Lys Val Lys Ile Ala Val Ser Asn
            980                 985                 990
Asp Pro Ile Asn Asn Pro Gln Ala Pro Thr Leu Lys Gln Tyr Ile Ala
        995                 1000                1005
Gln Ile Gln Gly Val Gln Ser Val Asp Ser Ile Asp Gln Ala Gly Gly
    1010                1015                1020
Asn Gln Ala Ile Asn Trp Leu Asn Lys Ile Phe Glu Thr Lys Gly Ser
1025                1030                1035                1040
Pro Leu Phe Ala Pro Tyr Tyr Leu Glu Ser His Ser Thr Lys Asp Leu
                1045                1050                1055
Thr Thr Ile Ala Gly Asp Ile Ala Asn Thr Leu Glu Val Ile Ala Asn
            1060                1065                1070
Pro Asn Phe Lys Asn Asp Ala Thr Asn Ile Leu Gln Ile Asn Thr Tyr
        1075                1080                1085
Thr Gln Gln Met Ser Arg Leu Ala Lys Leu Ser Asp Thr Ser Thr Phe
    1090                1095                1100
Ala Arg Ser Asp Phe Leu Glu Arg Leu Glu Ala Leu Lys Asn Lys Arg
1105                1110                1115                1120
Phe Ala Asp Ala Ile Pro Asn Ala Met Asp Val Ile Leu Lys Tyr Ser
                1125                1130                1135
Gln Arg Asn Arg Val Lys Asn Asn Val Trp Ala Thr Gly Val Gly Gly
            1140                1145                1150
Ala Ser Phe Ile Ser Gly Gly Thr Gly Thr Leu Tyr Gly Ile Asn Val
        1155                1160                1165
Gly Tyr Asp Arg Phe Ile Lys Gly Val Ile Val Gly Gly Tyr Ala Ala
    1170                1175                1180
Tyr Gly Tyr Ser Gly Phe His Ala Asn Ile Thr Gln Ser Gly Ser Ser
1185                1190                1195                1200
Asn Val Asn Val Gly Val Tyr Ser Arg Ala Phe Ile Lys Arg Ser Glu
                1205                1210                1215
Leu Thr Met Ser Leu Asn Glu Thr Trp Gly Tyr Asn Lys Thr Phe Ile
            1220                1225                1230
Asn Ser Tyr Asp Pro Leu Leu Ser Ile Ile Asn Gln Ser Tyr Arg Tyr
        1235                1240                1245
Asp Thr Trp Thr Thr Asp Ala Lys Ile Asn Tyr Gly Tyr Asp Phe Met
    1250                1255                1260
Phe Lys Asp Lys Ser Val Ile Phe Lys Pro Gln Val Gly Leu Ser Tyr
1265                1270                1275                1280
Tyr Tyr Ile Gly Leu Ser Gly Leu Arg Gly Ile Met Asp Asp Pro Ile
                1285                1290                1295
Tyr Asn Gln Phe Arg Ala Asn Ala Asp Pro Asn Lys Lys Ser Val Leu
            1300                1305                1310
Thr Ile Asn Phe Ala Leu Glu Ser Arg His Tyr Phe Asn Lys Asn Ser
        1315                1320                1325
Tyr Tyr Phe Val Ile Ala Asp Val Gly Arg Asp Leu Phe Ile Asn Ser
    1330                1335                1340
Met Gly Asp Lys Met Val Arg Phe Ile Gly Asn Asn Thr Leu Ser Tyr
```


This Sheet Has Been Replaced



```
1345                1350                1355                1360
Arg Asp Gly Gly Arg Tyr Asn Thr Phe Ala Ser Ile Ile Thr Gly Gly
                1365                1370                1375
Glu Ile Arg Leu Phe Lys Thr Phe Tyr Val Asn Ala Gly Ile Gly Ala
            1380                1385                1390
Arg Phe Gly Leu Asp Tyr Lys Asp Ile Asn Ile Thr Gly Asn Ile Gly
        1395                1400                1405
Met Arg Tyr Ala Phe
    1410
```

(2) INFORMATION FOR SEQ ID NO:1590:

(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:1590

```
Arg Asp Asn Met Glu Leu Ile Leu Gly Ser Gln Ser Ser Ala Arg Ala
1               5                   10                  15
Asn Leu Leu Lys Glu His Gly Ile Lys Phe Glu Gln Lys Ala Leu Tyr
            20                  25                  30
Phe Asp Glu Glu Ser Leu Lys Thr Thr Asp Pro Arg Glu Phe Val Tyr
        35                  40                  45
Leu Ala Cys Lys Gly Lys Leu Glu Lys Ala Lys Glu Leu Leu Ala Asn
    50                  55                  60
Asn Cys Ala Ile Val Val Ala Asp Ser Val Val Ser Val Gly Asn Arg
65                  70                  75                  80
Met Gln Arg Lys Ala Lys Asn Lys Arg Glu Ala Leu Glu Phe Leu Lys
                85                  90                  95
Arg Gln Asn Gly Asn Glu Ile Glu Val Leu Thr Cys Ser Ala Leu Ile
            100                 105                 110
Ser Pro Val Leu Glu Trp Leu Asp Leu Ser Val Phe Arg Ala Arg Leu
        115                 120                 125
Lys Ala Phe Asp Cys Ser Glu Ile Glu Lys Tyr Leu Glu Ser Gly Leu
    130                 135                 140
Trp Gln Gly Ser Ala Gly Cys Val Arg Leu Glu Asp Phe His Lys Pro
145                 150                 155                 160
Tyr Ile Lys Ser Ser Ser Lys Asn Leu Ser Val Gly Leu Gly Leu Asn
                165                 170                 175
Val Glu Gly Leu Leu Gly Ala Leu Lys Leu Gly Val Lys Leu Ser Leu
            180                 185                 190
Leu
```

(2) INFORMATION FOR SEQ ID NO:1591:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:1591

```
Arg Met Ala Leu Phe Gly Ser Lys Ser Lys Met Leu Glu Thr Tyr Ala
1               5                  10                  15
Leu Lys Ser Gly Ala Val Phe Ile Ser Asp Ala His Phe Leu Pro Lys
            20                  25                  30
Ser Pro His Leu Ile His Thr Leu Lys Glu Leu Leu Ser Ala Lys Pro
        35                  40                  45
Pro Gln Val Phe Phe Met Gly Asp Ile Phe His Val Leu Val Gly Tyr
    50                  55                  60
Leu Pro Leu Asp Lys Glu Gln Gln Lys Ile Ile Asp Leu Ile His Ala
65                  70                  75                  80
Leu Ser Glu Ile Ser Gln Val Phe Tyr Phe Glu Gly Asn His Asp Phe
                85                  90                  95
Ser Met Arg Phe Val Phe Asn Ser Lys Val Met Val Phe Glu Arg Gln
            100                 105                 110
Asn Gln Pro Ala Leu Phe Gln Tyr Asp Asn Lys Arg Phe Leu Leu Ala
        115                 120                 125
His Gly Asp Leu Phe Ile Thr Lys Ala Tyr Glu Phe Tyr Ile Thr Gln
    130                 135                 140
Leu Thr Ser Thr Trp Ala Arg Phe Phe Leu Thr Phe Leu Asn Leu Leu
145                 150                 155                 160
Ser Phe Lys Thr Leu Tyr Pro Phe
                165
```

(2) INFORMATION FOR SEQ ID NO:1592:

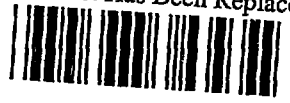
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1592

```
Asn Asp Asp Glu Asn Lys Val Ile Glu Leu Lys Thr Arg Asn Asn Met
1               5                  10                  15
Arg Ile Val Phe Met Gly Thr Pro Ser Phe Ala Glu Val Ile Leu Arg
            20                  25                  30
Ala Leu Val Glu Asn Glu Asp Lys Lys Ile Glu Val Val Gly Leu Phe
        35                  40                  45
Thr Gln Arg Asp Lys Pro Phe Gly Arg Lys Lys Glu Leu Lys Ala Pro
```

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

(2) INFORMATION FOR SEQ ID NO:1593:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1593

```
Lys Ser Thr Arg Lys Thr Ile Met Glu Ala Gln Leu Arg Phe Thr Gly
1               5                   10                  15
Val Gly Gly Gln Gly Val Leu Leu Ala Gly Glu Ile Leu Ala Glu Ala
            20                  25                  30
Lys Ile Val Ser Gly Gly Tyr Gly Thr Lys Thr Ser Thr Tyr Thr Ser
        35                  40                  45
Gln Val Arg Gly Gly Pro Thr Lys Val Asp Ile Leu Leu Asp Lys Asp
    50                  55                  60
Glu Ile Ile Phe Pro Tyr Ala Lys Glu Gly Glu Ile Asp Phe Met Leu
65                  70                  75                  80
```

```
Ser Val Ala Gln Ile Ser Tyr Asn Gln Phe Lys Ser Asp Ile Lys Lys
                85                  90                  95
Gly Gly Ile Val Val Ile Asp Pro Asn Leu Val Thr Pro Thr Lys Glu
            100                 105                 110
Asp Glu Glu Lys Tyr Gln Leu Tyr Lys Ile Pro Ile Ile Ser Ile Ala
        115                 120                 125
Lys Asp Glu Val Gly Asn Ile Ile Thr Gln Ser Val Val Ala Leu Ala
    130                 135                 140
Ile Thr Val Glu Leu Thr Lys Cys Val Glu Glu Asn Ile Val Leu Asp
145                 150                 155                 160
Thr Met Leu Lys Lys Val Pro Cys Lys Ser Arg
                165                 170
```

(2) INFORMATION FOR SEQ ID NO:1594:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 428 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1594

```
Ala Cys Leu Lys Gln Glu Asn Ile Thr Asn Thr Gln Ile Leu His Ile
1               5                   10                  15
Gly Asp Asn Ser Trp Ala Asp Asp Ala Met Pro Lys Ser Leu Gly Ile
            20                  25                  30
Ala Thr Leu Phe Arg Lys Ser Val Leu Lys Gln Leu Glu Glu Val Phe
        35                  40                  45
Pro Lys Tyr Lys Thr Phe Asn Pro Thr Ser Val Ala Gln Ser Phe Ile
    50                  55                  60
Leu Gly Ser Leu Cys Val Phe Tyr Lys Asn Tyr Ile Gln Lys His Glu
65                  70                  75                  80
Lys Phe Asp Tyr Trp Phe Leu Leu Gly Ala Met Gln Ala Gly Ile Ala
                85                  90                  95
Ala Val Ala Tyr Cys Gln Phe Ile Tyr Lys Glu Ile His Lys Arg Asn
            100                 105                 110
Ile Asp Thr Leu Val Phe Val Ala Arg Asp Gly Tyr Leu Leu Gln Lys
        115                 120                 125
Ile Phe Asn Ile Leu Tyr Pro Asn Ser Tyr Lys Thr Thr Tyr Val Tyr
    130                 135                 140
Ala Pro Arg Ile Leu Lys Lys Ala Val Phe Leu Glu Val Val Glu Gly
145                 150                 155                 160
Glu Ser Leu Glu Ile Leu Arg Ile Leu Glu Gly Glu Glu Glu Val Lys
                165                 170                 175
Lys Lys Gln Ile Thr Thr Asn Gln Gln Ala Tyr Val Tyr Leu Tyr Ser
            180                 185                 190
Asn Phe Glu His Cys Arg His Leu Ala Leu Lys Cys Leu Asp Asn Tyr
        195                 200                 205
Arg Lys Tyr Leu Phe Ser Ser Asn Leu Glu Gly Asn Ile Ala Ile Val
    210                 215                 220
Asp Thr Ile Thr Leu Gly Tyr Ser Ser Gln Gly Leu Ile Gln Lys Ala
225                 230                 235                 240
Leu Asn Lys Glu Val Phe Gly Cys Tyr Val Asp Leu Leu Arg Ile Leu
```

```
                245                 250                 255
Asn Tyr Asp Cys Val Ser Phe Leu Pro Phe Ser His Pro Lys Pro Val
            260                 265                 270
Tyr Phe His Asn Trp Asp Phe Met Glu Phe Leu Leu Thr Ser Pro Glu
        275                 280                 285
Tyr Pro Ile Leu Asn Val Glu Asn Gly Val Pro Ile Tyr Gln Lys Asp
    290                 295                 300
Val Ser Ser Cys Glu Lys His Arg Ser Lys Ala Tyr Glu Lys Ile Val
305                 310                 315                 320
Glu Gly Ala Val Gly Tyr Ala Ser Tyr Phe Lys Glu Ser Gln Ile Ser
                325                 330                 335
Leu Asp Ile His Asp Val Ile Glu Trp Val Asn Phe Phe Ile Asp Asn
            340                 345                 350
Pro Ser Ile Gln Asp Gln Glu Gln Phe Arg Gln Ile Tyr Phe Leu Pro
        355                 360                 365
Asp Ala Thr His Lys Asn Ala Leu Pro Leu Phe Cys Asn Asp Val Ser
    370                 375                 380
Leu Leu Ser Cys Ile Leu Lys Pro Ser Gln Ser Tyr Ser Val Leu Lys
385                 390                 395                 400
Arg Ser Leu Arg Thr Asn Lys Gln Glu Arg Leu Phe Lys Ile Leu Ser
                405                 410                 415
Leu Ile Lys Lys Ile Tyr Gly Lys Leu Lys Lys Lys
            420                 425
```

(2) INFORMATION FOR SEQ ID NO:1595:

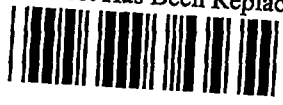
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 375 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1595

```
Gly Leu Leu Ala Cys Leu Leu Val Leu Leu Asn Leu Lys Ile Thr Pro
1               5                  10                  15
Asn Leu Met Trp Pro Leu Asp Ile Ile Val Val Val Ala Trp Val Leu
            20                  25                  30
Trp Gly Val Asn Met Phe Gly Ser Met Ser Val Arg Arg Glu Asn Thr
        35                  40                  45
Ile Tyr Val Ser Leu Trp Tyr Tyr Ile Ala Thr Tyr Val Gly Ile Ala
    50                  55                  60
Val Met Tyr Ile Phe Asn Asn Leu Ser Ile Pro Thr Tyr Phe Val Ala
65                  70                  75                  80
Asp Met Gly Ser Val Trp His Ser Ile Ser Met Tyr Ser Gly Ser Asn
                85                  90                  95
Asp Ala Leu Ile Gln Trp Trp Trp Gly His Asn Ala Val Ala Phe Val
            100                 105                 110
Phe Thr Ser Gly Val Ile Gly Thr Ile Tyr Tyr Phe Leu Pro Lys Glu
        115                 120                 125
Ser Gly Gln Pro Ile Phe Ser Tyr Lys Leu Thr Leu Phe Ser Phe Trp
    130                 135                 140
Ser Leu Met Phe Val Tyr Ile Trp Ala Gly Gly His His Leu Ile Tyr
145                 150                 155                 160
```

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

(2) INFORMATION FOR SEQ ID NO:1596:

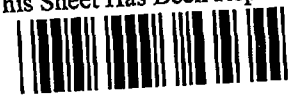
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1596

```
Gly Phe Asp Asp Asp Met Glu Ile Arg Asn Ile Lys Glu Phe Glu Lys
1               5                   10                  15
Ala Ser Lys Lys Leu Gln Lys Asp Thr Leu Lys Ile Ala Leu Ala Leu
            20                  25                  30
Leu Phe Leu Ile Gly Ala Ala Leu Leu Ala Leu Ile Phe Gly Gln Ala
        35                  40                  45
Asn Ser Lys Gly Leu Leu Leu Ile Phe Ala Ala Val Ile Gly Gly Tyr
    50                  55                  60
Met Ala Met Asn Ile Gly Ala Asn Asp Val Ser Asn Asn Val Gly Pro
65                  70                  75                  80
Ser Val Gly Ser Lys Ala Ile Ser Met Gly Gly Ala Ile Leu Ile Ala
                85                  90                  95
Ala Val Cys Glu Met Leu Gly Ala Ile Ile Ala Gly Gly Glu Val Val
            100                 105                 110
Ser Thr Ile Lys Gly Arg Ile Val Ser Pro Glu Phe Ile Asn Asp Ala
```

```
        115                 120                 125
His Val Phe Ile Asn Val Met Leu Ala Ser Leu Leu Ser Gly Ala Leu
    130                 135                 140
Trp Leu His Val Ala Thr Leu Ile Gly Ala Pro Val Ser Thr Ser His
145                 150                 155                 160
Ser Val Val Gly Gly Ile Met Gly Ala Gly Met Ala Ala Ala Gly Met
                165                 170                 175
Ser Ala Ile Asn Trp His Phe Leu Ser Gly Ile Val Ala Ser Trp Val
            180                 185                 190
Ile Ser Pro Leu Met Gly Ala Leu Ile Ala Met Phe Phe Leu Met Leu
        195                 200                 205
Ile Lys Lys Thr Ile Ala Tyr Lys Glu Asp Lys Lys Ser Ala Ala Leu
    210                 215                 220
Lys Val Val Pro Tyr Leu Val Ala Leu Met Ser Leu Ala Phe Ser Trp
225                 230                 235                 240
Tyr Leu Ile Val Lys Val Leu Lys Arg Leu Tyr Ala Val Gly Phe Glu
                245                 250                 255
Ile Gln Leu Ala Cys Gly Cys Val Leu Ala Leu Leu Ile Phe Ile Leu
            260                 265                 270
Phe Lys Arg Phe Val Leu Lys Lys Ala Pro Gln Leu Glu Asn Ser His
        275                 280                 285
Glu Ser Val Asn Glu Leu Phe Asn Val Pro Leu Ile Phe
    290                 295                 300
```

(2) INFORMATION FOR SEQ ID NO:1597:

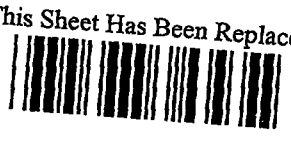
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1597

```
Arg Met Lys Leu Lys Lys Thr Leu Thr Tyr Gln His His Ala Tyr Ser
1               5                   10                  15
Phe Leu Ser Asp Asn Thr Asn Glu Val Leu Glu Asn Pro Lys Glu Ile
            20                  25                  30
Leu Phe Val Lys Thr Pro Leu Asn Glu Lys Tyr Ala Pro Leu Ile Ala
        35                  40                  45
Glu Lys Asn Leu Ala Ile Leu Asp Phe Asn Glu Leu Lys Asn Tyr Phe
    50                  55                  60
Asp Phe Lys Ile Lys Ile Val Gly Ile Thr Gly Thr Asn Gly Lys Thr
65                  70                  75                  80
Thr Thr Ala Ser Leu Met Tyr Ser Leu Leu Leu Asp Leu Asn Lys Lys
                85                  90                  95
Thr Ala Leu Leu Gly Thr Arg Gly Phe Phe Ile Asp Asp Lys His Ile
            100                 105                 110
Lys Glu Lys Gly Leu Thr Thr Pro Thr Leu Leu Glu Leu Tyr Ser Asp
        115                 120                 125
Leu Glu Glu Ala Ile Arg Leu Lys Cys Glu Tyr Phe Ile Met Glu Val
    130                 135                 140
Ser Ser His Ala Ile Val Gln Lys Arg Ile Ala Gly Leu Asp Phe Ala
145                 150                 155                 160
```

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

(2) INFORMATION FOR SEQ ID NO:1598:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1598

```
Arg Leu Leu Ser Gln Phe Lys Thr Arg Ile Asn Met Gln Glu Phe Ser
1               5                   10                  15
Leu Trp Cys Asp Phe Ile Glu Arg Asp Phe Leu Glu Asn Asp Phe Leu
            20                  25                  30
Lys Leu Ile Asn Lys Gly Ala Ile Cys Gly Ala Thr Ser Asn Pro Ser
        35                  40                  45
Leu Phe Cys Glu Ala Ile Thr Lys Ser Ala Phe Tyr Gln Asp Glu Ile
    50                  55                  60
Ala Lys Leu Lys Gly Lys Lys Ala Lys Glu Ile Tyr Glu Thr Leu Ala
```

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

(2) INFORMATION FOR SEQ ID NO:1599:

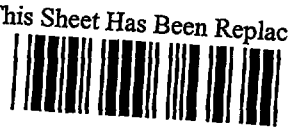
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1599

```
Gly Phe Lys Val Arg Leu Phe Arg Phe Val Gly Trp Tyr Tyr Phe Lys
1               5                   10                  15
Tyr Phe Leu Ile Val Leu Leu Ala Leu Glu Leu Phe Phe Val Gly Ile
            20                  25                  30
Asp Ser Leu Lys Tyr Ala Asp Lys Met Pro Asp Ser Ala Asn Met Ile
        35                  40                  45
Ile Leu Phe Phe Thr Tyr Asp Ile Leu Phe Ala Leu Asn Tyr Thr Leu
    50                  55                  60
Pro Ile Ser Leu Leu Leu Ala Met Val Leu Phe Tyr Ile Thr Phe Ile
65                  70                  75                  80
```

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

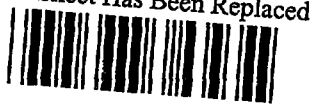
(2) INFORMATION FOR SEQ ID NO:1600:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 459 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1600

```
Lys Arg Arg Val Val Lys Phe Tyr Thr Tyr Ser Gly Glu Thr Ala Ala
1               5                  10                  15
Glu Ala Leu Lys Ile Ala Gln Ser His His Gly Val Asp Thr Leu Val
            20                  25                  30
Phe Lys Thr Gln Glu Ile Arg Lys Lys Thr Leu Thr Ser Ser Gly Leu
        35                  40                  45
Tyr Glu Ile Val Val Ala Val Glu Glu Glu Glu Asn Lys Lys Ala Pro
```

```
    50                  55                  60
Leu Ile Pro Glu Ser Leu Tyr Asp Glu Glu Leu Asn Glu Glu Asp Val
65                  70                  75                  80
Val Met Gln Leu Ser Ser Thr Val Glu Glu Met Arg Lys Leu Ala Gly
                85                  90                  95
Val Ser Ser Asn Gln Arg Asn Tyr Thr Phe Ser Lys Asn Lys Thr Leu
            100                 105                 110
Leu Glu Lys Asp Ala Pro Leu Glu Asp Thr Pro Leu Glu Ala Asn Lys
        115                 120                 125
Gln Asp Ala Leu Leu Gln Ala Leu Lys Asp Glu Ala Asn His Lys Lys
    130                 135                 140
Glu Arg Glu Lys Arg Glu Val Lys Gln Glu Glu Glu Ile Lys Asp Ile
145                 150                 155                 160
Asn Ala Gln Leu Ser Lys Ile Arg Asp Ser Leu Lys Leu Ile Gln Asn
                165                 170                 175
Met Phe Trp Asp Glu Lys Asn Pro Asn Ser Val Asn Ile Pro Gln Glu
            180                 185                 190
Phe Ala Glu Ile Tyr Lys Leu Ala Lys Gln Ser Gly Met Lys Ser Ser
        195                 200                 205
His Leu Asp Glu Ile Met Gln Leu Ser Leu Glu Leu Met Pro Leu Arg
    210                 215                 220
Met Arg Glu Asn Ser Val Thr Ile Lys Arg Tyr Phe Arg Glu Val Leu
225                 230                 235                 240
Arg Lys Ile Ile Leu Cys Arg Pro Glu Asp Leu Asn Leu Arg Gln Lys
                245                 250                 255
Arg Ile Leu Met Leu Val Gly Pro Thr Gly Val Gly Lys Thr Thr Thr
            260                 265                 270
Leu Ala Lys Leu Ala Ala Arg Tyr Ser Arg Met Leu Ala Lys Lys Tyr
        275                 280                 285
Lys Val Gly Ile Ile Thr Leu Asp Asn Tyr Arg Ile Gly Ala Leu Glu
    290                 295                 300
Gln Leu Ser Trp Tyr Ala Asn Lys Met Lys Met Ser Ile Glu Ala Val
305                 310                 315                 320
Ile Asp Ala Lys Asp Phe Ala Lys Glu Ile Glu Ala Leu Glu Tyr Cys
                325                 330                 335
Asp Phe Ile Leu Val Asp Thr Thr Gly His Ser Gln Tyr Asp Lys Glu
            340                 345                 350
Lys Ile Ala Gly Leu Lys Glu Phe Ile Asp Gly Gly Tyr Asn Ile Asp
        355                 360                 365
Val Ser Leu Val Leu Ser Val Thr Thr Lys Tyr Glu Asp Met Lys Asp
    370                 375                 380
Ile Tyr Asp Ser Phe Gly Val Leu Gly Ile Asp Thr Leu Ile Phe Thr
385                 390                 395                 400
Lys Leu Asp Glu Ser Arg Gly Leu Gly Asn Leu Phe Ser Leu Val His
                405                 410                 415
Glu Ser Gln Lys Pro Ile Ser Tyr Leu Ser Val Gly Gln Glu Val Pro
            420                 425                 430
Met Asp Leu Lys Val Ala Thr Asn Glu Tyr Leu Val Asp Cys Met Leu
        435                 440                 445
Asp Gly Phe Ser Asn Pro Asn Lys Glu Gln Ala
    450                 455
```

(2) INFORMATION FOR SEQ ID NO:1601:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

This Sheet Has Been Replaced



(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1601

```
Ile Met Ala Asp Ile Leu Ser Gln Glu Glu Ile Asp Ala Leu Leu Glu
1               5                  10                  15
Val Val Asp Glu Asn Val Asp Ile Gln Asn Val Gln Lys Lys Asp Ile
            20                  25                  30
Ile Pro Gln Arg Ser Val Thr Leu Tyr Asp Phe Lys Arg Pro Asn Arg
        35                  40                  45
Val Ser Lys Glu Gln Leu Arg Ser Phe Arg Ser Ile His Asp Lys Met
    50                  55                  60
Ala Arg Asn Leu Ser Ser Gln Val Ser Ser Ile Met Arg Ser Ile Val
65                  70                  75                  80
Glu Ile Gln Leu His Ser Val Asp Gln Met Thr Tyr Gly Glu Phe Leu
                85                  90                  95
Met Ser Leu Pro Ser Pro Thr Ser Phe Asn Val Phe Ser Met Lys Pro
            100                 105                 110
Met Gly Gly Thr Gly Val Leu Glu Ile Asn Pro Ser Ile Ala Phe Pro
        115                 120                 125
Met Ile Asp Arg Leu Leu Gly Gly Lys Gly Ser Ala Tyr Asp Gln Asn
    130                 135                 140
Arg Glu Phe Ser Asp Ile Glu Leu Asn Leu Leu Asp Thr Ile Leu Arg
145                 150                 155                 160
Gln Val Met Gln Ile Leu Lys Glu Val Trp Ser Pro Val Val Glu Met
                165                 170                 175
Tyr Pro Thr Ile Asp Ala Lys Glu Ser Ser Ala Asn Val Val Gln Ile
            180                 185                 190
Val Ala Gln Asn Glu Ile Ser Ile Met Val Val Leu Glu Ile Ile Ile
        195                 200                 205
Gly His Ser Arg Gly Met Met Asn Ile Cys Tyr Pro Val Ile Ser Ile
    210                 215                 220
Glu Ser Ile Leu Ser Lys Met Gly Ser Arg Asp Phe Met Leu Ser Glu
225                 230                 235                 240
Thr Asn Ser Lys Lys Ser Arg Asn Lys Glu Leu Gln Ala Leu Leu Ser
                245                 250                 255
Gly Val Ser Val Asp Met Met Val Phe Leu Gly Ala Val Glu Leu Ser
            260                 265                 270
Leu Lys Glu Met Leu Asp Leu Asp Val Gly Asp Thr Ile Arg Leu Asn
        275                 280                 285
Lys Val Ala Asn Asp Glu Val Ser Val Tyr Val His Lys Lys Lys Arg
    290                 295                 300
Tyr Leu Ala Ser Val Gly Phe Gln Gly Tyr Arg Lys Thr Ile Gln Ile
305                 310                 315                 320
Lys Glu Val Val Tyr Ser Glu Lys Glu Arg Thr Lys Glu Ile Leu Glu
                325                 330                 335
Met Leu Glu Glu Gln Arg Arg Gly Lys Val Gly Asp Ile Met Lys Ile
            340                 345                 350
Glu Glu Glu
        355
```

(2) INFORMATION FOR SEQ ID NO:1602:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1602

```
Gly Thr Ser Met Ser Asn Gln Ala Ser His Leu Asp Asn Phe Met Asn
1               5                  10                  15
Ala Lys Asn Pro Lys Ser Phe Phe Asp Asn Lys Gly Asn Thr Lys Phe
            20                  25                  30
Ile Ala Ile Thr Ser Gly Lys Gly Gly Val Gly Lys Ser Asn Ile Ser
        35                  40                  45
Ala Asn Leu Ala Tyr Ser Leu Tyr Lys Lys Gly Tyr Lys Val Gly Val
    50                  55                  60
Phe Asp Ala Asp Ile Gly Leu Ala Asn Leu Asp Val Ile Phe Gly Val
65                  70                  75                  80
Lys Thr His Lys Asn Ile Leu His Ala Leu Lys Gly Glu Ala Lys Leu
                85                  90                  95
Gln Glu Ile Ile Cys Glu Ile Glu Pro Gly Leu Cys Leu Ile Pro Gly
            100                 105                 110
Asp Ser Gly Glu Glu Ile Leu Lys Tyr Ile Ser Gly Ala Glu Ala Leu
        115                 120                 125
Asp Arg Phe Val Asp Glu Glu Gly Val Leu Ser Ser Leu Asp Tyr Ile
    130                 135                 140
Val Ile Asp Thr Gly Ala Gly Ile Gly Ala Thr Thr Gln Ala Phe Leu
145                 150                 155                 160
Asn Ala Ser Asp Cys Val Val Ile Val Thr Thr Pro Asp Pro Ser Ala
                165                 170                 175
Ile Thr Asp Ala Tyr Ala Cys Ile Lys Ile Asn Ser Lys Asn Lys Asp
            180                 185                 190
Glu Leu Phe Leu Ile Ala Asn Met Val Ala Gln Pro Lys Glu Gly Arg
        195                 200                 205
Ala Thr Tyr Glu Arg Leu Phe Lys Val Ala Lys Asn Asn Ile Ala Ser
    210                 215                 220
Leu Glu Leu His Tyr Leu Gly Ala Ile Glu Asn Ser Ser Leu Leu Lys
225                 230                 235                 240
Arg Tyr Val Arg Glu Arg Lys Ile Leu Arg Lys Ile Ala Pro Asn Asp
                245                 250                 255
Leu Phe Ser Gln Ser Ile Asp Gln Ile Ala Ser Leu Leu Val Ser Lys
            260                 265                 270
Leu Glu Thr Gly Thr Leu Glu Ile Pro Lys Glu Gly Leu Lys Ser Phe
        275                 280                 285
Phe Lys Arg Leu Leu Lys Tyr Leu Gly
    290                 295
```

(2) INFORMATION FOR SEQ ID NO:1603:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 531 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



SUBSTITUTE SHEET (RULE 26)

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1603

```
Ile Ser Glu Phe Asn His Arg Ser Ala Pro Leu Ile Ile Asn Tyr Val
1               5                  10                  15
Asn Thr Ile Phe Lys Lys Ala Tyr Gln Asn Ser Pro Thr Ala Tyr Leu
            20                  25                  30
Glu Gln Lys Tyr Pro Lys Thr Ser Asn Asn Lys His Val Thr Glu Gly
        35                  40                  45
Tyr Val Lys Val Ser Leu Val Ala Asp Glu Lys Glu Leu Leu Leu Glu
    50                  55                  60
Gln Ile Leu Gln Glu Ala Gln Asn Leu Leu Glu His Arg Ile Asp Pro
65                  70                  75                  80
Lys Asp Ile Thr Ile Leu Cys Ala Thr Asn Lys Asp Ala Leu Glu Ile
                85                  90                  95
Lys Asn Tyr Leu Gln Glu Tyr Leu Ser Ala Ile Arg Pro Ser Thr Glu
            100                 105                 110
Ser Ser Ala Lys Leu Ser Gln Leu Val Glu Ser Lys Ile Ile Lys Asn
        115                 120                 125
Ala Leu Glu Tyr Ala Leu Ala Glu Glu Pro Tyr Lys Pro Phe Tyr Lys
    130                 135                 140
His Ser Val Leu Lys Leu Ala Gly Tyr Leu His Asp Asp Val Ile Ala
145                 150                 155                 160
Leu Pro Gly Phe Asn Pro Lys Lys Glu Ser Val Ala Ser Phe Val Trp
                165                 170                 175
Lys Ile Met Glu Gln Phe Lys Leu Tyr Glu Glu Pro Ala Gln Ser Cys
            180                 185                 190
Leu Glu Leu Ala Val Gly Cys Glu Asp Ala Asp Gly Phe Leu Glu Lys
        195                 200                 205
Leu Glu Ala Lys Glu Ile Ala Ser Phe Asn Pro Lys Gly Ala Gln Ile
    210                 215                 220
Met Thr Ile His Lys Ser Lys Gly Met Gln Phe Pro Tyr Val Ile Val
225                 230                 235                 240
Cys Glu Arg Leu Gly Asn Pro Asn Ser Ser His Ala Asn Gln Leu Leu
                245                 250                 255
Glu Glu Tyr Asp Gly Thr Glu Leu Ala Arg Leu Tyr Tyr Arg Met Lys
            260                 265                 270
Asn Arg Glu Val Val Asp Lys Asp Tyr Ala Arg Ala Leu Asp Lys Glu
        275                 280                 285
Glu Ala Ala Lys Asp His Glu Glu Ile Asn Val Tyr Tyr Val Ala Phe
    290                 295                 300
Thr Arg Ala Glu Leu Gly Leu Ile Val Val Ala Lys Asp Lys Lys Glu
305                 310                 315                 320
Ser Lys Lys Glu Ser Lys Asn Lys Lys Met His Glu Gln Leu Glu Leu
                325                 330                 335
Ala Pro Leu Glu Glu Gly Glu Ile Ala Pro Val Ile Ser Pro Gln Lys
            340                 345                 350
Glu Pro Leu Met Thr Ser Val Val Ile Lys Pro His Ala Tyr Gly Glu
        355                 360                 365
Gln Val Gln Glu Ile Glu Glu Glu Ser Asp Ser Asp Tyr Glu Lys Asn
    370                 375                 380
Asn Asp Gln Glu Ala Ile Asn Phe Gly Ile Ala Leu His Lys Gly Leu
385                 390                 395                 400
Glu Tyr Gln Tyr Ala Tyr Asn Ile Pro Lys Gln Ser Val Leu Glu Tyr
                405                 410                 415
Leu Asn Tyr His Tyr Gly Phe Tyr Gly Leu Asp Tyr Gln Ala Leu Glu
            420                 425                 430
Glu Ser Leu Glu Leu Phe Glu Asn Asp Ala Gly Ile Gln Ala Leu Phe
        435                 440                 445
Lys Asn His Ala Leu Lys Gly Glu Ala Ala Phe Leu Phe Gln Gly Val
    450                 455                 460
Val Ser Arg Ile Asp Val Leu Leu Trp Asp Arg Gly Gln Asn Leu Tyr
```

```
465                 470                 475                 480
Val Leu Asp Tyr Lys Ser Ser Gln Asn Tyr Gln Gln Ser His Lys Ala
                485                 490                 495
Gln Val Ser His Tyr Ala Glu Phe Leu Arg Thr Gln Ala Pro His Phe
            500                 505                 510
Lys Ile Gln Ala Gly Ile Ile Tyr Ala His Lys Arg Leu Leu Glu Lys
        515                 520                 525
Leu Trp Val
    530
```

(2) INFORMATION FOR SEQ ID NO:1604:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1604

```
Leu Ser Thr Ala Tyr Gln Ala Val Glu Leu His Trp Phe Leu Lys Ala
1               5                  10                  15
Val Leu Val Leu Glu Arg Ser Pro Ser Ser Pro Glu Ile Lys Gly Ile
            20                  25                  30
Trp Asp Arg Asp Tyr His Thr Pro Ile Thr Ser Ser Phe Thr Leu Asp
        35                  40                  45
Val Ser Tyr Asp Asn Thr Asp Asp Tyr Tyr Phe Pro Arg Asn Gly Val
    50                  55                  60
Ile Phe Ser Ser Tyr Ala Thr Met Ser Gly Leu Pro Ser Ser Gly Thr
65                  70                  75                  80
Leu Asn Ser Trp Asn Gly Leu Gly Gly Asn Val Arg Asn Thr Lys Val
                85                  90                  95
Tyr Gly Lys Phe Ala Ala Tyr His His Leu Gln Lys Tyr Leu Leu Ile
            100                 105                 110
Asp Leu Ile Ala Arg Phe Lys Thr Gln Gly Gly Tyr Ile Phe Arg Tyr
        115                 120                 125
Asn Thr Asp Asp Tyr Leu Pro Leu Asn Ser Thr Phe Tyr Met Gly Gly
    130                 135                 140
Val Thr Thr Val Arg Gly Phe Arg Asn Gly Ser Ile Thr Pro Lys Asp
145                 150                 155                 160
Glu Phe Gly Leu Trp Leu Gly Gly Asp Gly Ile Phe Thr Ala Ser Thr
                165                 170                 175
Glu Leu Ser Tyr Gly Val Leu Lys Ala Ala Lys Met Arg Leu Ala Trp
            180                 185                 190
Phe Phe Asp Phe Gly Phe Leu Thr Phe Lys Thr Pro Thr Arg Gly Ser
        195                 200                 205
Phe Phe Tyr Asn Ala Pro Thr Thr Thr Ala Asn Phe Lys Asp Tyr Gly
    210                 215                 220
Val Val Gly Ala Gly Phe Glu Arg Ala Thr Trp Arg Ala Ser Thr Gly
225                 230                 235                 240
Leu Gln Ile Glu Trp Ile Ser Pro Met Gly Pro Trp Cys
                245                 250
```

This Sheet Has Been Replaced

INFORMATION FOR SEQ ID NO:1605:

(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:1605

```
Ala Arg Ile Met Leu Asp Lys Arg Ile Lys Thr Leu Leu Leu Phe Phe
1               5                  10                  15
Gly Leu Asn Met Val Cys Leu Ser Val Ser Phe Thr Asn Lys Pro His
            20                  25                  30
Leu Cys Phe Trp Phe Leu Val Leu Gly Cys Tyr Leu Val Tyr Glu Trp
        35                  40                  45
Gln Lys Lys Gln Lys Lys Asp Phe Gln Ser Ala Lys Ser Leu Lys Phe
    50                  55                  60
Asp Ser Val Ser Glu Leu Glu Lys Asp Leu Asn Met Glu Val Thr Asn
65                  70                  75                  80
Asp Glu Trp Asp Thr His
                85
```

(2) INFORMATION FOR SEQ ID NO:1606:

(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:1606

```
Ser Arg Ser Val Glu Met Asn Tyr Pro Asn Leu Pro Asn Ser Ala Leu
1               5                  10                  15
Glu Ile Ser Glu Gln Pro Glu Val Lys Glu Ile Thr Asn Glu Leu Leu
            20                  25                  30
Lys Gln Leu Gln Asn Ala Leu Arg Ser Asn Ala His Phe Ser Glu Gln
        35                  40                  45
Val Glu Leu Ser Leu Lys Cys Ile Val Arg Ile Leu Glu Val Leu Leu
    50                  55                  60
Ser Leu Asp Phe Phe Lys Asn Ala Asn Glu Ile Asp Ser Ser Leu Arg
65                  70                  75                  80
Asn Ser Ile Glu Trp Leu Thr Asn Ala Gly Glu Ser Leu Lys Leu Lys
```

```
                85                  90                  95
Met Lys Glu Tyr Glu Arg Phe Phe Ser Glu Phe Asn Thr Ser Met His
            100                 105                 110
Ala Asn Glu Gln Glu Val Thr Asn Thr Leu Asn Ala Asn Ala Glu Asn
        115                 120                 125
Ile Lys Ser Glu Ile Lys Lys Leu Glu Asn Gln Leu Ile Glu Thr Thr
    130                 135                 140
Thr Arg Leu Leu Thr Ser Tyr Gln Ile Phe Leu Asn Gln Ala Arg Asp
145                 150                 155                 160
Asn Ala Asn Asn Gln Ile Thr Lys Asn Lys Thr Gln Ser Leu Glu Ala
                165                 170                 175
Ile Thr Gln Ala Lys Asn Asn Ala Asn Asn Glu Ile Ser Asn Thr Gln
            180                 185                 190
Thr Gln Ala Ile Thr Asn Ile Thr Glu Ala Lys Thr Asn Ala Asn Asn
        195                 200                 205
Glu Ile Ser Asn Asn Gln Thr Gln Ala Ile Thr Asn Ile Asn Glu Ala
    210                 215                 220
Lys Glu Ser Ala Thr Thr Gln Ile Asn Ala Asn Lys Gln Glu Ala Ile
225                 230                 235                 240
Asn Asn Ile Thr Gln Glu Lys Thr Gln Ala Thr Ser Glu Ile Thr Glu
                245                 250                 255
Ala Lys Lys Thr Asp His Tyr Gln Asn Ile Asp Phe Phe Glu Phe Glu
            260                 265                 270
```

(2) INFORMATION FOR SEQ ID NO:1607:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 443 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1607

```
Gly Leu Ser Val Leu Glu Arg Tyr Ala Asn Glu Glu Met Lys Ala Leu
1               5                   10                  15
Trp Asn Glu Gln Thr Lys Phe Glu Thr Tyr Leu Glu Val Glu Lys Ala
            20                  25                  30
Val Val Arg Ala Trp Asn Lys Leu Gly Gln Ile Gln Asp Ser Asp Cys
        35                  40                  45
Glu Lys Ile Cys Leu Lys Ala Ala Phe Asn Leu Glu Arg Ile Lys Glu
    50                  55                  60
Ile Glu Lys Thr Thr Lys His Asp Leu Ile Ala Phe Thr Thr Cys Val
65                  70                  75                  80
Ala Glu Ser Leu Gly Glu Glu Ser Arg Phe Phe His Tyr Gly Ile Thr
                85                  90                  95
Ser Ser Asp Cys Ile Asp Thr Ala Met Ala Leu Leu Met Thr Lys Ser
            100                 105                 110
Leu Lys Leu Ile Gln Lys Gly Val Lys Asn Leu Tyr Glu Thr Leu Lys
        115                 120                 125
Asn Arg Ala Leu Glu His Gln Asp Thr Leu Met Val Gly Arg Ser His
    130                 135                 140
Gly Val Phe Gly Glu Pro Ile Thr Phe Gly Leu Val Leu Ala Leu Phe
145                 150                 155                 160
```

This Sheet Has Been Replaced



```
Ala Asp Glu Ile Lys Arg His Leu Lys Ala Leu Asp Leu Thr Met Glu
                165                 170                 175
Phe Ile Ser Val Trp Ala Ile Ser Gly Gly Leu Gly Asn Phe Ala His
            180                 185                 190
Ala Pro Leu Glu Leu Glu Glu Leu Ala Cys Gly Phe Leu Gly Leu Lys
        195                 200                 205
Thr Ala Asn Ile Ser Asn Gln Val Ile Gln Arg Asp Arg Tyr Ala Arg
    210                 215                 220
Leu Ala Cys Asp Leu Ala Leu Leu Ala Ser Ser Cys Glu Lys Ile Ala
225                 230                 235                 240
Val Asn Ile Arg His Leu Gln Arg Ser Glu Val Tyr Glu Val Glu Glu
                245                 250                 255
Ala Phe Ser Ala Gly Gln Lys Gly Ser Ser Ala Met Pro His Lys Arg
            260                 265                 270
Asn Pro Ile Leu Ser Glu Asn Ile Thr Gly Leu Cys Arg Val Ile Arg
        275                 280                 285
Ser Phe Thr Thr Pro Met Leu Glu Asn Val Ala Leu Trp His Glu Arg
    290                 295                 300
Asp Met Ser His Ser Ser Val Glu Arg Phe Ala Leu Pro Asp Leu Phe
305                 310                 315                 320
Ile Thr Ser Asp Phe Met Leu Ser Arg Leu Asn Ser Val Ile Glu Asn
                325                 330                 335
Leu Val Val Tyr Pro Lys Asn Met Leu Lys Asn Leu Ala Leu Ser Gly
            340                 345                 350
Gly Leu Val Phe Ser Gln Arg Val Leu Leu Glu Leu Pro Lys Lys Gly
        355                 360                 365
Leu Ser Arg Glu Glu Ser Tyr Ser Ile Val Gln Glu Asn Ala Met Lys
    370                 375                 380
Ile Trp Glu Val Leu Gln Gln Gly Ala Phe Lys Asn Ala Asp Glu Asn
385                 390                 395                 400
Leu Phe Leu Asn Ala Leu Leu Asn Asp Glu Arg Leu Lys Lys Tyr Leu
                405                 410                 415
Asn Glu Ser Glu Ile Arg Ala Cys Phe Asp Tyr Ser Tyr Tyr Thr Lys
            420                 425                 430
Asn Val Gly Ala Ile Phe Lys Arg Val Phe Gly
        435                 440
```

(2) INFORMATION FOR SEQ ID NO:1608:

(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:1608

```
Asn Asp Ser Gly Ser Lys His Phe Ile Leu Pro Phe Leu Thr Leu Leu
1               5                   10                  15
Leu Gln Met Tyr Leu Ser Arg Thr Arg Glu Tyr Met Ala Asp Ser Gly
            20                  25                  30
Ala Ala Phe Leu Met His Asp Asn Lys Pro Met Ile Arg Ala Leu Gln
        35                  40                  45
Lys Ile Ser Asn Asp Tyr Thr Asn Asn Asp Tyr Lys Glu Ile Asp Lys
```

This Sheet Has Been Replaced



```
    50                  55                  60
Asn Ser Thr Arg Ser Ala Ala Tyr Leu Phe Asn Ala Glu Met Phe Ser
65                  70                  75                  80
Thr His Pro Ser Ile Lys Asn Arg Ile Gln Ser Leu Arg Lys Arg Val
                85                  90                  95
Ile
```

(2) INFORMATION FOR SEQ ID NO:1609:

(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:1609

```
Met Glu Lys Phe Phe Asn Gln Phe Phe Glu Asn Ile Gly Glu Asp Lys
1               5                  10                  15
Asn Arg Glu Gly Leu Lys Glu Thr Pro Lys Arg Val Gln Glu Leu Trp
            20                  25                  30
Lys Phe Leu Tyr Lys Gly Tyr Lys Glu Asp Pro Arg Val Ala Leu Lys
        35                  40                  45
Ser Ala Tyr Phe Gln Gly Val Cys Asp Glu Met Ile Val Ala Gln Asn
    50                  55                  60
Ile Glu Phe Tyr Ser Thr Cys Glu His His Leu Leu Pro Phe Phe Gly
65                  70                  75                  80
Asn Ile Ser Val Gly Tyr Ile Pro Lys Glu Lys Ile Val Gly Ile Ser
                85                  90                  95
Ala Ile Ala Lys Leu Ile Glu Ile Tyr Ser Lys Arg Leu Gln Ile Gln
            100                 105                 110
Glu Arg Leu Thr Thr Gln Ile Ala Glu Thr Phe Asp Glu Ile Ile Glu
        115                 120                 125
Pro Arg Gly Val Ile Val Val Cys Glu Ala Lys His Leu Cys Met Ser
    130                 135                 140
Met Gln Gly Val Gln Lys Gln Asn Ala Ile Ile Lys Thr Ser Val Leu
145                 150                 155                 160
Arg Gly Leu Phe Lys Lys Asp Pro Lys Thr Arg Ala Glu Phe Met Gln
                165                 170                 175
Leu Leu Lys Ser
            180
```

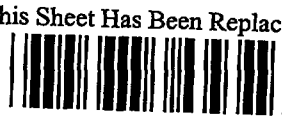
(2) INFORMATION FOR SEQ ID NO:1610:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1610

```
Val Ile Ile Leu Gly Met Ser Asn Pro Asn Leu Ser Phe Tyr Cys Asn
1               5                  10                  15
Glu Cys Glu Arg Phe Glu Ser Phe Leu Lys Asn His Tyr Leu His Leu
            20                  25                  30
Glu Gly Phe His Pro Tyr Leu Glu Lys Ala Phe Phe Glu Met Val Leu
        35                  40                  45
Asn Gly Gly Lys Arg Phe Arg Pro Lys Leu Phe Leu Ala Val Leu Cys
    50                  55                  60
Ser Leu Val Gly Lys Lys Asp Tyr Ser Asn Gln Gln Thr Glu Tyr Phe
65                  70                  75                  80
Lys Ile Ala Leu Ser Ile Glu Cys Leu His Thr Tyr Ser Leu Ile His
                85                  90                  95
Asp Asp Leu Pro Cys Met Asp Asn Ala Ile Leu Arg Arg Asn His Pro
            100                 105                 110
Thr Leu His Ala Lys Tyr Asp Glu Thr Thr Ala Val Leu Ile Gly Asp
        115                 120                 125
Ala Leu Asn Thr Tyr Ser Phe Glu Leu Leu Ser Asn Ser Leu Leu Glu
    130                 135                 140
Ser Arg Ile Ile Val Glu Leu Val Lys Ile Leu Ser Ala Asn Gly Gly
145                 150                 155                 160
Ile Lys Gly Met Ile Leu Gly Gln Ala Leu Asp Cys Tyr Phe Glu Asn
                165                 170                 175
Thr Pro Leu Asn Leu Glu Gln Leu Thr Phe Leu His Glu His Lys Thr
            180                 185                 190
Ala Lys Leu Ile Ser Ala Ser Leu Ile Met Gly Leu Val Ala Ser Gly
        195                 200                 205
Ile Asn Asp Glu Glu Leu Leu Lys Trp Leu Gln Ala Phe Gly Leu Lys
    210                 215                 220
Met Gly Leu Cys Phe Gln Val Leu Asp Asp Ile Ile Asp Val Thr Gln
225                 230                 235                 240
Asp Glu Lys Glu Ser Gly Lys Thr Thr His Leu Asp Ser Ala Lys Asn
                245                 250                 255
Ser Phe Val Asn Leu Leu Gly Leu Lys Lys Ala Ser Gly Tyr Ala Gln
            260                 265                 270
Thr Leu Lys Thr Glu Ile Leu Asn Asp Leu Asn Ala Leu Glu Pro Thr
        275                 280                 285
Tyr Leu Ser Leu Gln Glu Asn Leu Asn Ala Leu Leu Asn Thr Leu Phe
    290                 295                 300
Lys Gly Lys Thr
305
```

(2) INFORMATION FOR SEQ ID NO:1611:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1611

```
Leu Leu Asn Thr Ser Lys Lys Lys Arg Asn Leu Asn Trp Asn Phe Thr
1               5                  10                  15
Cys Leu Lys Gly Val Met Arg Ala Arg Cys Ser Lys Lys Ser Ser Met
            20                  25                  30
Arg Lys Glu Lys Ile Met Thr Asn Phe Glu Lys Ile Ile Ala Gln Asn
        35                  40                  45
Arg Leu Lys Thr Asn Ala Val Leu Thr Thr Tyr Cys Ala Ile Phe Ala
    50                  55                  60
Phe Ile Gly Leu Leu Val Asp Ala Ile Arg Ile Asn Ala Asn Asp Leu
65                  70                  75                  80
Gly Ile Ala Leu Phe Lys Leu Met Thr Phe Gln Ile Phe Pro Thr Ile
                85                  90                  95
Thr Ile Val Met Phe Val Val Ala Phe Val Ile Ile Leu Val Cys Ile
            100                 105                 110
Gln Asn Phe Ser Ser Ile Met Leu Ser Gly Asp Glu Tyr Lys Leu Ile
        115                 120                 125
Asp Pro Ser Lys Val Leu Ser Ser Lys Glu Asn Gln Ile His Arg Leu
    130                 135                 140
Leu Leu Glu Leu Leu Glu Glu Ala Lys Leu His Phe Glu Pro Lys Leu
145                 150                 155                 160
Tyr Ile Ile Asn Ala Pro Tyr Met Asn Ala Phe Ala Ser Gly Trp Asp
                165                 170                 175
Glu Ser Asn Ser Leu Ile Ala Leu Thr Ser Ala Leu Ile Glu Arg Leu
            180                 185                 190
Asp Arg Asp Glu Leu Lys Ala Val Ile Ala His Glu Leu Ser His Ile
        195                 200                 205
Arg His Asn Asp Ile Arg Leu Thr Met Cys Val Gly Ile Leu Ser Asn
    210                 215                 220
Ile Met Leu Leu Val Ala Asn Phe Ser Val Tyr Phe Phe Met Gly Asn
225                 230                 235                 240
Arg Lys Asn Ser Gly Ala Asn Leu Ala Arg Met Ile Leu Trp Val Leu
                245                 250                 255
Gln Ile Ile Leu Pro Phe Leu Thr Leu Leu Leu Gln Met Tyr Leu Ser
            260                 265                 270
Arg Thr Arg Glu Tyr Met Ala Asp Ser Gly Ala Ala Phe Leu Met His
        275                 280                 285
Asp Asn Lys Pro Met Ile Arg Ala Leu Gln Lys Ile Ser Asn Asp Tyr
    290                 295                 300
Thr Asn Asn Asp Tyr Lys Glu Ile Asp Lys Asn Ser Thr Arg Ser Ala
305                 310                 315                 320
Ala Tyr Leu Phe Asn Ala Glu Met Phe Ser Thr His Pro Ser Ile Lys
                325                 330                 335
Asn Arg Ile Gln Ser Leu Arg Lys Arg Val Ile
            340                 345
```

(2) INFORMATION FOR SEQ ID NO:1612:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

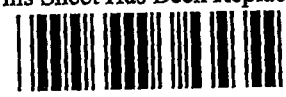
(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1612

```
Thr Gln Pro His Lys Asn Lys Arg Leu Asn Lys Arg Leu Asn Lys Arg
1               5                  10                  15
Leu Asn Lys Arg Leu Asn Lys Arg Leu Asn Lys Arg Leu Asn Lys Arg
            20                  25                  30
Leu Asn Lys Lys Leu Asn Lys Ser Lys Lys Lys Lys Ile Ser Leu Asn
        35                  40                  45
Lys Thr Val Ser Arg Pro Phe Lys Thr Ile Lys Lys Pro Pro Gln Pro
    50                  55                  60
Pro
65
```

(2) INFORMATION FOR SEQ ID NO:1613:

(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:1613

```
Gly Val Asn Met Leu Ile Leu Gly His Pro Leu Ile Pro Ser Ala Arg
1               5                  10                  15
Phe Val Phe Ile Lys Asn Thr Asp Ala Ile His Ser Ser Ala Asn Asn
            20                  25                  30
Asp Ile Val Cys Phe Glu Ala Asn Pro Lys Asn Leu Glu Leu Ala Gln
        35                  40                  45
Tyr Cys Cys Glu Asn Gly Val His Phe Ser Val Ile Phe Leu Ser His
    50                  55                  60
Lys Ile Glu Thr Asp Thr Phe Phe Leu Phe Asn Ala Phe Lys Pro Leu
65                  70                  75                  80
Tyr Cys Ile Phe Lys Asp Ile Lys Gln Ala Ile Leu Ala Gln Gln His
                85                  90                  95
Ala Thr Asn Tyr Leu Leu Asp Ser Lys Ile Leu Phe Ser Met Asp Phe
            100                 105                 110
Asn Asp Thr Glu Ser Trp Glu Ile Cys Ala Lys Asn Gln Ile Asp Gly
        115                 120                 125
Val Ile Ser Lys Asp Ser Leu Leu Leu Lys
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:1614:

(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:1614

```
Phe Lys Cys Asn Leu Lys Arg Arg Ser Ala Leu Lys Leu Leu Val Val
1               5                  10                  15
Asp Asp Ser Ser Thr Met Arg Arg Ile Ile Lys Asn Thr Leu Ser Arg
            20                  25                  30
Leu Gly Tyr Glu Asp Val Leu Glu Ala Glu His Gly Val Glu Ala Trp
        35                  40                  45
Glu Lys Leu Asp Ala Asn Ala Asp Thr Lys Val Leu Ile Thr Asp Trp
    50                  55                  60
Asn Met Pro Glu Met Asn Gly Leu Asp Leu Val Lys Lys Val Arg Ala
65                  70                  75                  80
Asp Asn Arg Phe Lys Glu Ile Pro Ile Ile Met Ile Thr Thr Glu Gly
                85                  90                  95
Gly Lys Ala Glu Val Ile Thr Thr Leu Lys Ala Gly Val Asn Asn Tyr
            100                 105                 110
Ile Val Lys Pro Phe Thr Pro Gln Val Leu Lys Glu Lys Leu Glu Val
        115                 120                 125
Val Leu Gly Thr Asn Asp
    130
```

(2) INFORMATION FOR SEQ ID NO:1615:

(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:1615

```
Arg Val Met Ala Val Arg Ile Met Ala Thr Val Trp Thr Asn Ser Cys
1               5                  10                  15
Lys Glu Phe Gly Leu Val Ser Leu Phe Leu Ser Leu Leu Val Leu Val
            20                  25                  30
Val Val Gly Arg Phe Phe Ile Lys Gly Ala Phe Tyr Gly Leu Lys Asn
        35                  40                  45
Gly Val Leu Gly Met Asp Leu Ser Val Ser Phe Gly Ala Leu Ser Ala
    50                  55                  60
Phe Val Tyr Ser Leu Tyr Ala Met Leu Val Ser Gln Glu Thr Tyr Phe
65                  70                  75                  80
```

This Sheet Has Been Replaced



```
Glu Ala Ser Ser Thr Ile Leu Thr Leu Val Phe Gly Ser Lys Phe Leu
                85                  90                  95
Glu Leu Lys Ala Arg Leu Phe Ala Asn Glu Lys Cys Leu Ala Leu Glu
            100                 105                 110
Ser His Glu Ile His Ser Val Ile Val Val Glu Asn Gly Lys Gln Ile
        115                 120                 125
Glu Lys His Pro Lys Asp Val Ala Ile Gly Ser Val Val Trp Val Pro
    130                 135                 140
Ser Gly Ala Lys Ile Ala Leu Asp Gly Val Leu Leu Asn Ser Ala Ser
145                 150                 155                 160
Val Asp Ala Ser Leu Ile Ser Gly Glu Phe Lys Pro Leu Glu Leu Gly
                165                 170                 175
Val Asn Asp Pro Ile Leu Gly Gly Tyr Val Asn Val Gly Val Pro Phe
            180                 185                 190
Ser Tyr Gln Val Ser Ala Thr Phe Gln Asn Ser Arg Leu Ser Ser Leu
        195                 200                 205
Leu Glu Thr Leu Lys Lys Ser Phe Leu Glu Lys Pro Leu Ile Glu Ser
    210                 215                 220
Ser Ala Asn Lys Ile Ala Asp Ile Phe Ser Lys Ala Val Leu Phe Leu
225                 230                 235                 240
Ala Phe Val Ser Phe Leu Leu Trp Gln Phe Gly Leu Gly Gly Asn Phe
                245                 250                 255
Glu Lys Ala Leu Met Val Cys Ile Ser Val Leu Val Ile Ser Cys Pro
            260                 265                 270
Cys Ala Phe Ala Arg Leu Arg Pro
        275                 280
```

(2) INFORMATION FOR SEQ ID NO:1616:

(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:1616

```
Arg Ala Ser His Lys Leu Pro Leu Arg Val Arg Ser Ala Thr Pro Ile
1               5                  10                  15
Ala Leu Val Ile Gly Val Phe Lys Asn Pro Leu Ile Val Phe Lys Glu
            20                  25                  30
Ala Leu Phe Leu Glu Thr Leu Ala Lys Val Lys Lys Ile Phe Ile Asp
        35                  40                  45
Lys Thr Gly Thr Leu Thr Gln Lys Glu Val Leu Leu Lys Glu Lys Ile
    50                  55                  60
Ile His Glu Glu Phe Asp Glu Arg Leu Leu Lys Ser Leu Leu Lys Thr
65                  70                  75                  80
Arg Glu His Leu Ala His Asn Ala Ile Leu Lys Thr Leu Asp Gly Asp
                85                  90                  95
Glu Val Asp Leu Glu Lys Ile Glu Phe Phe Ala His Gly Leu Lys Ala
            100                 105                 110
Ser Tyr Gln Asn Glu Thr Leu Leu Val Gly Ser Leu Lys Phe Leu Asn
        115                 120                 125
Ala Met Gly Val Asp Leu Lys Val Lys Glu Ser Ala Asn Ile Met Val
```

This Sheet Has Been Replaced

```
    130                 135                 140
Gly Phe Ala Lys Asn Lys Thr Leu Cys Ala Leu Phe Ile Leu Glu Glu
145                 150                 155                 160
Arg Leu Lys Ala Asn Ala Lys Glu Val Ile Gln Ala Leu Gln Asn Gln
                165                 170                 175
Gly Leu Glu Leu Glu Ile Leu Ser Gly Asp Asn Glu Ser Ser Val Lys
            180                 185                 190
Glu Cys Ala Lys
        195
```

(2) INFORMATION FOR SEQ ID NO:1617:

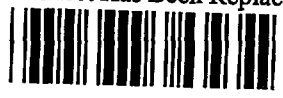
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 667 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1617

```
Thr Pro Thr Lys Ala Pro Lys Ile Val Gln Glu Gln Val Thr Tyr Pro
1               5                   10                  15
Leu Val Ser Thr Phe Met Ser Ile Ala Asn Ile Asp Thr Val Arg Gly
            20                  25                  30
Ile Ser Ser Tyr Glu Ser Gly Leu Ile Tyr Ile Ile Phe Lys Asp Gly
        35                  40                  45
Val Asn Leu Tyr Trp Ala Arg Asp Arg Val Leu Glu Gln Leu Asn Arg
    50                  55                  60
Val Ser Asn Leu Pro Lys Asp Ala Lys Val Glu Ile Gly Ser Asp Ser
65                  70                  75                  80
Thr Ser Ile Gly Trp Ala Tyr Gln Tyr Ala Leu Ser Ser Asp Ser Lys
                85                  90                  95
Asn Leu Ser Asp Leu Lys Val Leu Gln Asp Phe Tyr Tyr Arg Tyr Ala
            100                 105                 110
Leu Leu Gly Val Asp Gly Val Ser Glu Val Ala Ser Val Gly Gly Phe
        115                 120                 125
Val Lys Asp Tyr Glu Val Thr Leu Gln Asn Asp Ser Leu Ile Arg Tyr
    130                 135                 140
Asn Leu Ser Leu Glu Gln Val Ala Asn Ala Ile Lys Asn Ser Asn Asn
145                 150                 155                 160
Asp Thr Gly Gly Gly Val Ile Leu Glu Asn Gly Phe Glu Lys Ile Ile
                165                 170                 175
Arg Ser His Gly Tyr Ile Gln Ser Leu Asn Asp Leu Glu Glu Ile Val
            180                 185                 190
Val Lys Lys Glu Gly Ala Ile Pro Leu Lys Ile Lys Asp Ile Ala Ser
        195                 200                 205
Val Arg Leu Ala Pro Lys Pro Arg Arg Gly Ala Ala Asn Leu Asn Gly
    210                 215                 220
Asp Lys Glu Val Val Gly Gly Ile Val Met Val Arg Tyr His Ala Asp
225                 230                 235                 240
Thr Tyr Lys Val Leu Lys Ala Ile Lys Glu Lys Ile Ala Thr Leu Gln
                245                 250                 255
Ala Ser Asn Pro Asp Val Lys Ile Thr Ser Val Tyr Asp Arg Ser Glu
            260                 265                 270
```

```
Leu Ile Glu Lys Gly Ile Asp Asn Leu Ile His Thr Leu Ile Glu Glu
        275                 280                 285
Ser Val Ile Val Leu Val Ile Ile Ala Ile Phe Leu Leu His Phe Arg
    290                 295                 300
Ser Ala Leu Val Val Ile Ile Thr Leu Pro Leu Ser Val Cys Ile Ser
305                 310                 315                 320
Phe Leu Leu Met Arg Tyr Phe Asn Ile Glu Ala Ser Ile Met Ser Leu
                325                 330                 335
Gly Gly Ile Ala Ile Ala Ile Arg Ala Met Val Asp Ala Ala Ile Val
            340                 345                 350
Met Val Glu Asn Ala His Lys His Leu Gln His Ile Asp Thr Arg Asp
        355                 360                 365
Asn Thr Gln Arg Val Asn Ala Ile Met Gln Gly Val Lys His Val Gly
    370                 375                 380
Gly Ala Ile Phe Phe Ala Leu Met Ile Ile Val Val Ser Phe Leu Pro
385                 390                 395                 400
Ile Phe Ala Leu Thr Gly Gln Glu Glu Lys Leu Phe Ala Pro Leu Ala
                405                 410                 415
Tyr Thr Lys Thr Phe Ala Met Leu Val Gly Ala Leu Leu Ser Ile Thr
            420                 425                 430
Ile Val Pro Val Leu Met Val Trp Leu Ile Lys Gly Arg Ile Leu Glu
        435                 440                 445
Glu Ser Glu Ser Pro Val Asn Ala Phe Phe Met Lys Ile Tyr Gly Val
    450                 455                 460
Ser Leu Arg Val Val Leu Lys Phe Arg Tyr Ala Phe Leu Ile Ala Ser
465                 470                 475                 480
Val Leu Gly Leu Gly Gly Leu Val Val Ala Tyr Lys Lys Leu Asn Trp
                485                 490                 495
Glu Phe Ile Pro Gln Ile Asn Glu Gly Val Ile Met Tyr Met Pro Val
            500                 505                 510
Thr Ile Asn Gly Val Gly Ile Asp Thr Ala Leu Glu Tyr Leu Lys Lys
        515                 520                 525
Ser Asn Ala Ala Ile Lys Gln Leu Asp Phe Val Lys Gln Val Phe Gly
    530                 535                 540
Lys Val Gly Arg Ala Asn Thr Ser Thr Asp Ala Ala Gly Leu Gly Met
545                 550                 555                 560
Ile Glu Thr Tyr Ile Glu Leu Lys Pro Gln Asn Glu Trp Lys Glu Lys
                565                 570                 575
Leu Ser Tyr Lys Glu Val Arg Asp Lys Leu Glu Lys Thr Leu Gln Leu
            580                 585                 590
Lys Gly Leu Thr Asn Ser Trp Thr Tyr Pro Ile Arg Gly Arg Thr Asp
        595                 600                 605
Met Leu Leu Thr Gly Ile Arg Thr Pro Leu Gly Ile Lys Leu Tyr Gly
    610                 615                 620
Asn Asp Thr Asp Lys Leu Gln Glu Leu Ala Ile Leu Met Glu Gln Gln
625                 630                 635                 640
Leu Lys Thr Leu Lys Glu Ser Leu Ser Gly Phe Ala Glu Arg Ser Asn
                645                 650                 655
Asn Gly Tyr Tyr Ile Thr Leu Asp Leu Glu Arg
            660                 665
```

(2) INFORMATION FOR SEQ ID NO:1618:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1618

```
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:1619:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1619

```
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
        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:1620:

(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:1620

```
Asn Lys Ile Leu Ala Ser Glu Leu Glu Phe Lys Phe Leu Ile Lys Gly
1               5                  10                  15
Val Ile Met Ala His His Glu Glu Gln His Gly Gly His His His His
            20                  25                  30
His His His Thr His His His His Tyr His Gly Gly Glu His His His
        35                  40                  45
His His His Ser Ser His His Glu Glu Gly Cys Cys Ser Thr Ser Asp
    50                  55                  60
Ser His His Gln Glu Glu Gly Cys Cys His Gly His His Glu
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:1621:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1621

```
Gly Val Leu Ile Arg Thr Pro Lys His Leu Thr Lys Gln Glu Ser Val
1               5                  10                  15
Asn Leu Gly Ala Tyr Tyr Thr Pro Pro Tyr Leu Val Asp Cys Ala Tyr
            20                  25                  30
Lys Leu Leu Lys Lys His Val Gly Ile Glu Asn Tyr Thr Leu Leu Asp
        35                  40                  45
Thr Ala Cys Gly Asn Lys Glu Phe Leu Lys Leu His His Pro Lys Lys
```

```
    50                  55                  60
Ile Gly Ala Asp Ile Asp Pro Lys Cys Asp Ala Leu Ile Ile Asn Ala
65                  70                  75                  80
Leu Ala Asn Pro Lys Arg Glu Asn Tyr Gly Ile Ser Gln Asp Glu Pro
                85                  90                  95
Leu Ile Ile Val Gly Asn Pro Pro Tyr Asn Asp Arg Thr Ser Phe Ile
            100                 105                 110
Lys Gln Asp Ile Lys Asn Lys Asp Phe Ile Phe Glu Ile Asp Asn Asp
        115                 120                 125
Leu Lys Ser Arg Asp Leu Gly Ile Ser Phe Leu Lys Ser Phe Ala Ile
    130                 135                 140
Leu Lys Pro Ala Phe Ile Cys Val Leu His Pro Leu Ser Tyr Leu Ile
145                 150                 155                 160
Lys Glu Ala Asn Phe Lys Gln Leu Lys Leu Phe Lys Asp His Tyr Arg
                165                 170                 175
Leu Leu Asp Ala Phe Val Val Ser Ser Lys Ser Phe Thr Lys Ser Asn
            180                 185                 190
Glu Phe Pro Ile Val Ile Ala Leu Tyr Glu Arg Gly Arg Met Asp Tyr
        195                 200                 205
Ala Gly Ile Arg Arg Phe Val Phe Pro Thr Asp Cys Asp Thr Thr Leu
    210                 215                 220
Cys Leu Asn Asp Phe Asp Tyr Ile Ala Asn Tyr Val Asp Lys Tyr Pro
225                 230                 235                 240
Asn Ala Lys Lys Val Gly Ala Cys Val Gly Tyr Phe Phe Pro Met Arg
                245                 250                 255
Asp Ile Asn Ala Leu Lys Arg Asn Lys Thr Phe Leu Asn Ala Pro Ser
            260                 265                 270
Glu Asn Ala Val Arg Ile Ser Gln Asp Lys Leu Ile Tyr Tyr Gln Tyr
        275                 280                 285
Ile His Tyr Phe Lys Glu Ile Ala Pro Lys Ile Pro Tyr Tyr Phe Gly
    290                 295                 300
Asn Leu Asp Ile Ile Ile Asp His Phe Ala Phe Leu Glu Ile Lys Asp
305                 310                 315                 320
Ala Phe Leu Lys Asp Lys Arg Ala Arg Leu Glu Tyr Phe Lys Lys Leu
                325                 330                 335
Phe Gln Gly His Pro Cys Glu Phe Asp
            340                 345
```

(2) INFORMATION FOR SEQ ID NO:1622:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 262 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1622

```
Asn Ile Leu Lys Asn Cys Phe Lys Asp Thr Leu Val Ser Leu Ile Lys
1               5                   10                  15
Val Ser Gly Asp Lys Lys Val Ile Glu Val Ser Ile Pro Leu Thr Ser
            20                  25                  30
Ile Ser Gly Lys Ala Arg Val Lys Ile Arg His Ala Phe Ser Asp Tyr
        35                  40                  45
```

This Sheet Has Been Replaced



```
Gly Ile Ser Thr Ala Thr Arg Lys Ile Pro Phe Ser Leu Lys His Tyr
    50                  55                  60
Val Glu Trp Gln Ile Gly Tyr Asp Val Pro Ile Lys Asp Lys Glu Lys
65                  70                  75                  80
Phe Glu Leu Thr Thr Leu Lys Asp Glu Lys Tyr His Phe Leu Gly Ala
                85                  90                  95
Asn Asn Lys Val Lys Thr Leu Tyr Glu Leu Ser Glu Met Ile Tyr Tyr
            100                 105                 110
Ala Lys Arg Leu Gly Leu Ile Ser Leu Glu Asn Leu Glu Asn Thr Leu
        115                 120                 125
Lys Phe Leu Glu Lys Gln Lys Gln Phe Ile Glu Asp Asn Phe Met Ile
    130                 135                 140
Thr Arg Glu Arg Phe Arg Ser His Gln Phe Gly Gly Met Asp Phe Glu
145                 150                 155                 160
Leu Leu Arg Ile Ser Tyr Pro Leu Leu Ile His Ser Phe Asp Asp Asn
                165                 170                 175
Glu Leu Ser Glu Ile Val Ile Lys Glu Gln Gln Tyr Gly Ser Lys Thr
            180                 185                 190
Gln Ala Met Leu Tyr Phe Cys Phe Ser Ile Leu Glu Leu Lys Thr Ala
        195                 200                 205
Thr Pro Leu Leu Asn Arg Thr Ala Met Pro Lys Glu His Ala Leu Leu
    210                 215                 220
Ile Ile His Glu Thr Asn Ala Leu Val Phe Leu Glu Met Leu Lys Ile
225                 230                 235                 240
Phe Gly Leu Leu Ser Gln Val His His Asn Asp Val Leu Lys Ile Leu
                245                 250                 255
Glu Lys Ile Leu Gln Asn
            260
```

(2) INFORMATION FOR SEQ ID NO:1623:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 413 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

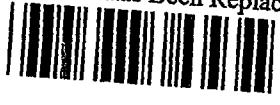
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...413

This Sheet Has Been Replaced



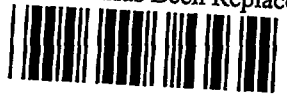
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1623

```
Leu Lys Ala Leu Asn Asp Cys Met Val Phe Phe His Lys Lys Ile Ile
1               5                   10                  15
Leu Asn Phe Ile Tyr Ser Leu Met Val Ala Phe Leu Phe His Leu Ser
            20                  25                  30
Tyr Gly Val Leu Leu Lys Ala Asp Gly Met Ala Lys Lys Gln Thr Leu
        35                  40                  45
Leu Val Gly Glu Arg Leu Val Trp Asp Lys Leu Thr Leu Leu Gly Phe
    50                  55                  60
Leu Glu Lys Asn His Ile Pro Gln Lys Leu Tyr Tyr Asn Leu Ser Ser
65                  70                  75                  80
Gln Asp Lys Glu Leu Ser Ala Glu Ile Gln Ser Asn Val Thr Tyr Tyr
                85                  90                  95
Thr Leu Arg Asp Ala Asn Asn Thr Leu Ile Gln Ala Leu Ile Pro Ile
            100                 105                 110
Ser Gln Asp Leu Gln Ile His Ile Tyr Lys Lys Gly Glu Asp Tyr Phe
```

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

(2) INFORMATION FOR SEQ ID NO:1624:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(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

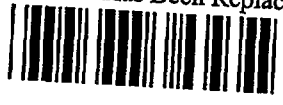
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1624

```
Gly Cys Leu Met Lys Ser Ile Leu Leu Phe Met Ile Phe Val Val Cys
1               5                   10                  15
Gln Leu Glu Gly Lys Lys Phe Ser Gln Asp Asn Phe Lys Val Asp Tyr
            20                  25                  30
Asn Tyr Tyr Leu Arg Lys Gln Asp Leu His Ile Ile Lys Thr Gln Asn
        35                  40                  45
```

```
Asp Leu Ser Asn Ala Trp Tyr Leu Pro Pro Gln Lys Ala Pro Lys Glu
    50                  55                  60
His Ser Trp Val Asp Phe Ala Lys Lys Tyr Leu Asn Met Met Asp Tyr
65                  70                  75                  80
Leu Gly Thr Tyr Phe Leu Pro Phe Tyr His Ser Phe Thr Pro Ile Phe
                85                  90                  95
Gln Trp Tyr His Pro Asn Ile Asn Pro Tyr Gln Arg Asn Glu Phe Lys
            100                 105                 110
Phe Gln Ile Ser Phe Arg Val Pro Val Phe Arg His Ile Leu Trp Thr
        115                 120                 125
Lys Gly Thr Leu Tyr Leu Ala Tyr Thr Gln Thr Asn Trp Phe Gln Ile
    130                 135                 140
Tyr Asn Asp Pro Gln Ser Ala Pro Met Arg Met Ile Asn Phe Met Pro
145                 150                 155                 160
Glu Leu Ile Tyr Val Tyr Pro Ile Asn Phe Lys Pro Phe Gly Gly Lys
                165                 170                 175
Ile Gly Asn Phe Ser Glu Ile Trp Ile Gly Trp Gln His Ile Ser Asn
            180                 185                 190
Gly Val Gly Gly Ala Gln Cys Tyr Gln Pro Phe Asn Lys Glu Gly Asn
        195                 200                 205
Pro Glu Asn Gln Phe Pro Gly Gln Pro Val Ile Val Lys Asp Tyr Asn
    210                 215                 220
Gly Gln Lys Asp Val Arg Trp Gly Gly Cys Arg Ser Val Ser Ala Gly
225                 230                 235                 240
Asn Ala Leu Cys Phe Val Trp Cys Gly Lys Arg Glu Ala
                245                 250
```

(2) INFORMATION FOR SEQ ID NO:1625:

This Sheet Has Been Replaced



(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:1625

```
Met Asn Arg Ala Trp Ile Lys Lys Lys Met Lys Lys Ile Lys Leu Thr
1               5                   10                  15
Lys Arg Met Ile Ala Thr Ala Lys Lys Ala Leu Ser Lys Ser Tyr Gly
            20                  25                  30
Tyr Cys Leu Val Gly Arg Phe Leu Ile Phe Phe Leu Arg Phe Cys Ile
        35                  40                  45
Phe Phe Trp His Ala Gly Lys Lys Ser Tyr Cys Pro Ser Leu Ala Val
    50                  55                  60
Lys Lys Thr Arg Lys Pro Gly Cys Arg Gly Ile Glu Ser Phe Tyr Gln
65                  70                  75                  80
Pro Ser Lys
```

(2) INFORMATION FOR SEQ ID NO:1626:

(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:1626

```
Arg Ile Glu Trp Gly Asn Arg His Cys Gly Ala Leu Ser His Ala Asn
1               5                  10                  15
Ser Val Ser Met Leu Leu Leu Phe Gly Ala Phe Leu Ser Ile Asn Leu
            20                  25                  30
Gly Ile Leu Asn Leu Leu Pro Ile Pro Ala Leu Asp Gly Ala Gln Met
        35                  40                  45
Leu Gly Val Val Phe Lys Asn Ile Phe His Ile Ala Leu Pro Thr Pro
    50                  55                  60
Ile Gln Asn Ala Leu Trp Leu Val Gly Val Gly Phe Leu Val Phe Val
65                  70                  75                  80
Met Phe Leu Gly Leu Phe Asn Asp Ile Thr Arg Leu Leu
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:1627:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 424 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1627

```
Asn Leu Gly Gly Ala Ala Asn Val Ala Asn Asn Leu Thr Ser Leu Lys
1               5                  10                  15
Ala Lys Val Phe Leu Cys Gly Val Val Gly Asp Asp Leu Lys Gly Lys
            20                  25                  30
His Phe Ile Ser Thr Leu Asn Ser Ile Arg Ile Asp Thr Ser Gly Val
        35                  40                  45
Leu Ile Asp Lys Thr Arg Cys Thr Thr Leu Lys Thr Arg Ile Ile Ala
    50                  55                  60
Gln Asn Gln Gln Ile Val Arg Val Asp Lys Glu Ile Lys Asp Pro Leu
65                  70                  75                  80
Asn Ala Asp Leu Arg Lys Asn Leu Leu Asp Phe Ile Ala Glu Lys Ile
                85                  90                  95
Gln Glu Ile Asp Gly Val Ile Leu Ser Asp Tyr Asn Lys Gly Val Leu
            100                 105                 110
```

```
Asp Phe Glu Leu Thr Gln Thr Ile Ile Thr Leu Ala Asn Lys His His
        115                 120                 125
Lys Leu Ile Leu Cys Asp Pro Lys Gly Lys Asp Tyr Ser Lys Tyr Ser
    130                 135                 140
His Ala Ser Leu Ile Thr Pro Asn Arg Ala Glu Leu Glu Gln Ala Leu
145                 150                 155                 160
His Leu Lys Leu Asp Ser His Ala Asn Leu Ser Lys Ala Leu Gln Ile
                165                 170                 175
Leu Gln Glu Thr Tyr His Ile Ala Met Pro Leu Val Thr Leu Ser Glu
            180                 185                 190
Gln Gly Ile Ala Phe Leu Glu Lys Gly Glu Leu Val Asn Cys Pro Thr
        195                 200                 205
Ile Ala Lys Glu Val Tyr Asp Val Thr Gly Ala Gly Asp Thr Val Ile
    210                 215                 220
Ala Ser Leu Thr Leu Ser Leu Leu Glu Ser Lys Ser Leu Lys Glu Ala
225                 230                 235                 240
Cys Glu Phe Ala Asn Ala Ala Ala Ala Val Val Val Gly Lys Met Gly
                245                 250                 255
Ser Ala Leu Ala Ser Leu Glu Glu Ile Ala Leu Ile Leu Asn Gln Thr
            260                 265                 270
His Pro Lys Ile Leu Pro Leu Glu Lys Leu Leu Glu Thr Leu Glu Arg
        275                 280                 285
Asn Gln Gln Lys Ile Val Phe Thr Asn Gly Cys Phe Asp Ile Leu His
    290                 295                 300
Lys Gly His Ala Ser Tyr Leu Gln Lys Ala Lys Ala Leu Gly Asp Ile
305                 310                 315                 320
Leu Val Val Gly Leu Asn Ser Asp Asn Ser Ile Lys Arg Leu Lys Gly
                325                 330                 335
Asp Lys Arg Pro Ile Val Ser Glu Lys Asp Arg Ala Phe Leu Leu Ala
            340                 345                 350
Ser Leu Ser Cys Val Asp Tyr Val Val Val Phe Gly Glu Asp Thr Pro
        355                 360                 365
Ile Lys Leu Ile Gln Ala Leu Lys Pro Asp Ile Leu Val Lys Gly Ala
    370                 375                 380
Asp Tyr Leu Asn Lys Glu Val Ile Gly Ser Glu Leu Ala Lys Glu Thr
385                 390                 395                 400
Arg Leu Ile Glu Phe Glu Glu Gly Tyr Ser Thr Ser Ala Ile Ile Glu
                405                 410                 415
Lys Ile Lys Arg Thr His Asn Asp
            420
```

(2) INFORMATION FOR SEQ ID NO:1628:

This Sheet Has Been Replaced



(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:1628

```
Gly Ser Leu Met Val Asn Val Phe Phe Lys Gln Gln Lys Phe Val Ile
1               5                   10                  15
Lys Lys Arg Phe Asn Asp Phe Asn Gly Phe Asp Ile Glu Glu Asn Glu
```

```
            20                  25                  30
Val Leu Trp Phe Glu Leu Ile Asn Pro Thr Pro Asn Glu Leu Ala Thr
        35                  40                  45
Leu Ser Gln Glu Tyr Ala Ile His Tyr Asn Thr Asp His Ser Gln Arg
    50                  55                  60
Val Ser Ser Val Thr Lys Tyr Trp Glu Asp Ser Ser Ser Val Thr Ile
65                  70                  75                  80
Asn Ala Phe Phe Thr Asn Gln Asp Glu Asn Glu Thr Phe His Met Glu
                85                  90                  95
Met Ala Thr Phe Ile Leu Ser Asn Asn Ile Leu Phe Thr Ile Tyr Tyr
            100                 105                 110
Gly Thr Leu Glu Ile Phe Asp Ser Ile Gln Lys Lys Val Leu Ala Ser
        115                 120                 125
Pro Lys Lys Phe Glu Asp Gly Phe Asp Ile Leu Thr Lys Ile Phe Glu
    130                 135                 140
Val Tyr Phe Glu Lys Gly Val Glu Cys Leu Glu Trp Ile Asn Lys Gln
145                 150                 155                 160
Thr Ser Leu Leu Arg Lys Asn Ile Ile Phe Lys Glu Thr Ser Thr His
                165                 170                 175
Asp Asp Ile Leu Val Arg Leu Ser Asn Leu Gln Glu Phe Asn Val Ala
            180                 185                 190
Leu Arg Asp Ser Phe Phe Asp Lys Arg Arg Ile Ile Thr Ala Leu Leu
        195                 200                 205
Arg Ser Asn Lys Val Asp Ser Asp Thr Lys Asn Asn Leu Asn Ile Ile
    210                 215                 220
Leu Thr Asp Phe Ser Ser Leu Val Glu Ser Thr Thr Val Asn Leu Asn
225                 230                 235                 240
Ser Leu Asp Asn Ile Gln Asn Leu Phe Ala Ser Gln Val Asn Val Glu
                245                 250                 255
Gln Asn Lys Ile Ile Lys Leu Phe Thr Val Ala Thr Met Ala Met Met
            260                 265                 270
Pro Pro Thr Leu Ile Gly Thr Ile Tyr Gly Met Asn Phe Lys Phe Met
        275                 280                 285
Pro Glu Leu Glu Trp Gln Tyr Gly Tyr Leu Phe Ala Leu Ile Val Met
    290                 295                 300
Ala Ile Ser Thr Ile Leu Pro Val Ile Tyr Phe Lys Lys Lys Gly Trp
305                 310                 315                 320
Leu
```

(2) INFORMATION FOR SEQ ID NO:1629:

This Sheet Has Been Replaced



(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:1629

```
Pro Phe Met Glu Phe Leu Ser Ser Leu Leu Asp Ala Leu Ser Thr Pro
1               5                   10                  15
His Gly Ile Val Ser Leu Ala Thr Leu Thr Leu Leu Glu Ile Val Leu
            20                  25                  30
```

```
Gly Ile Asp Asn Ile Ile Phe Ile Thr Val Met Val Tyr Lys L
        35                  40                  45
Lys His Gln Gln Asn Lys Val Met Ile Leu Gly Leu Gly Leu Ala Met
    50                  55                  60
Ile Thr Arg Ile Gly Leu Leu Gly Ser Leu Phe Phe Ile Ser His Leu
65                  70                  75                  80
Gln Lys Pro Leu Phe Ala Ile Ala Gly Met Ser Phe Ser Trp Arg Asp
                85                  90                  95
Val Val Leu Leu Leu Gly Gly Ala Phe Leu Ala Phe Lys Ala Leu Val
            100                 105                 110
Glu Leu Lys Glu Gln Ile Tyr Pro Lys Glu Lys Arg Gln Glu Lys Ala
        115                 120                 125
Phe Gly Phe Phe Ile Thr Leu Ile Glu Ile Met Phe Leu Asp Ile Val
    130                 135                 140
Phe Ser Leu Asp Ser Val Ile Thr Ala Ile Gly Ile Ala Lys His Leu
145                 150                 155                 160
Glu Val Met Ala Leu Ala Ile Ile Leu Ser Val Ile Val Met Met Phe
                165                 170                 175
Phe Ser Lys Ile Val Gly Asp Phe Ile Glu Lys His Tyr Arg Val Lys
            180                 185                 190
Thr Leu Ala Phe Val Phe Leu Leu Val Val Gly Val Phe Leu Phe Leu
        195                 200                 205
Glu Gly Leu His Leu His Ile Asn Lys Asn Tyr Leu Tyr Ala Gly Ile
    210                 215                 220
Gly Phe Ala Leu Leu Ile Glu Cys Leu Asn Ile Phe Ile Glu Lys Lys
225                 230                 235                 240
Met Lys Lys Ser
```

(2) INFORMATION FOR SEQ ID NO:1630:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

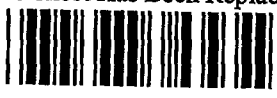
(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1630

This Sheet Has Been Replaced



```
Val Tyr Gly Phe Trp Ala Cys Val Leu Cys Gly Phe Lys Phe Gly Phe
1               5                   10                  15
Val Tyr Phe Ala Gln Thr Arg Ala Phe Gln Phe Arg Gln Asn His Ser
            20                  25                  30
Phe His Arg Tyr Gln Asn Glu His Asp Phe Arg Pro Val His Ala His
        35                  40                  45
Ser Arg Glu Phe Leu Arg Trp Gly Val Gly Glu Ile Leu Gly Ala Leu
    50                  55                  60
Leu Gly Val Gly Pro Arg Asn Leu Gly Val Asp Phe Tyr Leu Arg Leu
65                  70                  75                  80
Cys Leu Asp Leu Ala Phe Ala Phe Phe Arg Leu Ser Lys Leu Ala Leu
                85                  90                  95
Tyr Phe Ser Glu Gln Gln Arg Ala Arg Val Leu Phe Gly Phe Asn Asp
            100                 105                 110
Leu Phe Trp Arg Glu Leu Leu Pro Phe Trp Leu Ala Gln Leu Cys Arg
```

```
        115                 120                 125
Arg Ser Phe Ala Asp Pro Tyr Phe Phe Ile Leu Phe Gly Ser Asp Thr
    130                 135                 140
Phe Arg Ser Arg Ile Leu Ala Tyr Phe Lys Arg His
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:1631:

(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:1631

```
Arg Tyr Ser Asp Gln Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile Glu
1               5                   10                  15
Ala Ala Arg Ala Gly Glu His Gly Arg Gly Phe Ala Val Val Ala Asp
            20                  25                  30
Glu Val Arg Asn Leu Ala Gly Arg Thr Gln Lys Ser Leu Ala Glu Ile
        35                  40                  45
Asn Ser Thr Ile Met Val Ile Val Gln Glu Ile Asn Asp Val Ser Ser
    50                  55                  60
Gln Met Asn Leu Asn Ser Gln Lys Met Glu Arg Leu Ser Asp Met Ser
65                  70                  75                  80
Lys Ser Val Gln Glu Thr Tyr Glu Lys Met Ser Ser Asn Leu Ser Ser
                85                  90                  95
Val Val Leu Asp Ser Asn Gln Ser Met Asp Asp Tyr Ala Lys Ser Gly
            100                 105                 110
His Gln Ile Glu Ala Met Val Ser Asp Phe Ala Glu Val Glu Lys Val
        115                 120                 125
Ala Ser Lys Thr Leu Ala Asp Ser Ser Asp Ile Leu Asn Ile Ala Thr
    130                 135                 140
His Val Ser Gly Thr Thr Met Asn Leu Asp Lys Gln Val Asn Leu Phe
145                 150                 155                 160
Lys Thr
```

(2) INFORMATION FOR SEQ ID NO:1632:

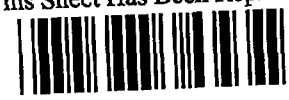
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1632

```
Ile Cys Leu Lys Leu Asn Gln Gly Gly Val Tyr Gln Lys Arg Val Gly
1               5                  10                  15
Leu Leu Lys Val Ser Val Ile Thr Ala Cys Phe Asn Ser Glu Lys Thr
            20                  25                  30
Ile Glu Asp Thr Ile Leu Ser Val Leu Asn Gln Thr Tyr Lys Asn Ile
        35                  40                  45
Glu Tyr Ile Ile Ile Asp Gly Ala Ser Ala Ile Ala Leu
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:1633:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 664 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1633

```
Asn His Ile Val Arg Gly Val Asp Cys Asp Arg Gly Val Ser Ile Leu
1               5                  10                  15
Gly Val Ser Leu Asn Ser Arg Val Lys Glu Ile Leu Lys Glu Ser Ala
            20                  25                  30
Leu His Ser Met Gln Asp Ser Leu His Phe Lys Val Lys Glu Val Gln
        35                  40                  45
Ser Val Leu Glu Asn Thr Tyr Thr Ser Met Gly Ile Val Lys Glu Met
    50                  55                  60
Leu Pro Glu Asp Thr Lys Arg Glu Ile Lys Ile Gln Leu Leu Lys Asn
65                  70                  75                  80
Phe Ile Leu Ala Asn Ser His Val Ala Gly Val Ser Met Phe Phe Lys
                85                  90                  95
Asp Arg Glu Asp Leu Arg Leu Thr Leu Leu Arg Asp Asn Asp Thr Ile
            100                 105                 110
Lys Leu Met Glu Asn Pro Ser Leu Gly Ser Asn Pro Leu Val Gln Lys
        115                 120                 125
Ala Met Lys Asn Lys Glu Ile Ser Lys Ser Leu Pro Tyr Tyr Arg Lys
    130                 135                 140
Met Pro Asn Gly Ala Glu Val Tyr Gly Val Asp Ile Leu Leu Pro Leu
145                 150                 155                 160
Phe Lys Glu Asn Thr Gln Glu Val Val Gly Val Leu Met Ile Phe Phe
                165                 170                 175
Ser Ile Asp Ser Phe Ser Asn Glu Ile Thr Lys Asn Arg Ser Asp Leu
            180                 185                 190
Phe Leu Ile Gly Val Lys Gly Lys Val Leu Leu Ser Ala Asn Lys Ser
        195                 200                 205
Leu Gln Asp Lys Ser Ile Thr Glu Ile Tyr Lys Ser Val Pro Lys Ala
    210                 215                 220
Thr Asn Glu Val Met Ala Ile Leu Glu Asn Gly Ser Lys Ala Thr Leu
```

```
225                 230                 235                 240
Glu Tyr Leu Asp Pro Phe Ser His Lys Glu Asn Phe Leu Ala Val Glu
                245                 250                 255
Thr Phe Lys Met Leu Gly Lys Thr Glu Ser Lys Asp Asn Leu Asn Trp
            260                 265                 270
Met Ile Ala Leu Ile Ile Glu Lys Asp Lys Val Tyr Glu Gln Val Gly
        275                 280                 285
Ser Val Arg Phe Val Val Val Ala Ala Ser Ala Ile Met Val Leu Ala
    290                 295                 300
Leu Ile Ile Ala Ile Thr Leu Leu Met Arg Ala Ile Val Ser Asn Arg
305                 310                 315                 320
Leu Glu Val Val Ser Ser Thr Leu Ser His Phe Phe Lys Leu Leu Asn
                325                 330                 335
Asn Gln Ala His Ser Ser Asp Ile Lys Leu Val Glu Ala Arg Ser Asn
            340                 345                 350
Asp Glu Leu Gly Arg Met Gln Thr Ala Ile Asn Lys Asn Ile Leu Gln
        355                 360                 365
Thr Gln Lys Thr Met Gln Glu Asp Trp Gln Ala Val Gln Asp Thr Ile
    370                 375                 380
Lys Val Val Ser Asp Val Lys Ala Gly Asn Phe Ala Val Arg Ile Thr
385                 390                 395                 400
Ala Glu Pro Ala Ser Pro Asp Leu Lys Glu Leu Arg Asp Ala Leu Met
                405                 410                 415
Asp His Ala Leu Phe Ala Arg Lys Arg Gly Thr His Met Pro Ser Ile
            420                 425                 430
Phe Lys Ile Phe Glu Ser Tyr Ser Gly Leu Asp Phe Arg Gly Arg Ile
        435                 440                 445
Gln Asn Ala Ser Gly Arg Val Glu Leu Val Thr Asn Ala Leu Gly Gln
    450                 455                 460
Glu Ile Gln Lys Met Leu Glu Thr Ser Ser Asn Phe Ala Lys Asp Leu
465                 470                 475                 480
Ala Asn Asp Ser Ala Asn Leu Lys Glu Cys Val Gln Asn Leu Glu Lys
                485                 490                 495
Ala Ser Asn Ser Gln His Lys Ser Leu Met Glu Thr Ser Lys Thr Ile
            500                 505                 510
Glu Asn Ile Thr Thr Ser Ile Gln Gly Val Ser Ser Gln Ser Glu Ala
        515                 520                 525
Met Ile Glu Gln Gly Lys Asp Ile Lys Ser Ile Val Glu Ile Ile Arg
    530                 535                 540
Asp Ile Ala Asp Gln Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile Glu
545                 550                 555                 560
Ala Ala Arg Ala Gly Glu His Gly Arg Gly Phe Ala Val Val Ala Asp
                565                 570                 575
Glu Val Arg Lys Leu Ala Glu Arg Thr Gln Lys Ser Leu Ser Glu Ile
            580                 585                 590
Glu Ala Asn Ile Asn Ile Leu Val Gln Ser Ile Ser Asp Thr Ser Glu
        595                 600                 605
Ser Ile Lys Asn Gln Val Lys Glu Val Glu Glu Ile Asn Ala Ser Ile
    610                 615                 620
Glu Ala Leu Arg Ser Val Thr Glu Gly Asn Leu Lys Ile Ala Ser Asp
625                 630                 635                 640
Ser Leu Glu Ile Ser Gln Glu Ile Asp Lys Val Ser Asn Asp Ile Leu
                645                 650                 655
Glu Asp Val Asn Lys Lys Gln Phe
            660
```

(2) INFORMATION FOR SEQ ID NO:1634:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 425 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1634

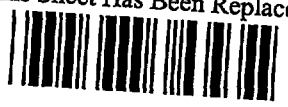
```
Arg Gly Glu Cys Tyr Phe Glu Arg Glu Ile Gly Leu Met Arg Lys Ile
1               5                  10                  15
Phe Ser Tyr Ile Ser Lys Val Leu Leu Phe Ile Gly Val Val Tyr Ala
            20                  25                  30
Glu Pro Asp Ser Lys Val Glu Ala Leu Glu Gly Arg Lys Gln Glu Ser
        35                  40                  45
Ser Leu Asp Lys Lys Ile Arg Gln Glu Leu Lys Ser Lys Glu Leu Lys
    50                  55                  60
Asn Lys Glu Leu Lys Asn Lys Asp Leu Lys Asn Lys Glu Glu Lys Lys
65                  70                  75                  80
Glu Thr Lys Ala Lys Arg Lys Pro Arg Ala Glu Val His His Gly Asp
                85                  90                  95
Ala Lys Asn Pro Thr Pro Lys Ile Thr Pro Pro Lys Ile Lys Gly Ser
            100                 105                 110
Ser Lys Gly Val Gln Asn Gln Gly Val Gln Asn Asn Ala Pro Lys Pro
        115                 120                 125
Glu Glu Lys Asp Thr Thr Pro Gln Ala Thr Glu Lys Asn Lys Glu Thr
    130                 135                 140
Ser Pro Ser Ser Gln Phe Asn Ser Ile Phe Gly Asn Pro Asn Asn Ala
145                 150                 155                 160
Thr Asn Asn Thr Leu Glu Asp Lys Val Val Gly Gly Ile Ser Leu Leu
                165                 170                 175
Val Asn Gly Ser Pro Ile Thr Leu Tyr Gln Ile Gln Glu Glu Gln Glu
            180                 185                 190
Lys Ser Lys Val Ser Lys Ala Gln Ala Arg Asp Arg Leu Ile Ala Glu
        195                 200                 205
Arg Ile Lys Asn Gln Glu Ile Glu Arg Leu Lys Ile His Val Asp Asp
    210                 215                 220
Asp Lys Leu Asn Gln Glu Met Ala Met Met Ala Gln Gln Gln Gly Met
225                 230                 235                 240
Asp Leu Asp His Phe Lys Gln Met Leu Met Ala Glu Gly His Tyr Lys
                245                 250                 255
Leu Tyr Arg Asp Gln Leu Lys Glu His Leu Glu Met Gln Glu Leu Leu
            260                 265                 270
Arg Asn Ile Leu Leu Thr Asn Val Asp Thr Ser Ser Glu Thr Lys Met
        275                 280                 285
Arg Glu Tyr Tyr Asn Lys His Lys Glu Gln Phe Ser Ile Pro Thr Glu
    290                 295                 300
Ile Glu Thr Val Arg Tyr Thr Ser Thr Asn Gln Glu Asp Leu Glu Arg
305                 310                 315                 320
Ala Met Ala Asp Pro Asn Leu Glu Val Pro Gly Val Ser Lys Ala Asn
                325                 330                 335
Glu Lys Ile Glu Met Lys Thr Leu Asn Pro Gln Ile Ala Gln Val Phe
            340                 345                 350
Ile Ser His Glu Gln Gly Ser Phe Thr Pro Val Met Asn Gly Gly Gly
        355                 360                 365
Gly Gln Phe Ile Thr Phe Tyr Ile Lys Glu Lys Arg Gly Lys Asn Glu
    370                 375                 380
Val Ser Phe Ser Gln Ala Lys Gln Phe Ile Ala Gln Lys Leu Val Glu
385                 390                 395                 400
Glu Ser Lys Asp Lys Ile Leu Glu Glu His Phe Glu Lys Leu Arg Val
                405                 410                 415
Lys Ser Arg Ile Val Met Ile Arg Glu
```


This Sheet Has Been Replaced



420 425

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1635:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

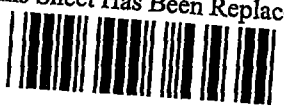
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1635

```
Ile Val Gln His Phe Asn Phe Leu Tyr Lys Asp Ser Leu Phe Ser Ile
1               5                  10                  15
Ala Leu Phe Thr Phe Ile Ile Ala Leu Val Ile Leu Leu Glu Gln Ala
            20                  25                  30
Arg Ala Tyr Phe Thr Arg Lys Arg Asn Lys Lys Phe Leu Gln Lys Phe
        35                  40                  45
Ala Gln Asn Gln Asn Ala Tyr Ala Ser Ser Glu Asn Leu Asp Glu Leu
    50                  55                  60
Leu Lys His Ala Lys Ile Ser Ser Leu Met Phe Leu Ala Arg Ala Tyr
65                  70                  75                  80
Ser Lys Ala Asp Val Glu Met Ser Ile Glu Ile Leu Lys Gly Leu Leu
                85                  90                  95
Asn Arg Pro Leu Lys Asp Glu Glu Lys Ile Ala Val Leu Asp Leu Leu
            100                 105                 110
Ala Lys Asn Tyr Phe Ser Val Gly Tyr Leu Gln Lys Thr Lys Asp Thr
        115                 120                 125
Val Lys Glu Ile Leu Arg Phe Ser Pro Arg Asn Val Glu Ala Leu Leu
    130                 135                 140
Lys Leu Leu His Ala Tyr Glu Leu Glu Lys Asp Tyr Ser Lys Ala Leu
145                 150                 155                 160
Glu Thr Leu Glu Cys Leu Glu Glu Leu Glu Val Pro Lys Ile Glu Thr
                165                 170                 175
Ile Lys Asn Tyr Leu Tyr Leu Met His Leu Ile Glu Asn Lys Glu Asp
            180                 185                 190
Ala Ala Lys Ile Leu His Val Ser Lys Ala Ser Leu Asp Leu Lys Lys
        195                 200                 205
Ile Ala Leu Asn His Leu Lys Ser His Asp Glu Asn Leu Phe Trp Gln
    210                 215                 220
Glu Ile Asp Thr Thr Glu Arg Leu Glu Asn Val Ile Asp Leu Leu Trp
225                 230                 235                 240
Asp Met Asn Ile Pro Ala Phe Ile Leu Glu Lys His Ala Leu Leu Gln
                245                 250                 255
Asp Ile Ala Arg Ser Gln Gly Leu Leu Leu Asp His Lys Pro Cys Gln
            260                 265                 270
Ile Phe Glu Leu Glu Val Leu Arg Ala Leu Leu His Ser Pro Ile Lys
        275                 280                 285
Ala Ser Leu Thr Phe Glu Tyr Arg Cys Lys His Cys Lys Gln Ile Phe
    290                 295                 300
Pro Phe Glu Ser His Arg Cys Pro Val Cys Tyr Gln Leu Ala Phe Met
305                 310                 315                 320
Asp Met Val Leu Lys Ile Ser Lys Lys Thr His Ala Met Gly Val Asp
                325                 330                 335
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1636:

(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:1636

```
Ile Arg Gly Ala Lys Thr Gly Gln Asn Asp His Leu Lys Gly Lys Met
1               5                  10                  15
Met Lys Asn Lys Arg Ser Gln Asn Ser Pro Tyr Val Thr Pro Asp Asn
            20                  25                  30
Pro Tyr Leu Thr Leu Glu Lys Ala Leu Gly Tyr Ser Phe Lys Asp Lys
        35                  40                  45
Arg Leu Leu Glu Gln Ala Leu Thr His Lys Ser Cys Lys Leu Ala Leu
    50                  55                  60
Asn Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Val Leu Gly Leu Val
65                  70                  75                  80
Ile Gly Glu Leu Leu Tyr His Lys Phe Tyr Gln Tyr Asp Glu Gly Lys
                85                  90                  95
Leu Ser Lys Leu Arg Ala Ser Ile Val Ser Ala His Gly Phe Thr Lys
            100                 105                 110
Leu Ala Lys Ala Ile Ala Leu Gln Asp Tyr Leu Arg Val Ser Ser Ser
        115                 120                 125
Glu Glu Ile Ser Lys Gly Arg Glu Lys Pro Ser Ile Leu Ser Ser Ala
    130                 135                 140
Phe Glu Ala Leu Met Ala Gly Val Tyr Leu Glu Ala Gly Leu Ala Lys
145                 150                 155                 160
Val Arg Lys Ile Ile Gln Asn Leu Leu Asn Arg Ala Tyr Lys Arg Leu
                165                 170                 175
Asp Leu Glu His Leu Phe Met Asp Tyr Lys Thr Ala Leu Gln Glu Leu
            180                 185                 190
Thr Gln Ala Gln Phe Cys Val Ile Pro Thr Tyr Gln Leu Leu Gln Glu
        195                 200                 205
Lys Gly Pro Asp His His Lys Glu Phe Glu Met Ala Leu Tyr Ile Gln
    210                 215                 220
Asp Lys Met Tyr Ala Thr Ala Lys Gly Lys Ser Lys Lys Glu Ala Glu
225                 230                 235                 240
Gln Gln Cys Ala Tyr Gln Ala Leu Gln Lys Leu Lys Glu Val Lys
                245                 250                 255
```

(2) INFORMATION FOR SEQ ID NO:1637:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(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:1637

```
Ala His Gln Ser Ser Arg Gly Val Ser Met Ile Leu Ala Cys Asp Val
1               5                  10                  15
Gly Leu Lys Arg Ile Gly Ile Ala Ala Leu Leu Asn Gly Val Ile Leu
            20                  25                  30
Pro Leu Glu Ala Ile Leu Arg His Asn Arg Asn Gln Ala Ser Arg Asp
        35                  40                  45
Leu Ser Asp Leu Leu Arg Lys Lys Asp Ile Gln Val Leu Val Val Gly
    50                  55                  60
Lys Pro Asn Glu Ser Tyr Ala Asp Thr His Ala Arg Ile Glu His Phe
65                  70                  75                  80
Ile Lys Leu Val Asp Phe Lys Gly Glu Ile Val Phe Ile Asn Glu Asp
                85                  90                  95
Asn Ser Ser Val Glu Ala Tyr Glu Asn Leu Glu His Leu Gly Lys Lys
            100                 105                 110
Asn Lys Arg Ile Ala Thr Lys Asp Gly Arg Leu Asp Ser Leu Ser Ala
        115                 120                 125
Cys Arg Ile Leu Glu Arg Tyr Cys Gln Gln Val Leu Lys Lys Gly
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:1638:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 577 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1638

```
Lys Asn Glu Asn Phe Ile Lys Val Leu Ile Leu Asp Leu Lys Val Leu
1               5                  10                  15
Leu Gln Arg Ile Val Asp Phe Phe Ile Lys Leu Asn Lys Lys Gln Lys
            20                  25                  30
Ile Ala Leu Ile Ala Ala Gly Val Leu Ile Thr Ala Leu Leu Val Phe
        35                  40                  45
Leu Leu Leu Tyr Pro Phe Lys Glu Lys Asp Tyr Ala Gln Gly Gly Tyr
    50                  55                  60
Gly Val Leu Phe Glu Arg Leu Asp Ser Ser Asp Asn Ala Leu Ile Leu
65                  70                  75                  80
Gln His Leu Gln Gln Asn Gln Ile Pro Tyr Lys Val Leu Lys Asp Asp
                85                  90                  95
Thr Ile Leu Val Pro Lys Asp Lys Val Tyr Glu Glu Arg Ile Thr Leu
            100                 105                 110
```

```
Ala Ser Gln Gly Ile Pro Lys Thr Ser Lys Val Gly Phe Glu Ile Phe
        115                 120                 125
Asp Thr Lys Asp Phe Gly Ala Thr Asp Phe Asp Gln Asn Ile Lys Leu
    130                 135                 140
Ile Arg Ala Ile Glu Gly Glu Leu Ser Arg Thr Ile Glu Ser Leu Asn
145                 150                 155                 160
Pro Ile Leu Lys Ala Asn Val His Ile Ala Ile Pro Lys Asp Ser Val
                165                 170                 175
Phe Val Ala Lys Glu Val Pro Pro Ser Ala Ser Val Met Leu Lys Leu
            180                 185                 190
Lys Pro Asp Met Lys Leu Ser Pro Thr Gln Ile Leu Gly Ile Lys Asn
        195                 200                 205
Leu Ile Ala Ala Ala Val Pro Lys Leu Thr Ile Glu Asn Val Lys Ile
    210                 215                 220
Val Asn Glu Asn Gly Glu Ser Ile Gly Glu Gly Asp Ile Leu Glu Asn
225                 230                 235                 240
Ser Lys Glu Leu Ala Leu Glu Gln Leu Arg Tyr Lys Gln Asn Phe Glu
                245                 250                 255
Asn Ile Leu Glu Asn Lys Ile Val Asn Ile Leu Ala Pro Ile Val Gly
            260                 265                 270
Gly Lys Asn Lys Val Val Ala Arg Val Asn Ala Glu Phe Asp Phe Ser
        275                 280                 285
Gln Lys Lys Ser Thr Lys Glu Thr Phe Asp Pro Asn Asn Val Val Arg
    290                 295                 300
Ser Glu Gln Asn Leu Glu Glu Lys Lys Glu Gly Ala Pro Lys Lys Gln
305                 310                 315                 320
Val Gly Gly Val Pro Gly Val Val Ser Asn Ile Gly Pro Val Gln Gly
                325                 330                 335
Leu Lys Asp Asn Lys Glu Pro Glu Lys Tyr Glu Lys Ser Gln Asn Thr
            340                 345                 350
Thr Asn Tyr Glu Val Gly Lys Thr Ile Ile Glu Ile Lys Gly Glu Phe
        355                 360                 365
Gly Thr Leu Met Arg Leu Asn Ala Ala Val Val Val Asp Gly Lys Tyr
    370                 375                 380
Lys Ile Ala Leu Glu Asp Gly Ala Asn Ala Leu Glu Tyr Glu Pro Leu
385                 390                 395                 400
Ser Asp Glu Ser Leu Lys Lys Ile Asn Ala Leu Val Lys Gln Ala Ile
                405                 410                 415
Gly Asp Asn Gln Asn Arg Gly Asp Asp Val Ala Val Ser Asn Phe Glu
            420                 425                 430
Phe Asn Pro Met Ala Pro Met Ile Asp Asn Ala Thr Leu Ser Glu Lys
        435                 440                 445
Ile Met His Lys Thr Gln Lys Ile Leu Gly Ser Phe Thr Pro Leu Ile
    450                 455                 460
Lys Tyr Ile Leu Val Phe Ile Val Leu Phe Ile Phe Tyr Lys Lys Val
465                 470                 475                 480
Ile Val Pro Phe Ser Glu Arg Met Leu Glu Val Val Pro Asp Glu Asp
                485                 490                 495
Lys Glu Val Lys Ser Met Phe Glu Glu Met Asp Glu Glu Glu Asp Glu
            500                 505                 510
Leu Asn Lys Leu Gly Asp Leu Arg Lys Lys Val Glu Asp Gln Leu Gly
        515                 520                 525
Leu Asn Ala Ser Phe Ser Glu Glu Glu Val Arg Tyr Glu Ile Ile Leu
    530                 535                 540
Glu Lys Ile Arg Gly Thr Leu Lys Glu Arg Pro Asp Glu Ile Ala Thr
545                 550                 555                 560
Leu Phe Lys Leu Leu Ile Lys Asp Glu Ile Ser Ser Asp Ser Ala Lys
                565                 570                 575
Gly
```

(2) INFORMATION FOR SEQ ID NO:1639:

(i) SEQUENCE CHARACTERISTICS:

This Sheet Has Been Replaced



(A) LENGTH: 199 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1639

```
Lys Trp Cys Gly Tyr Cys Glu Arg Arg Ser Val Arg Arg Gly Tyr Tyr
1               5                  10                  15
Arg Ser Arg Lys Arg Leu Thr Lys Asn His His Ala Phe Ala Cys Ser
            20                  25                  30
Leu Asp Phe Ile Tyr Pro Thr Asn Asn His Lys Val Ile Gln Glu Ile
        35                  40                  45
Ala Gln Asn Gly Leu Ile Leu Ser Glu His Glu Lys Asp Phe Met Phe
    50                  55                  60
Ile Lys Gly Phe Phe Leu Val Arg Asn Cys Leu Val Ile Ala Leu Thr
65                  70                  75                  80
Asp Ala Val Ile Ile Pro Gln Ala Asp Leu Lys Ser Gly Ser Met Ser
                85                  90                  95
Ser Val Arg Leu Ala Gln Lys Tyr Gln Lys Pro Leu Phe Val Leu Pro
            100                 105                 110
Gln Arg Leu Asn Glu Ser Asp Gly Thr Asn Glu Leu Leu Glu Lys Gly
        115                 120                 125
Gln Ala Gln Gly Ile Phe Asn Ile Gln Asn Phe Ile Asn Thr Leu Leu
    130                 135                 140
Lys Asp Tyr His Leu Lys Glu Met Pro Glu Met Lys Asp Glu Phe Leu
145                 150                 155                 160
Glu Tyr Cys Ala Lys Asn Pro Ser Tyr Glu Glu Ala Tyr Leu Lys Phe
                165                 170                 175
Gly Asp Lys Leu Leu Glu Tyr Glu Leu Leu Gly Lys Ile Lys Arg Ile
            180                 185                 190
Asn His Leu Val Val Leu Ala
        195
```

(2) INFORMATION FOR SEQ ID NO:1640:

(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:1640

This Sheet Has Been Replaced



```
Arg Leu Lys Met Ala Thr Lys Leu Thr Pro Lys Gln Lys Ala Gln Leu
1               5                  10                  15
Asp Glu Leu Ser Met Ser Glu Lys Ile Ala Ile Leu Leu Ile Gln Val
            20                  25                  30
Gly Glu Asp Thr Thr Gly Glu Ile Leu Arg His Leu Asp Ile Asp Ser
        35                  40                  45
Ile Thr Glu Ile Ser Lys Gln Ile Val Gln Leu Asn Gly Thr Asp Lys
    50                  55                  60
Gln Ile Gly Ala Ala Val Leu Glu Glu Phe Phe Ala Ile Phe Gln Ser
65                  70                  75                  80
Asn Gln Tyr Ile Asn Thr Gly Gly Leu Glu Tyr Ala Arg Glu Leu Leu
                85                  90                  95
Thr Arg Thr Leu Gly Ser Glu Glu Ala Arg Lys Val Met Asp Lys Leu
            100                 105                 110
Thr Lys Ser Leu Gln Thr Gln Lys Asn Phe Ala Tyr Leu Gly Lys Ile
        115                 120                 125
Lys Pro Gln Gln Leu Ala Asp Phe Ile Ile Asn Glu His Pro Gln Thr
    130                 135                 140
Ile Ala Leu Ile Leu Ala His Met Glu Ala Pro Asn Ala Ala Glu Thr
145                 150                 155                 160
Leu Ser Tyr Phe Pro Asp Glu Met Lys Ala Glu Ile Ser Ile Arg Met
                165                 170                 175
Ala Asn Leu Gly Glu Ile Ser Pro Gln Val Val Lys Arg Val Ser Thr
            180                 185                 190
Val Leu Glu Asn Lys Leu Glu Ser Leu Thr Ser Tyr Lys Ile Glu Val
        195                 200                 205
Gly Gly Leu Arg Ala Val Ala Glu Ile Phe Asn Arg Leu Gly Gln Lys
    210                 215                 220
Ser Ala Lys Thr Thr Leu Ala Arg Ile Glu Ser Val Asp Asn Lys Leu
225                 230                 235                 240
Ala Gly Ala Ile Lys Glu Met Met Phe Thr Phe Glu Asp Ile Ala Lys
                245                 250                 255
Leu Asp Asn Phe Ala Ile Met Arg Asp Phe Lys Ser Gly Gly Leu Lys
            260                 265                 270
Lys Thr Gly Leu
        275
```

(2) INFORMATION FOR SEQ ID NO:1641:

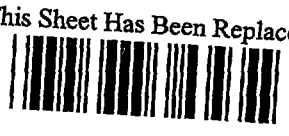
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 194 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1641

```
Arg Ser Leu Gly Lys Gly Arg Pro Met Asn Lys Lys Asn Ser Val Ile
1               5                  10                  15
Ser Gly Leu Met Asn Phe Phe Ser Glu Lys Asn Glu Arg Trp Leu Leu
            20                  25                  30
Ala His Arg His Thr Arg Gly Phe Val Ile Val Ala Trp Leu Phe Arg
        35                  40                  45
Phe Lys Ser Ile Ala Phe Ser Ile Leu Ile Thr Leu Leu Val Ile Leu
```

```
    50                  55                  60
Val Asp Ile Trp Val Tyr Ser Asp Val Arg Gln Phe Leu Leu Asp Thr
65                  70                  75                  80
Ser Ser Ser Phe Ile Trp Leu Leu Ile Ala Leu Leu Ile Lys Trp Gly
                85                  90                  95
Val Ile Val Ile Ser Ala Arg Lys Cys Tyr Gln Phe Ser Gln Lys Met
            100                 105                 110
Phe Ala Leu Ile Gln Arg Lys Arg Gln Ile Arg Glu Asn Leu Lys Asn
        115                 120                 125
Arg Ser Asn Arg Lys Asp Ala Lys Asn Phe Glu Lys Leu Ser Asn Ile
    130                 135                 140
Ala Glu Glu Ile Ile Ser Lys Lys Gln Glu Glu Ser His His Lys Glu
145                 150                 155                 160
Asp Ser Asn Asp Glu Asn His Lys Asp Lys Leu Ser Asn Ile Thr Glu
                165                 170                 175
Glu Met Ile Leu Lys Lys Gln Glu Glu Leu Lys Ala Arg Lys Asp Lys
            180                 185                 190
Gly Asp
```

(2) INFORMATION FOR SEQ ID NO:1642:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 539 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1642

```
Leu Met Asp Arg Ala Lys Phe Ile Phe Val Thr Gly Gly Val Leu Ser
1               5                   10                  15
Ser Leu Gly Lys Gly Ile Ser Ser Ser Ser Ile Ala Thr Leu Leu Gln
            20                  25                  30
His Cys Asn Tyr Gln Val Ser Ile Leu Lys Ile Asp Pro Tyr Ile Asn
        35                  40                  45
Ile Asp Pro Gly Thr Met Ser Pro Leu Glu His Gly Glu Val Phe Val
    50                  55                  60
Thr Ser Asp Gly Ala Glu Thr Asp Leu Asp Ile Gly His Tyr Glu Arg
65                  70                  75                  80
Phe Leu Asn Arg Asn Leu Thr Arg Leu Asn Asn Phe Thr Thr Gly Gln
                85                  90                  95
Ile Phe Ser Ser Val Ile Glu Asn Glu Arg Lys Gly Glu Tyr Leu Gly
            100                 105                 110
Lys Thr Ile Gln Ile Val Pro His Val Thr Asp Glu Ile Lys Arg Arg
        115                 120                 125
Ile Lys Ser Ala Ala Lys Gly Leu Asp Phe Leu Ile Val Glu Val Gly
    130                 135                 140
Gly Thr Val Gly Asp Met Glu Gly Met Phe Tyr Val Glu Pro Ile Arg
145                 150                 155                 160
Gln Leu Lys Leu Glu Leu Arg Asn Lys Ala Leu Ile Asn Met His Val
                165                 170                 175
Thr Leu Met Pro Tyr Ile Arg Ala Thr Ser Glu Leu Arg Ser Arg Pro
            180                 185                 190
```

```
Thr Gln His Ser Val Gln Glu Leu Arg Arg Leu Gly Val Thr Pro Gln
        195                 200                 205
Ile Ile Leu Ala Arg Ser Pro Lys Pro Leu Asp Lys Glu Leu Lys Lys
    210                 215                 220
Lys Ile Ala Leu Ser Cys Asp Val Glu Gln Asp Ser Val Ile Val Ala
225                 230                 235                 240
Thr Asp Thr Lys Ser Ile Tyr Ala Cys Pro Ile Leu Phe Leu Gln Glu
                245                 250                 255
Gly Ile Leu Thr Pro Ile Ala Arg Arg Phe Asn Leu Asn Lys Leu His
            260                 265                 270
Pro Lys Met Ala Ala Trp Asn Thr Leu Val Glu Lys Ile Ile Ala Pro
        275                 280                 285
Lys His Lys Val Lys Ile Gly Phe Val Gly Lys Tyr Leu Ser Leu Lys
    290                 295                 300
Glu Ser Tyr Lys Ser Leu Ile Glu Ala Leu Ile His Ala Gly Ala His
305                 310                 315                 320
Leu Asp Thr Gln Val Asn Ile Glu Trp Leu Asp Ser Glu Asn Phe Asn
                325                 330                 335
Glu Lys Thr Asp Leu Glu Gly Val Asp Ala Ile Leu Val Pro Gly Gly
            340                 345                 350
Phe Gly Glu Arg Gly Ile Glu Gly Lys Ile Cys Ala Ile Gln Arg Ala
        355                 360                 365
Arg Leu Glu Lys Leu Pro Phe Leu Gly Ile Cys Leu Gly Met Gln Leu
    370                 375                 380
Ala Ile Val Glu Phe Cys Arg Asn Val Leu Gly Leu Lys Gly Ala Asn
385                 390                 395                 400
Ser Thr Glu Phe Asn Gln Arg Cys Glu Tyr Pro Val Val Tyr Leu Ile
                405                 410                 415
Glu Asp Phe Met Asp Gln Asn His Gln Lys Gln Val Arg Thr Tyr Asn
            420                 425                 430
Ser Pro Leu Gly Gly Thr Met Arg Leu Gly Glu Tyr Glu Cys Glu Ile
        435                 440                 445
Met Pro Asn Ser Leu Leu Glu Lys Ala Tyr Lys Lys Pro Asn Ile Lys
    450                 455                 460
Glu Arg His Arg His Arg Tyr Glu Ile Asn Pro Lys Tyr Arg Gln Glu
465                 470                 475                 480
Trp Glu Asn Lys Gly Leu Lys Val Val Gly Phe Gly Ala Asn His Leu
                485                 490                 495
Ile Glu Ala Ile Glu Leu Glu Asp His Pro Phe Phe Val Gly Val Gln
            500                 505                 510
Phe His Pro Glu Phe Thr Ser Arg Leu Gln Ser Pro Asn Pro Ile Ile
        515                 520                 525
Leu Asp Phe Ile Lys Ser Ala Leu His Lys Ser
    530                 535
```

(2) INFORMATION FOR SEQ ID NO:1643:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 369 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1643

```
Ile Trp Arg Gly Cys Gly Ser His Asp Arg Val His Asp Glu Phe Val
1               5                  10                  15
Phe Ala Arg Tyr Thr Lys Ala Asn Tyr Glu Asn Thr Tyr Tyr Asp Thr
            20                  25                  30
Glu Phe Ser His Leu Lys Glu Ala Ser Ala Tyr Phe Pro Asp Ile Asp
        35                  40                  45
Glu Ala Ser Leu Phe Thr Asp Leu Gln Asp Tyr Phe Asn Ser Trp Lys
    50                  55                  60
Glu Leu Ser Lys Asn Ala Lys Asp Ser Ala Gln Lys Gln Ala Leu Ala
65                  70                  75                  80
Gln Lys Thr Glu Ala Leu Thr His Asn Ile Lys Asp Thr Arg Glu Arg
                85                  90                  95
Leu Thr Thr Leu Gln His Lys Ala Ser Glu Glu Leu Lys Ser Val Ile
            100                 105                 110
Lys Glu Val Asn Ser Leu Gly Ser Gln Ile Ala Glu Ile Asn Lys Arg
        115                 120                 125
Ile Lys Glu Val Glu Asn Asn Lys Ser Leu Lys His Ala Asn Glu Leu
    130                 135                 140
Arg Asp Lys Arg Asp Glu Leu Glu Phe His Leu Arg Glu Leu Leu Gly
145                 150                 155                 160
Gly Asn Val Phe Lys Ser Ser Ile Lys Thr His Ser Leu Thr Asp Lys
                165                 170                 175
Asp Ser Ala Asp Phe Asp Glu Ser Tyr Asn Leu Asn Ile Gly His Gly
            180                 185                 190
Phe Asn Ile Ile Asp Gly Ser Ile Phe His Pro Leu Val Val Lys Glu
        195                 200                 205
Ser Glu Asn Lys Gly Gly Leu Asn Gln Val Tyr Phe Gln Ser Asp Asp
    210                 215                 220
Phe Lys Leu Thr Asn Ile Thr Asp Lys Leu Asn Gln Gly Lys Val Gly
225                 230                 235                 240
Ala Leu Leu Asn Val Tyr Asn Asp Gly Ser Asn Gly Thr Leu Lys Gly
                245                 250                 255
Lys Leu Gln Asp Tyr Ile Asp Leu Leu Asp Ser Phe Ala Arg Gly Leu
            260                 265                 270
Ile Glu Ser Thr Asn Ala Ile Tyr Ala Gln Ser Ala Ser His His Ile
        275                 280                 285
Glu Gly Glu Pro Val Glu Phe Asn Ser Asp Glu Ala Phe Lys Asp Thr
    290                 295                 300
Asn Tyr Asn Ile Lys Asn Gly Ser Phe Asp Leu Ile Ala Tyr Asn Thr
305                 310                 315                 320
Asp Gly Lys Glu Ile Ala Arg Lys Thr Ile Ala Ile Thr Pro Ile Thr
                325                 330                 335
Thr Met Asn Asp Ile Ile Gln Val Ile Asn Ala Asn Thr Asp Asp Asn
            340                 345                 350
Gln Asp Asn Asn Thr Glu Asn Asp Phe Asp Glu Leu Phe His Ser Glu
        355                 360                 365
Leu
```

(2) INFORMATION FOR SEQ ID NO:1644:

This Sheet Has Been Replaced



(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:1644

```
Lys Thr Lys Leu Val Phe Met Ile Lys Ala Arg Phe Lys Lys Arg Leu
1               5                  10                  15
Leu Gly Ser Arg Gly Ala Phe Asp Leu Asn Ile Asp Leu Glu Ile Lys
            20                  25                  30
Glu Ala Glu Val Val Ala Leu Leu Gly Glu Ser Gly Ala Gly Lys Ser
        35                  40                  45
Thr Ile Leu Arg Ile Leu Ala Gly Leu Glu Ala Val Ser Ser Gly Tyr
    50                  55                  60
Ile Glu Ala Asn His Ser Val Trp Leu Asp Thr Gln Lys Lys Ile Phe
65                  70                  75                  80
Leu Lys Pro Gln Gln Arg Lys Ile Gly Phe Val Phe Gln Asp Tyr Ala
                85                  90                  95
Leu Phe Pro His Leu Asn Val Tyr Gln Asn Ile Ala Phe Ala His Pro
            100                 105                 110
Lys Asp Lys Asn Lys Ile His Glu Val Leu Arg Leu Met Arg Leu Glu
        115                 120                 125
Asn Leu Ser Gln Gln Lys Ile Pro Lys Leu Ser Gly Gly Gln Ala Gln
    130                 135                 140
Arg Val Ala Leu Ala Arg Ala Leu Ile Ala Ala Lys Asn Leu Leu Leu
145                 150                 155                 160
Leu Asp Glu Pro Leu Asn Ala Leu Asp Asn Ala Leu Lys Asn Glu Val
                165                 170                 175
Gln Gln Gly Leu Leu Asp Phe Ile Lys Arg Glu Asn Leu Ser Val Leu
            180                 185                 190
Leu Val Ser His Asp Pro Asn Glu Ile Thr Lys Leu Ala Arg Thr Phe
        195                 200                 205
Leu Phe Leu Asn Asn Gly Val Ile Asp Pro Asn Gln Glu Asn Arg Leu
    210                 215                 220
Phe Ser Asn Arg Leu Leu Val Lys Pro Leu Phe Glu Asp Glu Asn Tyr
225                 230                 235                 240
Cys His Tyr Glu Val Ile Pro Gln Thr Ile Ser Leu Pro Lys Asp Cys
                245                 250                 255
Leu Asn Pro Thr Phe Lys Leu Asp Phe Ile Gln Asn Lys Lys Phe
            260                 265                 270
```

(2) INFORMATION FOR SEQ ID NO:1645:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1645

```
Gly Leu Ser Ala Thr Ile Leu Gly Met Trp Ile Met Ser Ser Leu Ser
1               5                  10                  15
Ser Ser Phe Phe His Ser Leu Phe Phe Ile Lys Ser Asn Pro Gly Gln
```

```
            20                  25                  30
Leu Leu Lys Gly Trp Gly Ser Lys Ile Phe Phe Ile Asn Arg Lys Phe
        35                  40                  45
Val Leu Ala Gln Tyr Asn Pro Ser Val Ser Ile Phe Ile Leu Leu Asn
    50                  55                  60
Arg Val Phe Gly Val Gly Val
65                  70
```

(2) INFORMATION FOR SEQ ID NO:1646:

(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:1646

```
Ile Gln Arg Ser His Gln Leu Phe Asn Leu Gln Glu Lys Lys Gly Ile
1               5                   10                  15
Leu Gly Phe Leu His Gln Lys Asn Ile Leu Asn Ile Ala Gln Asn Asp
            20                  25                  30
Ile His Gln Leu Leu Ile Leu Met Val Val Phe Ser Met Leu Ala Thr
        35                  40                  45
Pro Phe Ile Leu Lys Tyr Leu Glu Ser Ile Ala Gln Phe Ile Leu His
    50                  55                  60
Gln Lys Ser Gln Glu Asn Glu Pro Ala Lys Lys
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:1647:

(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:1647

```
Gly Leu Met Arg Ile Ile Ile Arg Leu Leu Ser Phe Lys Met Asn Ala
1               5                   10                  15
Phe Leu Lys Leu Ala Leu Ala Ser Leu Met Gly Gly Leu Trp Tyr Ala
            20                  25                  30
```

This Sheet Has Been Replaced



```
Phe Asn Gly Glu Gly Ser Glu Ile Val Ala Ile Gly Ile Phe Val Leu
        35                  40                  45
Ile Leu Phe Val Phe Phe Ile Arg Pro Val Ser Phe Gln Asp Pro Glu
    50                  55                  60
Lys Arg Glu Glu Tyr Ile Glu Arg Leu Lys Lys Asn His Glu Arg Lys
65                  70                  75                  80
Met Ile Leu Gln Asp Lys Gln Lys Glu Glu Gln Met Arg Leu Tyr Gln
                85                  90                  95
Ala Lys Lys Glu Arg Glu Ser Arg Gln Lys Gln Asp Leu Lys Glu Gln
            100                 105                 110
Met Lys Lys Tyr Ser
        115
```

(2) INFORMATION FOR SEQ ID NO:1648:

(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:1648

```
Arg Lys Lys Met Glu Ile Ile Leu Leu Ile Val Ala Ala Val Val Leu
1               5                   10                  15
Phe Tyr Phe Tyr Asn Thr Leu Lys Glu Tyr Leu Lys Asn Pro Leu Asn
            20                  25                  30
Pro Lys Thr Lys Thr Glu Glu Tyr Asp Leu Lys Asn Asp Pro Tyr Leu
        35                  40                  45
Leu Val Gln Ser Ser Pro Leu Asp Lys Phe Lys Gln Thr Gln Ile Gly
    50                  55                  60
Ala Tyr Met Arg Leu Leu Lys Phe Leu Asp Ile Gln Lys Asn Ala Leu
65                  70                  75                  80
Asp Asn Ala Leu Arg Thr Leu Phe Ile His Glu Leu Glu Gln Pro Leu
                85                  90                  95
Asn Ser Glu Gln Gln Asn Leu Gly Gln Arg Ala Ser Gln
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:1649:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 543 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

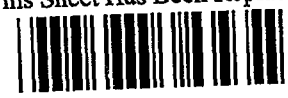
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

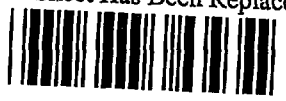
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(A) NAME/KEY: misc_feature
(B) LOCATION 1...543

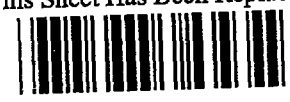
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1649

```
Met Pro Asn Asn Ala Leu Leu Gln Ile Lys Gln Asp Thr Leu Ser Leu
1               5                  10                  15
Ile Asp Asp Leu Lys Val Ile Cys Lys Asp Ala Gly Leu Ala Gly Asp
            20                  25                  30
Gly Asn Gly Tyr Lys Ile Ile Thr Gln Cys Phe Leu Tyr Lys Phe Leu
        35                  40                  45
Cys Asp Lys Phe Glu Phe Phe Phe Glu Gln Lys Phe Pro Asn Lys Thr
    50                  55                  60
Ile Arg Asp Tyr Lys Asp Phe Asn Glu Glu Glu Lys Glu Tyr Phe Phe
65                  70                  75                  80
Leu Thr Leu Ser Asp Lys Lys Leu Pro Lys Leu Ala Tyr Asp Glu Leu
                85                  90                  95
Leu Asn Tyr Leu Phe Glu Lys His Phe Tyr Asp Asn Asp Leu His Leu
            100                 105                 110
Lys Leu Asp Ala Ile Phe Asn Arg Ile Ser Ser Asn Asn Ala Glu Leu
        115                 120                 125
Phe Asn Thr Lys Ser Thr Asp Glu Thr Thr Ile Ala Leu Phe Glu Ser
    130                 135                 140
Val Ser Gln Tyr Ile Asn Glu Gly Ser Lys Arg Ala Asn Phe Thr Arg
145                 150                 155                 160
Ser Leu Leu Asp Lys Leu Lys Asn Phe Asn Phe Lys Gln Ala Phe Leu
                165                 170                 175
Asn Leu Gln Asn Gln Gln Gly Tyr Asp Phe Phe Ala Pro Ile Phe Glu
            180                 185                 190
Tyr Leu Leu Lys Asp Tyr Asn Asn Asn Ser Gly Gly Thr Tyr Ala Glu
        195                 200                 205
Tyr Tyr Thr Pro Leu Ser Ile Ala Ser Ile Ile Ala Lys Leu Leu Val
    210                 215                 220
Asn Lys Pro Thr Gln Ser Val Lys Ile Tyr Asp Pro Ser Ala Gly Thr
225                 230                 235                 240
Gly Thr Leu Leu Met Ala Leu Ala His Gln Ile Gly Thr Asp Ser Cys
                245                 250                 255
Thr Leu Tyr Ala Gln Asp Ile Ser Gln Lys Ser Leu Arg Met Leu Lys
            260                 265                 270
Leu Asn Leu Ile Leu Asn Asp Leu Thr His Ser Leu Arg His Ala Ile
        275                 280                 285
Glu Gly Asn Thr Leu Thr Asn Pro Tyr His Ser Lys Asp His Lys Gly
    290                 295                 300
Lys Met Asp Phe Ile Val Ser Asn Pro Pro Phe Lys Leu Asp Phe Ser
305                 310                 315                 320
Asn Glu His Ala Glu Ile Ser Gln Asn Lys Asn Asp Phe Phe Leu Gly
                325                 330                 335
Val Pro Asn Ile Pro Lys Asn Asp Lys Ser Lys Met Pro Ile Tyr Thr
            340                 345                 350
Leu Phe Phe Gln His Cys Leu Asn Met Leu Ser Pro Lys Gly Lys Gly
        355                 360                 365
Ala Ile Ile Val Pro Thr Gly Phe Ile Ser Ala Lys Ser Gly Val Asn
    370                 375                 380
Asn Lys Asn Val Arg His Leu Val Asp Glu Arg Leu Val Tyr Gly Val
385                 390                 395                 400
Ile Cys Met Pro Ser Gln Val Phe Ala Asn Thr Gly Thr Asn Val Ser
                405                 410                 415
Ile Ile Phe Phe Gln Lys Thr Pro Ser Ala Lys Glu Val Ile Leu Ile
            420                 425                 430
Asp Ala Ser Lys Leu Gly Glu Glu Tyr Thr Glu Asn Lys Asn Lys Lys
        435                 440                 445
Thr Arg Leu Arg Pro Ser Asp Met Asp Leu Ile Leu Glu Thr Phe Gln
    450                 455                 460
Asn Lys Ala Pro Lys Ser Asp Phe Cys Ala Leu Val Ser Phe Asp Glu
465                 470                 475                 480
```

```
Ile Thr Glu Lys Asn Tyr Ser Leu Asn Pro Gly Gln Tyr Phe Thr Ile
                485                 490                 495
Glu Asp Thr Ser Glu Thr Ile Ser Gln Ala Glu Phe Glu Asn Leu Met
            500                 505                 510
Gln Gln Tyr Ser Ser Glu Leu Ala Ser Leu Phe Asp Glu Ser Gln Asn
        515                 520                 525
Leu Gln Gln Glu Ile Leu Glu Thr Leu Lys Gly Val Arg Phe Glu
    530                 535                 540
```

(2) INFORMATION FOR SEQ ID NO:1650:

This Sheet Has Been Replaced



(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:1650

```
Lys Gly Asp Phe Met Lys Glu Gln Glu Trp Asp Leu Ser Ala Leu Phe
1               5                  10                  15
Glu Asn Lys Glu Ser Ala Glu Glu Phe Leu Lys Thr Leu Gln Thr Glu
            20                  25                  30
Val Gln Glu Phe Glu Asn Ala Tyr Gln Asn Asn Leu Lys Asn Leu Asp
        35                  40                  45
Ala Ala Lys Phe Ala Asn Thr Leu Lys His Tyr Glu Asn Leu Ser Glu
    50                  55                  60
Lys Ile Ser Arg Ala Met Ala Tyr Ala Gln Leu Leu Phe Ala Lys Asn
65                  70                  75                  80
Thr Lys Glu Ala Lys Phe Tyr Ser Gln Cys Glu Met Ala Cys Ala Asn
                85                  90                  95
Ile Gln Gln His Leu Leu Phe Phe Glu Ile Glu Phe Lys Asn Leu Asp
            100                 105                 110
Ala Lys Lys Gln Leu Ala Phe Ile Lys Lys Cys Lys Asp His Ala Phe
        115                 120                 125
Tyr Leu Asn Asn Leu Ile Glu Lys Lys Lys His Thr Leu Asn Leu Asp
    130                 135                 140
Glu Glu Lys Ile Ala Leu Ala Leu Ser Pro Val Gly Val Gly Ala Phe
145                 150                 155                 160
Ser Phe Val Met Asp Glu His Leu Phe Ser Leu Asn Ile Ser Leu His
                165                 170                 175
Arg Ile Asn Phe Lys Arg Arg Ile Asn Phe Ser Pro Leu Ala Gln Pro
            180                 185                 190
```

(2) INFORMATION FOR SEQ ID NO:1651:

(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:1651

```
Ala Lys Glu Leu Leu Asn Glu Pro Val Asp Lys Lys Glu Asn Phe Glu
1               5                  10                  15
Ser Leu Cys Gln Glu Ile Ala Asp His Thr His Gly Glu Tyr Thr Lys
            20                  25                  30
Arg Leu Lys Leu Val Glu Phe Leu Met Leu Leu Ala Tyr Ala Asp Gly
        35                  40                  45
Ile Leu Asp Ser Lys Glu Lys Glu Leu Phe Leu Asp Val Gly Ala Phe
    50                  55                  60
Leu Gln Ile Asp Asn Gln Asp Phe Asn Glu Leu Tyr Asp Asn Phe Glu
65                  70                  75                  80
His Phe Asn Ser Ile Glu Ile Pro Met Ser Leu Glu Glu Ala Lys Asn
                85                  90                  95
Leu Phe Glu Ile Gln Thr His Thr Thr Met Gln Asp Leu Glu Lys Lys
            100                 105                 110
Ala Leu Asp Leu Ser Ala Pro Tyr Tyr His Lys Met Asn Asp Asn Lys
        115                 120                 125
Arg Tyr Ser Glu Gln Asp Phe Ile Ser Leu Lys Lys Ile Ala Leu Ala
    130                 135                 140
Ser Gln Leu Leu Glu Asn Asp Leu Lys Asp Ser
145                 150                 155
```

This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:1652:

(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:1652

```
Met Pro Phe Leu Lys Ala Leu Ala Ser Phe Asp Ala Pro Phe Leu Glu
1               5                  10                  15
Lys Glu Ile Ser Lys Arg Phe Arg Asp Asn Leu Val Phe Phe Lys Ser
            20                  25                  30
Tyr His Pro Asn Leu Phe Asn Ala Leu Asn Thr Pro Phe Lys Asn Tyr
        35                  40                  45
Gln Leu Leu Phe Glu Thr Asn His Leu Asn Leu Leu His Thr Pro Thr
    50                  55                  60
Asn Ala Leu Ser Tyr Pro Lys His Gln Met Ile Glu Thr Ala Phe Asn
65                  70                  75                  80
Met Ala Lys Asn Pro Leu Asn Asn Pro Arg Trp Ser Leu Asp Asn Asn
                85                  90                  95
```

```
His Leu Ser Leu His Tyr Leu Lys Ser Gln Asn Asn His Lys Leu Pro
            100                 105                 110
Leu Thr Leu Lys Ala Thr His Ala Ile Ser Asn Phe Leu Asp Asn His
        115                 120                 125
Gln Thr Pro Cys Ser Leu Lys Lys Phe Leu Pro Pro Thr Met Ile Tyr
    130                 135                 140
Gly Val Leu Asp Gly Leu Phe Leu Ala Ile Leu Gln Ala Gln Asn Tyr
145                 150                 155                 160
Arg Phe His Ser Leu Tyr Leu Phe Glu Glu Asn Leu Asp Leu Phe Lys
                165                 170                 175
Ile Ser Cys Tyr Phe Ala Arg Tyr Glu Asp Leu Ile Lys Lys Gly Ala
            180                 185                 190
Lys Leu Phe Ile Gln Gly Phe Phe Asn Pro Asn Glu Leu Lys Met Asp
        195                 200                 205
Phe Leu Lys Arg Pro Ile Thr His Ser Phe Leu Lys Leu Glu Ile Met
    210                 215                 220
Pro Tyr Lys Ser Ala Phe Asn Leu Arg Met Arg Glu Asn Ile Gln Ser
225                 230                 235                 240
Tyr Tyr Lys Gln Ala Leu Arg Gly Trp Gly Ser Phe Glu Asp Glu Leu
                245                 250                 255
Leu Gly Val Lys Asn Thr Leu Lys Asn Leu Pro Leu Cys Gln Thr Leu
            260                 265                 270
Lys Thr Lys Pro Lys Lys Ile Asn Ala Pro Ile Cys Val Val Gly Asn
        275                 280                 285
Gly Pro Ser Leu Asp Leu Leu Leu Asp Phe Leu Lys Glu Asn Glu Glu
    290                 295                 300
Lys Phe Ile Ile Phe Ser Cys Gly Thr Ala Leu Lys Pro Leu Lys Ala
305                 310                 315                 320
His Gly Val Lys Val Asp Phe Gln Ile Glu Val Glu Arg Ile Asp Tyr
                325                 330                 335
Leu Lys Glu Val Leu Glu Arg Ala Pro Leu Glu Asp Thr Pro Leu Met
            340                 345                 350
Gly Ala Asn Met Leu Asn Pro Asn Ala Phe Asp Leu Ala Lys Glu Ala
        355                 360                 365
Leu Met Phe Met Arg Gly Gly Ser Ala Cys Ala Tyr Lys Pro Phe Glu
    370                 375                 380
Tyr Arg Ile Arg Ser Ala Phe Cys Gly Gln Cys Arg Gly Gly Phe Ser
385                 390                 395                 400
Gly Phe Asp Glu Arg
                405
```

(2) INFORMATION FOR SEQ ID NO:1653:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 413 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...413

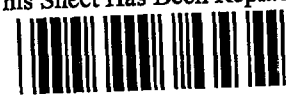
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1653

```
Lys Gly Leu Gly Leu Ser Glu Trp Gln Thr Phe Cys Leu Lys Asp Leu
1               5                   10                  15
Gly Lys Ile Val Gly Gly Ala Thr Pro Pro Thr Asn Asn Pro Lys Asn
```

```
          20                  25                  30
Tyr Gly Asn Lys Ile Ala Trp Ile Thr Pro Lys Asp Leu Ser Thr Leu
      35                  40                  45
Gln Gly Arg Tyr Ile Lys Lys Gly Ser Arg Ser Ile Ser Arg Leu Gly
  50                  55                  60
Phe Lys Ser Cys Ser Cys Val Leu Leu Pro Lys His Ala Ile Leu Phe
65                  70                  75                  80
Ser Ser Arg Ala Pro Ile Gly Tyr Val Ala Ile Ala Glu Lys Arg Leu
                85                  90                  95
Cys Thr Asn Gln Gly Phe Lys Ser Ile Ile Pro Asn Lys Lys Ile Tyr
            100                 105                 110
Phe Glu Phe Leu Tyr Tyr Leu Leu Lys Tyr Tyr Lys Asp Asn Ile Ser
        115                 120                 125
Asn Ile Gly Gly Gly Thr Thr Phe Lys Glu Val Ser Gly Ala Thr Leu
    130                 135                 140
Gly Leu Phe Gln Val Lys Ile Pro Pro Thr Tyr Tyr Glu Gln Gln Lys
145                 150                 155                 160
Ile Ala His Thr Leu Ser Ile Leu Asp Gln Lys Ile Glu Asn Asn His
                165                 170                 175
Lys Ile Asn Glu Leu Leu His Lys Ile Leu Glu Leu Leu Tyr Glu Gln
            180                 185                 190
Tyr Phe Val Arg Phe Asp Phe Leu Asp Glu Asn Asn Lys Pro Tyr Gln
        195                 200                 205
Thr Ser Gly Gly Lys Met Lys Phe Ser Lys Glu Leu Asn Arg Leu Ile
    210                 215                 220
Pro Asn Asp Phe Lys Val Lys Thr Leu Gly Glu Leu Ile Thr Trp Ile
225                 230                 235                 240
Ser Gly Ser Gln Pro Pro Lys Ser Cys His Ile Tyr Glu Tyr Lys Glu
                245                 250                 255
Gly Tyr Ile Arg Phe Ile Gln Asn Arg Asp Tyr Ser Ser Asn Asn Tyr
            260                 265                 270
Val Thr Tyr Ile Pro Ile Ser Lys Asn Asn Lys Ile Cys Tyr Gln Tyr
        275                 280                 285
Asp Ile Met Met Asp Lys Tyr Gly Glu Ala Gly Ser Val Arg Phe Gly
    290                 295                 300
Leu Gln Gly Ala Tyr Asn Val Ala Leu Ser Lys Ile Ser Val Leu Asn
305                 310                 315                 320
Gln Ser Met Gln Glu Tyr Ile Arg Ser Tyr Leu Asn Ser Lys Pro Ile
                325                 330                 335
Lys Lys Tyr Leu Ser Asn Ala Cys Met Ala Ser Thr Arg Ala Ser Leu
            340                 345                 350
Asn Glu Asn His Ile Tyr Ser Leu Met Leu Pro Ile Pro Pro Ile Asn
        355                 360                 365
Leu Leu Gln Lys Tyr Glu Lys Ile Ala Lys Asn Ile Ile Thr Ala Ile
    370                 375                 380
Ile Lys Asn Asn Gln Ser Thr Gln Thr Leu Thr Ala Leu Arg Asp Phe
385                 390                 395                 400
Leu Leu Pro Leu Leu Leu Lys Gln Gln Val Lys Pro Gln
                405                 410
```

(2) INFORMATION FOR SEQ ID NO:1654:

This Sheet Has Been Replaced



(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:1654

```
Gly Val Thr Leu Ile Gln Gln Glu Gly Phe Ile Met Ile Lys Arg Ile
1               5                  10                  15
Ala Cys Ile Leu Ser Leu Ser Ala Ser Leu Ala Leu Ala Gly Glu Val
            20                  25                  30
Asn Gly Phe Phe Met Gly Ala Gly Tyr Gln Gln Gly Arg Tyr Gly Pro
        35                  40                  45
Tyr Asn Ser Asn Tyr Ser Asp Trp Arg His Gly Asn Asp Leu Tyr Gly
    50                  55                  60
Leu Asn Phe Lys Leu Gly Phe Val Gly Phe Ala Asn Lys Trp Phe Gly
65                  70                  75                  80
Ala Arg Val Tyr Gly Phe Leu Asp Trp Phe Asn Thr Ser Gly Thr Glu
                85                  90                  95
His Thr Lys Thr Asn Leu Leu Thr Tyr Gly Gly Gly Gly Asp Leu Ile
            100                 105                 110
Val Asn Leu Ile Pro Ser Asp Lys Phe Ala Leu Gly Leu Ile Gly Gly
        115                 120                 125
Val Gln Leu Ala Gly Asn Thr Trp Met Phe Pro Tyr Asp Val Asn Gln
    130                 135                 140
Thr Arg Phe Gln Phe Leu Trp Asn Leu Gly Gly Arg Met Arg Val Gly
145                 150                 155                 160
Asp Arg Ser Ala Phe Glu Ala Gly Val Lys Phe Pro Met Val Asn Gln
                165                 170                 175
Gly Ser Lys Asp Val Gly Leu Ile Arg Tyr Tyr Ser Trp Tyr Val Asp
            180                 185                 190
Tyr Val Phe Thr Phe
        195
```

(2) INFORMATION FOR SEQ ID NO:1655:

This Sheet Has Been Replaced



(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:1655

```
Phe Arg Phe Tyr Phe Phe Lys Ala Asn Arg Ser Tyr Trp Gly Lys Val
1               5                  10                  15
Phe Met Val Asn Ser Thr Leu Tyr Ile Val Ile Ala Gly Leu Trp Leu
            20                  25                  30
Ala Val Gly Phe Gly Ile Phe Leu Lys Lys Leu Asp Met Pro Val Ile
        35                  40                  45
Ile Gly Tyr Ile Cys Thr Gly Thr Val Leu Ala Ala Phe Phe Lys Ile
    50                  55                  60
Asn Asp Phe Asn Leu Leu Ser Asp Ile Gly Glu Phe Gly Ile Val Phe
65                  70                  75                  80
Leu Met Phe Met Ile Gly Ile Glu Phe Asn Phe Asp Lys Leu Lys Ser
```

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

(2) INFORMATION FOR SEQ ID NO:1656:

This Sheet Has Been Replaced



(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:1656

```
Cys Leu Cys Val Gly Gly Ala Leu Ala His Ile Ser Pro Leu Ser Ile
1               5                   10                  15
Glu Tyr Ala Ala Pro Phe Val Gly Asn Ala Gly Val Ala Leu Ala Gly
            20                  25                  30
Leu Met Ser Asp Glu Ile Tyr Leu Cys Ala Leu Asp Cys Ala Tyr Ile
        35                  40                  45
Lys Gly Phe Lys Lys His Ala Gln Asn Ser Tyr Tyr Gly Asp Glu Lys
    50                  55                  60
```

```
Glu Ile Asp Thr Ser Ser Leu Ile Ser Val Glu Gly Asn Val Glu Gly
65                  70                  75                  80
Tyr Glu Thr Phe Ser Asp Ser Leu Phe Leu Leu Ser Lys Glu Arg Ile
                85                  90                  95
Glu Glu Ala Leu His Tyr Tyr Gln Pro Lys Lys Val Tyr Asn Leu Ser
            100                 105                 110
Tyr Gly Ala Lys Ile Lys His Ala Val Ser Leu Asn His Ser Gln Val
        115                 120                 125
Lys Leu Lys Gln Ile Asn Lys Gln Asp Ala Ile Val Arg Ile Lys Ser
    130                 135                 140
Met Phe Ser Pro Arg Ser Asn His Ala Lys Asp Leu Lys Asn Leu Gln
145                 150                 155                 160
Lys Asn Leu Ile Arg Phe Lys Glu Asp Phe Phe Thr His Leu Asn Thr
                165                 170                 175
Pro Cys Lys Thr Lys Gln Glu Ala Phe Glu Trp Val Asp Ser Leu Ser
            180                 185                 190
Gly Phe Cys Gln Thr Ala Ser Ala Lys Thr Pro Thr Ile Gly Ile Leu
        195                 200                 205
Phe Glu Gly Ser Val Ala His Ile Leu Gln Ser Val Leu Ile Val Ser
    210                 215                 220
Leu His Leu Lys Glu Asn Glu Leu Thr Leu Leu Ser Asn Ser Leu Lys
225                 230                 235                 240
Thr Pro
```

(2) INFORMATION FOR SEQ ID NO:1657:

This Sheet Has Been Replaced



(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:1657

```
Ile Leu Leu Val Glu Leu Lys Leu His Pro Lys Ile Gly Tyr Phe Ser
1               5                   10                  15
Lys Arg Phe Asn Phe Leu Ser Lys Met Arg Val Leu Glu Trp Lys Tyr
            20                  25                  30
Trp Leu Asn Thr Asp Lys Trp Asp Thr Pro Thr Asn Lys Pro Pro Gln
        35                  40                  45
Thr Phe Lys Ile Gln Ile Phe Lys Ile Gln Ile Gly Ile Ile Asn Asn
    50                  55                  60
Phe Asn His Leu Ile Lys Gly Ser Ser Met Lys Asn Ala Phe Lys Ala
65                  70                  75                  80
Phe Ala Leu Leu Ile Val Phe Phe Ser Asn Ala Leu Leu Ala Gln Asp
                85                  90                  95
Leu Lys Ile Ala Ala Ala Ala Asn Leu Thr Arg Ala Leu Lys Ala Leu
            100                 105                 110
Val Lys Glu Phe Gln Lys Glu His Pro Lys Asp Ala Ile Asn Ile Ser
        115                 120                 125
Phe Asn Ser Ser Gly Lys Leu Tyr Ala Gln Ile Ala Gln Asn Ala Pro
    130                 135                 140
Phe Asp Leu Phe Ile Ser Ala Asp Ile Ala Arg Pro Lys Lys Leu Tyr
```

```
145                 150                 155                 160
Asp Glu Lys Ile Thr Pro Phe Lys Glu Glu Val Tyr Ala Lys Gly Val
                165                 170                 175
Leu Val Leu Trp Ser Glu Asn Leu Lys Met Asp Ser Leu Glu Ile Leu
            180                 185                 190
Lys Asp Pro Lys Ile Lys Arg Ile Ala Met Ala Asn Pro Lys Leu Ala
        195                 200                 205
Pro Tyr Gly Lys Ala Ser Met Glu Val Leu Asp Arg Leu Lys Leu Thr
    210                 215                 220
Pro Ser Leu Lys Ser Lys Ile Ile Tyr Gly Ala Ser Ile Ser Gln Ala
225                 230                 235                 240
His Gln Phe Ile Ala Thr Lys Asn Ala Gln Ile Gly Phe Gly Ala Leu
                245                 250                 255
Ser Leu Ile Asp Lys Lys Asp Lys Asn Leu Ser Tyr Phe Ile Ile Asp
            260                 265                 270
Lys Thr Leu Tyr Asn Pro Ile Glu Gln Ala Leu Ile Ile Thr Lys Asn
        275                 280                 285
Gly Ala Asn Asn Pro Leu Ala Lys Val Phe Lys Asp Phe Leu Phe Ser
    290                 295                 300
Pro Lys Ala Arg Ala Ile Phe Lys Glu Tyr Gly Tyr Ile Val Asp
305                 310                 315
```

(2) INFORMATION FOR SEQ ID NO:1658:

This Sheet Has Been Replaced



(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:1658

```
Lys Arg Arg Thr Met Asp His Glu Phe Leu Ile Thr Met Arg Leu Ser
1                   5                  10                  15
Phe Ser Leu Ala Leu Ile Thr Thr Leu Ile Leu Leu Pro Ile Gly Ile
            20                  25                  30
Phe Leu Gly Tyr Phe Leu Ser Leu Lys Arg Asn Leu Leu Thr Ser Leu
        35                  40                  45
Thr Glu Thr Leu Val Tyr Met Pro Leu Val Leu Pro Pro Ser Val Leu
    50                  55                  60
Gly Phe Tyr Leu Leu Leu Ile Phe Ser Pro Ser Ser Phe Leu Gly Ala
65                  70                  75                  80
Phe Leu Gln Asp Val Leu Asn Val Lys Leu Val Phe Ser Phe Gln Gly
                85                  90                  95
Leu Ile Leu Gly Ser Val Ile Phe Ser Leu Pro Phe Met Val Ser Pro
            100                 105                 110
Ile Lys Ser Ala Leu Ile Ser Leu Pro Thr Ser Leu Lys Glu Ala Ser
        115                 120                 125
Tyr Ser Leu Gly Lys Gly Glu Tyr Tyr Thr Leu Phe Phe Val Leu Leu
    130                 135                 140
Pro Asn Ile Lys Pro Ser Val Leu Met Ala Ile Ile Thr Thr Phe Met
145                 150                 155                 160
His Thr Ile Gly Glu Phe Gly Val Val Met Met Leu Gly Gly Asp Ile
                165                 170                 175
```

```
Leu Gly Glu Thr Arg Val Ala Ser Ile Thr Ile Phe Asn Glu Ala Glu
            180                 185                 190
Ala Leu Asn Tyr Ser Lys Ala His Gln Tyr Ala Leu Thr Leu Thr Leu
        195                 200                 205
Ile Ser Phe Ser Leu Leu Phe Val Thr Leu Phe Leu Asn Lys Lys Gln
    210                 215                 220
Ser Ser Phe Leu
225
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1659:

(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:1659

```
Asn Phe Ile Phe Gly Glu Phe Ile Met Lys Arg Ser Ser Val Phe Ser
1               5                   10                  15
Phe Leu Val Ala Phe Leu Leu Val Val Gly Cys Ser His Lys Met Asp
            20                  25                  30
Asn Lys Thr Val Ala Gly Asp Val Ser Thr Lys Ala Val Gln Thr Ala
        35                  40                  45
Pro Val Thr Thr Glu Pro Ala Pro Glu Lys Glu Glu Pro Lys Gln Glu
    50                  55                  60
Pro Ala Pro Val Val Glu Glu Lys Pro Ala Ile Glu Ser Gly Thr Ile
65                  70                  75                  80
Ile Ala Ser Ile Tyr Phe Asp Phe Asp Lys Tyr Glu Ile Lys Glu Ser
                85                  90                  95
Asp Gln Glu Thr Leu Asp Glu Ile Val Gln Lys Ala Lys Glu Asn His
            100                 105                 110
Met Gln Val Leu Leu Glu Gly Asn Thr Asp Glu Phe Gly Ser Ser Glu
        115                 120                 125
Tyr Asn Gln Ala Leu Gly Val Lys Arg Thr Leu Ser Val Lys Asn Ala
    130                 135                 140
Leu Val Ile Lys Gly Val Glu Lys Asp Met Ile Lys Thr Ile Ser Phe
145                 150                 155                 160
Gly Glu Ser Lys Pro Lys Cys Val Gln Lys Thr Arg Glu Cys Tyr Arg
                165                 170                 175
Glu Asn Arg Arg Val Asp Val Lys Leu Val Lys
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:1660:

(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:1660

```
Lys Arg Ile Lys Arg Gly Phe Phe Met Gln Glu Ala Leu Leu Arg Phe
1               5                  10                  15
Gln Glu Gly Phe Lys Glu Trp Gly Tyr Leu Ile Leu Phe Leu Tyr Ser
            20                  25                  30
Leu Gly Gly Gly Tyr Val Gly Ile Val Ile Ala Ser Ile Leu Ser Ala
        35                  40                  45
Thr Thr His Ala Leu Asp Ile Lys Ile Thr Ile Leu Val Ala Phe Leu
    50                  55                  60
Gly Asn Leu Ile Gly Ser Gly Ala Leu Val Ile Phe Ala Arg Tyr Gln
65                  70                  75                  80
Lys Arg Glu Phe Leu Lys Tyr Phe Gln Lys His Arg Arg Lys Leu Ala
                85                  90                  95
Leu Ala Ser Leu Trp Val Lys Arg Tyr Ala Leu Leu Met Ile Phe Val
            100                 105                 110
Asn Lys Tyr Leu Tyr Gly Ile Lys Ser Val Val Pro Leu Ala Ile Gly
        115                 120                 125
Phe Ser Lys Tyr Pro Leu Lys Lys Phe Leu Trp Leu Asn Val Phe Ser
    130                 135                 140
Ser Phe Leu Trp Ala Leu Ile Val Gly Ser Val Ser Phe Gln Ala Ser
145                 150                 155                 160
Asp Trp Val Lys Thr Leu Tyr Glu Arg Leu Ser His Tyr Thr Ser Phe
                165                 170                 175
Phe Val Ile Ser Phe Val Leu Ile Ala Leu Leu Ile Trp Phe Leu Leu
            180                 185                 190
Lys Arg Tyr Ser Arg Lys Met Gly Phe
        195                 200
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1661:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...394

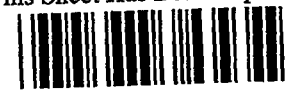
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1661

```
Ala Ser Phe Asn Tyr Asn Phe Gln Met Leu Arg Lys Asn Ile Leu Ala
1               5                  10                  15
Tyr Tyr Gly Ala Asn Phe Leu Leu Ile Ile Ala Gln Ser Leu Pro His
            20                  25                  30
Ala Ile Leu Thr Pro Leu Leu Leu Ser Lys Gly Leu Ser Leu Ser Glu
        35                  40                  45
```

```
Ile Leu Leu Val Gln Thr Phe Phe Ser Phe Cys Val Leu Val Ala Glu
    50                  55                  60
Tyr Pro Ser Gly Val Leu Ala Asp Leu Met Ser Arg Lys Asn Leu Phe
65                  70                  75                  80
Leu Val Ser Asn Val Phe Leu Ile Ala Ser Phe Ser Phe Val Leu Phe
                85                  90                  95
Phe Asp Ser Phe Ile Leu Met Leu Leu Ala Trp Gly Leu Tyr Gly Leu
            100                 105                 110
Tyr Ser Ala Cys Ser Ser Gly Thr Ile Glu Ala Ser Leu Ile Thr Asp
        115                 120                 125
Ile Lys Glu Asn Lys Lys Asp Leu Ser Lys Phe Leu Ala Lys Asn Asn
    130                 135                 140
Gln Ile Thr Tyr Leu Gly Met Ile Ile Gly Ser Ser Leu Gly Ser Phe
145                 150                 155                 160
Leu Tyr Leu Lys Val His Ala Met Leu Tyr Val Val Gly Ile Phe Leu
                165                 170                 175
Ile Met Leu Cys Ala Leu Thr Ile Ile Ile Tyr Phe Lys Glu Lys Glu
            180                 185                 190
Gly Asp Phe Lys Ser Gln Lys Asn Leu Lys Leu Leu Lys Glu Gln Val
        195                 200                 205
Lys Gly Ser Leu Lys Glu Leu Lys Asp Asn Pro Lys Leu Lys Ile Leu
    210                 215                 220
Leu Val Gly His Leu Ile Thr Pro Val Phe Phe Met Ser His Phe Gln
225                 230                 235                 240
Met Trp Gln Ala Tyr Phe Leu Lys Gln Gly Val Lys Glu Gln Tyr Leu
                245                 250                 255
Phe Val Phe Tyr Ile Ala Phe Gln Val Ile Ser Ile Leu Ile His Phe
            260                 265                 270
Leu Lys Ala Lys Asn Tyr Ser Gln Lys Ile Ala Leu Ser Ser Leu Leu
        275                 280                 285
Val Leu Leu Gly Val Ser Pro Leu Leu Leu Ser Asn Ile Pro Tyr Cys
    290                 295                 300
Phe Ile Gly Val Tyr Ala Leu Met Val Ala Phe Phe Ala Tyr Met Ser
305                 310                 315                 320
Tyr Cys Leu Gly Tyr Gln Phe Ser Lys Phe Val Ser Lys Asn Asn Ile
                325                 330                 335
Ser Ser Leu Ser Ser Leu Leu Ser Ser Cys Val Arg Val Val Ser Val
            340                 345                 350
Leu Ile Leu Ser Leu Ser Ser Leu Glu Leu Arg Tyr Phe Ser Pro Leu
        355                 360                 365
Thr Ile Ile Thr Met His Phe Ala Leu Thr Leu Ile Ile Leu Phe Phe
    370                 375                 380
Phe Leu Tyr Lys Ala Lys Pro Phe Asp Glu
385                 390
```

(2) INFORMATION FOR SEQ ID NO:1662:

This Sheet Has Been Replaced



(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:1662

```
Arg Arg Asn Leu Thr Arg Gln His Gly Ser Val Lys Lys Arg Glu Lys
1               5                  10                  15
Arg Phe Lys Thr His Ala Ser Leu Cys Asp Ser Val Arg Ser Gly Lys
            20                  25                  30
Arg Leu Gly Tyr Thr Asn Gln Val Ile Thr Asp Ile Val Asn Ile Gly
        35                  40                  45
Ile Gly Gly Ser Asp Leu Gly Ala Leu Met Val Cys Thr Ala Leu Lys
    50                  55                  60
Arg Tyr Gly His Pro Arg Leu Glu Met His Phe Val Ser Asn Val Asp
65                  70                  75                  80
Gly Thr Gln Ile Leu Asp Val
                85
```

(2) INFORMATION FOR SEQ ID NO:1663:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

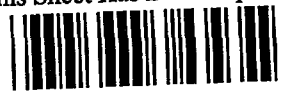
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1663

```
Gln His Tyr Pro Asn Asn Leu Lys Asp Ile Glu Met Asn Thr Glu Ile
1               5                  10                  15
Leu Thr Ile Met Leu Val Val Ser Val Leu Met Gly Leu Val Gly Leu
            20                  25                  30
Ile Ala Phe Leu Trp Gly Val Lys Ser Gly Gln Phe Asp Asp Glu Lys
        35                  40                  45
Arg Met Leu Glu Ser Val Leu Tyr Asp Ser Ala Ser Asp Leu Asn Glu
    50                  55                  60
Ala Ile Leu Gln Glu Lys Arg Gln Lys Asn
65                  70
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1664:

(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:1664

```
Glu Met Gln  he Leu His Ala His Leu Leu Ser Val Val Ile Phe Phe
1               5                  10                  15
Pro Met Leu Ser Ala Leu Leu Ala Phe Phe Met Ser Asp Gln Ala Ser
            20                  25                  30
Arg Ala Tyr Ala Ile Val Ile Ala Leu Ile Glu Leu Leu Leu Val Leu
        35                  40                  45
Leu Leu Trp His Gly Phe Asp Ile Gln Thr Ala Gly Met Gln Phe Glu
    50                  55                  60
Glu Met Lys Glu Leu Ala Tyr Gln Ile Gly Val Asn Tyr His Val Gly
65                  70                  75                  80
Val Asp Gly Ile Ala Leu Phe Leu Leu Leu Leu Asn Ala Ile Val Val
                85                  90                  95
Leu Leu Ser Val Ile Tyr Val Lys Glu Arg Arg Lys Asp Phe Val Ile
            100                 105                 110
Cys Leu Leu Leu Leu Glu Gly Ile Leu Met Gly Val Phe Ser Ser Leu
        115                 120                 125
Asn Val Ile Phe Phe Tyr Ala Phe Trp Glu Ile Ser Leu Leu Pro Val
    130                 135                 140
Leu Tyr Leu Ile Gly Arg Phe Gly Arg Asn Asn Lys Ile Tyr Ser Gly
145                 150                 155                 160
Met Lys Phe Phe Leu Tyr Thr Phe Leu Ala Ser Leu Cys Met Leu Leu
                165                 170                 175
Gly Ile Leu Tyr Ile Gly Tyr Asp Tyr Ala Asn Asn Tyr Gly Met Met
            180                 185                 190
Ser Phe Asp Ile Leu Asp Trp Tyr Gln Leu Asn Phe Ser Ser Gly Ile
        195                 200                 205
Lys Thr Trp Leu Phe Val Ala Phe Leu Ile Gly Ile Ala Val Lys Ile
    210                 215                 220
Pro Leu Phe Pro Phe Thr His Gly Cys Leu Met Arg Ile Leu Thr Pro
225                 230                 235                 240
Pro Leu
```

(2) INFORMATION FOR SEQ ID NO:1665:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 496 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1665

```
Lys Arg Ser Leu Met Leu Ile Asp Ile Leu His Ile Ser Phe Asp Ser
1               5                  10                  15
Phe Ser Phe Glu Ser Ile Leu Pro Met Leu Val Leu Val Cys Gly Gly
            20                  25                  30
Ile Phe Thr Leu Leu Ile Asn Ala Phe Thr Ser Arg Phe Ser Arg Asn
        35                  40                  45
Leu Asn Val Phe Leu Cys Met Leu Phe Leu Val Leu Asp Phe Leu Val
    50                  55                  60
Val Ser Gly Leu Glu Glu Gln Glu Asn Ala Phe Phe Gly Phe Leu Ser
```

```
65                  70                  75                  80
Leu Asp Thr Leu Ser Leu Ile Ser Gln Ser Ile Val Leu Ile Ser Ala
                85                  90                  95
Phe Phe Leu Ile Phe Leu Ala Leu Ser Lys Glu Arg Phe Asn Glu Phe
            100                 105                 110
Gln Thr Ala Glu Phe Tyr Ser Leu Tyr Leu Phe Ile Val Ala Gly Phe
        115                 120                 125
Gln Phe Met Val Ser Ser Asn Gln Phe Val Val Ile Leu Ile Gly Leu
    130                 135                 140
Glu Thr Ala Pro Leu Pro Leu Cys Val Leu Met Ala Leu Ser Asp Lys
145                 150                 155                 160
Arg Tyr Gly Leu Glu Ala Gly Ile Lys Tyr Phe Thr Met Gly Ala Met
                165                 170                 175
Ala Ser Ala Phe Phe Ala Met Gly Ala Met Ala Phe Tyr Leu Leu Thr
            180                 185                 190
Gly Ser Leu Asn Leu Glu Val Ile Thr Leu Tyr Leu His Thr Glu Gly
        195                 200                 205
Ile Thr Asn Pro Met Leu Phe Ala Met Gly Thr Ile Phe Leu Ile Gly
    210                 215                 220
Ala Ile Gly Phe Lys Val Ser Leu Val Pro Phe His Thr Trp Met Pro
225                 230                 235                 240
Asp Val Tyr Glu Gly Asn Asn Pro Val Phe Ala Ser Tyr Ile Ser Ile
                245                 250                 255
Val Pro Lys Ile Ala Gly Phe Val Val Ala Thr Arg Leu Phe Gly Ala
            260                 265                 270
Phe Ile Asp Thr His Thr Ala Trp Val Glu Asp Ile Phe Tyr Val Leu
        275                 280                 285
Ile Leu Met Thr Ile Thr Ile Pro Asn Phe Ile Ala Leu Trp Gln Glu
    290                 295                 300
Asp Val Lys Arg Met Leu Ala Tyr Ser Ser Ile Ser His Ser Gly Phe
305                 310                 315                 320
Ala Leu Ala Cys Val Phe Ile His Thr Glu Asp Ser Gln Gln Ala Met
                325                 330                 335
Phe Val Tyr Trp Phe Met Phe Ala Phe Thr Tyr Ile Gly Ala Phe Gly
            340                 345                 350
Leu Leu Trp Leu Leu Lys Ser Arg Glu Lys Thr Trp Asp Glu Arg Tyr
        355                 360                 365
Asp His Pro Tyr Ser Lys Phe Asn Gly Leu Ile Lys Thr His Pro Leu
    370                 375                 380
Val Ala Ile Leu Gly Ala Ile Phe Val Phe Gly Leu Ala Gly Ile Pro
385                 390                 395                 400
Pro Phe Ser Val Phe Trp Gly Lys Phe Leu Ala Val Glu Ser Ala Leu
                405                 410                 415
Glu Ser Asn His Ile Leu Leu Ala Val Val Met Leu Val Asn Ser Ala
            420                 425                 430
Val Ala Ala Phe Tyr Tyr Phe Arg Trp Leu Val Ala Met Phe Phe Asn
        435                 440                 445
Lys Pro Leu Gln Thr Gln Ser Tyr Ala Gln Asn Asp Ile Tyr Thr Gln
    450                 455                 460
Asn Ala Thr Met Pro Ile Tyr Ala Val Ile Ile Ala Met Ala Leu Ala
465                 470                 475                 480
Cys Leu Phe Ser Val Phe Met Met Arg Gly Leu Leu Glu Phe Val Ala
                485                 490                 495
```

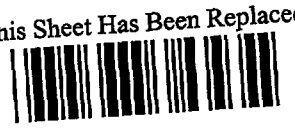
(2) INFORMATION FOR SEQ ID NO:1666:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



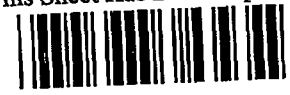
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1666

```
Asn Pro Ala Leu Ser Leu His Thr Trp Leu Pro Tyr Ala Tyr Ser Asn
1               5                  10                  15
Ala Pro Thr Leu Gly Ser Val Met Leu Ser Ala Leu Leu Ser Lys Met
            20                  25                  30
Gly Thr Tyr Ala Leu Leu Arg Phe Leu Leu Pro Leu Phe Pro Glu Leu
        35                  40                  45
Ser Glu Ile Tyr Leu Thr Pro Ile Ala Ile Val Ala Leu Cys Met Ile
    50                  55                  60
Ile Tyr Gly Gly Phe Leu Ala Tyr Ala Gln Lys Asp Leu Lys Thr Leu
65                  70                  75                  80
Ile Ala Tyr Ser Ser Phe Ser His Met Gly Val Val Val Leu Gly Val
                85                  90                  95
Phe Ser Phe Asn Val Glu Gly Val Ser Gly Ala Val Phe Met Met Phe
            100                 105                 110
Ala His Gly Val Ile Val Met Gly Leu Phe Leu Leu Ala Gly Ile Leu
        115                 120                 125
Glu Glu Arg Ala Ser Ser Leu Glu Ile Ala Arg Phe Gly Ser Ile Ala
    130                 135                 140
Lys Ser Ala Pro Val Phe Ala Ala Phe Phe Met Ile Val Leu Met Ala
145                 150                 155                 160
Asn Val Gly Met Pro Leu Ser Ile Gly Phe Val Gly Glu Phe Leu Ser
                165                 170                 175
Leu Leu Gly Phe Phe Ala Thr Tyr Pro Leu Leu Ala Ile Ile Ala Gly
            180                 185                 190
Thr Ser Ile Ile Leu Ser Ala Val Tyr Met Leu Thr Ser Tyr Lys Asp
        195                 200                 205
Val Phe Phe Gly Asn Leu Lys Thr Gly Asn Asn Gln Ile Ser Val Phe
    210                 215                 220
Glu Asp Leu Asn Ala Arg Glu Val Gly Val Leu Ser Val Ile Leu Ala
225                 230                 235                 240
Leu Ile Leu Ile Leu Gly Ile Tyr Pro Lys Ala Leu Leu Lys Pro Ile
                245                 250                 255
Glu Gln Gly Phe Lys Gln Leu Leu Glu Val Ile Glu Ile Arg Ser Leu
            260                 265                 270
Leu Phe Leu Gly Ser Leu Asp Thr Lys Ile Lys Glu Val Ser Tyr Val
        275                 280                 285
Asn Arg Tyr Ser Pro His Leu Phe
    290                 295
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1667:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 468 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

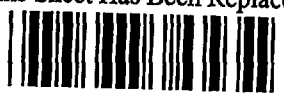
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

This Sheet Has Been Replaced

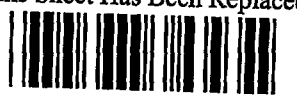


(A) NAME/KEY: misc_feature
(B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1667

```
Ile Tyr Ser Lys Thr Arg Ser His Asp Met Asp Ile Ser Ile Phe Arg
1               5                  10                  15
Glu Tyr Asp Ile Arg Gly Ile Tyr Pro Thr Thr Leu Asp Glu Asn Thr
            20                  25                  30
Ala Phe Ser Ile Gly Val Glu Leu Gly Lys Ile Met Arg Glu Tyr Asp
        35                  40                  45
Lys Ser Val Phe Val Gly His Asp Ala Arg Val His Gly Arg Phe Leu
    50                  55                  60
Phe Glu Val Leu Ser Ala Gly Leu Gln Ser Ser Gly Leu Lys Val Tyr
65                  70                  75                  80
Asp Leu Gly Leu Ile Pro Thr Pro Val Ala Tyr Phe Ala Ala Phe Asn
                85                  90                  95
Glu Ile Asp Asn Ile Gln Cys Pro Asn Ser Ile Met Ile Thr Gly Ser
            100                 105                 110
His Asn Pro Lys Glu Tyr Asn Gly Phe Lys Ile Thr Leu Asn Gln Asn
        115                 120                 125
Pro Phe Tyr Gly Lys Asp Ile Gln Ala Leu Lys Asn Thr Leu Leu Asn
    130                 135                 140
Ala Lys His Glu Ile Lys Pro Leu Lys Glu Thr Pro Glu Lys Val Asn
145                 150                 155                 160
Ala Leu Glu Ala Tyr His Arg Tyr Leu Ile Lys Asp Phe Lys His Leu
                165                 170                 175
Lys Asn Leu Lys Tyr Lys Ile Ala Leu Asp Phe Gly Asn Gly Val Gly
            180                 185                 190
Ala Leu Gly Leu Glu Pro Ile Leu Lys Ala Leu Asn Ile Asp Phe Ser
        195                 200                 205
Ser Leu Tyr Ser Asp Pro Asp Gly Asp Phe Pro Asn His His Pro Asp
    210                 215                 220
Pro Ser Glu Ala Lys Asn Leu Lys Asp Leu Glu Lys His Met Arg Glu
225                 230                 235                 240
Asn Ala Ile Leu Ile Gly Phe Ala Phe Asp Gly Asp Ala Asp Arg Ile
                245                 250                 255
Ala Met Leu Ser Ser His His Ile Tyr Ala Gly Asp Glu Leu Ala Ile
            260                 265                 270
Leu Phe Ala Lys Arg Leu His Ala Gln Gly Ile Thr Pro Phe Val Ile
        275                 280                 285
Gly Glu Val Lys Cys Ser Gln Val Met Tyr Asn Ala Ile Asn Thr Phe
    290                 295                 300
Gly Lys Thr Leu Met Tyr Lys Thr Gly His Ser Asn Leu Lys Ile Lys
305                 310                 315                 320
Leu Lys Glu Thr Asn Ala His Phe Ala Ala Glu Met Ser Gly His Ile
                325                 330                 335
Phe Phe Lys Glu Arg Tyr Phe Gly Tyr Asp Asp Ala Leu Tyr Ala Cys
            340                 345                 350
Leu Arg Ala Leu Glu Leu Leu Leu Glu Gln Ser Pro Ser Asp Leu Glu
        355                 360                 365
Asn Thr Ile Lys Asn Leu Pro Tyr Ser Tyr Thr Thr Pro Glu Glu Lys
    370                 375                 380
Ile Ala Val Ser Glu Glu Glu Lys Phe Glu Ile Ile Arg Asn Leu Gln
385                 390                 395                 400
Glu Ala Leu Lys Asn Pro Pro Ser His Phe Pro Thr Ile Lys Glu Ile
                405                 410                 415
Ile Ser Ile Asp Gly Val Arg Val Val Phe Glu His Gly Phe Gly Leu
            420                 425                 430
Ile Arg Ala Ser Asn Thr Thr Pro Tyr Leu Val Ser Arg Phe Glu Gly
        435                 440                 445
Lys Asp Glu Thr Thr Ala Leu Glu Tyr Lys Arg Ala Leu Leu Gly Leu
    450                 455                 460
Leu Glu Lys Leu
465
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1668:

(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:1668

```
Gly Ile Phe Met Asn Glu Ile Ile Leu Ile Thr Gly Ala Tyr Gly Met
1               5                  10                  15
Val Gly Gln Asn Thr Ala Leu Tyr Phe Lys Lys Asn Lys Pro Asp Val
            20                  25                  30
Thr Leu Leu Thr Pro Lys Lys Ser Glu Leu Tyr Leu Leu Asp Lys Asp
        35                  40                  45
Asn Val Gln Ala Tyr Leu Lys Glu Tyr Lys Pro Thr Gly Ile Ile His
    50                  55                  60
Cys Ala Gly Arg Val Gly Gly Ile Val Ala Asn Met Asn Asp Leu Ser
65                  70                  75                  80
Thr Tyr Met Val Glu Asn Leu Leu Met Gly Leu Tyr Leu Phe Ser Ser
                85                  90                  95
Ala Leu Asp Leu Gly Val Lys Lys Ala Ile Asn Leu Ala Ser Ser Cys
            100                 105                 110
Ala Tyr Pro Lys Tyr Ala Pro Asn Pro Leu Lys Glu Ser Asp Leu Leu
        115                 120                 125
Asn Gly Ser Leu Glu Pro Thr Asn Glu Gly Tyr Ala Leu Ala Lys Leu
    130                 135                 140
Ser Val Met Lys Tyr Cys Glu Tyr Val Ser Ala Glu Lys Gly Val Phe
145                 150                 155                 160
Tyr Lys Thr Leu Val Pro Cys Asn Leu Tyr Gly Glu Phe Asp Lys Phe
                165                 170                 175
Glu Glu Lys Ile Ala His Met Ile Pro Gly Leu Ile Ala Arg Met His
            180                 185                 190
Thr Ala Lys Leu Lys Asn Glu Lys Asn Phe Ala Met Trp Gly Asp Gly
        195                 200                 205
Thr Ala Glu Glu Ser Ile
    210
```

(2) INFORMATION FOR SEQ ID NO:1669:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1669

```
Ala His Ala Asn Arg Thr Ile Ile His Arg Ile Asp Asp Ser Ile Ala
1               5                  10                  15
Gln Arg Val Asp Asn Ala Ile Arg Pro Met Arg Leu Val Arg Gly Phe
            20                  25                  30
Ala Pro Leu Tyr Leu Thr Leu Pro Lys Arg Ser Phe Asn Ala Pro Lys
        35                  40                  45
Lys Ile Leu Ala Leu Gly Ala Glu Gln Lys Gly His Phe Ser Leu Leu
    50                  55                  60
Asp Ser Glu Thr Ser Val Leu Leu Leu Ser Pro Phe Cys Gly Asp Leu
65                  70                  75                  80
Ser Val Leu Glu Asn Glu Lys His Phe Lys Glu Thr Leu Asn Phe Phe
                85                  90                  95
Leu Lys Thr Tyr Asp Phe Lys Pro Thr Leu Leu Ala Cys Asp Glu His
            100                 105                 110
Gln Asn Tyr Thr Thr Thr Lys Met Ala Phe Asp Phe Asn Thr Pro Leu
        115                 120                 125
Leu Gln Val Gln His His His Ala His Phe Leu Ala Ser Val Leu Asp
    130                 135                 140
Ala Leu Leu Gln Asp Pro His Leu Asn His Pro Phe Ile Gly Ile Val
145                 150                 155                 160
Trp Asp Gly Ser Gly Ala Tyr Glu Asn Lys Ile Tyr Gly Ala Glu Cys
                165                 170                 175
Phe Val Gly Asp Leu Glu Arg Ile Glu Glu Val Ala Arg Phe Glu Glu
            180                 185                 190
Phe Trp Leu Leu Gly Gly Gln Lys Ala Ile Lys Glu Pro Arg Arg Leu
        195                 200                 205
Val Leu Glu Ile Ala Leu Lys His Gln Leu Asn Lys Leu Leu Lys Arg
    210                 215                 220
Val Gln Lys His Phe Lys Glu Asp Glu Leu Gly Ile Phe Lys Gln Met
225                 230                 235                 240
His Asp Lys Lys Ile Gln Ser Val Ala Thr Asn Ser Ile Gly Arg Leu
                245                 250                 255
Phe Asp Ile Val Ala Phe Ser Leu Gly Val Val Gly Thr Ile Ser Phe
            260                 265                 270
Glu Ala Glu Ser Gly Gln Val Leu Glu Asn Leu Ala Leu Gln Ser Asp
        275                 280                 285
Glu Ile Ala Phe Tyr Pro Phe Glu Ile Lys Asn Ser Val Val Arg Leu
    290                 295                 300
Lys Glu Phe Tyr Gln Ala Phe Glu Lys Asp Leu Gly Val Leu Glu Pro
305                 310                 315                 320
Lys Arg Ile Ala Lys Lys Phe Phe Asn Ser Leu Val Glu Ile Ile Thr
                325                 330                 335
Ala Leu Ile Ala Pro Phe Lys Gly His Val Val Val Cys Ser Gly Gly
            340                 345                 350
Val Phe Cys Asn Gln Leu Leu Cys Glu Gln Leu Ala Lys Arg Leu Lys
        355                 360                 365
Lys Leu Gln Arg Glu Tyr Phe Phe His Lys His Phe Pro Pro Asn Asp
    370                 375                 380
Ser Ser Ile Pro Val Gly Gln Ala Leu Met Ala Tyr Phe Asn Pro Thr
385                 390                 395                 400
Ile Ile Lys Lys Gly
                405
```

(2) INFORMATION FOR SEQ ID NO:1670:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 446 amino acids

This Sheet Has Been Replaced



(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1670

```
Arg Phe Glu Cys Gly Ala Ser Asp Met Ser Gly Trp Leu Leu Met Gly
1               5                  10                  15
Leu Pro Gly Ala Leu Tyr Val Gly Gly Leu Ile Asn Ser His Ile Ala
            20                  25                  30
Ile Gly Leu Ser Leu Gly Ala Leu Ile Asn Trp Val Phe Val Ala Lys
        35                  40                  45
Arg Leu Arg Ile Tyr Thr Ser Val Ile Ala Asn Ser Ile Thr Ile Ser
    50                  55                  60
Asp Tyr Phe Glu Thr Arg Phe Ser Asp Asp Lys His Ile Leu Arg Leu
65                  70                  75                  80
Ile Ser Ala Phe Val Ile Leu Ile Leu Lys Ile Phe Tyr Phe Ser Ser
                85                  90                  95
Gly Leu Val Ser Gly Ala Lys Leu Phe Glu Pro Thr Phe Gly Ile Gln
            100                 105                 110
Tyr Thr Tyr Ala Leu Ser Ile Gly Thr Leu Ile Ile Val Ser Tyr Thr
        115                 120                 125
Phe Leu Gly Arg Tyr Lys Ala Val Cys Trp Thr Asp Leu Ile Gln Gly
    130                 135                 140
Leu Leu Met Met Ser Ala Leu Ile Val Val Pro Ile Val Met Ile Ile
145                 150                 155                 160
His Leu Gly Gly Ile Gly Glu Gly Ile Lys Ile Ile Lys Glu Ile Lys
                165                 170                 175
Pro Glu Asn Leu Ser Phe Leu Gln Gly Ser Ser Val Val Ala Ile Ile
            180                 185                 190
Ser Ser Leu Ala Trp Gly Leu Gly Tyr Phe Gly Gln Pro His Ile Leu
        195                 200                 205
Val Arg Phe Met Ser Ile Arg Ser Ile Arg Asp Val Pro Lys Ala Thr
    210                 215                 220
Thr Ile Gly Ile Ser Trp Met Val Ile Ser Leu Ile Gly Ala Cys Val
225                 230                 235                 240
Met Gly Leu Leu Gly Val Ala Tyr Val His Lys Phe Asp Leu Ser Leu
                245                 250                 255
Glu Asp Pro Glu Lys Ile Phe Ile Val Met Ser Gln Leu Leu Phe Asn
            260                 265                 270
Pro Trp Ile Thr Gly Ile Leu Leu Ser Ala Ile Leu Ala Ala Val Met
        275                 280                 285
Ser Thr Ala Ser Ser Gln Leu Leu Val Ser Ser Ser Thr Ile Ala Glu
    290                 295                 300
Asp Phe Tyr Ala Thr Ile Phe Asn Lys Asn Ala Pro Gln Lys Leu Val
305                 310                 315                 320
Met Thr Ile Ser Arg Leu Ser Val Leu Gly Val Ala Cys Ile Ala Phe
                325                 330                 335
Phe Ile Ser Thr Asp Lys Asn Ala Ser Ile Leu Ser Ile Val Ser Tyr
            340                 345                 350
Ala Trp Ala Gly Phe Gly Ala Ser Phe Gly Ser Val Ile Leu Phe Ser
        355                 360                 365
Leu Phe Trp Ser Arg Met Thr Arg Ile Gly Ala Ile Ala Gly Met Leu
    370                 375                 380
Ser Gly Ala Ser Thr Val Ile Leu Tyr Asp Lys Phe Gly Lys Ser Phe
```

```
385                 390                 395                 400
Leu Asp Ile Tyr Glu Ile Val Pro Gly Phe Ile Val Ala Ser Val Ala
                405                 410                 415
Ile Val Ala Phe Ser Leu Phe Ser Ser Val Arg Ser Gly Thr Lys Glu
            420                 425                 430
Ala Phe Glu Thr Met Leu Lys Glu Ile Glu Ser Leu Lys His
        435                 440                 445
```

(2) INFORMATION FOR SEQ ID NO:1671:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 375 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

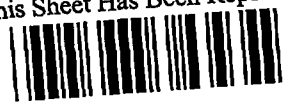
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1671

```
Asn Lys Trp Ile Lys Gly Ala Val Val Phe Val Gly Gly Phe Ala Thr
1               5                  10                  15
Ile Thr Thr Phe Ser Leu Ile Tyr His Gln Lys Pro Lys Ala Pro Leu
            20                  25                  30
Asn Asn Gln Pro Ser Leu Leu Asn Asp Asp Glu Val Lys Tyr Pro Leu
        35                  40                  45
Gln Asp Tyr Thr Phe Thr Gln Asn Pro Gln Pro Thr Asn Thr Glu Ser
    50                  55                  60
Ser Lys Asp Ala Thr Ile Lys Ala Leu Gln Glu Gln Leu Lys Ala Ala
65                  70                  75                  80
Leu Lys Ala Leu Asn Ser Lys Glu Met Asn Tyr Ser Lys Glu Glu Thr
                85                  90                  95
Phe Thr Ser Pro Pro Met Asp Pro Lys Thr Thr Pro Pro Lys Lys Asp
            100                 105                 110
Phe Ser Pro Lys Gln Leu Asp Leu Leu Ala Ser Arg Ile Thr Pro Phe
        115                 120                 125
Lys Gln Ser Pro Lys Asn Tyr Glu Glu Asn Leu Ile Phe Pro Val Asp
    130                 135                 140
Asn Pro Asn Gly Ile Asp Ser Phe Thr Asn Leu Lys Glu Lys Asp Ile
145                 150                 155                 160
Ala Thr Asn Glu Asn Lys Leu Leu Arg Thr Ile Thr Ala Asp Lys Met
                165                 170                 175
Ile Pro Ala Phe Leu Ile Thr Pro Ile Ser Ser Gln Ile Ala Gly Lys
            180                 185                 190
Val Ile Ala Gln Val Glu Ser Asp Ile Phe Ala Ser Met Gly Lys Ala
        195                 200                 205
Val Leu Ile Pro Lys Gly Ser Lys Val Ile Gly Tyr Tyr Ser Asn Asn
    210                 215                 220
Asn Lys Met Gly Glu Tyr Arg Leu Asp Ile Val Trp Ser Arg Ile Ile
225                 230                 235                 240
Thr Pro His Gly Ile Asn Ile Met Leu Thr Asn Ala Lys Gly Ala Asp
                245                 250                 255
Ile Lys Gly Tyr Asn Gly Leu Val Gly Glu Leu Ile Glu Arg Asn Phe
            260                 265                 270
Gln Arg Tyr Gly Val Pro Leu Leu Leu Ser Thr Leu Thr Asn Gly Leu
        275                 280                 285
```

This Sheet Has Been Replaced



```
Leu Ile Gly Ile Thr Ser Ala Leu Asn Asn Arg Gly Asn Lys Glu Glu
    290                 295                 300
Val Thr Asn Phe Phe Gly Asp Tyr Leu Leu Leu Gln Leu Met Arg Gln
305                 310                 315                 320
Ser Gly Met Gly Ile Asn Gln Val Val Asn Gln Ile Leu Arg Asp Lys
                325                 330                 335
Ser Lys Ile Ala Pro Ile Val Val Ile Arg Glu Gly Ser Arg Val Phe
            340                 345                 350
Ile Ser Pro Asn Thr Asp Ile Phe Phe Pro Ile Pro Arg Glu Asn Glu
        355                 360                 365
Val Ile Ala Glu Phe Leu Lys
    370                 375
```

(2) INFORMATION FOR SEQ ID NO:1672:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1672

```
Lys Ala Ala Phe Cys Ile Gly Ile Phe Phe Tyr Gly Ala Tyr Tyr Phe
1               5                   10                  15
Leu Asp Glu Phe Leu Ile Lys Leu Tyr Leu Gln Pro Ser Glu Gln Asp
            20                  25                  30
Ala Leu Phe Met Gln Glu Thr Lys Arg Ala Met Asn Ile Tyr Tyr Val
        35                  40                  45
Gly Tyr Val Phe Leu Gly Met Thr Leu Leu Cys Ala Val Phe Phe Gln
    50                  55                  60
Ser Ile Gln Arg Thr Lys Ser Ser Phe Ile Ile Thr Ile Ser His Thr
65                  70                  75                  80
Leu Gly Phe Ile Val Ile Leu Leu Pro Ile Leu Ser His Phe Tyr Gly
                85                  90                  95
Val Asn Gly Ile Trp Val Thr Tyr Pro Ile Ala Gln Phe Leu Ala Val
            100                 105                 110
Phe Gly Ser Val Arg Gly Asn Leu Leu
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:1673:

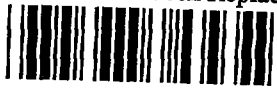
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1673

```
Met Leu Lys Lys Lys Ile Asp Leu His Lys Asp Ser Ile Arg Lys Leu
1               5                  10                  15
Phe Phe Tyr Tyr Phe Ile Pro Leu Val Phe Ser Met Ile Ser Leu Ser
            20                  25                  30
Thr Tyr Ser Met Val Asp Asp Met Phe Val Gly Lys Lys Leu Gly Lys
        35                  40                  45
Glu Ala Ile Ala Ala Val Asn Ile Ala Trp Pro Ile Phe Pro Gly Leu
    50                  55                  60
Ile Ala Tyr Glu Leu Leu Phe Gly Phe Gly Ala Ala Ser Ile Val Gly
65                  70                  75                  80
Tyr Phe Leu Gly Gln Asn Lys Thr His Arg Ala Arg Leu Val Phe Ser
                85                  90                  95
Ser Val Phe Tyr Phe Val Ala Leu Ser Ala Phe Ile Leu Ser Met Ala
            100                 105                 110
Leu Leu Pro Phe Ser Glu Asn Ile Ala Arg Phe Leu Gly Ala Met Thr
        115                 120                 125
Leu Tyr
    130
```

(2) INFORMATION FOR SEQ ID NO:1674:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1674

```
Asn His Phe Asn Gly Cys Val Phe Arg Val Gln His Leu Leu Ala Asp
1               5                  10                  15
Val Phe Val Val Asn Asp Lys Arg Pro Val Leu Ala Met Val Ala Met
            20                  25                  30
Leu Ile Gly Ser Leu Ala Asn Ile Phe Phe Asn Tyr Leu Phe Ile Phe
        35                  40                  45
Val Leu Glu Val Gly Val Gln Gly Ser Ala Ile Ala Thr Val Ile Gly
    50                  55                  60
His Ala Ile Gly Val Leu Val Leu Met Gln His Phe Trp Arg Lys Lys
65                  70                  75                  80
Gly Gln Leu Tyr Phe Ile Lys Arg Phe Ser Leu Ser Ser Val Ile Ser
                85                  90                  95
Ser Ala Lys Ser Gly Val Pro Gln Ser Thr Ala Glu Phe Ser Ala Ser
            100                 105                 110
Ile Met Ile Leu Leu Phe Asn Thr Ala Ile Met His Thr Ala Gly Glu
        115                 120                 125
Arg Phe Val Ser Met Tyr Gly Ile Val Met Tyr Asn Ala Ile Ile Phe
    130                 135                 140
```

Phe Thr Thr Leu Phe Ala Ile Ser Gln Gly Ile Gln Pro Ile Ala Glu
145 150 155 160
Leu

(2) INFORMATION FOR SEQ ID NO:1675:

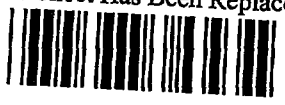
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1675

Phe Leu Asn Ile Arg Asp Leu Thr Met Ile Phe Ser Ser Leu Phe Ser
1 5 10 15
Val Val Gly Met Ala Val Leu Phe Leu Ile Ala Trp Val Phe Ser Gly
20 25 30
Asn Lys Arg Ala Ile Asn Tyr Arg Thr Ile Val Ser Ala Phe Val Ile
35 40 45
Gln Val Ala Leu Gly Ala Leu Ala Leu Tyr Val Pro Leu Gly Arg Glu
50 55 60
Ile Leu Gln Gly Leu Ala Ser Gly Ile Gln Ser Val Ile Gly Tyr Gly
65 70 75 80
Tyr Glu Gly Val Arg Phe Leu Phe Gly Asn Leu Ala Pro Asn Ala Lys
85 90 95
Gly Asp Gln Gly Ile Gly Gly Phe Ile Phe Ala Ile Asn Val Leu Ala
100 105 110
Ile Ile Ile Phe Phe Ala Ser Leu Ile Ser Leu Leu Tyr Tyr Leu Lys
115 120 125
Ile Met Pro Leu Val Ile Asn Leu Ile Gly Gly Ala Leu Gln Lys Cys
130 135 140
Leu Gly Thr Ser Lys Ala Glu Ser Met Ser Ala Ala Ala Asn Ile Phe
145 150 155 160
Val Ala His Thr Glu Ala Pro Leu Val Ile Lys Pro Tyr Leu Lys Ser
165 170 175
Met Ser Asp Ser Glu Ile Phe Ala Val Met Cys Val Gly Met Ala Ser
180 185 190
Val Ala Gly Pro Val Leu Ala Gly Tyr Ala Ser Met Gly Ile Pro Leu
195 200 205
Pro Tyr Leu Ile Ala Ala Ser Phe Met Ser Ala Pro Gly Gly Leu Leu
210 215 220
Phe Ala Lys Ile Ile Tyr Pro Gln Asn Glu Thr Ile Ser Ser His Ala
225 230 235 240
Asp Val Ser Ala Glu Glu His Val Asn Ile Ile Glu Ala Ile Ala Asn
245 250 255
Gly Ala Ser Thr Gly Leu His Leu Ala Leu His Val Gly Ala Met Leu
260 265 270
Leu Ala Phe Val Gly Met Leu Ala Leu Val Asn Gly Leu Leu Gly Val
275 280 285
Val Gly Gly Phe Leu Gly Met Glu His Leu Ser Leu Gly Val Val Leu
290 295 300
Gly Thr Leu Leu Lys Pro Leu Ala Phe Met Leu Gly Val Pro Trp Ser

```
305                 310                 315                 320
Gln Ala Gly Ile Ala Gly Glu Ile Ile Gly Ile Lys Ile Ala Leu Asn
                325                 330                 335
Glu Phe Val Gly Tyr Met Gln Leu Leu Pro Tyr Leu Gly Asp Asn Pro
            340                 345                 350
Pro Leu Ile Leu Ser Glu Lys Thr Lys Ala Ile Ile Thr Phe Ala Leu
        355                 360                 365
Cys Gly Phe Ala Asn Leu Ser Ser Val Ala Met Leu Ile Gly Gly Leu
    370                 375                 380
Gly Ser Leu Val Pro Lys Lys Lys Asp Phe Ile Ala Arg Leu Ala Leu
385                 390                 395                 400
Lys Ala Val Leu Val Gly Thr Leu Ser Asn Phe Met Ser Ala Thr Ile
                405                 410                 415
Ala Gly Leu Phe Ile Gly Leu Ser Ala Asn
            420                 425
```

(2) INFORMATION FOR SEQ ID NO:1676:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1676

```
Thr Leu Ser Lys Glu Glu Gly Leu Met Pro Gln Asn Gln Leu Val Ile
1               5                   10                  15
Thr Ile Ile Asp Glu Ser Gly Ser Lys Gln Leu Lys Phe Ser Lys Asn
            20                  25                  30
Leu Lys Arg Asn Leu Ile Ile Ser Val Val Ile Leu Leu Leu Ile Val
        35                  40                  45
Gly Leu Gly Val Gly Phe Leu Lys Phe Leu Ile Ala Lys Met Asp Thr
    50                  55                  60
Met Thr Ser Glu Arg Asn Ala Val Leu Arg Asp Phe Arg Gly Leu Tyr
65                  70                  75                  80
Gln Lys Asn Tyr Ala Leu Ala Lys Glu Ile Lys Asn Lys Arg Glu Glu
                85                  90                  95
Leu Phe Ile Val Gly Gln Lys Ile Arg Gly Leu Glu Ser Leu Ile Glu
            100                 105                 110
Ile Lys Lys Gly Ala Asn Gly Gly Gly His Leu Tyr Asp Glu Val Asp
        115                 120                 125
Leu Glu Asn Leu Ser Leu Asn Gln Lys His Leu Ala Leu Met Leu Ile
    130                 135                 140
Pro Asn Gly Met Pro Leu Lys Thr Tyr Ser Ala Ile Lys Pro Thr Lys
145                 150                 155                 160
Glu Arg Asn His Pro Ile Lys Lys Ile Lys Gly Val Glu Ser Gly Ile
                165                 170                 175
Asp Phe Ile Ala Pro Leu Asn Thr Pro Val Tyr Ala Ser Ala Asp Gly
            180                 185                 190
Ile Val Asp Phe Val Lys Thr Arg Ser Asn Ala Gly Tyr Gly Asn Leu
        195                 200                 205
Val Arg Ile Glu His Ala Phe Gly Phe Ser Ser Ile Tyr Thr His Leu
    210                 215                 220
```

```
Asp His Val Asn Val Gln Pro Lys Ser Phe Ile Gln Lys Gly Gln Leu
225                 230                 235                 240
Ile Gly Tyr Ser Gly Lys Ser Gly Asn Ser Gly Gly Glu Lys Leu His
                245                 250                 255
Tyr Glu Val Arg Phe Leu Gly Lys Ile Leu Asp Ala Glu Lys Phe Leu
            260                 265                 270
Ala Trp Asp Leu Asp His Phe Gln Ser Ala Leu Glu Glu Asn Lys Phe
        275                 280                 285
Ile Glu Trp Lys Asn Leu Phe Trp Val Leu Glu Asp Ile Val Gln Leu
    290                 295                 300
Gln Glu His Val Asp Lys Asp Thr Leu Lys Gly Gln
305                 310                 315
```

(2) INFORMATION FOR SEQ ID NO:1677:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1677

```
Gly Phe Leu Val Phe Leu Asp Arg Arg Leu Ile Val Met Val Thr Asp
1                   5                  10                  15
Ser Lys Gly Ser Arg Tyr Ile Asn Val His Ile Leu Phe Arg Gln Ile
            20                  25                  30
Ser Leu Tyr Ala Leu Leu Ser Val Val Gly Ser Leu Leu Phe Leu Gly
        35                  40                  45
Val Ser Leu Leu Val Leu Asn Lys Glu Ile Lys Asn Ile Glu Lys Gln
    50                  55                  60
His Ala Leu Ile Thr Lys Glu Phe Glu Lys Lys Arg Glu Thr Asn Glu
65                  70                  75                  80
Lys Leu Ser Leu Gln Met Asp Glu Phe Leu Asp Asp Leu Gln Leu Ser
                85                  90                  95
Gly Glu Arg Ile Asn Asp Leu Glu Glu Val Val Gly Val Asn Arg Pro
            100                 105                 110
Glu Glu Glu Lys Glu Glu Gly Asn Phe Ser Ser Arg Leu Asp Val Ala
        115                 120                 125
Gly Ile Thr Gly Leu Gln Lys Ser Phe Ile Met Arg Leu Ile Pro Asn
    130                 135                 140
Asp Tyr Pro Leu Glu Ser Tyr Arg Arg Val Ser Ala Ala Phe Asn Lys
145                 150                 155                 160
Arg Met His Pro Ile Leu His Val Leu His Asn His Thr Gly Leu Asp
                165                 170                 175
Leu Ser Thr Ala Ile Asn Thr Pro Val Tyr Ala Ser Ala Ser Gly Val
            180                 185                 190
Val Gly Leu Ala Ser Lys Gly Trp Asn Gly Gly Tyr Gly Asn Leu Ile
        195                 200                 205
Lys Val Phe His Pro Phe Gly Phe Lys Thr Tyr Tyr Ala His Leu Asn
    210                 215                 220
Lys Ile Val Val Lys Thr Gly Glu Phe Val Lys Lys Gly Gln Leu Ile
225                 230                 235                 240
Gly Tyr Ser Gly Asn Thr Gly Met Ser Thr Gly Pro His Leu His Tyr
```

```
                245                 250                 255
Glu Val Arg Phe Leu Asp Gln Pro Ile Asn Pro Met Ser Phe Thr Lys
            260                 265                 270
Trp Asn Met Lys Asp Phe Glu Glu Val Phe Asn Lys Glu Arg Ser Ile
        275                 280                 285
Arg Trp Gln Ser Leu Ile Thr Ile Ile Asn Arg Leu Met Gln Lys Gln
    290                 295                 300
Asp Gln Arg Leu Ser Ser Leu Lys Ala Pro Lys
305                 310                 315
```

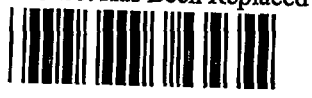
(2) INFORMATION FOR SEQ ID NO:1678:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 460 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

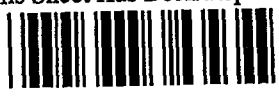
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1678

```
Asp Ile Glu Phe Ala Asn Leu Tyr His Ile Pro Ile Lys Val Ile Thr
1               5                   10                  15
Gln Ser Pro Gln Asn Leu Pro His Thr Lys Glu Glu Ile Leu Lys Asn
            20                  25                  30
Ser Gly Glu Trp Ser Asp Leu Ser Ser Ser Leu Ala Arg Lys Lys Ile
        35                  40                  45
Leu Pro Tyr Phe Asp Lys Glu Asn Leu Gly Lys Arg Val Ile Asn Tyr
    50                  55                  60
Arg Leu Gln Asn Trp Gly Val Ser Arg Gln Arg Tyr Trp Gly Ala Pro
65                  70                  75                  80
Ile Pro Met Ile His Cys Lys His Cys Gly Ile Val Pro Glu Thr Gln
                85                  90                  95
Leu Pro Val Thr Leu Pro Glu Asp Ile Val Ile Asp Gly Glu Gly Asn
            100                 105                 110
Pro Leu Lys Lys His Ala Ser Trp Arg Phe Ala Gln Cys Pro Arg Cys
        115                 120                 125
His Lys Asp Ala Leu Val Glu Thr Asp Thr Met Asp Thr Phe Ile Gln
    130                 135                 140
Ser Ser Trp Tyr Phe Leu Arg Tyr Thr Thr Pro Lys Asn Gln Arg Glu
145                 150                 155                 160
Asn Gln Ala Phe Asp Gln Asn Tyr Leu Lys Tyr Phe Met Pro Val Asp
                165                 170                 175
Thr Tyr Ile Gly Gly Ile Glu His Ala Ile Leu His Leu Leu Tyr Ala
            180                 185                 190
Arg Phe Phe Thr Lys Ala Leu Arg Asp Leu Gly Tyr Leu His Leu Asp
        195                 200                 205
Glu Pro Phe Lys Gln Leu Ile Thr Gln Gly Met Val Leu Lys Asp Gly
    210                 215                 220
Ala Lys Met Ser Lys Ser Lys Gly Asn Val Val Ser Pro Lys Glu Ile
225                 230                 235                 240
Leu Lys Lys Tyr Gly Ala Asp Ala Val Arg Leu Phe Ile Leu Phe Ala
                245                 250                 255
Ala Pro Pro Ala Lys Glu Leu Glu Trp Asn Asp Asn Ala Leu Glu Gly
            260                 265                 270
```

```
Ala His Arg Phe Ile Lys Arg Leu Tyr Asp Lys Ala Asn Ala Ile Thr
        275                 280                 285
Pro Thr Thr Ser Lys Pro Glu Phe Lys Glu Val Gly Leu Asn Glu Ala
    290                 295                 300
Gln Lys Leu Ala Arg Lys Lys Val Tyr Glu Ala Leu Lys Lys Ser His
305                 310                 315                 320
Glu Ile Phe Asn Lys Ala Glu Ser Ala Tyr Ala Phe Asn Thr Leu Ile
                325                 330                 335
Ala Ser Cys Met Glu Ala Leu Asn Ala Leu Asn Ala Gln Ser Asp Glu
            340                 345                 350
Gln Ile Leu Cys Glu Gly Tyr Phe Val Leu Leu Gln Ile Leu Glu Pro
        355                 360                 365
Met Ile Pro His Thr Ala Trp Glu Leu Ser Glu Arg Leu Phe Lys Arg
    370                 375                 380
Glu Asn Phe Lys Pro Ile Glu Val Asp Glu Ser Ala Leu Ile Glu Asp
385                 390                 395                 400
Phe Met Thr Leu Gly Leu Thr Ile Asn Gly Lys Arg Arg Ala Glu Leu
                405                 410                 415
Lys Val Asn Ile Asn Ala Ser Lys Glu Glu Ile Ile Ile Leu Ala Lys
            420                 425                 430
Lys Glu Leu Glu Lys Tyr Leu Glu Asn Ala Ser Val Lys Lys Glu Ile
        435                 440                 445
Tyr Val Pro Asn Lys Leu Val Asn Phe Val Thr Ala
    450                 455                 460
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1679:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 403 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1679

```
Leu Asn Leu Trp Leu Lys Ser Leu Met Arg Gly Asn Ser Ile Met Lys
1               5                   10                  15
Asn Ser His Gly Leu Lys Ala Phe Leu Glu Thr Lys Pro Lys Glu Tyr
            20                  25                  30
His Lys Phe Asp Pro Ser Arg Phe Ile Gln Ile Tyr Lys Asp Phe Lys
        35                  40                  45
Asn Ala Phe Phe Glu Ile Gln Ala Lys Val Ile His Val Val Gly Thr
    50                  55                  60
Asn Gly Lys Gly Ser Thr Gly Arg Phe Leu Thr Leu Leu Leu Ala Asp
65                  70                  75                  80
Gln Gly Phe Lys Val Leu His Phe Thr Ser Pro His Val Phe Glu Phe
                85                  90                  95
Arg Glu Arg Phe Tyr Leu Asn Gly Ser Val Val Lys Glu Ser Val Leu
            100                 105                 110
Glu Asn Ala His Gln Gln Leu Gln Ser His Ala Phe Ser Asn Ala Cys
        115                 120                 125
Ser Tyr Phe Glu Tyr Ala Thr Leu Leu Ala Val Met Leu Ala Lys Asp
    130                 135                 140
Cys Asp Tyr Leu Val Leu Glu Ala Gly Leu Gly Gly Glu Phe Asp Ser
```

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

(2) INFORMATION FOR SEQ ID NO:1680:

(i). SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

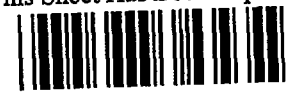
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1680

```
Ser Val Ser Ser His Ser Gly Ser Ala Asp Leu Leu Glu Asn Leu Gly
1               5                   10                  15
Val Asn Ile Glu Met Asn Pro Met Gln Leu Glu Asn Cys Phe Lys Gln
            20                  25                  30
Ser His Phe Gly Phe Leu Phe Ala Pro Leu Tyr His Gln Ser Phe Lys
        35                  40                  45
Lys Ser Ala Pro Leu Arg Lys Glu Leu Phe Thr Lys Thr Ile Phe Asn
    50                  55                  60
Cys Leu Gly Pro Leu Ile Asn Pro Leu Arg Pro Lys Ile Gln Leu Leu
65                  70                  75                  80
```

This Sheet Has Been Replaced



```
Gly Val Tyr Asp Lys Ser Leu Cys Lys Thr Met Ala Leu Ala Leu Lys
                85                  90                  95
Ala Leu Gly Val Lys Arg Ala Met Val Val Asn Gly Gly Gly Thr Asp
            100                 105                 110
Glu Ile Val Leu His Asp Ile Thr His Ala Cys Glu Leu Lys Asn Asn
        115                 120                 125
Glu Ile Leu Glu Tyr Asp Leu Ser Ala Lys Asp Phe Asp Leu Pro Pro
    130                 135                 140
Tyr Asp Leu Lys Glu Leu Gln Ile Glu Asn Ala Lys Glu Ser Val Gln
145                 150                 155                 160
Ala Cys Leu Asp Ile Leu Glu Asn Lys Gly Lys Asp Ser His Thr Met
                165                 170                 175
Val Val Ala Ala Asn Val Ala Ser Leu Leu Tyr Leu Ser His Arg Ala
            180                 185                 190
Lys Gly Phe Lys Arg Gly Arg Glu His Asp Phe Arg Ala Phe Lys Asn
        195                 200                 205
Gln Ser Ala Leu Cys Ala Phe Thr Lys Asn His Lys Ala Lys Pro Cys
    210                 215                 220
Leu Ala Cys
225
```

(2) INFORMATION FOR SEQ ID NO:1681:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 294 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...294

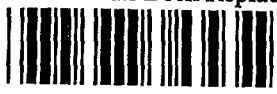
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1681

```
Asn Leu Val Val Ser Val Pro Ala Thr Ser Ala Asn Leu Gly Pro Gly
1               5                   10                  15
Phe Asp Cys Leu Gly Leu Ser Leu Asn Leu Arg Asn Arg Phe Phe Ile
            20                  25                  30
Glu Pro Ser Asn Ile His Ala Val Lys Leu Val Gly Glu Gly Glu Gly
        35                  40                  45
Ile Pro Lys Phe Leu Thr Asn Asn Ile Phe Thr Lys Val Phe Tyr Glu
    50                  55                  60
Ile Leu Lys Lys His Gly Asn Asp Gly Ser Phe Lys Phe Leu Leu His
65                  70                  75                  80
Asn Lys Val Pro Ile Thr Arg Gly Met Gly Ser Ser Ser Ala Met Ile
                85                  90                  95
Val Gly Ala Val Ala Ser Ala Phe Ala Phe Leu Gly Phe Ala Phe Asp
            100                 105                 110
Arg Glu Asn Ile Leu Asn Thr Ala Leu Ile Tyr Glu Asn His Pro Asp
        115                 120                 125
Asn Ile Thr Pro Ala Val Phe Gly Gly Tyr Asn Ala Ala Phe Val Glu
    130                 135                 140
Lys Lys Lys Val Ile Ser Leu Lys Thr Lys Ile Pro Ser Phe Leu Lys
145                 150                 155                 160
Ala Val Met Val Ile Pro Asn Arg Val Ile Ser Thr Lys Gln Ser Arg
                165                 170                 175
His Leu Leu Pro Lys Arg Tyr Ser Val Gln Glu Ser Val Phe Asn Leu
```

```
            180                 185                 190
Ser His Ala Ser Leu Met Thr Met Ala Ile Val Gln Gly Lys Trp Asp
        195                 200                 205
Leu Leu Arg Cys Cys Ser Lys Asp Arg Met His Gln Tyr Lys Arg Met
    210                 215                 220
Gln Thr Tyr Pro Val Leu Phe Ala Ile Gln Lys Leu Ala Leu Glu Asn
225                 230                 235                 240
Asn Ala Leu Met Ser Thr Leu Ser Gly Ser Gly Ser Ser Phe Phe Asn
                245                 250                 255
Met Cys Tyr Glu Glu Asp Ala Pro Lys Leu Lys Gln Val Leu Ser Lys
            260                 265                 270
Lys Phe Pro Lys Phe Arg Val Ala Val Leu Asp Phe Asp Asn Asp Gly
        275                 280                 285
Val Leu Ile Glu Lys Asp
    290
```

(2) INFORMATION FOR SEQ ID NO:1682:

This Sheet Has Been Replaced



(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:1682

```
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:1683:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1683

```
Tyr His Arg Thr Asn Thr Thr Ile Arg Ile Ile Ile Met Gln Asp Leu
1               5                   10                  15
Pro Pro Cys Pro Lys Arg Asn Asp Ala Tyr Thr Tyr His Asp Gly Thr
            20                  25                  30
Gln Phe Val Cys Ser Ser Cys Leu Tyr Glu Trp Asn Gly Asn Glu Ile
        35                  40                  45
Ser Asn Glu Glu Leu Ile Val Lys Asp Cys His Asn Asn Leu Leu Gln
    50                  55                  60
Asn Gly Asp Ser Val Ile Leu Ile Lys Asp Leu Lys Val Lys Gly Ser
65                  70                  75                  80
Ser Leu Val Leu Lys Lys Gly Thr Lys Ile Lys Asn Ile Lys Leu Val
                85                  90                  95
Asn Ser Asp His Asn Val Asp Cys Lys Val Glu Gly Gln Ser Leu Ser
            100                 105                 110
Leu Lys Ser Glu Phe Leu Lys Lys Ala
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:1684:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

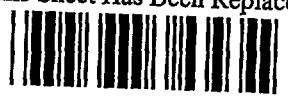
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

This Sheet Has Been Replaced



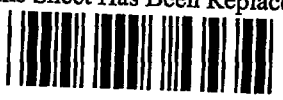
(A) NAME/KEY: misc_feature
(B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1684

```
Lys Gly Cys Phe Met Arg Glu Phe Phe Lys Lys Leu Gly Thr Glu Tyr
1               5                  10                  15
Ala Ser Lys Leu Phe Leu Val Tyr Trp Leu Arg Trp Met Leu Ser Ala
            20                  25                  30
Leu Val Met Leu Pro Phe Met Glu Val Phe Tyr Tyr Phe Asn Phe Pro
        35                  40                  45
Leu Trp Leu Asn Leu Phe Leu Gly Gln Thr Ile Gly Ala Val Ile Phe
    50                  55                  60
Phe Lys Leu Asp Lys Leu Ile Phe Ser Lys Lys
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:1685:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 497 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1685

```
Phe Phe Lys Arg Tyr Glu Arg Leu Ser Met Gln Tyr Ser Ser Leu Leu
1               5                  10                  15
Ser Val Val Leu Phe Leu Pro Leu Ile Gly Ala Val Tyr Ala Gly Leu
            20                  25                  30
Phe Gly Ala Lys Ala Lys Ala Leu His Val Gly Val Phe Asn Ser Leu
        35                  40                  45
Cys Val Leu Val Ser Phe Ile Gly Ala Val Val Leu Phe Ile Gln Ala
    50                  55                  60
Trp His His Gln Ser Tyr Glu Lys Tyr Leu Phe Asp Trp Ile Val Val
65                  70                  75                  80
Gly Asn Phe Lys Val Gly Phe Ser Leu Met Leu Asp Asn Ile Asn Ala
                85                  90                  95
Val Met Ile Val Val Val Thr Leu Val Ser Phe Leu Val His Val Tyr
            100                 105                 110
Ser Ile Gly Tyr Met Glu His Asp Thr Gly Phe Asn Arg Tyr Phe Ser
        115                 120                 125
Tyr Leu Ser Gly Phe Val Phe Ser Met Leu Val Leu Val Leu Ser Asp
    130                 135                 140
Asn Phe Leu Gly Leu Phe Ile Gly Trp Glu Gly Val Gly Leu Cys Ser
145                 150                 155                 160
Tyr Leu Leu Ile Gly Phe Trp Tyr His Lys Lys Ser Ala Asn Asn Ala
                165                 170                 175
Ser Ile Glu Ala Phe Val Met Asn Arg Ile Thr Asp Leu Gly Met Leu
            180                 185                 190
Met Gly Ile Ile Leu Ile Phe Trp Asn Phe Gly Thr Leu Gln Tyr Lys
        195                 200                 205
Glu Val Phe Ser Met Leu Asn Asn Ala Asp Tyr Ser Met Leu Phe Tyr
    210                 215                 220
```

```
Ile Ser Val Phe Leu Phe Ile Gly Ala Met Gly Lys Ser Ala Gln Phe
225                 230                 235                 240
Pro Met His Thr Trp Leu Ala Asn Ala Met Glu Gly Pro Thr Pro Val
                245                 250                 255
Ser Ala Leu Ile His Ala Ala Thr Met Val Thr Ala Gly Val Tyr Leu
            260                 265                 270
Ile Ile Arg Ala Asn Pro Leu Tyr Ser Ala Val Phe Glu Val Gly Tyr
        275                 280                 285
Phe Ile Ala Cys Leu Gly Ala Phe Val Ala Leu Phe Gly Ala Ser Met
    290                 295                 300
Ala Leu Val Asn Lys Asp Leu Lys Arg Ile Val Ala Tyr Ser Thr Leu
305                 310                 315                 320
Ser Gln Leu Gly Tyr Met Phe Val Ala Ala Gly Leu Gly Ala Tyr Ala
                325                 330                 335
Ile Ala Leu Phe His Leu Phe Thr His Ala Phe Phe Lys Ser Leu Leu
            340                 345                 350
Phe Leu Gly Ser Gly Asn Val Met His Ala Met Glu Asp Asn Leu Asp
        355                 360                 365
Ile Thr Lys Met Gly Ala Leu Tyr Lys Pro Met Arg Ile Thr Ala Val
    370                 375                 380
Phe Met Ile Ile Gly Ser Val Ala Leu Cys Gly Ile Tyr Pro Phe Ala
385                 390                 395                 400
Gly Tyr Phe Ser Lys Asp Lys Ile Leu Glu Val Ala Phe Gly Met His
                405                 410                 415
His His Ile Leu Trp Phe Val Leu Leu Ile Gly Ala Ile Phe Thr Ala
            420                 425                 430
Phe Tyr Ser Phe Arg Leu Ile Met Leu Val Phe Phe Ala Pro Lys Gln
        435                 440                 445
His Glu Ile Asn His Pro His Glu Gly Gln Lys Phe His Ala Phe Glu
    450                 455                 460
His Ala Thr Val Arg Gly Phe Gly Gly His Cys Arg Phe Phe Arg Arg
465                 470                 475                 480
Ala Val Phe Ser Phe Tyr Leu Ser Ser Glu Phe Leu Val Leu Glu Ser
                485                 490                 495
Ile
```

(2) INFORMATION FOR SEQ ID NO:1686:

This Sheet Has Been Replaced



(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

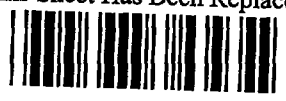
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686

```
Asn Lys Pro Asn Lys Gly Ala Val Leu Glu Lys Thr Lys Lys Arg Gln
1               5                  10                  15
Leu Leu Gln Lys Lys Thr Lys Lys Arg Ile Lys Gln Lys Arg Leu Pro
            20                  25                  30
Gln Lys Lys Ile Lys Gln Lys Thr Arg Gln Arg Leu Lys Arg Lys Ile
        35                  40                  45
Glu Val Pro Thr Lys Thr Thr Tyr Leu Leu Leu Glu Glu Ala Gly Ile
```

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

(2) INFORMATION FOR SEQ ID NO:1687:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1687

```
Gly Gly Phe Met Ala Lys Gln Glu Tyr Lys Gln Leu Pro Lys Arg Ala
1               5                   10                  15
Glu Val His Ser Ala Thr Glu Gln Phe Lys Asp Thr Ile Lys Thr Ser
            20                  25                  30
Leu Gly Leu Asp Leu Phe Lys Gly Leu Gly Leu Thr Ile Lys Glu Phe
        35                  40                  45
Phe Ser Pro Ser Val Thr Ile His Tyr Pro Met Glu Gln Leu Pro Leu
    50                  55                  60
Ser Pro Arg Tyr Arg Ala Val His His Leu Gln Arg Leu Leu Asp Ser
65                  70                  75                  80
Gly Ser Glu Arg Cys Ile Gly Cys Gly Leu Cys Glu Lys Ile Cys Thr
                85                  90                  95
Ser Asn Cys Ile Arg Ile Ile Thr His Lys Gly Glu Asp Asn Arg Lys
            100                 105                 110
```

```
Lys Ile Asp Ser Tyr Thr Ile Asn Leu Gly Arg Cys Ile Tyr Cys Gly
        115                 120                 125
Leu Cys Ala Glu Val Cys Pro Glu Leu Ala Ile Val Met Gly Asn Arg
    130                 135                 140
Phe Glu Asn Ala Ser Thr Gln Arg Ser Gln Tyr Gly Ser Lys Ser Glu
145                 150                 155                 160
Phe Leu Thr Ser Glu Gln Asp Ala Lys Asn Cys Ser His Ala Glu Phe
                165                 170                 175
Leu Gly Phe Gly Ala Val Ser Pro Asn Tyr Asn Glu Arg Met Gln Ala
            180                 185                 190
Thr Pro Leu Asp Tyr Val Gln Glu Pro Ser Lys Glu Glu Ser Lys Glu
        195                 200                 205
Glu Ser Pro Thr Ser Pro Glu Ser His Lys Gly Asp Glu Asn Val
    210                 215                 220
```

(2) INFORMATION FOR SEQ ID NO:1688:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1688

```
Ile Met Ser Lys Asn Leu Gln Lys Lys Asn Pro Lys Lys Ser Leu Gln
1               5                   10                  15
Gln Ala Gln Lys Ala Ile Arg Glu Met Lys Met Phe Glu Thr Ile Ala
            20                  25                  30
Phe Tyr Phe Phe Ala Ile Leu Thr Leu Ser Met Ala Leu Val Val Ile
        35                  40                  45
Thr Thr Thr Asn Ile Leu Tyr Ala Ile Thr Ala Leu Ala Ser Ser Met
    50                  55                  60
Val Phe Ile Ser Ala Phe Phe Phe Leu Leu Asp Ala Glu Phe Leu Gly
65                  70                  75                  80
Val Val Gln Ile Thr Val Tyr Val Gly Ala Val Ile Val Met Tyr Ala
                85                  90                  95
Phe Gly Met Met Phe Phe Asn Ser Ala Ala Glu Val Val Glu Arg Lys
            100                 105                 110
Gln Ser Pro Lys Ile Leu Cys Val Leu Ser Phe Gly Val Ala Leu Leu
        115                 120                 125
Leu Thr Leu Ile Leu Ser Ala Pro Ser Ile Gly Glu Asn Leu Ser Lys
    130                 135                 140
Gln Val Asn Ser Asn Ala Ile Asp Ala Gln Ile Pro Asn Ile Lys Ala
145                 150                 155                 160
Ile Gly Tyr Val Leu Phe Thr Asn Tyr Leu Ile Pro Phe Glu Ala Ala
                165                 170                 175
Ala Leu Met Leu Leu Val Ala Met Val Gly Gly Ile Ala Thr Gly Ile
            180                 185                 190
Gln Lys Ile His Gly Lys Asn His Thr Gln Phe Ile Lys Glu Ser Leu
        195                 200                 205
```

(2) INFORMATION FOR SEQ ID NO:1689:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

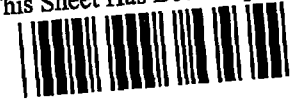
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1689

```
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
Asn Ala Asn Ser Val Ile Thr Ile Asn Ser Val Ser Leu Asn Gly Glu
225                 230                 235                 240
Tyr Leu Gln Phe Phe Ser
                245
```

(2) INFORMATION FOR SEQ ID NO:1690:

This Sheet Has Been Replaced



(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:1690

```
Val Phe Thr Pro Arg Val Lys Arg Phe Phe Ile Phe Leu Phe Leu Phe
1               5                  10                  15
Leu Ile Leu His Glu Ile Leu Asn Thr Glu Leu Ala Pro Leu Asn Gly
            20                  25                  30
Ile Ser Leu Ala Leu Gly Tyr Leu Cys Leu Phe Ile Leu Val Leu Ser
        35                  40                  45
Ala Ser Leu Ile Phe Glu Lys Val Leu Ser Lys Gln Tyr Leu Gln Thr
    50                  55                  60
Ala Lys Asp Lys Ile Ala Ser Leu Lys Asn Leu Lys Val Ile Ala Ile
65                  70                  75                  80
Thr Gly Ser Phe Gly Lys Thr Ser Thr Lys Asn Phe Leu His Gln Ile
                85                  90                  95
Leu Gln Thr Gln Phe Asn Ala His Ala Ser Pro Lys Ser Val Asn Thr
            100                 105                 110
Leu Leu Gly Ile Ala Asn Asp Ile Asn Gln Asn Leu Asp Asp Arg Ser
        115                 120                 125
Glu Ile Tyr Ile Ala Glu Ala Gly Ala Arg Asn Lys Gly Asp Ile Lys
    130                 135                 140
Glu Ile Thr Arg Leu Ile Glu Pro His Leu Ala Val Val Ala Glu Val
145                 150                 155                 160
Gly Glu Gln His Leu Glu Tyr Phe Lys Thr Leu Glu Asn Ile Cys Glu
                165                 170                 175
Thr Lys Ala Glu Leu Leu Asp Ser Lys Arg Leu Glu Lys Ala Phe Cys
            180                 185                 190
Tyr Ser Val Glu Lys Ile Lys Pro Tyr Ala Pro Lys Asp Ser Pro Leu
        195                 200                 205
Ile Asp Tyr Ser Ser Leu Val Arg Asn Val Gln Ser Thr Leu Lys Gly
    210                 215                 220
Thr Ser Phe Glu Thr Leu Ile Asn Gly Val Trp Glu Ser Phe Glu Thr
225                 230                 235                 240
Lys Val Leu Gly Glu Phe Asn Ala Tyr Asn Ile Ala Ser Ala Ile Leu
                245                 250                 255
Ile Ala Lys His Leu Gly Leu Glu Thr Glu Arg Ile Lys Arg Leu Val
            260                 265                 270
Phe Glu Leu Lys Pro Ile Asn His Arg Leu Gln Leu Leu Glu Ala Asn
        275                 280                 285
Gln Lys Ile Ile Ile Asp Asp Ser Phe Asn Gly Asn Leu Lys Gly Met
    290                 295                 300
Leu Glu Gly Ile Arg Leu Ala Ser Leu His Gln Gly Arg Lys Val Ile
305                 310                 315                 320
Val Thr Pro Gly Leu Val Glu Ser Asn Thr Glu Ser Asn Glu Ala Leu
                325                 330                 335
Ala Gln Lys Ile Asp Gly Val Phe Asp Val Ala Ile Ile Thr Gly Glu
            340                 345                 350
Leu Asn Ser Lys Thr Ile Ala Ser Lys Leu Lys Thr Pro Gln Lys Ile
        355                 360                 365
Leu Leu Lys Asp Lys Ala Gln Leu Glu Asn Ile Leu Gln Ala Thr Thr
    370                 375                 380
Ile Gln Gly Asp Leu Ile Leu Phe Ala Thr Asp Ala Pro Asn Tyr Ile
385                 390                 395                 400
```

(2) INFORMATION FOR SEQ ID NO:1691:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 717 amino acids
(B) TYPE: amino acid

This Sheet Has Been Replaced



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1691

```
Tyr Ala Leu Lys Ser Leu Arg Gln Ala Tyr Phe Phe Ser Gln Ser Val
1               5                  10                  15
Phe Val Gly Leu Tyr His Gly Ala Ser Ile Phe Asp Leu Lys Phe Glu
            20                  25                  30
Val Tyr Leu Thr Met Leu Ile Ser Leu Met Pro Phe Val Ala Thr Ile
        35                  40                  45
Tyr Ile Asn Phe Pro Lys Thr Thr Glu Thr Ser His Gly Tyr Ala Arg
    50                  55                  60
Trp Ala Asn Val Lys Asp Ile Glu Cys Phe Lys Ile Phe Ser Lys Glu
65                  70                  75                  80
Gly Phe Cys Lys Val Val His Arg Leu Gly Val Gln Phe Asp Asn Gly
                85                  90                  95
Phe Ile Leu Gly Lys Phe Gly Phe Pro Lys Leu Arg Asn Val Cys Tyr
            100                 105                 110
Asp Lys Pro Leu Gly Thr Met Ile Val Ala Pro Pro Gly Ala Gly Lys
        115                 120                 125
Thr Ala Cys Val Ala Leu Pro Asn Leu Leu Thr Leu Pro Asn Ser Cys
    130                 135                 140
Ile Ile Thr Asp Ile Lys Gly Glu Leu Arg Asp Lys Thr Ala Gly Tyr
145                 150                 155                 160
Arg Gln Lys Phe Leu Asn Asn Arg Ile Leu Ile Phe Asn Pro Tyr Gly
                165                 170                 175
Asp Asp Asn Thr Cys Tyr Phe Asn Pro Phe Asp Lys Arg Ile Val Glu
            180                 185                 190
Lys Met Thr Phe Ala Glu Gln Leu Arg His Val Lys Ala Val Gly Asp
        195                 200                 205
Gly Ile Phe Val Asp Glu Glu Asp His Trp Val Ser Lys Ala Lys Glu
    210                 215                 220
Leu Phe Val Phe Phe Ala Leu Leu Gln Val Val Thr Lys Gly His Ser
225                 230                 235                 240
Ser Phe Tyr Asp Val Ser Ile Ala Pro Ala Asn Asp Tyr Ala Pro Leu
                245                 250                 255
Ile His Pro Lys Ser Pro Tyr Tyr Lys Gln Leu Tyr Gln His Asp Lys
            260                 265                 270
Lys Thr Gly Glu Val Ile Leu Asp Pro Gln Thr Asn Ala Pro Met Lys
        275                 280                 285
Asn Pro Gln Ala Asn Val Leu Lys Leu Phe Leu Asn Gln Val Ala Asp
    290                 295                 300
Gln Lys Tyr Ile Asp Met Asn Asp Glu Lys Asn Tyr Asp Pro Arg Glu
305                 310                 315                 320
Pro Glu Pro Pro Tyr Gly Thr Lys Gly Ala Leu Asp Glu Ile Ile Arg
                325                 330                 335
Thr Asp Ala Arg Ser Trp Ala Asn Thr Pro Asp Asp Glu Phe Gly Ser
            340                 345                 350
Ile Met Ser Ser Phe Lys Arg Phe Met Tyr Val Tyr Lys Asp Pro Lys
        355                 360                 365
Val Arg Glu Ala Thr Ser Lys Met Ser Phe Asp Tyr Glu Glu Leu Arg
    370                 375                 380
Thr Gly Asn Ile Ser Ile Tyr Ile Val Ile Ala Gln Ile Asp Ile Gly
385                 390                 395                 400
```

```
Thr Leu Ser Ser Leu Val Arg Ala Phe Leu Glu Ser Ile Ala Lys Asn
                405                 410                 415
Leu Met Val Lys Glu Ser Ser Lys Pro Glu Glu Arg Ile Phe Ile Ile
            420                 425                 430
Ala Asp Glu Phe Val Arg Phe Gly Lys Leu Pro Phe Leu Glu Met
        435                 440                 445
Pro Ala Leu Cys Arg Ser Tyr Asn Val Val Pro Leu Phe Ile Thr Gln
    450                 455                 460
Asp Tyr Ala Met Ile Arg Lys Tyr Tyr Ser Asp Asp Asp Leu Lys Ile
465                 470                 475                 480
Leu Lys Gly Val Val His Tyr Asn Ile Val Phe Lys Met Asn Ser Ala
                485                 490                 495
Glu Asp Ala Glu Ile Val Ser Lys Glu Val Gly Glu Phe Thr Arg Arg
            500                 505                 510
Ser Lys Asn Tyr Ser Thr Glu Lys Gly Gln Leu Val Phe Gly Gly Ser
        515                 520                 525
Ser Ser Tyr Ser His Glu Gly Arg Asn Leu Leu Thr Ala Gln Asp Ile
    530                 535                 540
Met Asn Ile Asn Ser Asp Glu Val Ile Val Ile Val Thr Gly Ala Lys
545                 550                 555                 560
Ala Thr Pro Leu Lys Leu Lys Ala Asn Tyr Trp Phe Lys Asp Lys Glu
                565                 570                 575
Leu Leu Lys Arg Ala Asn Leu Pro Ile Asp Leu Glu Val Glu Arg Gln
            580                 585                 590
Arg Val Glu Glu Pro Ile Gln Pro Thr Thr Glu Ile Glu Thr Thr Pro
        595                 600                 605
Asn Gln Asn Lys Ala Asp Leu Glu Pro Ser Asn Lys Gly Glu Lys Val
    610                 615                 620
Glu Asn Glu Ser Asn Glu Arg Asn Thr Asn Glu Asn Asn Pro Thr Thr
625                 630                 635                 640
Pro Gln Glu Leu Glu Asn Ser Asn Leu Lys Glu Ser Glu Lys Asp Asn
                645                 650                 655
Glu Ser Pro Ile Thr Leu Glu Asn Ala Asn Glu Asn Ile Glu Gln Gly
            660                 665                 670
Asn His Asn Glu Ile Asp Glu Ile Leu Lys Lys Pro Leu Ser Glu Ile
        675                 680                 685
Ser Met Glu Glu Lys Arg Ala Leu Phe Lys Lys Met Gln Gln Ser Asp
    690                 695                 700
Glu Glu Ser Glu Gln Glu Val Thr Gln Ser Thr Gln Ser
705                 710                 715
```

(2) INFORMATION FOR SEQ ID NO:1692:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2440 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1692

```
Tyr Asn His Pro Asn Leu Ser Val Ala Asp Leu Glu Leu Glu Gln Gln
1               5                   10                  15
Asn Leu Gly Glu Gln Asn Gly Lys Glu Arg Thr Asn Arg Ala Asp Glu
```

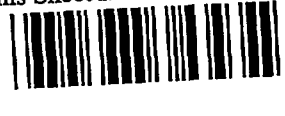
```
            20                  25                  30
Pro Asn Gly Thr Arg Ala Gly Ile Pro Gln Glu Ile His Arg Arg Ser
        35                  40                  45
Glu Pro Arg Gly Gln Gln Glu Gly Met Glu Arg Ser Ser Asp Glu Asp
    50                  55                  60
Leu Ser His Gln Asp Pro Ser Leu Phe Ile Glu Ser Arg Glu Gln Gly
65                  70                  75                  80
Gly Thr Arg Gly Val Tyr Arg Ser Ser Asp Gln Gln Ala Val Ser Glu
                85                  90                  95
Glu Ser His Arg Glu Arg Asp Arg Ile His Glu His Val Ser Arg Gly
            100                 105                 110
Asp Gly Val Ser Ala Arg Ala Asp Ala Arg Ala Asn Ser Asn Gly Ala
        115                 120                 125
Ser Ser Pro Ala Ser Arg Met Glu Asn Gly Ala Arg Ser Glu Glu Lys
    130                 135                 140
Gly Asp Asn Pro Ser Asp Glu Arg Gly Ile Pro Gln Thr Pro Gln Ser
145                 150                 155                 160
Pro Ser His Gln Gln Asn Ser Ser Arg Asp Leu Gly Leu Ser Leu Ser
                165                 170                 175
Arg Glu Gln Pro Gly Gln Thr Gly Arg Leu Arg Leu Phe Asp His Gly
            180                 185                 190
Gln Met Gly Ser Leu Phe Pro Thr Asp His Glu Asn Gln Arg Lys Arg
        195                 200                 205
Ser Asp Asn Glu Leu Asp Arg Arg Ser Asp Lys Ala Asn Glu Asn Gly
    210                 215                 220
Asp Lys Ser Pro Arg Gln Asn Gly Ser Ala Asn Gln Glu Ser Ala Arg
225                 230                 235                 240
Ser Glu Arg Tyr Gly Ile Ala Gln Gly Ser Ser Asn Gln Ser Val Leu
                245                 250                 255
Leu Pro Ala Gln Ser Arg Leu His His Ala Gly Leu Ser Ala Gln Asn
            260                 265                 270
Gly Leu Arg Asp Leu Glu Glu Asn Arg Asp Gln Glu Gly Arg Leu Leu
        275                 280                 285
Ser Asn Leu Asp Asn Leu Glu Ser Leu Leu Asn Ala Ile Arg Asn Asn
    290                 295                 300
Thr Ile Ala Ser Glu Pro Asp Phe Arg Ser Arg Leu Leu Glu Ala Ile
305                 310                 315                 320
Gln Asn Asn Asp Pro Leu Lys Asp Ser Ile Val Gly Ala Gln Leu Leu
                325                 330                 335
Lys Asp Pro Thr Thr Lys Ile Phe Tyr Asp Lys Phe Gln Leu Lys Ile
            340                 345                 350
Ser Pro Lys Lys Val Leu Glu Ile Leu Glu Asn Arg Leu Lys Lys Ser
        355                 360                 365
Ile Glu Thr Thr Asn Glu Thr Leu Asn Ala Phe Asn Val Leu Asp Ser
    370                 375                 380
Gln Ala Ile Asp Leu Asn Ala Ile Ser Asn Ser Val Gly Leu Asn Pro
385                 390                 395                 400
Thr Gln Glu Ser Lys Ile Thr Asp Asn Ser Val Glu Leu Asn Asn Ala
                405                 410                 415
Gln Glu Gln Thr Ala Gln Glu Gln Thr Thr Gln Glu Gln Thr Thr Gln
            420                 425                 430
Glu Gln Thr Thr Gln Glu Gln Thr Thr Gln Glu Gln Thr Thr Gln Glu
        435                 440                 445
Gln Thr Thr Gln Glu Gln Thr Thr Gln Glu Gln Asp Thr Gln Glu Asn
    450                 455                 460
Ala Pro Thr Thr Ile Lys Gln Glu Thr Pro Ile Thr Pro Ala Ile Pro
465                 470                 475                 480
Leu Asn Pro Lys Ile Asp Phe Lys Pro Ser Glu Glu Val Leu Ile Lys
                485                 490                 495
Gly Ala Lys Thr Arg Tyr Lys Ala Asn Ile Lys Ala Ile Glu Leu Leu
            500                 505                 510
Lys Glu Leu Gln Ala Lys Gln Glu Ile Leu Lys Gly Asp Tyr Tyr Ala
        515                 520                 525
Thr Leu Lys Glu Gln Glu Ile Leu Ala Gln Phe Ser Gly Trp Gly Gly
    530                 535                 540
```

This Sheet Has Been Replaced

SUBSTITUTE SHEET (RULE 26)

Leu Glu Ser Tyr Phe Lys Lys Ala Gln His Pro Glu Glu Phe Lys Glu
545 550 555 560
Leu Asn Ala Leu Leu Thr Lys Asp Glu Phe Arg Arg Ala Tyr Leu Ser
565 570 575
Ala Arg Asp Ala Tyr Tyr Thr Pro Lys Leu Val Ile Asp Ser Ile Tyr
580 585 590
Gln Gly Leu Asp Gln Leu Gly Phe Asn Asn Asp Asn His Pro Lys Lys
595 600 605
Ile Phe Glu Pro Ser Leu Gly Thr Gly Lys Phe Ile Ala His Ala Pro
610 615 620
Ser Asp Lys Asn Tyr Arg Phe Ile Gly Thr Glu Leu Asp Pro Ile Ser
625 630 635 640
Ala Asn Leu Ser Lys Phe Leu Tyr Pro Asn Gln Val Ile Gln Asn Thr
645 650 655
Ala Leu Glu Asn Tyr Gln Phe Tyr Gln Glu Tyr Asp Ala Phe Val Gly
660 665 670
Asn Pro Pro Tyr Gly Asn His Lys Ile Tyr Ser Ser Asn Asp Lys Glu
675 680 685
Leu Ser Asn Glu Ser Ile His Asn Tyr Phe Leu Gly Lys Ala Ile Lys
690 695 700
Glu Leu Lys Asp Asp Gly Ile Gly Ala Phe Val Val Ser Ser Trp Phe
705 710 715 720
Met Asp Ala Lys Asn Pro Lys Met Arg Glu His Ile Ala Lys Asn Ala
725 730 735
Thr Phe Leu Gly Ala Ile Arg Leu Pro Asn Ser Val Phe Lys Ala Thr
740 745 750
Gly Ala Glu Val Thr Ser Asp Ile Val Phe Phe Lys Lys Gly Val Glu
755 760 765
Lys Ala Thr Asn Gln Ser Phe Thr Lys Ala Met Pro Tyr Tyr Asp Lys
770 775 780
Ile Leu Asn Ser Leu Asp Asp Asp Thr Leu Phe Ala Leu Gln Asn Asn
785 790 795 800
Arg Phe Asp Ser Phe Ile Pro Ser Asp Gln Leu Lys Ile Val Asn Ala
805 810 815
Val Ala Asn His Phe Gly Phe Lys Gln Glu Lys Leu Gln Arg Trp Tyr
820 825 830
Glu Lys Ile Asp Thr Ala Asn Phe Gly Tyr Ser Thr Gln Asp Tyr Lys
835 840 845
Ile Ile Lys Asp Phe Ile Asp Lys Val Gly Lys Asn Ser Ile Asn Leu
850 855 860
Asn Glu Gln Thr Leu Asn Glu Tyr Phe Ile His His Pro Glu Asn Ile
865 870 875 880
Leu Gly His Leu Ser Leu Glu Lys Thr Arg Tyr Arg Phe Glu Thr Asn
885 890 895
Gly Glu Gln Ile Tyr Lys Tyr Asp Leu Gln Ala Leu Glu Asp Glu Ser
900 905 910
Leu Asp Leu Ser Gln Ala Leu Lys Gln Ala Ile Glu Lys Leu Pro Lys
915 920 925
Asp Val Tyr Gln Tyr His Lys Thr Thr Leu Lys Thr Asp Val Leu Ile
930 935 940
Ile Asp Ser Ser Asn Glu Arg Tyr Gln Glu Val Gln Lys Leu Ile Lys
945 950 955 960
Asn Leu Glu Arg Arg Glu Leu Val Lys Trp Asp Asn Leu Tyr Phe Gln
965 970 975
Leu Glu Gln Asn Asn Glu Met Gly Ile Phe Leu Lys Pro Thr Lys Ile
980 985 990
Asn Ser Lys Val Gln Asp Ser Arg Leu Lys Ala Tyr Phe Lys Ile Lys
995 1000 1005
Asp Ala Leu Asn Asp Leu Thr Ser Ala Glu Leu Asn Pro Leu Ser Ser
1010 1015 1020
Asp Leu Glu Leu Glu Asn Lys Arg Ala Lys Leu Asn Leu Val Tyr Asp
1025 1030 1035 1040
Glu Phe Val Lys Lys Phe Gly Tyr Leu Asn Glu Asn Lys Asn Arg Lys
1045 1050 1055
Asp Ile Arg Gln Asp Leu Tyr Gly Ala Lys Val Leu Gly Leu Glu Lys

This Sheet Has Been Replaced



1060 1065 1070
Asp Phe Glu Lys Glu Ile Thr Pro Arg Ser Ala Lys Met Gln Asn Ile
1075 1080 1085
Glu Pro Arg Gln Ala Gln Ala Lys Lys Ala Gln Ile Phe Phe Glu Arg
1090 1095 1100
Thr Leu Asn Pro Lys Lys Glu Leu Ile Ile Thr Asn Ala Lys Glu Ala
1105 1110 1115 1120
Leu Ile Ala Ser Ile Asn Gln Lys Gly Gly Leu Asp Leu His Phe Ile
1125 1130 1135
Arg Asp His Phe Thr Thr Gln Ser Leu Glu Thr Thr Ile Lys Glu Leu
1140 1145 1150
Leu Glu Gln Lys Leu Ile Tyr Lys Asp His Lys Asp Asn Gly Gly Tyr
1155 1160 1165
Ile Leu Ala Asn Asp Tyr Leu Ser Gly Asn Val Lys Arg Lys Leu Lys
1170 1175 1180
Glu Val Lys Glu Ala Ile Asn Gln Gly Val Glu Gly Leu Glu Ala Asn
1185 1190 1195 1200
Val Lys Asp Leu Glu Leu Ile Ile Pro Lys Asp Leu Lys Ala Thr Glu
1205 1210 1215
Ile Met Ala Asn Ile Asn Ser Pro Trp Ile Pro Thr Gln Tyr Leu Glu
1220 1225 1230
Glu Phe Leu Met Glu Leu Ser Ala Asn His Tyr Glu Lys Gln Tyr Gly
1235 1240 1245
Asp Lys Met Thr Asp Tyr Gln Leu Ser Asn Leu Lys Glu Asp Ile Lys
1250 1255 1260
Ile Glu His Leu Ser Gly Ala Tyr Glu Val Phe Val Arg Asn Asn Glu
1265 1270 1275 1280
Leu Asn Glu Leu Tyr Gly Ile Arg His Lys Asp Lys Pro His Ser Tyr
1285 1290 1295
Lys Val Pro Phe Glu Ser Leu Leu Asn Lys Val Leu Asn Asn Lys Asp
1300 1305 1310
Leu Ser Val Lys Tyr Ala Gln Val Asp Pro Asn Asp Pro Lys Lys Glu
1315 1320 1325
Ile Phe Ile Thr Asp Glu Glu Gln Ser Asn Leu Ala Arg Gln Lys Ala
1330 1335 1340
Glu Glu Leu Lys Glu Ala Phe Lys Asp Trp Ile Tyr Lys Asp Tyr Ser
1345 1350 1355 1360
Arg Arg Thr His Leu Glu Gln Ile Tyr Asn Asp Thr Phe Asn Asn Phe
1365 1370 1375
Val Leu Lys Thr Tyr Asp Gly Ser Gln Leu Glu Leu Glu Gly Phe Asn
1380 1385 1390
Tyr His Ile Ser Leu Arg Pro His Gln Lys Asn Ala Ile Phe Arg Thr
1395 1400 1405
Ile Gln Asp Arg Ala Val Cys Leu Asp His Gln Val Gly Ala Gly Lys
1410 1415 1420
Thr Leu Cys Ala Ile Ala Ser Cys Met Glu Gln Lys Arg Met Gly Leu
1425 1430 1435 1440
Val Asn Lys Thr Leu Ile Ala Val Pro Asn His Leu Thr Lys Gln Trp
1445 1450 1455
Gly Asp Glu Phe Tyr Lys Ala Tyr Pro Asn Ala Asn Val Leu Val Val
1460 1465 1470
Asp Ser Lys Asp Thr Thr Glu Lys Glu Arg Glu Leu Leu Phe Asn Gln
1475 1480 1485
Ile Ala Asn Asn Asn Tyr Asp Ala Val Val Ile Ala His Thr His Leu
1490 1495 1500
Glu Leu Leu Ser Asn Pro Arg Gly Ile Ile Glu Glu Leu Lys Glu Glu
1505 1510 1515 1520
Glu Leu Val Asn Ala Glu Lys Asn Phe Glu Arg Gln Glu Leu Ala Tyr
1525 1530 1535
Lys Asn Asn Pro Arg Glu Thr Lys Lys Pro Asn Glu Arg Ala Phe Lys
1540 1545 1550
Asn Lys Leu Asp Lys Ile Arg Ala Lys Tyr Asp Ala Ile Leu Glu Lys
1555 1560 1565
Gln Gly Ser His Ile Asp Ile Ser Gln Met Gly Ile Asp Asn Leu Ile
1570 1575 1580

This Sheet Has Been Replaced



Val Asp Glu Ala His Leu Phe Lys Asn Leu Ala Phe Glu Thr Ser Met
1585 1590 1595 1600
Glu Lys Ile Ala Gly Leu Gly Asn Gln Gln Gly Ser Asn Arg Ala Arg
1605 1610 1615
Asp Leu Phe Ile Lys Thr Arg Tyr Leu His Gln Asn Asp Lys Lys Ile
1620 1625 1630
Met Phe Leu Thr Gly Thr Pro Ile Ala Asn Ser Leu Ser Glu Met Tyr
1635 1640 1645
His Leu Gln Arg Tyr Leu Thr Pro Asp Val Leu Lys Glu Arg Gly Leu
1650 1655 1660
Glu Phe Phe Asp Asp Trp Ala Lys Thr Tyr Gly Glu Val Val Asn Asp
1665 1670 1675 1680
Phe Glu Leu Asp Thr Ser Ala Gln Ser Tyr Lys Met Val Asn Arg Phe
1685 1690 1695
Ser Lys Phe Ser Asp Val Gln Gly Leu Ser Thr Met Tyr Arg Ala Phe
1700 1705 1710
Ala Asp Ile Val Ser Asn Asp Asp Ile Leu Lys His Asn Pro His Phe
1715 1720 1725
Val Pro Lys Val Tyr Gly Asp Lys Pro Ile Asn Val Val Val Lys Arg
1730 1735 1740
Ser Glu Glu Val Ala Gln Phe Ile Gly Val Ala Leu Glu Asn Gly Lys
1745 1750 1755 1760
Tyr Asn Glu Gly Ser Ile Ile Asp Arg Met Gln Lys Cys Glu Gly Lys
1765 1770 1775
Lys Ser Gln Lys Gly Gln Asp Asn Ile Leu Ser Cys Thr Thr Asp Ala
1780 1785 1790
Arg Lys Val Ala Leu Asp Tyr Arg Leu Ile Asp Pro Asn Ala Lys Val
1795 1800 1805
Glu Lys Glu Phe Ser Lys Ser Tyr Ala Met Ala Lys Asn Ile Tyr Glu
1810 1815 1820
Asn Tyr Leu Glu Thr His Ala Thr Lys Gly Thr Gln Leu Gly Phe Ile
1825 1830 1835 1840
Gly Leu Ser Thr Pro Lys Thr His Ser Gln Lys Val Ser Leu Glu Ala
1845 1850 1855
Leu Asp Asn Ala His Glu Thr Glu Asn Lys Asn Pro Leu Asp Lys Ala
1860 1865 1870
Gln Glu Leu Leu Glu Ser Leu Ser Ser Tyr Asp Glu Lys Gly Asn Leu
1875 1880 1885
Ile Ala Pro Ser Lys Lys Glu Leu Glu Asn Glu Leu Lys Glu Lys Glu
1890 1895 1900
Ala Lys Ser Val Asn Leu Asp Glu Glu Ile Ala Lys Gly Cys Ser Phe
1905 1910 1915 1920
Asp Val Tyr Ser Asp Val Leu Arg His Leu Val Gln Met Gly Ile Pro
1925 1930 1935
Gln Asn Glu Ile Ala Phe Ile His Asp Ala Lys Thr Glu Glu Gln Lys
1940 1945 1950
Gln Asp Leu Phe Lys Lys Leu Asn Arg Gly Gly Val Arg Val Leu Leu
1955 1960 1965
Gly Ser Pro Ala Lys Met Gly Val Gly Thr Asn Val Gln Glu Arg Leu
1970 1975 1980
Val Ala Met His Glu Leu Asp Cys Pro Trp Arg Pro Asp Glu Leu Leu
1985 1990 1995 2000
Gln Met Glu Gly Arg Gly Ile Arg Gln Gly Asn Ile Leu His Gln Asn
2005 2010 2015
Asp Pro Glu Asn Phe Arg Met Lys Ile Tyr Arg Tyr Ala Thr Glu Lys
2020 2025 2030
Thr Tyr Asp Ser Arg Met Trp Gln Ile Ile Glu Thr Lys Ser Lys Gly
2035 2040 2045
Ile Glu Gln Phe Arg Asn Ala His Lys Leu Gly Leu Asn Glu Leu Glu
2050 2055 2060
Asp Phe Asn Met Gly Ser Ser Asn Ala Ser Glu Met Lys Ala Glu Ala
2065 2070 2075 2080
Thr Gly Asn Pro Leu Ile Ile Glu Glu Val Lys Leu Arg Ala Glu Ile
2085 2090 2095
Lys Ser Glu Glu Ser Lys Tyr Lys Ala Phe Asn Lys Glu His Tyr Phe

This Sheet Has Been Replaced

```
           2100                2105                2110
Asn Glu Glu Ser Leu Lys Asn Asn Ala Ser Lys Leu Asp Tyr Leu Lys
       2115                2120                2125
Gln Glu Leu Lys Asp Leu Glu Thr Leu Gln Arg Ser Val Ile Ile Pro
   2130                2135                2140
Thr His Thr Glu Ile Lys Leu Tyr Asp Leu Lys Asn Glu Glu Ser Lys
2145                2150                2155                2160
Asp Tyr Glu Leu Ile Lys Val Lys Glu Val Glu Pro Leu Lys Glu Asn
                2165                2170                2175
Ala Ser Met Ser Glu Glu Leu Thr His Lys Lys Leu Lys Glu Gln Asn
            2180                2185                2190
Lys Gln Ile Ala Glu Gln Asn Lys Glu Lys Leu Asp Ala Ile Lys Lys
        2195                2200                2205
Gln Phe Ala Ser Asn Leu Asn Thr Leu Phe Val Asn Glu Glu Glu Asp
    2210                2215                2220
Tyr Lys Leu Leu Glu Tyr Lys Gly Phe Val Val Asn Ala Tyr Lys Thr
2225                2230                2235                2240
Lys Tyr Gln Val Glu Phe Ser Leu Ser Pro Lys Asp Asn Pro Asn Ile
                2245                2250                2255
Ala Tyr Ser Pro Ser Asn Met Val Tyr Lys Asn Asp Thr Ile Asn Met
            2260                2265                2270
Phe Ser Ser Tyr Asn Phe Cys Ala Glu Ile Lys Phe Asp Gly Phe Leu
        2275                2280                2285
Lys Arg Leu Asp Asn Ala Ile Thr Lys Leu Pro Glu Lys Ile Lys Glu
    2290                2295                2300
Leu Glu Asn Ser Ile Glu Ile Thr Lys Lys Asn Ile Ala Lys Tyr Thr
2305                2310                2315                2320
Arg Leu Val Glu Gln Lys Pro Ser Tyr Pro Arg Leu Glu Tyr Leu Gln
                2325                2330                2335
Ala Leu Lys Trp Asp His Lys Thr Leu Ile Asp Asp Leu Ala Lys Met
            2340                2345                2350
Ser Lys Asp Arg Asn Tyr Lys Pro Ala Phe Asn Pro Lys Ser Lys Glu
        2355                2360                2365
Val Leu Lys Asn Leu Asn Ala Glu Lys Arg Ala Ser Leu Glu Asn Glu
    2370                2375                2380
Arg Glu Glu Gln Gly Val Lys Gly Asn Thr Lys Ser His Asp Glu Ile
2385                2390                2395                2400
Glu Pro Ala Thr Glu Gln Val Ile Glu Lys Glu Ile Glu Lys Gly Asp
                2405                2410                2415
Glu Ile Ala Asn Asn Val Asp Tyr Tyr Glu Asn Glu Gln Glu Val Glu
            2420                2425                2430
Ile Thr Lys Ser Met Gly Arg Arg
        2435                2440
```

(2) INFORMATION FOR SEQ ID NO:1693:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 425 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1693

This Sheet Has Been Replaced



```
Arg Glu Gly Ala Met Asn Phe Phe Asp Thr Leu Met Gly Met Phe Val
1               5                  10                  15
Glu Pro Ser Gln Lys Val Ala Lys Ser Leu Ala Glu His Val Gly Ser
            20                  25                  30
Phe Phe His Ala Gln Leu Ile Leu Asn Thr Ile Ile Thr Ile Leu Phe
        35                  40                  45
Met Ile Trp Ala Tyr Lys Arg Val Lys Glu Gly Asp Met Phe Glu Phe
    50                  55                  60
Lys Thr Ala Met Gly Val Val Val Phe Ile Ala Phe Val Gly Phe Ile
65                  70                  75                  80
Asn Trp Gly Ile Lys Asn Pro Asn Asp Phe Asn Thr Tyr Phe Ile Asn
                85                  90                  95
Thr Ile Phe Tyr Pro Ser Glu Lys Leu Ala Ile Leu Ile Ala Gln Ser
            100                 105                 110
Leu Asn Asp Gly Leu Glu Ile Pro Thr Asn Thr Asn Leu Ser Pro Ser
        115                 120                 125
Glu Ile Phe Ser Ile Gly Asn Leu Ala Ser Ser Ala Tyr Ala Met Ile
    130                 135                 140
Val Asn Leu Trp Asp Asn Ala Phe Asp Gly Ile Asn Met Phe Asn Trp
145                 150                 155                 160
Leu Thr Met Ile Pro Lys Ile Ile Met Phe Phe Leu Val Ile Leu Gly
                165                 170                 175
Glu Leu Leu Phe Leu Gly Leu Leu Leu Ile Ile Val Leu Leu Val Thr
            180                 185                 190
Ala Glu Ile Phe Met Trp Ser Ala Leu Gly Leu Ile Val Leu Pro Leu
        195                 200                 205
Gly Leu Ile Pro Gln Thr Lys Gly Met Leu Phe Ser Tyr Leu Lys Lys
    210                 215                 220
Leu Ile Ser Leu Thr Leu Tyr Lys Pro Cys Met Met Leu Val Ala Phe
225                 230                 235                 240
Phe Asn Tyr Gly Ile Ile Tyr Lys Val Asn Thr Leu Ile Pro Thr Lys
                245                 250                 255
His Glu Val Thr Gln Gly Phe Tyr Gly Asn Ala Asp Lys Met Ala Asn
            260                 265                 270
Glu Gly Lys Ile Ile Asp Val Phe Gly Asn Val Leu Lys Gly Asp Trp
        275                 280                 285
Asn Ser Tyr Ile Ala His Ser Ser Ile Val Gly Phe Leu Thr Ile Ile
    290                 295                 300
Val Leu Gly Ser Val Ile Cys Phe Phe Leu Val Lys Arg Val Pro Asp
305                 310                 315                 320
Phe Ile Asn Asn Ile Phe Gly Thr Ser Gly Gly Val Gly Ala Val Thr
                325                 330                 335
Glu Met Met Gln Lys Ile Gly Met Thr Ile Gly Gly Ala Val Phe Gly
            340                 345                 350
Gly Ser Ala Val Met Val Ala Asn Gln Val Lys Gln Ala Tyr Gln Ser
        355                 360                 365
Ala Gly Gly Gly Leu Ala Gly Leu Gln Ala Gly Ala Lys Ala Phe Gly
    370                 375                 380
Leu Gly Ala Ile Ser Gly Gly Ala Ser Ala Met Ala Asn His Arg Ser
385                 390                 395                 400
Val Lys Ala Gly Val Lys His Phe Val Ala Ser Val Lys Ser Gly Phe
                405                 410                 415
Gly Phe Asp Asn Asp Lys Asn Asn Lys
            420                 425
```

(2) INFORMATION FOR SEQ ID NO:1694:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 442 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: YES

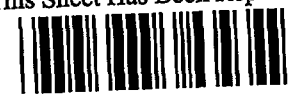
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1694

```
Lys Glu Gln Gln Met Ala Tyr Lys Pro Asn Lys Lys Lys Leu Lys Glu
1               5                  10                  15
Leu Arg Glu Gln Pro Asn Leu Phe Ser Ile Leu Asp Lys Gly Asp Val
            20                  25                  30
Ala Thr Asn Asn Pro Val Glu Glu Ser Asp Lys Ala Asn Lys Ile Gln
        35                  40                  45
Glu Pro Leu Pro Tyr Val Val Lys Thr Gln Ile Asn Lys Ala Ser Met
    50                  55                  60
Ile Ser Arg Asp Pro Ile Glu Trp Ala Lys Tyr Leu Ser Phe Glu Lys
65                  70                  75                  80
Arg Val Tyr Lys Asp Asn Ser Lys Glu Asp Val Asn Phe Phe Ala Asn
                85                  90                  95
Gly Glu Ile Lys Glu Ser Ser Arg Val Tyr Glu Ala Asn Lys Glu Gly
            100                 105                 110
Phe Glu Arg Arg Ile Thr Lys Arg Tyr Asp Leu Ile Asp Arg Asn Ile
        115                 120                 125
Asp Arg Asn Arg Glu Phe Phe Ile Lys Glu Ile Glu Ile Leu Thr His
    130                 135                 140
Thr Asn Ser Leu Lys Glu Leu Lys Glu Gln Gly Leu Glu Ile Gln Leu
145                 150                 155                 160
Thr His His Asn Glu Thr His Lys Lys Ala Leu Glu Asn Gly Asn Glu
                165                 170                 175
Ile Val Lys Glu Tyr Asp His Leu Lys Asp Ile Tyr Gln Glu Val Glu
            180                 185                 190
Arg Thr Lys Asp Gly Gly Leu Val Arg Glu Ile Ile Pro Ser Ile Ser
        195                 200                 205
Ser Ala Glu Tyr Phe Lys Leu Tyr Asn Lys Leu Pro Phe Glu Ser Ile
    210                 215                 220
Asn Asn Glu Asn Thr Lys Leu Asn Thr Asn Asp Asn Glu Glu Val Lys
225                 230                 235                 240
Lys Leu Glu Phe Glu Leu Ala Lys Glu Val His Ile Leu Ile Leu Glu
                245                 250                 255
Gln Gln Leu Leu Ser Ala Thr Asn Tyr Tyr Ser Trp Ile Asp Lys Asp
            260                 265                 270
Asp Asn Ala Asn Phe Ala Trp Lys Met His Arg Leu Ile Asn Glu Asn
        275                 280                 285
Lys Leu Lys Glu Asn His Leu Ser Ala Asn Asn Ala Asn Lys Ile Lys
    290                 295                 300
Gln Phe Phe Phe Asn Asn Gly Ser Ile Leu Gly Trp Thr Lys Glu Glu
305                 310                 315                 320
Gln Ser Ala Ile Gln Glu Asn Arg Asp Tyr Ser Leu Arg Ser Ala Leu
                325                 330                 335
Leu Ser Leu Glu Glu Ile Ala Gln Ala Lys Ile Glu Leu Gln Lys Tyr
            340                 345                 350
Tyr Glu Ser Val Tyr Val Asn Gly Asp Gly Asn Lys Arg Glu Ile Lys
        355                 360                 365
Pro Phe Lys Glu Ile Leu Arg Asp Thr Asn Asn Phe Glu Lys Ala Tyr
    370                 375                 380
Lys Glu Arg Tyr Asp Lys Leu Val Ser Leu Ser Ala Ala Ile Ile Gln
385                 390                 395                 400
Ala Lys Glu Gly Gly Asn Glu Arg Gln Asn Ser Ser Ala Asn Asn Asn
                405                 410                 415
Asn Pro Ile Lys Asn Thr Ile Glu Thr Asn Thr Ser Asn Asn Ile Ile
            420                 425                 430
```

This Sheet Has Been Replaced



```
Gln Asn Asn Asp Asn Ile Ile Ile Gln Ile
        435                 440
```

(2) INFORMATION FOR SEQ ID NO:1695:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1695

```
Ile Lys His Tyr Lys Gln Tyr Gly Thr Gly Leu His Leu Phe Arg His
1               5                  10                  15
Ser Phe Ala Thr Leu Ile Tyr Gln Glu Thr Gln Asp Leu Val Leu Thr
            20                  25                  30
Ser Arg Ala Leu Gly His Ser Ser Leu Leu Ser Thr Lys Ile Tyr Ile
        35                  40                  45
His Thr Thr Gln Glu His Asn Lys Lys Val Ala Leu Val Phe Asp Ser
    50                  55                  60
Leu Ile Glu Asn Lys Lys
65                  70
```

(2) INFORMATION FOR SEQ ID NO:1696:

(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

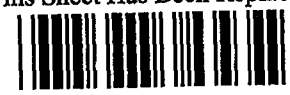
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1696

```
Lys Lys Arg Lys Tyr Met Arg Phe Arg Arg Val Lys Lys His Lys Asn
1               5                  10                  15
Lys His Asn Lys Glu His Thr Ser Met Asp Leu Gln Gln Ile Asp Glu
            20                  25                  30
Leu Glu Lys Lys Phe Glu Glu Gln Glu Glu Gln Ala Gln Asp Thr Pro
        35                  40                  45
Leu Lys Gln Glu Pro Ser Thr Lys Glu Val Lys Ile Pro Lys Lys Arg
    50                  55                  60
Gly Arg Lys Lys Ser Leu Leu Asp Glu Asp Lys Lys Lys Ser Phe Asn
```

```
65                  70                  75                  80
Ile Ala Phe Ser Pro Cys Val Ile Lys Glu Leu Asn Glu Phe Leu Leu
                85                  90                  95
Glu Phe Gly Ser Phe Lys Glu Thr Arg Ser Thr Phe Ile Glu Glu Ala
            100                 105                 110
Leu Ile Arg His Leu Lys His Arg Lys Asn Thr Gln Glu Gln Lys Leu
        115                 120                 125
Leu Lys Gln Leu Glu Arg Leu Gln Asn Lys Glu Lys Gly Asn Asn Glu
    130                 135                 140
Asn Asn Glu Leu Glu
145
```

(2) INFORMATION FOR SEQ ID NO:1697:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 373 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1697

```
Leu Asn Thr Asp Lys Ile Thr Lys Tyr Leu Ile Ile Ile Asp Ile Phe
1               5                  10                  15
Leu Lys Leu Tyr Val Ile Met Ile Ser Glu Ile Ile Lys Phe Gln Leu
            20                  25                  30
Lys Gly Ile Lys Met Ile Arg Leu Lys Gly Leu Asn Lys Thr Leu Lys
        35                  40                  45
Thr Ser Leu Leu Ala Gly Val Leu Leu Gly Ala Thr Ala Pro Leu Met
    50                  55                  60
Ala Lys Pro Leu Leu Ser Asp Glu Asp Leu Leu Lys Arg Val Lys Leu
65                  70                  75                  80
His Asn Ile Lys Glu Asp Thr Leu Thr Ser Cys Asn Ala Lys Val Asp
                85                  90                  95
Gly Ser Gln Tyr Leu Asn Ser Gly Trp Asn Leu Ser Lys Glu Phe Pro
            100                 105                 110
Gln Glu Tyr Arg Glu Lys Ile Phe Glu Cys Val Glu Glu Glu Lys His
        115                 120                 125
Lys Gln Ala Leu Asn Leu Ile Asn Lys Glu Asp Thr Lys Asp Lys Glu
    130                 135                 140
Glu Leu Ala Lys Lys Ile Lys Glu Ile Lys Glu Lys Ala Lys Val Leu
145                 150                 155                 160
Arg Gln Lys Phe Met Ala Phe Glu Met Lys Glu His Ser Lys Glu Phe
                165                 170                 175
Pro Asn Lys Lys Gln Leu Gln Thr Met Leu Glu Asn Ala Phe Asp Asn
            180                 185                 190
Gly Ala Glu Ser Phe Ile Asp Asp Trp His Glu Arg Phe Gly Gly Ile
        195                 200                 205
Ser Arg Glu Asn Thr Tyr Lys Ala Leu Gly Ile Lys Glu Tyr Ser Asp
    210                 215                 220
Glu Gly Lys Ile Leu Ala Phe Gly Glu Arg Ser Tyr Ile Arg Gln Tyr
225                 230                 235                 240
Lys Lys Asp Phe Glu Glu Ser Thr Tyr Asp Thr Arg Gln Thr Leu Ser
                245                 250                 255
```

```
Ala Met Ala Asn Met Ser Gly Glu Asn Asp Tyr Lys Ile Thr Trp Leu
            260                 265                 270
Lys Pro Lys Tyr Gln Leu His Ser Ser Asn Asn Ile Lys Pro Leu Met
        275                 280                 285
Ser Asn Thr Glu Leu Leu Asn Met Ile Glu Leu Thr Asn Ile Lys Lys
    290                 295                 300
Glu Tyr Val Met Gly Cys Asn Met Glu Ile Asp Gly Ser Lys Tyr Pro
305                 310                 315                 320
Ile His Lys Asp Trp Gly Phe Phe Gly Lys Ala Lys Val Pro Glu Thr
                325                 330                 335
Trp Arg Asn Lys Ile Trp Glu Cys Ile Lys Asn Lys Val Lys Ser Tyr
            340                 345                 350
Asp Asn Thr Thr Ala Glu Ile Gly Ile Val Trp Lys Lys Asn Thr Tyr
        355                 360                 365
Ser Ile Ser His His
    370
```

(2) INFORMATION FOR SEQ ID NO:1698:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

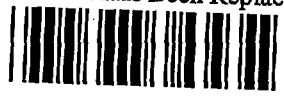
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1698

```
Lys Asp Tyr Lys Thr Lys Lys Arg Ala Ile Met Lys Thr Met Asn Leu
1               5                   10                  15
Asn Glu Phe Phe Thr His Lys Ile Ile Tyr Lys Asp Thr Pro Leu Lys
            20                  25                  30
Phe Lys Asp Thr Leu Glu Gln Glu Ile Ser Gln Ala Ser Leu Val Glu
        35                  40                  45
Lys Leu Ile Leu Ala Asn Ile Leu Ala Asn Met Val Phe Ala Lys Ile
    50                  55                  60
Ser Asn Glu Asn Ala Pro Lys Ile Leu Ile Ser Arg Leu Met Cys Lys
65                  70                  75                  80
Phe Ser Pro Ile Asp Tyr Glu Ser Thr Ile Pro Ser Asp Phe Lys Pro
                85                  90                  95
Ile Asp Glu Glu Glu Tyr Glu Asp Asp Leu Glu Trp Leu Asn Glu Glu
            100                 105                 110
Lys Glu Asp Arg Leu Phe Asn Tyr Tyr Leu Phe Leu Asn Gly Ile Lys
        115                 120                 125
Glu Ser Asp Val Glu Glu Val Phe Asn Glu Ser Val Glu Ile Tyr Asp
    130                 135                 140
Glu Cys Leu Ile Glu Ile Ala Gln Asn Val Leu Lys Asp Lys Phe Ser
145                 150                 155                 160
Tyr Asp Ile Asp Leu Leu Gln Val Leu Val Lys Gly Tyr Ala Lys Glu
                165                 170                 175
Ile Arg Glu Phe Leu Ser Tyr Lys Pro Ile Lys Glu Ile Lys Asp Phe
            180                 185                 190
Lys Asp Lys Asp Thr Ala Leu Tyr Ile Ser Leu Gly Lys Asp Tyr Asp
        195                 200                 205
Lys Glu Lys Glu Pro Phe Ser Lys Lys Leu Gln Gln Cys Phe Lys Glu
```

This Sheet Has Been Replaced



```
    210                 215                 220
Ile Leu Glu Ser Lys Gly Ile
225                 230
```

(2) INFORMATION FOR SEQ ID NO:1699:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 421 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1699

```
Met Lys Gly Leu Thr Met Lys Lys Leu Val Phe Ser Met Leu Leu Cys
1               5                  10                  15
Cys Lys Ser Val Phe Ala Glu Gly Glu Thr Pro Leu Ile Val Asn Asp
            20                  25                  30
Pro Glu Thr His Val Ser Gln Ala Thr Ile Ile Gly Lys Met Val Asp
        35                  40                  45
Ser Ile Lys Arg Tyr Glu Glu Ile Ile Ser Lys Ala Gln Ala Gln Val
    50                  55                  60
Asn Gln Leu Gln Lys Val Asn Asn Met Ile Asn Thr Thr Asn Ser Leu
65                  70                  75                  80
Ile Ser Ser Ser Ala Ile Thr Leu Ala Asn Pro Met Gln Val Leu Gln
                85                  90                  95
Asn Ala Gln Tyr Gln Ile Glu Ser Ile Arg Tyr Asn Tyr Glu Asn Leu
            100                 105                 110
Lys Gln Ser Ile Glu Asn Trp Asn Ala Gln Asn Leu Leu Arg Asn Lys
        115                 120                 125
Tyr Leu Gln Gln Gln Cys Pro Trp Leu Asn Val Asn Ala Leu Thr Asn
    130                 135                 140
Asn Lys Ile Val Asn Leu Lys Asp Leu Asn Asn Leu Ile Thr Lys Asn
145                 150                 155                 160
Gly Glu Gln Thr Gln Thr Ala Arg Asp Val Gln Asn Leu Ile Gln Ser
                165                 170                 175
Ile Ser Gly Ser Gly Tyr Gly Asn Met Gln Ser Leu Ala Gly Glu Leu
            180                 185                 190
Ser Gly Arg Ala Trp Gly Glu Met Leu Cys Lys Met Val Asn Asp Ser
        195                 200                 205
Asn Tyr Glu Ser Glu Gln Ala Leu Leu Ala Thr Gly Asn Asn Pro Glu
    210                 215                 220
Glu Gln Lys Arg Arg Phe Leu Leu Arg Val Lys Lys Lys Val Asn Asp
225                 230                 235                 240
Asn Lys Gln Leu Lys Asp Lys Leu Asp Pro Phe Leu Lys Arg Leu Asp
                245                 250                 255
Val Leu Gln Thr Glu Phe Gly Val Thr Asp Pro Thr Ala Asn His Asn
            260                 265                 270
Lys Gln Gly Ile His Tyr Cys Thr Glu Asn Lys Glu Thr Gly Lys Cys
        275                 280                 285
Asp Pro Ile Lys Asn Val Phe Arg Thr Thr Arg Leu Asp Asn Glu Leu
    290                 295                 300
Glu Gln Glu Ile Gln Thr Leu Thr Leu Asp Leu Thr Lys Ala Ser Asn
305                 310                 315                 320
```

```
Lys Asp Ala Gln Ser Gln Ala Tyr Ala Asn Phe Asn Gln Arg Ile Lys
                325                 330                 335
Leu Leu Thr Leu Lys Tyr Leu Lys Glu Ile Thr Asn Gln Met Leu Phe
            340                 345                 350
Leu Asn Gln Thr Met Ala Met Gln Ser Glu Ile Met Thr Asp Asp Tyr
        355                 360                 365
Phe Arg Gln Asn Asn Asp Gly Phe Gly Glu Lys Glu Asn His Ile Asp
    370                 375                 380
Lys Gln Leu Thr Gln Lys Arg Ile Asn Glu Arg Glu Arg Ala Arg Ile
385                 390                 395                 400
Tyr Phe Gln Asn Pro Asn Val Lys Phe Asp Gln Phe Gly Phe Pro Ile
                405                 410                 415
Phe Ser Ile Trp Asp
            420
```

(2) INFORMATION FOR SEQ ID NO:1700:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 446 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1700

```
Lys Arg Trp Trp Tyr Phe Val Arg Ala Phe Leu Asn Arg Ser Phe Ala
1               5                  10                  15
Pro Leu Leu Asn Pro Asn Glu Asn Leu Leu Asp Gln Val Lys Ser Ser
            20                  25                  30
Ile Ile Leu Lys Lys Gly Val Ser Tyr Phe Asp Trp Gly Ala Ser Gly
        35                  40                  45
Leu Ala Ser Ala Leu Val Glu Lys Arg Val Lys Ser Leu Leu Pro Tyr
    50                  55                  60
Tyr Ala Asn Ala His Ser Val Ala Ser Lys His Ala Ile Leu Met Gly
65                  70                  75                  80
Met Leu Leu Lys Glu Cys Gln Glu Lys Leu Lys Arg Ser Leu Asn Leu
                85                  90                  95
Ser Ala Asn His Cys Val Leu Ser Ala Gly Tyr Gly Ala Ser Ser Ala
            100                 105                 110
Ile Lys Lys Phe Gln Glu Ile Leu Gly Val Cys Ile Pro Ser Lys Thr
        115                 120                 125
Lys Lys Asn Leu Glu Pro Tyr Leu Lys Asp Met Ala Leu Lys Arg Val
    130                 135                 140
Ile Val Gly Pro Tyr Glu His His Ser Asn Glu Val Ser Trp Arg Glu
145                 150                 155                 160
Gly Leu Cys Glu Val Val Arg Ile Pro Leu Asn Glu His Gly Leu Leu
                165                 170                 175
Asp Leu Glu Ile Leu Glu Gln Thr Leu Lys Lys Thr Pro Asn Ser Leu
            180                 185                 190
Val Ser Val Ser Ala Ala Ser Asn Val Thr Gly Ile Leu Thr Pro Leu
        195                 200                 205
Lys Glu Val Ser Ser Leu Cys Lys Glu Tyr Arg Ala Ile Leu Ala Leu
    210                 215                 220
Asp Leu Ala Asn Phe Ser Ala His Ala Asn Pro Lys Asp Cys Glu Tyr
```

```
225                 230                 235                 240
Gln Thr Gly Phe Tyr Ala Pro His Lys Leu Leu Gly Gly Val Gly Gly
                245                 250                 255
Cys Gly Leu Leu Gly Ile Ser Lys Asp Leu Ile Asp Thr Gln Ile Pro
            260                 265                 270
Pro Ser Phe Ser Ala Gly Gly Val Ile Lys Tyr Ala Asn Arg Thr Arg
        275                 280                 285
His Glu Phe Ile Asp Glu Leu Pro Leu Arg Glu Glu Phe Gly Thr Pro
    290                 295                 300
Gly Leu Leu Gln Phe Tyr Arg Ser Ala Leu Ala Tyr Gln Leu Arg Asp
305                 310                 315                 320
Glu Cys Gly Leu Asp Phe Ile His Lys Lys Glu Asn Asn Leu Leu Arg
                325                 330                 335
Val Leu Val Tyr Gly Leu Lys Asp Leu Pro Ala Ile Asn Ile Tyr Gly
            340                 345                 350
Asn Leu Thr Ala Ser Arg Val Gly Val Val Ala Phe Asn Ile Gly Gly
        355                 360                 365
Ile Ser Pro Tyr Asp Leu Ala Arg Val Leu Ser Tyr Glu Tyr Ala Ile
    370                 375                 380
Glu Thr Arg Ala Gly Cys Ser Cys Ala Gly Pro Tyr Gly His Asp Leu
385                 390                 395                 400
Leu Asn Leu Asn Ala Gln Lys Ser Ser Asp Phe Asn Ala Lys Pro Gly
                405                 410                 415
Trp Leu Arg Val Ser Leu His Phe Thr His Ser Ile Asn Asp Ile Asp
            420                 425                 430
Tyr Leu Leu Asp Ser Leu Lys Lys Ala Val Lys Lys Leu Arg
        435                 440                 445
```

(2) INFORMATION FOR SEQ ID NO:1701:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 430 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1701

```
Tyr Val Ile Glu Leu Asp Ile Asn Ala Ser Asp Lys Ser Leu Ser His
1               5                   10                  15
Arg Ala Val Ile Phe Ser Leu Leu Ala Gln Lys Pro Cys Phe Val Arg
            20                  25                  30
Asn Phe Leu Met Gly Glu Asp Cys Leu Ser Ser Leu Glu Ile Ala Gln
        35                  40                  45
Asn Leu Gly Ala Lys Val Glu Asn Thr Ala Lys Asn Ser Phe Lys Ile
    50                  55                  60
Thr Pro Pro Thr Thr Ile Lys Glu Pro Asn Lys Ile Leu Asn Cys Asn
65                  70                  75                  80
Asn Ser Gly Thr Ser Met Arg Leu Tyr Ser Gly Leu Leu Ser Ala Gln
                85                  90                  95
Lys Gly Leu Phe Val Leu Ser Gly Asp Asn Ser Leu Asn Ala Arg Pro
            100                 105                 110
Met Lys Arg Ile Ile Glu Pro Leu Lys Ala Phe Gly Ala Lys Ile Leu
        115                 120                 125
```

```
Gly Arg Glu Asp Asn His Phe Ala Pro Leu Ala Ile Val Gly Gly Pro
    130                 135                 140
Leu Lys Ala Cys Asp Tyr Glu Ser Pro Ile Ala Ser Ala Gln Val Lys
145                 150                 155                 160
Ser Ala Phe Ile Leu Ser Ala Leu Gln Ala Gln Gly Ile Ser Ala Tyr
                165                 170                 175
Lys Glu Ser Glu Leu Ser Arg Asn His Thr Glu Ile Met Leu Lys Ser
            180                 185                 190
Leu Gly Ala Asn Ile Gln Asn Gln Asp Gly Val Leu Lys Ile Ser Pro
        195                 200                 205
Leu Glu Lys Pro Leu Glu Ser Phe Asp Phe Thr Ile Ala Asn Asp Pro
    210                 215                 220
Ser Ser Ala Phe Phe Leu Ala Leu Ala Cys Ala Ile Thr Pro Lys Ser
225                 230                 235                 240
Arg Leu Leu Leu Lys Asn Val Leu Leu Asn Pro Thr Arg Ile Glu Ala
                245                 250                 255
Phe Glu Val Leu Lys Lys Met Gly Ala His Ile Glu Tyr Val Ile Gln
            260                 265                 270
Ser Lys Asp Leu Glu Val Ile Gly Asp Ile Tyr Ile Glu His Ala Pro
        275                 280                 285
Leu Lys Ala Ile Ser Ile Asp Gln Asn Ile Ala Ser Leu Ile Asp Glu
    290                 295                 300
Ile Pro Ala Leu Ser Ile Ala Met Leu Phe Ala Lys Gly Lys Ser Met
305                 310                 315                 320
Val Arg Asn Ala Lys Asp Leu Arg Ala Lys Glu Ser Asp Arg Ile Lys
                325                 330                 335
Ala Val Val Ser Asn Phe Lys Ala Leu Gly Ile Glu Cys Glu Glu Phe
            340                 345                 350
Glu Asp Gly Phe Tyr Ile Glu Gly Leu Gly Asp Ala Ser Gln Leu Lys
        355                 360                 365
Gln His Phe Ser Lys Ile Lys Pro Pro Ile Ile Lys Ser Phe Asn Asp
    370                 375                 380
His Arg Ile Ala Met Ser Phe Ala Val Leu Thr Leu Ala Leu Pro Leu
385                 390                 395                 400
Glu Ile Asp Asn Leu Glu Cys Ala Asn Ile Ser Phe Pro Thr Phe Gln
                405                 410                 415
Leu Trp Leu Asn Leu Phe Lys Lys Arg Ser Leu Asn Gly Asn
            420                 425                 430
```

(2) INFORMATION FOR SEQ ID NO:1702:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

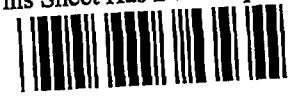
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1702

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

This Sheet Has Been Replaced



```
        35                  40                  45
Asn Ser Leu Ile Phe Gly Ser Leu Ile His Asn Ala Lys Glu Ile Asn
    50                  55                  60
Arg Leu Glu Lys Asn Phe Asn Val Lys Ile Glu Glu Asp Pro Lys Lys
65                  70                  75                  80
Ile Pro Lys Asn Lys Ser Val Ile Ile Arg Thr His Gly Ile Pro Lys
                85                  90                  95
Gln Asp Leu Glu Tyr Leu Lys Asn Lys Gly Val Lys Ile Thr Asp Ala
            100                 105                 110
Thr Cys Pro Tyr Val Ile Lys Pro Gln Gln Ile Val Glu Ser Met Ser
        115                 120                 125
Lys Glu Gly Tyr Gln Ile Val Leu Phe Gly Asp Ile Asn His Pro Glu
    130                 135                 140
Val Lys Gly Val Ile Ser Tyr Ala Thr Asn Gln Ala Leu Val Val Asn
145                 150                 155                 160
Ser Leu Glu Glu Leu Gln Glu Lys Lys Leu Gln Arg Lys Val Ala Leu
                165                 170                 175
Val Ser Gln Thr Thr Lys Gln Thr Pro Lys Leu Leu Gln Ile Ala Ser
            180                 185                 190
```

(2) INFORMATION FOR SEQ ID NO:1703:

(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:1703

```
Lys Leu Pro Ile His Ala Phe Val Leu Met Cys Leu Ala Ile Pro Ser
1               5                  10                  15
Lys Val Ile Ala Ile Asn Asp Asn Val Ala Leu Leu Glu Thr Leu Gly
            20                  25                  30
Val Gln Arg Glu Ala Ser Leu Asp Leu Met Gly Glu Ser Val Lys Val
        35                  40                  45
Gly Asp Tyr Val Leu Leu His Ile Gly Tyr Val Met Ser Lys Ile Asp
    50                  55                  60
Glu Lys Glu Ala Leu Glu Ser Ile Glu Leu Tyr Gln Glu Met Ile Ala
65                  70                  75                  80
Glu Val Asn Glu Thr His Glu
                85
```

(2) INFORMATION FOR SEQ ID NO:1704:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

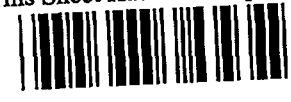
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1704

```
Lys Gly Thr Ser Met Ser Glu Gln Arg Lys Glu Ser Leu Gln Asn Asn
1               5                  10                  15
Pro Asn Leu Ser Lys Lys Asp Ile Lys Ile Val Glu Lys Ile Leu Ser
            20                  25                  30
Lys Asn Asp Ile Lys Ala Ala Glu Met Lys Glu Arg Tyr Leu Lys Glu
        35                  40                  45
Gly Ser Val Cys Val Asn Phe Met Ser Ser Pro Gly Ser Gly Lys Thr
    50                  55                  60
Thr Met Leu Glu Asn Leu Ala Asp Phe Lys Asp Phe Lys Phe Cys Val
65                  70                  75                  80
Val Glu Gly Asp Leu Gln Thr Asn Arg Asp Ala Asp Arg Leu Arg Lys
                85                  90                  95
Lys Gly Val Ser Ala His Gln Ile Thr Thr Gly Glu Ala Cys His Leu
            100                 105                 110
Glu Ala Ser Met Ile Glu Gly Ala Phe Asp Leu Leu Lys Asp Glu Gly
        115                 120                 125
Ala Leu Glu Lys Ser Asp Phe Leu Ile Ile Glu Asn Val Gly Asn Leu
    130                 135                 140
Val Cys Pro Ser Ser Tyr Asn Leu Gly Ala Ala Met Asn Ile Val Leu
145                 150                 155                 160
Leu Ser Val Pro Glu Gly Asp Asp Lys Val Leu Lys Tyr Pro Thr Met
                165                 170                 175
Phe Met Cys Ala Asp Ala Val Ile Ile Ser Lys Ala Asp Met Ile Glu
            180                 185                 190
Val Phe Asn Phe Arg Val Ser Gln Val Lys Glu Asp Met Gln Lys Leu
        195                 200                 205
Lys Pro Glu Ala Pro Ile Phe Leu Met Ser Ser Lys Asp Pro Lys Ser
    210                 215                 220
Leu Glu Asp Phe Lys Asn Phe Leu Leu Glu Lys Lys Arg Glu Asn Tyr
225                 230                 235                 240
Gln Ser Thr His Ser Phe
                245
```

(2) INFORMATION FOR SEQ ID NO:1705:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 957 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1705

```
Gly Lys Ile Met Ala Lys Lys Lys Gln Glu Val Arg Asn Asn Glu Ile
```

```
1               5                  10                  15
Phe Val Ala Gln Lys Leu Ala Glu Glu Glu Leu Asn Ala Asn Glu Ile
            20                  25                  30
Asn Asp Pro Leu Glu Met Leu Asp Phe Lys Ser Phe Asp Asp Asn Lys
        35                  40                  45
Glu Leu Leu Asp Tyr Gln Gln Gln Ala Leu Ile Asn Ala Phe Arg Val
    50                  55                  60
Leu Val Ala Tyr Phe Arg Asp Phe Lys Glu Ser Lys Lys Glu Phe Tyr
65                  70                  75                  80
Ala Phe Tyr Gln Lys His Tyr Ser Phe Ala Asn Cys Asp Phe Ala Lys
                85                  90                  95
Lys Lys Leu Asn His Leu Leu Lys Ser His Phe Lys Val Glu Asn His
            100                 105                 110
Cys Val Arg Phe Glu Asn Phe Ile Asn Arg Leu Ala Phe Tyr Met Ala
        115                 120                 125
Thr Gly Ser Gly Lys Thr Ile Val Ile Ile Lys Leu Val Glu Leu Leu
    130                 135                 140
Ser Val Ala Met Gly Met Gly Leu Ile Pro Lys Lys Asn Ile Met Phe
145                 150                 155                 160
Phe Ser Ala Asn Glu His Leu Ile Lys Gln Phe Glu Lys Glu Ile Glu
                165                 170                 175
Lys Tyr Asn Arg Asn Lys Asp Tyr Ser Lys Gln Ile Asp Phe Lys Asn
            180                 185                 190
Leu Lys Ser Val Lys Asn Lys Asp Phe Tyr Arg Ala Pro Lys Asp Ser
        195                 200                 205
Leu Met Lys Glu Ile Ala Leu Phe Tyr Tyr Arg Ala Asp Leu Met Ser
    210                 215                 220
Asp Glu Glu Ser Lys Glu Asn Leu Leu Asn Tyr Lys Asp Cys Trp Asp
225                 230                 235                 240
Asn Gly Glu Asn Tyr Val Ile Leu Asp Glu Ala His Lys Gly Asn Lys
                245                 250                 255
Thr Glu Ser Lys Arg Gln Ala Ile Phe Ser Leu Leu Ser Leu Lys Gly
            260                 265                 270
Phe Leu Phe Asn Phe Ser Ala Thr Phe Thr Glu Glu Ser Asp Leu Ile
        275                 280                 285
Thr Ala Val Tyr Asn Leu Ser Val Gly Glu Trp Val Lys Leu Gly Tyr
    290                 295                 300
Gly Lys Glu Ser Val Leu Leu Lys Lys Asn Asn Leu Asn Ala Phe Lys
305                 310                 315                 320
Glu Leu Lys Asp Leu Asn Asp Arg Glu Lys Glu Ile Ala Leu Leu Lys
                325                 330                 335
Ala Leu Leu Leu Leu Gly Met Gln Lys Arg Tyr Lys Val Glu Gly Tyr
            340                 345                 350
Phe His Asp Pro Leu Met Leu Val Phe Thr His Ser Val Asn Met Glu
        355                 360                 365
Asn Ser Asp Ala Glu Ile Phe Phe Lys Thr Leu Ala Arg Val Ile Glu
    370                 375                 380
Asn Asp Asp Glu Ser Asp Phe Ser Lys Ala Lys Asp Asp Leu Leu Glu
385                 390                 395                 400
Glu Leu Lys Asn Pro Glu Phe Leu Phe Ser Asp Gly Lys Asp Lys Glu
                405                 410                 415
Lys Asp Tyr Lys Ile Glu Val Phe Lys Glu Ser Leu Lys Gly Met Asp
            420                 425                 430
Phe Lys Gly Leu Lys Glu Ala Val Phe Tyr Ala Ser Asn Gly His Ile
        435                 440                 445
Glu Val Ile Ile Asn Pro Lys Asn Asn Gln Glu Ile Ala Phe Lys Leu
    450                 455                 460
Asn Thr Ser Asp Lys Val Phe Cys Leu Ile Arg Ile Gly Asp Ile Thr
465                 470                 475                 480
Glu Trp Ile Arg Glu Lys Leu Lys Ser Val Lys Val Val Ser Lys Asn
                485                 490                 495
Leu Ser Phe Lys Glu Glu Ser Tyr Phe Ser Gln Ile Asp Lys Ser Ser
            500                 505                 510
Ile Asn Ile Leu Val Gly Ser Arg Ala Phe Asp Thr Gly Trp Asp Ser
        515                 520                 525
```

This Sheet Has Been Replaced



```
Thr Arg Pro Ser Val Ile Leu Phe Leu Asn Ile Gly Leu Asp Asp Asp
    530                 535                 540
Ala Lys Lys Leu Val Lys Gln Ser Phe Gly Arg Gly Val Arg Ile Glu
545                 550                 555                 560
Ser Val Lys Asn Gln Arg Gln Arg Leu Ala Tyr Leu Glu Ile Asp Glu
                565                 570                 575
Ala Ile Lys Asp Lys Leu Lys Pro Asn Ala Ala Met Leu Glu Met Leu
            580                 585                 590
Phe Val Ile Pro Thr Asn His Ala Ser Leu Glu Ala Ile Leu Lys Phe
        595                 600                 605
Gln Lys Glu Ser Glu Asn Gly Gly Glu Asn Arg Gly Pro Trp Arg Glu
    610                 615                 620
Ile Lys Leu Glu Lys Thr Arg Ile Glu His Ala Leu Phe Val Pro Cys
625                 630                 635                 640
Tyr Arg Lys Glu Gln Thr Asn Ala Leu Lys Ile Ser Gln Ser Ala Ser
                645                 650                 655
Phe Lys Met Ser Glu Lys Asn Phe Lys Asp Leu Lys Glu His Phe His
            660                 665                 670
Leu Met Ser Glu Lys His Phe Ile Leu Lys His Glu Ile Tyr Asp Pro
        675                 680                 685
Lys Asp Tyr Ala Leu Leu Lys Glu Met Ile Gln Thr Ala His Phe Lys
    690                 695                 700
Lys Val Ser Thr Trp His Tyr Lys Asp Leu Asp Tyr Met Ile Ser Glu
705                 710                 715                 720
Ile Lys Gly Lys Leu Tyr Pro Asn Gln Lys Val Pro Lys Asp Glu Phe
                725                 730                 735
Asn Ala Leu Asp Asn Glu Lys Ile Val His Phe Lys Arg Val Lys Val
            740                 745                 750
Lys Ala Asp Lys Lys Glu Lys Leu Ile Gln Thr Ile Gln Glu Val Lys
        755                 760                 765
Glu His Ala Pro Leu Asp Lys Glu Thr Leu Arg Lys Lys Ile Ala Gln
    770                 775                 780
Gly Glu Ile Asp Pro Tyr Asp Thr Glu Lys His Lys Gln Asp Arg Thr
785                 790                 795                 800
Phe Lys Val Gly Asp Ala Glu Leu Leu Lys Leu Lys Glu His Tyr Tyr
                805                 810                 815
Thr Pro Leu Ile Lys Ala Lys Asn Cys Asp Trp Leu Lys His Val Val
            820                 825                 830
Lys Val Lys Ser Glu Ser Asp Phe Leu Glu Glu Leu Leu Lys Ile Thr
        835                 840                 845
Glu Thr Leu Gln Glu Asn Tyr Asp Phe Trp Ala Phe Ser Lys Ile Asp
    850                 855                 860
Glu His Leu Asp Asn Leu Phe Ile Pro Tyr Ile Asp Asn Ala Thr Glu
865                 870                 875                 880
Arg Arg Phe Phe Pro Asp Phe Ile Phe Trp Leu Gln Lys Gly Gly Thr
                885                 890                 895
Gln Ile Ile Cys Phe Ile Asp Pro Lys Gly Ser Lys His Thr Asp Tyr
            900                 905                 910
Glu His Lys Ala Asp Ala Tyr Gln Leu Phe Glu Asp Lys Val Phe Asn
        915                 920                 925
Pro Lys Asp Asp Pro Asn Leu Lys Ile Lys Val Val Leu Lys Phe Tyr
    930                 935                 940
Gly Asp Lys Asp Asp Val Gly Glu Arg Tyr Arg Asp Leu
945                 950                 955
```

(2) INFORMATION FOR SEQ ID NO:1706:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

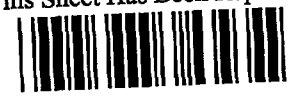
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1706

```
Cys Met Arg Phe Tyr Phe Lys Phe Leu Trp Leu Leu Gly Ile Phe Leu
1               5                  10                  15
Ile Phe Tyr Phe Leu Asp Ile Lys Gly Ser Ser Ser Tyr Ile Ser Asp
            20                  25                  30
Arg Val Lys Ser Ala Leu Met Ser Ala Lys Asn Ser Leu Leu Asp Asn
        35                  40                  45
Val Gln Ala Tyr Phe Phe Gln Ala Gln Asn Ile Lys Glu Phe Gln Lys
    50                  55                  60
Glu Arg Leu Ile Leu Glu Ala Leu Lys Leu Glu Asn Ala Asp Leu Lys
65                  70                  75                  80
Glu Arg Leu Asn Ser Ile Tyr Pro Leu Glu Asn Pro Lys Met Thr Tyr
                85                  90                  95
Thr Pro Thr Phe Met Thr Ser Phe Ile Asn Leu Glu Asp Thr His Ser
            100                 105                 110
Val Ser Leu Asn Pro Ile Val Asn Leu Glu Glu Asn Lys Ile Tyr Gly
        115                 120                 125
Leu Val Ser His Asn Gln Ala Ile Gly Ile Ala Val Leu Glu Lys Gly
    130                 135                 140
Arg Leu Asn Gly Phe Leu Asn Ala His Lys Arg Cys Ala Tyr Ser Val
145                 150                 155                 160
Met Ile Gly Gln Asn Gln Val Leu Gly Phe Ile Gly Thr Asn Phe Lys
                165                 170                 175
Gln Glu Leu Val Val Asp Phe Ile Val Pro Ser Ala Glu Ile Asn Ile
            180                 185                 190
Gly Asp Gln Val Leu Thr Ser Gly Leu Asp Gly Ile Phe Gly Ala Gly
        195                 200                 205
Val Phe Val Gly Glu Val Ser Ser Val Glu Asp His Tyr Thr Tyr Lys
    210                 215                 220
Ser Ala Val Leu Lys Asn Ala Phe Leu Ser Glu Ala Lys Leu Leu Arg
225                 230                 235                 240
His Val Phe Leu Ser Gly Val Lys Asn
                245
```

(2) INFORMATION FOR SEQ ID NO:1707:

This Sheet Has Been Replaced



(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:1707

```
Trp Tyr Phe Lys Lys Glu Arg Asn Pro Met Val Ile His Glu Lys Ile
1               5                  10                  15
Lys Ser Arg Phe Ser Arg Asn Trp Ser Leu Arg Asn Arg Gly Arg His
            20                  25                  30
Phe Ala Ser Ser Ser Val Tyr Phe Phe Ser Leu Leu Val Ile Thr Ala
        35                  40                  45
Val Asn Arg Ser Ser Ala Val Ala Trp Leu Leu Met Pro Glu His Leu
    50                  55                  60
Ile Gly Trp Phe Leu Ile Ser Phe Ser Gly Glu Phe Val Ala Asp Met
65                  70                  75                  80
Ala Phe Gly Lys Lys Ser Lys Ile Phe Lys Thr Arg Phe Gly Ile Ser
                85                  90                  95
Ile Val Ser Gly Val Ser Leu Leu Leu Gly Ala Leu Pro Ala His Leu
            100                 105                 110
Phe Phe Val Trp Phe Gly Phe Ile Asn Trp Trp Ala Val Phe Phe Ile
        115                 120                 125
Glu Ala Gly Ala Asp Leu Leu Val Gly Cys Val Ile Gln Lys Ile Phe
    130                 135                 140
Phe Gly Lys Tyr Trp Val Asp Arg Tyr Tyr
145                 150
```

(2) INFORMATION FOR SEQ ID NO:1708:

(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:1708

```
Trp Ala Lys Gly Ala Gly Ala Leu Val Leu Glu Glu Tyr Glu Ser Ala
1               5                  10                  15
Lys Lys Arg Gly Ala Lys Ile Tyr Ala Glu Phe Ala Gly Tyr Gly Glu
            20                  25                  30
Ser Gly Asp Ala Asn His Ile Thr Ala Pro Ala Pro Glu Gly Glu Arg
        35                  40                  45
Ala Phe Lys Ala Met Lys Met Ala Leu Glu Met Ala Lys Val Glu Val
    50                  55                  60
Cys Tyr Val Asn Ala His Gly Asp Lys His Ala Leu
65                  70                  75
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1709:

(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:1709

```
Thr Pro Met Gly Thr Ser Thr His Tyr Asn Asp Trp Tyr Glu Ser Ile
1               5                  10                  15
Ala Leu Lys Asn Val Phe Gly Ser Lys Glu Lys Val Pro Pro Val Ser
            20                  25                  30
Ser Thr Lys Gly Gln Ile Gly His Cys Leu Gly Ala Ala Gly Ala Leu
        35                  40                  45
Val Ala Val Ile Ser Ile Met Ala Met Asn Gln Gly Ile Leu Pro Pro
    50                  55                  60
Thr Ile Asn Gln Glu Thr Pro Asp Pro Glu Cys Asp Leu Asp Tyr Ile
65                  70                  75                  80
Pro Asn Thr Ala Arg Glu Lys Gln Val Asn Ala Val Met Ser Asn Ser
                85                  90                  95
Phe Gly Phe Gly Gly Thr Asn Gly Val Val Ile Phe Lys Lys Ala
            100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:1710:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1710

```
Gly Pro Ile Gln Ser Ala Pro Ala Met Asn Lys Leu Phe Leu Ala Phe
1               5                  10                  15
Ile Val Gly Gly Met Leu Leu Ser Ala Asp Ala Leu Asn Asp Lys Ile
            20                  25                  30
Glu Asn Leu Met Gly Glu Arg Ser Tyr His Met Asn Lys Leu Phe Leu
        35                  40                  45
Glu Arg Leu Phe Lys Asn Arg Lys Asp Phe Tyr Glu Met Gly Arg Leu
    50                  55                  60
Asp Ser Leu Lys Leu Leu Asn Thr Leu Lys Glu Asn Gly Leu Leu Ser
65                  70                  75                  80
Phe Asn Phe Asp Lys Pro Ser Val Leu Lys Ile Thr Phe Lys Ala Ser
                85                  90                  95
Ser Asn Pro Leu Ala Phe Ala Lys Ser Ile Asn Asn Ser Leu Asn Met
            100                 105                 110
Met Gly Tyr Ser Tyr Val Leu Pro Ile Arg Met Gln Ser Ser Ser Gly
        115                 120                 125
Glu Asn Val Phe Ser Tyr Glu Leu Lys Thr Glu Tyr Val Leu Asp Pro
    130                 135                 140
Asn Ile Leu Ile Glu Thr Met Lys Arg His Gly Phe Asp Phe Met Asp
145                 150                 155                 160
```

Ile Arg Arg Val Ser Leu Lys Glu Trp Glu Tyr Asp Phe Ala Leu Gln
165 170 175
Lys Ile Lys Leu Pro Asn Gly Glu Ser Leu Ser Phe Glu
180 185

(2) INFORMATION FOR SEQ ID NO:1711:

(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:1711

Met Glu Gln Asn Lys Lys Ser Leu Glu Asn Leu Asp Leu Ser Asp Val
1 5 10 15
Gln Asn Ile Ser Lys Asp Ile Ser Gly Thr Ala Leu Glu Glu Leu Ser
20 25 30
Leu Lys Asn Leu Asp Lys Asn Leu Gln Ile Leu Lys Glu Val Gly Ala
35 40 45
Ala Glu Ile Cys Lys Ala Thr Lys Ile Ala Ser Lys Asn Ile His Ser
50 55 60
Ile Leu Glu Lys Arg Tyr Glu Ser Leu Ser Arg Val His Ala Arg Gly
65 70 75 80
Phe Ile Gln Ile Leu Glu His Glu Tyr Lys Ile Asp Leu Ser Ala Trp
85 90 95
Val Lys Glu Phe Asp Lys Val Cys Val Phe Lys Glu Gly Val Gly Glu
100 105 110
Glu Gln Lys Gln Glu Thr Ser Pro Glu Glu Thr Ala Lys Lys Pro Leu
115 120 125
Lys Val Glu Leu Asp Tyr Ser Ile Asn Gln Ala Asn Thr Ser Leu Ser
130 135 140
Lys Lys Ser Ser Lys Trp Lys Pro Phe Val Ile Val Leu Gly Val Val
145 150 155 160
Val Ile Ile Leu Val Val Val Ile Ile Gln Asn Ser Ser Ser Leu Lys
165 170 175
Glu Glu Arg Glu Gln Glu Arg Ala Ile Lys Pro Asp Thr Lys Asn Asn
180 185 190
Ser Phe Asn Glu Thr Asn Pro Thr Glu Glu Lys Lys Leu Glu Pro Thr
195 200 205
Pro Lys Leu Glu Glu Lys His Lys Glu Gln Asp Lys Gln Gly Lys Glu
210 215 220
Ala Ile Lys Glu Asn Pro Asn Thr Ile Tyr Ile Ile Pro Lys Arg Asp
225 230 235 240
Ile Trp Val Glu Val Ile Asp Leu Asp Glu Lys Lys Asn Ser Phe Gln
245 250 255
Lys Val Phe Lys Lys Ser Tyr Pro Leu Glu Ala Lys Asn His Arg Leu
260 265 270
Leu Leu Arg Phe Gly His Gly His Leu Ile Leu Lys Asn Asn His Gln
275 280 285
Glu Gln Asp Tyr Asn Asp Ser Lys Thr Arg Arg Phe Leu Tyr Glu Pro
290 295 300
Asn Lys Gly Leu Thr Leu Ile Asn Glu Ala Gln Tyr Lys Ala Leu Gln

This Sheet Has Been Replaced



305 310 315 320
Gln

(2) INFORMATION FOR SEQ ID NO:1712:

(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:1712

Arg Ser Gly Asn Thr Thr Leu Pro Tyr Lys Arg Ser Ser Ser Leu Thr
1 5 10 15
Ala Arg Ala Leu Val Leu Ser Ser Asp Pro Val Glu Phe Lys Glu Ala
20 25 30
Ser Gly Lys Tyr Trp Leu Ser Val Asn Gln Asn Ala Tyr Leu Lys Ile
35 40 45
Ser Ser Asn Asn Pro Leu Trp Gln Pro Lys Ile Ile Phe Tyr Asp Glu
50 55 60
Asn Leu Lys Ile Ile Gln Ile Ile Ala Lys Glu Asn Arg Gln Gln Glu
65 70 75 80
Ile Ala Leu Asn Leu Leu Asp Gly Val Arg Phe Ile His Ile Thr Asp
85 90 95
Ala Lys Asn Pro Ile Ile Leu Lys Asn Gly Ile Ser Val Val Phe Asp
100 105 110
Ala Met Pro
115

(2) INFORMATION FOR SEQ ID NO:1713:

This Sheet Has Been Replaced

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1713

Arg Ser Leu Ala Cys Trp Leu Arg Leu Ser Leu Phe Lys Gly Ile Ile
1 5 10 15

```
Met Phe Asp Ser Ile Val Tyr Phe Phe Asn Lys Ser Gly Phe Val Thr
            20                  25                  30
Thr Leu Val Leu Val Trp Ile Ser Leu Tyr Leu Val Met Thr Leu Trp
        35                  40                  45
Val Phe Leu Tyr Lys Ser Ile Val Leu Lys Ile Glu Leu Arg Arg Glu
    50                  55                  60
Met Gln Ser Leu Ser Asn Ile Leu Asn Gly Ala Gln Asp Ala Gln Ser
65                  70                  75                  80
Ile Leu Cys Leu Ile Lys Lys Glu Met Met Arg Pro Lys Gly Ile Leu
                85                  90                  95
Met Asn Cys Cys Arg Ala Trp Lys His Gln Val Leu Lys Gln Ser Thr
            100                 105                 110
Thr Gly Leu Val Val Leu Ser Ile Ile Ser Ser Thr Ala Pro Phe Ile
        115                 120                 125
Gly Leu Phe Gly Thr Val Val Glu Ile Leu Glu Ala Phe Asn Asn Leu
    130                 135                 140
Gly Ala Leu Gly Gln Ala Ser Phe Gly Val Ile Ala Pro Ile Ile Ser
145                 150                 155                 160
Lys Ala Leu Ile Ala Thr Ala Ala Gly Ile Leu Ala Ala Ile Pro Ala
                165                 170                 175
Tyr Ser Phe Tyr Leu Ile Leu Lys Arg Lys Val Tyr Asp Leu Ser Val
            180                 185                 190
Tyr Val Gln Met Gln Val Asp Ile Leu Ser Ser Lys Lys
        195                 200                 205
```

(2) INFORMATION FOR SEQ ID NO:1714:

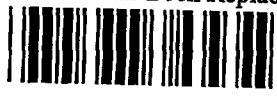
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1714

```
Lys Val Phe Met Asn Tyr Asp Asn Tyr Trp Asp Glu Asp Lys Pro Glu
1               5                   10                  15
Leu Asn Ile Thr Pro Leu Val Asp Val Met Leu Val Leu Leu Ala Ile
            20                  25                  30
Leu Met Val Thr Thr Pro Thr Leu Thr Tyr Lys Glu Glu Ile Ala Leu
        35                  40                  45
Pro Ser Gly Ser Lys Thr Ala Arg Ala Thr Gln Asp Lys Val Ile Glu
    50                  55                  60
Ile Arg Met Asp Lys Asp Ala Lys Ile Tyr Ile Asp Ser Gln Thr Tyr
65                  70                  75                  80
Glu Tyr Asn Ser Phe Pro Asp Thr Phe Asn Leu Leu Ser Lys Lys Tyr
                85                  90                  95
Asp Lys Asp Thr Arg Val Ser Ile Arg Ala Asp Lys Arg Leu Thr Tyr
            100                 105                 110
Asp Lys Val Ile Tyr Leu Leu Lys Thr Ile Lys Glu Ala Gly Phe Leu
        115                 120                 125
Lys Val Ser Leu Ile Thr Ser Pro
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:1715:

(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:1715

```
Lys Val Gly Pro Ile Cys Met Ser Lys Ser Ala Ile Phe Val Leu Ser
1               5                  10                  15
Gly Phe Leu Ala Phe Leu Leu Tyr Ala Leu Leu Leu Tyr Gly Leu Leu
            20                  25                  30
Leu Glu Arg His Asn Lys Glu Ala Glu Lys Ile Leu Leu Asp Leu Asn
        35                  40                  45
Lys Lys Asp Glu Gln Ala Ile Asp Leu Asn Leu Glu Asp Leu Pro Ser
    50                  55                  60
Glu Lys Lys Asn Glu Lys Ile Glu Lys Val Thr Glu Lys Gln Gly Asp
65                  70                  75                  80
Phe Leu Glu Pro Lys Glu Glu Pro Lys Glu Glu Pro Glu Glu Ser Leu
                85                  90                  95
Glu Asp Ile Phe Ser Ser Leu Asn Asp Phe Gln Glu Arg Gln Thr Lys
            100                 105                 110
Thr Leu Lys Lys Thr Ser Lys Lys Met Asn Lys Lys Asn Lys Gly Val
        115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:1716:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 215 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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

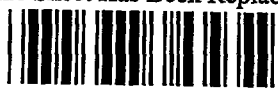
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1716

```
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
        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:1717:

This Sheet Has Been Replaced



(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:1717

```
Phe Leu Arg Gly Lys Phe Ile Gln Glu Arg Leu Lys Ala Leu Cys Cys
1               5                   10                  15
Gln Gly Val Glu Gly Glu Phe Gly Val Leu Tyr Gly His Ser Asn Met
            20                  25                  30
Ile Thr Leu Leu Gln Ala Gly Val Val Glu Ile Glu Thr Glu Asn Gln
        35                  40                  45
Lys Glu His Ile Ala Ile Asn Trp Gly Tyr Ala Glu Val Thr Asn Glu
    50                  55                  60
Arg Val Asp Ile Leu Ala Asp Gly Ala Val Phe Ile Lys Lys Gly Ser
65                  70                  75                  80
Asp Asp Arg Asp Asp Ala Ile Ser Arg Ala Lys Lys Leu Leu Glu Asp
                85                  90                  95
Ala Ser Ser Asp Arg Leu Ala Val Ser Ser Val Leu Ala Lys Ile Glu
            100                 105                 110
Ser Leu
```

(2) INFORMATION FOR SEQ ID NO:1718:

(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:1718

```
Lys Leu Ser Met Arg Ala Ile Ala Ile Val Leu Ala Arg Ser Ser Ser
1               5                  10                  15
Lys Arg Ile Lys Asn Lys Asn Met Ile Asp Phe Phe Asn Lys Pro Met
            20                  25                  30
Leu Ala Tyr Pro Ile Glu Thr Ala Leu Asn Ser Lys Leu Phe Glu Lys
        35                  40                  45
Val Phe Ile Ser Ser Asp Ser Met Glu Tyr Val Asn Leu Ala Lys Asn
    50                  55                  60
Tyr Gly Ala Ser Phe Leu Asn Leu Arg Pro Lys Asn Leu Ala Asp Glu
65                  70                  75                  80
Gln Gly His Asp Phe Arg Ser Asp Gly Leu Ser His Glu Arg Ile Arg
                85                  90                  95
Ile Lys Arg
```

(2) INFORMATION FOR SEQ ID NO:1719:

This Sheet Has Been Replaced



(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:1719

```
Ile Pro Pro Ser Thr Pro Phe Leu Asn Ile Leu His Val Phe Lys His
1               5                  10                  15
Tyr Arg Ser His Tyr Gly Lys Ile Asn Thr Cys Leu Asn Thr Leu Gly
            20                  25                  30
Asp Leu Ile Leu Ala Leu Pro Val Tyr Tyr Asp Lys Asp Ile Asp Leu
        35                  40                  45
Gly Val Ile Gln Ser Leu Gln Val Gly Ile Ile Gly Tyr Gly Val Gln
    50                  55                  60
Gly Glu Ala Gln Ala Leu Asn Leu Arg Asp Ser Lys Val Lys Val Arg
65                  70                  75                  80
Ile Gly Leu Tyr Gln Gly Ser Leu Ser Val Ser Lys Ala Lys Lys Glu
                85                  90                  95
```

```
Gly Phe Glu Val Leu Gly Val Lys Glu Leu Val Gln Gln Ser Asp Val
            100                 105                 110
Ile Met Ala Leu Leu Pro Asp Glu Leu His Lys Glu Val Leu Glu Lys
        115                 120                 125
Glu Val Ile Pro Phe Leu Lys Glu Gly Gln Ile Ile Gly Phe Ala His
    130                 135                 140
Gly Phe Ser Val His Phe Asn Gln Val Val Leu Pro Lys Gly Val Gly
145                 150                 155                 160
Ala Ile Leu Val Ala Pro Lys Gly Pro Gly Ser Ala Leu Arg Glu Glu
                165                 170                 175
Tyr Leu Lys Asn Arg Gly Leu Tyr His Leu Ile Ala Ile Glu Gln Glu
            180                 185                 190
Ser Ser Ile His Asn Ala Lys Ala Val Ala Leu Ser Tyr Ala Lys Ala
        195                 200                 205
Met Gly Gly Gly Arg Met Gly Val Leu Glu Thr Ser Phe Lys Glu Glu
    210                 215                 220
Cys Glu Ser Asp Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Leu
225                 230                 235                 240
Glu Ala Ile Val Arg Met Gly Phe Glu Thr Leu Ile Lys Ala Gly Tyr
                245                 250                 255
```

(2) INFORMATION FOR SEQ ID NO:1720:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

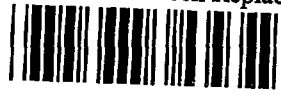
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...91

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1720

```
Gln Thr Ser Arg Ala Thr Thr Leu Glu Val Met Ala Tyr His Met Lys
1               5                   10                  15
Glu Leu Glu Leu Lys Asp Glu Asp Ile Ala Cys Cys Leu Tyr Gly Val
            20                  25                  30
Ser Val Phe Leu Gln Glu Lys His Leu Gln Asn Ala Phe Glu Thr Leu
        35                  40                  45
Lys Gln Asn Gln Asn Thr Asp Tyr Val Phe Thr Cys Ser Pro Phe Ser
    50                  55                  60
Ala Ser Pro Ile Val Leu Leu Ala Leu Lys Thr Ala Phe Lys Trp Leu
65                  70                  75                  80
Leu Lys Ser Ile Gln Thr Arg Ala Arg Lys Ile
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:1721:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

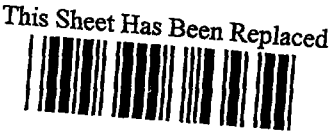
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...312

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1721

```
Met Lys Ser Asp Lys Pro Phe Leu Glu Arg Tyr Phe Tyr Asp Pro Thr
1               5                  10                  15
Leu Leu Gln Lys Gly Leu Ile Phe Ala Leu Tyr Pro Phe Ser Leu Ile
            20                  25                  30
Tyr Gln Cys Ile Ala Thr Ile Lys Arg Lys Thr Ala Lys Lys His Asp
        35                  40                  45
Phe Lys Ile Pro Ile Ile Ser Ile Gly Asn Leu Ile Ala Gly Gly Ser
    50                  55                  60
Gly Lys Thr Pro Phe Ile Leu Glu Ile Ala Pro Arg Tyr Gln Glu Val
65                  70                  75                  80
Ala Val Val Ser Arg Gly Tyr Gln Arg Asp Ser Lys Gly Leu Val Val
                85                  90                  95
Val Ser Val Lys Gly Asn Ile Leu Val Pro Gln Lys Thr Ala Gly Asp
            100                 105                 110
Glu Ala Tyr Leu Leu Ala Leu Asn Leu Lys Gln Ala Ser Val Ile Val
        115                 120                 125
Ser Glu Lys Arg Glu Leu Gly Val Leu Lys Ala Leu Glu Leu Gly Ser
    130                 135                 140
Lys Ile Val Phe Leu Asp Asp Gly Phe Arg Phe Asn Phe Asn Gln Phe
145                 150                 155                 160
Asn Ala Leu Leu Lys Pro Lys Val Pro Pro Tyr Tyr Pro Phe Cys Leu
                165                 170                 175
Pro Ser Gly Leu Tyr Arg Glu Asn Ile Lys Ser Tyr Lys Glu Ala His
            180                 185                 190
Leu Val Ile Thr Glu Asp Lys Asp Tyr Gln Arg Ile Thr Ser Ile Thr
        195                 200                 205
Asn Pro Thr Lys Arg Met Leu Leu Val Thr Ala Ile Ala Asn Pro Ser
    210                 215                 220
Arg Leu Asp Ala Phe Leu Pro Lys Glu Val Val Lys Lys Leu Tyr Phe
225                 230                 235                 240
Arg Asp His Ala Pro Phe Asp Leu Lys Leu Leu Glu Lys Glu Phe Tyr
                245                 250                 255
Gln Asn Asn Ala Thr Ser Leu Leu Val Thr Ser Lys Asp Leu Val Lys
            260                 265                 270
Leu Gln Asp Cys Lys Leu Pro Leu Ser Val Leu Asp Leu Lys Leu Glu
        275                 280                 285
Ile Cys Pro Lys Val Leu Glu Glu Ile Asp Arg Tyr Ile Leu Ser Tyr
    290                 295                 300
Pro Cys Asn Ile Lys Glu His Leu
305                 310
```

(2) INFORMATION FOR SEQ ID NO:1722:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

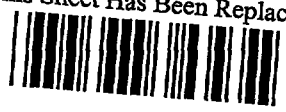
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1722

```
Lys Val Leu Trp Val Leu Tyr Phe Leu Thr Ser Leu Phe Ile Cys Ser
1               5                  10                  15
Leu Ile Val Leu Trp Ser Lys Lys Ser Met Leu Phe Val Asp Asn Ala
            20                  25                  30
Asn Lys Ile Gln Gly Phe His His Ala Arg Thr Pro Arg Ala Gly Gly
        35                  40                  45
Leu Gly Ile Phe Leu Ser Phe Ala Leu Ala Cys Tyr Leu Glu Pro Phe
    50                  55                  60
Glu Met Pro Phe Lys Gly Pro Phe Val Phe Leu Gly Leu Ser Leu Val
65                  70                  75                  80
Phe Leu Ser Gly Phe Leu Glu Asp Ile Asn Leu Ser Leu Ser Pro Lys
                85                  90                  95
Ile Arg Leu Ile Leu Gln Ala Val Gly Val Val Cys Ile Ile Ser Ser
            100                 105                 110
Thr Pro Leu Val Val Ser Asp Phe Ser Pro Leu Phe Ser Leu Pro Tyr
        115                 120                 125
Phe Ile Ala Phe Leu Phe Ala Ile Phe Met Leu Val Gly Ile Ser Asn
    130                 135                 140
Ala Ile Asn Ile Ile Asp Gly Phe Asn Gly Leu Ala Ser Gly Ile Cys
145                 150                 155                 160
Ala Ile Ala Leu Leu Val Ile His Tyr Ile Asp Pro Ser Ser Leu Ser
                165                 170                 175
Cys Leu Leu Ala Tyr Met Val Leu Gly Phe Met Val Leu Asn Phe Pro
            180                 185                 190
Ser Gly Lys Ile Phe
        195
```

(2) INFORMATION FOR SEQ ID NO:1723:

(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

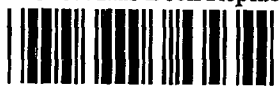
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1723

```
Gln Phe Val Leu Phe Ala Arg Leu His Gly Ala Trp Val Tyr Gly Val
1               5                  10                  15
Lys Phe Pro Phe Arg Lys Asp Phe Leu Gly Asp Gly Gly Ala Tyr Phe
            20                  25                  30
Leu Gly Leu Val Cys Gly Ile Ser Leu Leu His Leu Ser Leu Glu Gln
        35                  40                  45
Lys Ile Ser Val Phe Phe Gly Leu Asn Leu Met Leu Tyr Pro Val Ile
    50                  55                  60
Glu Val Leu Phe Ser Ile Leu Arg Arg Lys Ile Lys Arg Gln Lys Ala
```

```
65                  70                  75                  80
Thr Met Pro Asp Asn Leu His Leu His Thr Leu Leu Phe Lys Phe Leu
                85                  90                  95
Gln Gln Arg Ser Phe Asn Tyr Pro Asn Pro Leu Cys Ala Phe Ile Leu
            100                 105                 110
Ile Leu Cys Asn Leu Pro Phe Ile Leu Ile Ser Val Leu Phe Arg Leu
        115                 120                 125
Asp Ala Tyr Ala Leu Ile Val Ile Ser Leu Val Phe Ile Ala Cys Tyr
    130                 135                 140
Leu Ile Gly Tyr Ala Tyr Leu Asn Arg Gln Val Cys Ala Leu Glu Lys
145                 150                 155                 160
Arg Ala Phe
```

(2) INFORMATION FOR SEQ ID NO:1724:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(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:1724

```
Met Asn Lys Thr Ile Lys Ala Ala Ala Leu Ala Tyr Asn Met Gly Gln
1               5                   10                  15
Asp His Ala Pro Lys Val Ile Ala Ser Gly Val Gly Glu Val Ala Lys
            20                  25                  30
Arg Ile Ile Gln Lys Ala Lys Glu Tyr Asp Ile Ala Leu Phe Ser Asn
        35                  40                  45
Pro Met Leu Val Asp Ser Leu Leu Lys Val Glu Leu Asp Cys Ala Ile
    50                  55                  60
Pro Glu Glu Leu Tyr Glu Ser Val Val Gln Val Phe Leu Trp Leu Asn
65                  70                  75                  80
Ser Val Glu Asn Asn Ala Gln Met Ser Lys
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:1725:

(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:1725

```
Val Lys Lys Ser Asn Asn Met Val Val Glu Leu Lys Asn Ile Glu Lys
1               5                  10                  15
Ile Tyr Glu Asn Gly Phe His Ala Leu Lys Gly Val Asn Leu Glu Leu
            20                  25                  30
Lys Lys Gly Asp Ile Leu Gly Val Ile Gly Tyr Ser Gly Ala Gly Lys
        35                  40                  45
Ser Thr Leu Ile Arg Leu Ile Asn Cys Leu Glu Arg Pro Ser Ser Gly
    50                  55                  60
Glu Val Leu Val Asn Gly Val Asn Leu Leu Asn Leu Lys Pro Lys Glu
65                  70                  75                  80
Leu Gln Lys Ala Arg Gln Lys Ile Gly Met Ile Phe Gln His Phe Asn
                85                  90                  95
Leu Leu Ser Ala Lys Asn Val Phe Glu Asn Val Ala Phe Ala Leu Glu
            100                 105                 110
Ile Ala Arg Trp Glu Lys Thr Lys Ile Lys Ser Arg Val His Glu Leu
        115                 120                 125
Leu Glu Leu Val Gly Leu Glu Asp Lys Val His Phe Tyr Pro Lys Gln
    130                 135                 140
Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ser Leu Ala
145                 150                 155                 160
Asn Cys Pro Asn Leu Leu Leu Cys Asp Glu Ala Thr Ser Ala Leu Asp
                165                 170                 175
Ser Lys Thr Thr His Ser Ile Leu Thr Leu Leu Ser Gly Ile Gln Lys
            180                 185                 190
Lys Phe Asp Leu Ser Ile Val Phe Ile Thr His Gln Ile Glu Val Val
        195                 200                 205
Lys Glu Leu Cys Asn Gln Met Cys Val Ile Ser Ser Gly Glu Ile Val
    210                 215                 220
Glu Arg Gly Ser Val Glu Glu Ile Phe Ala Asn Pro Lys His Ala Val
225                 230                 235                 240
Thr Lys Glu Leu Leu Gly Ile Lys Asn Glu His Ala Asp Gln Lys Ser
                245                 250                 255
Gln Asp Ile Tyr Arg Ile Val Phe Leu Gly Glu His Leu Asp Glu Pro
            260                 265                 270
Ile Ile Ser Asn Leu Ile Arg Arg Phe Lys Ile Arg Arg
        275                 280                 285
```

(2) INFORMATION FOR SEQ ID NO:1726:

This Sheet Has Been Replaced



(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:1726

```
Leu Phe Cys Ser Cys Leu Tyr Gln Arg Phe Leu Ile Gly Thr Ser Ile
1               5                  10                  15
Gly Ser Ser Ala Ser Ile Ile Pro Leu Ala Ile Ser Ala Ile Pro Phe
```

```
            20                  25                  30
Val Val Lys Leu Phe Glu Asn Ser Leu Met Glu Val Glu His Gly Lys
        35                  40                  45
Ile Glu Thr Thr Leu Ser Leu Gly Ala Ser His Leu Glu Val Ile Lys
    50                  55                  60
Met Met Leu Leu Glu Ser Leu Pro Ser Leu Val Asn Asn Ile Thr Ile
65                  70                  75                  80
Thr Leu Ile Ser Leu Ile Gly Tyr Ser Ala Met Ala Gly Ala Leu Gly
                85                  90                  95
Ala Gly Gly Leu Gly Asp Leu Ala Ile Arg Ile Gly Tyr Gln Ser Tyr
            100                 105                 110
Arg Gly Asp Val Leu Phe Tyr Ala Val Val Val Ile Ile Val Leu Val
        115                 120                 125
Gln Ile Ile Gln Ser Ala Gly Asp Tyr Val Val Lys Arg Leu Arg Lys
    130                 135                 140
Asn Lys Tyr
145
```

(2) INFORMATION FOR SEQ ID NO:1727:

(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:1727

```
Ser Tyr Phe Cys Tyr Asn Leu Arg Leu Leu Ser Leu Val Lys Gly Lys
1               5                   10                  15
Thr Met Leu Arg Ser Leu Tyr Ser Ala Thr Ser Gly Met Leu Ala Gln
            20                  25                  30
Gln Thr His Ile Asp Thr Thr Ser Asn Asn Ile Ala Asn Val Asn Thr
        35                  40                  45
Thr Gly Phe Lys Lys Ser Arg Ala Asp Phe Asn Asp Leu Phe Tyr Gln
    50                  55                  60
Ala Met Gln Tyr Ala Gly Thr Asn Thr Ser Asn Thr Thr Leu Ser Pro
65                  70                  75                  80
Asp Gly Met Glu Val Gly Leu Gly Val Arg Pro Ser Ala Ile Thr Lys
                85                  90                  95
Met Phe Ser Gln Gly Ser Pro Lys Glu Thr Glu Asn Asn Leu Asp Ile
            100                 105                 110
Ala Ile Thr Gly Lys Gly Phe Phe Gln Val Gln Leu Pro Asp Gly Thr
        115                 120                 125
Thr Ala Tyr Thr Arg Ser Gly Asn Phe Lys Leu Asp Glu Gln Gly Asn
    130                 135                 140
Leu Val Thr Ser Glu Gly Tyr Leu Leu Ile Pro Gln Ile Thr Leu Pro
145                 150                 155                 160
Glu Asp Thr Thr Gln Val Asn Ile Gly Val Asp Gly Thr Val Ser Val
                165                 170                 175
Thr Gln Gly Leu Gln Thr Thr Ser Asn Val Ile Gly Gln Ile Thr Leu
            180                 185                 190
Ala Asn Phe Val Asn Pro Ala Gly Leu His Ser Met Gly Asp Asn Leu
        195                 200                 205
```

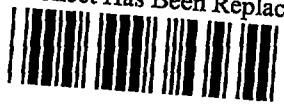
This Sheet Has Been Replaced



```
Phe Ser Ile Thr Asn Ala Ser Gly Asp Ala Ile Val Gly Asn Pro Asp
    210                 215                 220
Ser Gln Gly Leu Gly Lys Leu Arg Gln Gly Phe Leu Glu Leu Ser Asn
225                 230                 235                 240
Val Arg Leu Val Glu Glu Met Thr Asp Leu Ile Thr Ala Gln Arg Ala
                245                 250                 255
Tyr Glu Ala Asn Ser Lys Ser Ile Gln Thr Ala Asp Ala Met Leu Gln
            260                 265                 270
Thr Val Asn Ser Leu Lys Arg
        275
```

(2) INFORMATION FOR SEQ ID NO:1728:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1728

```
Lys Trp Arg Asn Ser Ser Ser Asp Lys Met Ala Lys Lys Lys Ile Ala
1               5                  10                  15
Ile Ser Cys Gly Asp Ile Gln Gly Val Gly Leu Glu Leu Ile Leu Lys
            20                  25                  30
Ser His Lys Glu Val Ser Ala Leu Cys Glu Pro Leu Tyr Leu Val His
        35                  40                  45
Ser Glu Leu Leu Glu Arg Ala Asn Gln Leu Leu Asp Asn Ala Tyr Glu
    50                  55                  60
Thr Lys Thr Leu Asn Ala Ile Ala Ile Asp Ala Pro Leu Pro Leu Leu
65                  70                  75                  80
Asn Ser Ser Thr Ile Gly Lys Val Ser Thr Gln Ser Gly Ala Tyr Ser
                85                  90                  95
Phe Glu Ser Phe Lys Lys Ala Cys Glu Leu Ala Asp Ser Lys Glu Val
            100                 105                 110
Asp Gly Ile Cys Thr Leu Pro Ile Asn Lys Leu Ala Trp Gln Gln Ala
        115                 120                 125
Gln Ile Pro Phe Val Gly His Thr Asp Phe Leu Lys Gln Arg Tyr Lys
    130                 135                 140
Asp His Gln Ile Ile Met Met Leu Gly Cys Ser Lys Leu Phe Val Gly
145                 150                 155                 160
Leu Phe Ser Asp His Val Pro Leu Ser Ala Val Ser Gln Leu Ile Gln
                165                 170                 175
Val Lys Ala Leu Val Lys Phe Leu Leu Ala Phe Gln Lys Ser Thr Gln
            180                 185                 190
Ala Lys Ile Val Gln Val Cys Gly Phe Asn Pro His Ala Gly Glu Glu
        195                 200                 205
Gly Leu Phe Gly Glu Glu Asp Glu Lys Ile Leu Lys Ala Ile Gln Glu
    210                 215                 220
Ser Asn Gln Thr Leu Gly Phe Glu Cys Phe Leu Gly Pro Leu Pro Ala
225                 230                 235                 240
Asp Ser Ala Phe Ala Pro Asn Lys Arg Lys Ile Thr Pro Phe Tyr Val
                245                 250                 255
Ser Met Ser His Asp Val Gly Leu Ala Pro Leu Lys Ala Leu Tyr Phe
```

```
            260                 265                 270
Asp Glu Ser Ile Asn Val Ser Leu Asn Ala Pro Ile Leu Arg Ala Ser
        275                 280                 285
Thr Asp His Gly Thr Ala Phe Asp Ile Ala Tyr Gln Asn Lys Ala Asn
    290                 295                 300
His Lys Ser Tyr Leu Asn Ala Ile Lys Tyr Leu Ala
305                 310                 315
```

(2) INFORMATION FOR SEQ ID NO:1729:

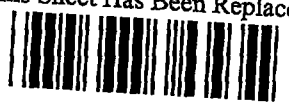
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1729

```
Gln Gly Ile Ile Gln Ala Lys Thr Pro Pro Lys Asp Lys Asp Met Ile
1               5                  10                  15
Leu Ser Ile Glu Ser Ser Cys Asp Asp Ser Ser Leu Ala Leu Thr Arg
            20                  25                  30
Ile Glu Asp Ala Lys Leu Ile Ala His Phe Lys Ile Ser Gln Glu Lys
        35                  40                  45
His His Ser Ser Tyr Gly Gly Val Val Pro Glu Ile Ala Ser Arg Leu
    50                  55                  60
His Ala Glu Asn Leu Pro Leu Leu Leu Glu Arg Val Lys Ile Ser Leu
65                  70                  75                  80
Asn Lys Asp Phe Ser Lys Ile Lys Ala Ile Ala Ile Thr Asn Gln Pro
                85                  90                  95
Gly Leu Ser Val Thr Leu Ile Glu Gly Leu Met Met Ala Lys Ala Leu
            100                 105                 110
Ser Leu Ser Leu Asn Leu Pro Leu Ile Leu Glu Asp His Leu Arg Gly
        115                 120                 125
His Val Tyr Ser Leu Phe Ile Asn Glu Lys Gln Thr Arg Met Pro Leu
    130                 135                 140
Ser Val Leu Leu Val Ser Gly Gly His Ser Leu Ile Leu Glu Ala Arg
145                 150                 155                 160
Asp Tyr Glu Asp Ile Lys Ile Val Ala Thr Ser Leu Asp Asp Ser Phe
                165                 170                 175
Gly Glu Ser Phe Asp Lys Val Ser Lys Met Leu Asp Leu Gly Tyr Pro
            180                 185                 190
Gly Gly Pro Ile Val Glu Lys Leu Ala Leu Asp Tyr Ala His Pro Asn
        195                 200                 205
Glu Pro Leu Met Phe Pro Ile Pro Leu Lys Asn Ser Pro Asn Leu Ala
    210                 215                 220
Phe Ser Phe Ser Gly Leu Lys Asn Ala Val Arg Leu Glu Val Glu Lys
225                 230                 235                 240
Asn Ala His Asn Leu Asn Asp Glu Val Lys Gln Lys Ile Gly Tyr His
                245                 250                 255
Phe Gln Ser Ala Ala Ile Glu His Leu Ile Gln Gln Thr Lys Arg Tyr
            260                 265                 270
Phe Lys Ile Lys Arg Pro Lys Ile Phe Gly Ile Val Gly Gly Ala Ser
        275                 280                 285
```

```
Gln Asn Leu Ala Leu Arg Lys Ala Phe Glu Asp Leu Cys Ala Glu Phe
    290                 295                 300
Asp Cys Glu Leu Val Leu Ala Pro Leu Glu Phe Cys Ser Asp Asn Ala
305                 310                 315                 320
Ala Met Ile Gly Arg Ser Ser Leu Glu Ala Tyr Gln Lys Lys Arg Phe
                325                 330                 335
Ile Pro Leu Glu Lys Ala Asp Ile Ser Pro Arg Thr Leu Leu Lys Asn
            340                 345                 350
Phe Glu
```

(2) INFORMATION FOR SEQ ID NO:1730:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

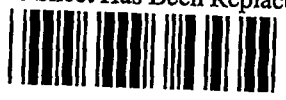
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1730

```
Arg Asn Asn Met Ala Tyr Lys Tyr Asp Arg Asp Leu Glu Phe Leu Lys
1               5                  10                  15
Gln Leu Glu Ser Ser Asp Leu Leu Asp Leu Phe Glu Val Leu Val Phe
            20                  25                  30
Gly Lys Asp Gly Glu Lys Arg His Asn Glu Lys Leu Thr Ser Ser Ile
        35                  40                  45
Glu Tyr Lys Arg His Gly Asp Asp Tyr Ala Lys Tyr Ala Glu Arg Ile
    50                  55                  60
Ala Glu Glu Leu Gln Tyr Tyr Gly Ser Asn Ser Phe Ala Ser Phe Ile
65                  70                  75                  80
Lys Gly Glu Gly Val Leu Tyr Lys Glu Ile Leu Cys Asp Val Cys Asp
                85                  90                  95
Lys Leu Lys Val Asn Tyr Asn Lys Lys Thr Glu Thr Thr Leu Ile Glu
            100                 105                 110
Gln Asn Met Leu Ser Lys Ile Leu Glu Arg Ser Leu Glu Glu Met Asp
        115                 120                 125
Asp Glu Glu Val Lys Glu Met Cys Asp Glu Leu Ser Ile Lys Asn Thr
    130                 135                 140
Asp Asn Leu Asn Arg Gln Ala Leu Ser Ala Ala Thr Leu Thr Leu Phe
145                 150                 155                 160
Lys Met Gly Gly Phe Lys Ser Tyr Gln Leu Ala Val Ile Val Ala Asn
                165                 170                 175
Ala Val Ala Lys Thr Ile Leu Gly Arg Gly Leu Ser Leu Ala Gly Asn
            180                 185                 190
Gln Val Leu Thr Arg Thr Leu Ser Phe Leu Thr Gly Pro Val Gly Trp
        195                 200                 205
Ile Ile Thr Gly Val Trp Thr Ala Ile Asp Ile Ala Gly Pro Ala Tyr
    210                 215                 220
Arg Val Thr Ile Pro Ala Cys Ile Val Val Ala Thr Leu Arg Leu Lys
225                 230                 235                 240
Thr Gln Gln Ala Asn Glu Asp Lys Lys Ser Leu Gln Ile Glu Ser Val
                245                 250                 255
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1731:

(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:1731

```
Val Ile Ile Phe Leu Leu Leu Phe Phe Leu Gly Asn Lys Val Phe Ser
1               5                  10                  15
Ile Tyr Leu Leu Leu Glu Ser Phe Leu Trp Val Ile Leu Thr Thr Trp
            20                  25                  30
Cys Cys Leu Val Met His Glu Asp Gln Arg Gln Lys Asp Met Glu Gln
        35                  40                  45
Leu Ile Asn Gly Ile Asp Arg Ile Ile Lys Ala Asn Ser Gly Lys Ser
    50                  55                  60
Leu His Gln Glu Thr Gln Gln Ala Asn Lys Thr Asp Lys Ala Trp Asp
65                  70                  75                  80
Leu Ala Ala Asn Val Phe Leu Ile Gly Leu Val Val Leu Ala Val Phe
                85                  90                  95
His Met Ile Lys Arg
            100
```

(2) INFORMATION FOR SEQ ID NO:1732:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1732

```
Ala Val Lys Lys Val Glu Ser Met Asn Val Val Pro Phe Ile Asp Ile
1               5                  10                  15
Met Leu Val Leu Leu Val Ile Val Leu Thr Thr Ala Ser Phe Val Gln
            20                  25                  30
Thr Ser Lys Leu Pro Ile Ser Ile Pro Gln Val Asp Lys Asp Ser Thr
        35                  40                  45
Asp Ser Lys Asp Val Leu Asp Lys Lys Gln Val Thr Ile Ala Ile Ser
    50                  55                  60
```

```
Asn Lys Gly Ser Phe Tyr Phe Asp Asp Lys Glu Ile Ser Phe Glu Asn
65                  70                  75                  80
Leu Lys His Lys Val Ser Thr Leu Ala Lys Asp Thr Pro Ile Val Leu
                85                  90                  95
Gln Gly Asp Lys Lys Ser Asn Leu Asp Asn Phe Ile Lys Val Val Asp
            100                 105                 110
Leu Leu Gln Leu Thr Ile
        115
```

(2) INFORMATION FOR SEQ ID NO:1733:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1733

```
Leu His Arg Gln Ala Gln Val Arg Ile Ser Leu Thr Gln Thr Thr Thr
1               5                   10                  15
Leu Val Ala Thr Ile Gly Ser Asn Ala Pro Tyr Ile Gly Leu Leu Gly
            20                  25                  30
Thr Val Met Gly Ile Met Leu Thr Phe Met Asp Leu Gly Ser Ala Ser
        35                  40                  45
Gly Ile Asp Thr Lys Ala Ile Met Thr Asn Leu Ala Leu Ala Leu Lys
    50                  55                  60
Ala Thr Gly Met Gly Leu Leu Val Ala Ile Pro Ala Ile Val Ile Tyr
65                  70                  75                  80
Asn Leu Leu Val Arg Lys Ser Glu Ile Leu Val Thr Lys Trp Asp Ile
                85                  90                  95
Phe His His Pro Val Asp Thr Gln Ser His Glu Val Tyr Ser Lys Ala
            100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:1734:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1734

```
Asn His Lys Ile Arg Gly Tyr Glu Lys Arg Met Ala Leu Asp Lys Arg
1               5                  10                  15
Ile Trp Met His Phe Asp Leu Leu Pro Phe Val Phe Ile Ile Pro Leu
            20                  25                  30
Leu Val Val Ser Phe Leu Leu Ile Phe Glu Ser Ser Ala Val Leu Ser
        35                  40                  45
Leu Lys Gln Gly Val Tyr Tyr Ala Ile Gly Phe Leu Leu Phe Trp Val
    50                  55                  60
Val Phe Phe Ile Pro Phe Arg Lys Leu Asp Arg Trp Leu Phe Ala Leu
65                  70                  75                  80
Tyr Trp Ala Cys Val Ile Leu Leu Ala Leu Val Asp Phe Met Gly Ser
                85                  90                  95
Ser Lys Leu Gly Ala Gln Arg Trp Leu Val Ile Pro Phe Thr Ser Ile
            100                 105                 110
Thr Leu Gln Pro Ser Glu Pro Val Lys Ile Ala Ile Leu Leu Leu Leu
        115                 120                 125
Ala Arg Phe Asp Gln Asn Gln Pro Thr Ser Phe
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:1735:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

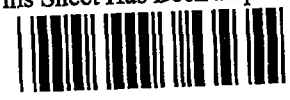
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...310

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1735

```
Phe Cys Gly Thr Leu Lys Ala Leu Lys Ile Lys Ile Thr Thr Thr Pro
1               5                  10                  15
Cys Lys Ala Leu Lys Lys Lys Trp Lys Ile Leu Leu Lys His Leu Met
            20                  25                  30
Lys Lys Lys Pro Leu Met Trp Arg Ile Cys Ala Leu Arg Arg Leu Leu
        35                  40                  45
Leu Gly Phe Lys Arg Glu Arg Glu Leu Leu Ser Phe Ala Lys His Trp
    50                  55                  60
Asn Ile Pro Thr Ile Val Val Phe Thr His Thr Gln Ala Glu Ala Gly
65                  70                  75                  80
Asp Ala Phe Val Gln Glu Thr Lys Gly Ile Ile Asp Glu Glu Trp Gly
                85                  90                  95
Phe Lys Gly Phe Val Arg Ala Tyr Val Arg Val Asn Ser Val Ala Phe
            100                 105                 110
Ser Phe Arg Gly Leu Lys Val Pro Val Glu Gly Leu Glu Glu Leu Val
        115                 120                 125
Asp Glu Thr Lys Lys Cys Leu Ser Asp Ala Glu Lys Asn Lys Lys Arg
    130                 135                 140
His Phe Leu Ser Ile Gln Arg Val Lys Ile Gln Glu Arg Lys Gln Ala
145                 150                 155                 160
Met Ile Glu Glu Cys Lys Thr Ile Ile His Val Ala Ser Gly Ala Ala
                165                 170                 175
Gly Val Ala Gly Leu Ile Pro Ile Pro Phe Ser Asp Ala Leu Ala Ile
            180                 185                 190
```

```
Ala Pro Ile Gln Ala Gly Met Ile Tyr Lys Met Asn Asp Ala Phe Gly
        195                 200                 205
Met Asp Leu Asp Lys Ser Val Gly Ala Ser Leu Val Ala Gly Leu Leu
    210                 215                 220
Gly Val Thr Ala Val Ala Gln Val Gly Arg Thr Leu Val Asn Gly Phe
225                 230                 235                 240
Leu Lys Phe Ile Pro Val Val Gly Ser Val Ala Gly Gly Ala Thr Ala
                245                 250                 255
Ala Val Ile Thr Glu Gly Ile Gly Phe Ala Tyr Leu Lys Val Leu Glu
            260                 265                 270
Lys Cys Phe Asn Asp Glu Thr Gly Glu Val Asn Leu Pro Gly Glu Val
        275                 280                 285
Gly Met Ile Thr Ser Leu Phe Lys Glu Asn Tyr Leu Asn Leu Asp Thr
    290                 295                 300
Ile Lys Lys Leu Lys Pro
305                 310
```

(2) INFORMATION FOR SEQ ID NO:1736:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 419 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1736

```
Met Arg Ser Trp Met Lys Lys Lys Tyr Phe Thr Leu Leu Leu Gln Ser
1               5                  10                  15
Ser Val Val Leu Ala Val Phe Ile Gly Cys Ser Ser Thr Arg Asn His
            20                  25                  30
Thr Phe Ser Ala Leu Ser Asn Gln Glu Asn Thr Asp Asp Lys Leu Pro
        35                  40                  45
Val Val His Ser Ile Lys Thr Ile Asn Asp Val Ser Ser Val Gly Phe
    50                  55                  60
Glu Trp Ser Lys Val Ala Asp Thr Tyr Asp Ile Asp Gly Phe Val Leu
65                  70                  75                  80
Tyr Arg Leu Lys Lys Asp Ser Lys Leu Lys Arg Ile Ala Thr Ile Lys
                85                  90                  95
Asn Pro Tyr Ala Thr His Tyr Tyr Asp Glu Gly Leu Glu Thr Glu Ser
            100                 105                 110
Ser Tyr Thr Tyr Gln Leu Ala Thr Tyr Lys Gly Asp Lys Ile Ser Lys
        115                 120                 125
Leu Ser Glu Pro Ile Leu Val Lys Thr Ser Phe Ile Asn Pro Val Glu
    130                 135                 140
Ser Val Phe Ala Ser Leu Glu Tyr Pro Lys Ser Val Lys Val Phe Trp
145                 150                 155                 160
Ser Pro His Pro Asn Pro Ser Val Ser Lys Tyr Ile Ile Gln Arg Gln
                165                 170                 175
Asn Lys Asp Gly Lys Phe Leu Asn Val Gly Ala Val Lys Asn Arg Leu
            180                 185                 190
Phe Val Glu Phe Phe Asp Lys Asp Leu Glu Asp Gly Gln Lys Tyr Arg
        195                 200                 205
Tyr Gln Ile Ile Ala Glu Asn Phe Met Gly Asp Lys Ser Arg Pro Ser
```

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

(2) INFORMATION FOR SEQ ID NO:1737:

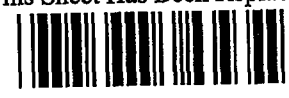
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1737

```
Leu Lys Asn Thr Leu Lys Gly Leu Leu Met Leu Asp Phe Asp Leu Val
1               5                   10                  15
Leu Phe Gly Ala Thr Gly Asp Leu Ala Met Arg Lys Leu Phe Val Ser
            20                  25                  30
Leu Tyr Glu Ile Tyr Ile His Tyr Gly Phe Lys Asn Asp Ser Arg Ile
        35                  40                  45
Ile Ala Ser Gly Arg Lys Glu Leu Ser Asn Glu Glu Phe Leu Ala Leu
    50                  55                  60
Leu Cys Glu Lys Thr Gln Leu His Ser Arg Glu Lys Gly Glu Glu Phe
65                  70                  75                  80
Leu Thr His Ile Ser Tyr Leu Arg Val Arg Leu Asp Asn Pro Lys Asp
                85                  90                  95
Phe Glu Glu Leu Ser Lys Ile Ala Thr Asn Asn Lys Pro Leu Ile Phe
            100                 105                 110
Tyr Phe Ser Ile Ser Pro Ser Phe Phe Ala Thr Thr Ala Gln Asn Leu
        115                 120                 125
```

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

(2) INFORMATION FOR SEQ ID NO:1738:

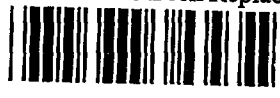
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 346 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1738

```
Gly Met Val Lys His Tyr Leu Phe Met Ala Val Ser Gln Val Phe Phe
1               5                  10                  15
Ser Phe Phe Leu Val Leu Phe Phe Ile Ser Ser Ile Val Leu Leu Ile
            20                  25                  30
Ser Ile Ala Ser Val Thr Leu Val Ile Lys Val Ser Phe Leu Asp Leu
        35                  40                  45
Val Gln Leu Phe Leu Tyr Ser Leu Pro Gly Thr Thr Phe Phe Ile Leu
    50                  55                  60
Pro Ile Thr Phe Phe Ala Ala Cys Ala Leu Gly Leu Ser Arg Leu Ser
65                  70                  75                  80
Tyr Asp His Glu Leu Leu Val Phe Phe Ser Leu Gly Val Ser Pro Lys
                85                  90                  95
Lys Met Thr Lys Ala Phe Val Pro Leu Ser Leu Leu Val Ser Ala Ile
            100                 105                 110
Leu Leu Ala Phe Ser Leu Ile Leu Ile Pro Thr Ser Lys Ser Ala Tyr
        115                 120                 125
Tyr Gly Phe Leu Arg Gln Lys Lys Asp Lys Ile Asp Ile Asn Ile Arg
    130                 135                 140
Ala Gly Glu Phe Gly Gln Lys Leu Gly Asp Trp Leu Val Tyr Val Asp
145                 150                 155                 160
Lys Thr Glu Asn Asn Ser Tyr Asp Asn Leu Val Leu Phe Ser Asn Lys
                165                 170                 175
Ser Leu Ser Gln Glu Ser Phe Ile Leu Ala Gln Lys Gly Asn Ile Asn
            180                 185                 190
Asn Gln Asn Gly Val Phe Glu Leu Asn Leu Tyr Asn Gly His Ala Tyr
```

```
        195                 200                 205
Phe Thr Gln Gly Asp Lys Met Arg Lys Val Asp Phe Glu Glu Leu His
    210                 215                 220
Leu Arg Asn Lys Leu Lys Ser Phe Asn Ser Asn Asp Ala Ala Tyr Leu
225                 230                 235                 240
Gln Gly Thr Asp Tyr Leu Gly Tyr Trp Lys Lys Ala Phe Gly Lys Asn
                245                 250                 255
Ala Asn Lys Asn Gln Lys Arg Arg Phe Ser Gln Ala Ile Leu Val Ser
            260                 265                 270
Leu Phe Pro Leu Ala Ser Val Phe Leu Ile Pro Leu Phe Gly Ile Ala
        275                 280                 285
Asn Pro Arg Phe Lys Thr Asn Trp Ser Tyr Phe His Val Leu Gly Ala
    290                 295                 300
Val Gly Val Tyr Phe Leu Met Val His Val Ile Ser Thr Asp Leu Phe
305                 310                 315                 320
Leu Met Thr Phe Phe Phe Pro Phe Ile Trp Ala Phe Ile Ser Tyr Leu
                325                 330                 335
Leu Phe Arg Lys Phe Ile Leu Lys Arg Tyr
            340                 345
```

(2) INFORMATION FOR SEQ ID NO:1739:

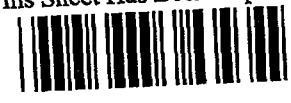
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 615 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1739

```
Ile Leu Ile Glu Gly Val Phe Met Pro Lys His Ser Leu Glu Gln Ile
1               5                  10                  15
Lys Glu Lys Ile Thr Glu Arg Ser Lys Lys Thr Arg Glu Leu Tyr Leu
            20                  25                  30
Glu Asn Thr Phe Asn Pro Lys Asn Gln Pro Lys Ile Glu Ser Leu Gly
        35                  40                  45
Cys Ala Asn Ile Ala His Val Thr Ala Ser Met Pro Glu His Leu Lys
    50                  55                  60
Met Pro Leu Gly Ser His Lys Arg Lys His Phe Ala Ile Ile Thr Ala
65                  70                  75                  80
Tyr Asn Asp Met Leu Ser Ala His Gln Pro Phe Lys Asn Tyr Pro Asp
                85                  90                  95
Leu Ile Lys Lys Glu Leu Gln Glu His Asn Ala Tyr Ala Ser Val Ala
            100                 105                 110
Ser Gly Val Pro Ala Met Cys Asp Gly Ile Thr Gln Gly Tyr Glu Gly
        115                 120                 125
Met Glu Leu Ser Leu Phe Ser Arg Asp Val Ile Ala Leu Ser Thr Ala
    130                 135                 140
Val Gly Leu Ser His Asn Val Phe Asp Gly Ala Phe Phe Leu Gly Val
145                 150                 155                 160
Cys Asp Lys Ile Val Pro Gly Leu Leu Ile Gly Ala Leu Ser Phe Gly
                165                 170                 175
Asn Leu Ala Ser Val Phe Val Pro Ser Gly Pro Met Val Ser Gly Ile
            180                 185                 190
```

```
Glu Asn Tyr Lys Lys Ala Lys Ala Arg Gln Asp Phe Ala Met Gly Lys
        195                 200                 205
Ile Asn Arg Glu Glu Leu Leu Lys Val Glu Met Gln Ser Tyr His Asp
    210                 215                 220
Val Gly Thr Cys Thr Phe Tyr Gly Thr Ala Asn Ser Asn Gln Met Met
225                 230                 235                 240
Met Glu Phe Met Gly Leu His Val Ala Asn Ser Ser Phe Ile Asn Pro
                245                 250                 255
Asn Asn Pro Leu Arg Lys Val Leu Val Glu Glu Ser Ala Lys Arg Leu
            260                 265                 270
Ala Ser Gly Lys Val Leu Pro Leu Ala Lys Leu Ile Asp Glu Lys Ser
        275                 280                 285
Ile Leu Asn Ala Leu Ile Gly Leu Met Ala Thr Gly Gly Ser Thr Asn
    290                 295                 300
His Thr Leu His Leu Ile Ala Ile Ala Arg Ser Cys Gly Val Ile Leu
305                 310                 315                 320
Asn Trp Asp Asp Phe Asp Ala Ile Ser Asn Leu Ile Pro Leu Leu Ala
                325                 330                 335
Lys Val Tyr Pro Asn Gly Ser Ala Asp Val Asn Ala Phe Glu Ala Cys
            340                 345                 350
Gly Gly Leu Ala Phe Val Ile Lys Glu Leu Leu Lys Glu Gly Leu Leu
        355                 360                 365
Phe Glu Asp Thr His Thr Ile Met Asp Thr Glu Thr Gln Lys Gly Met
    370                 375                 380
Gln Asn Tyr Thr Lys Thr Pro Phe Leu Glu Asn Asp Gln Leu Val Tyr
385                 390                 395                 400
Lys Asp Ala Val Ser His Ser Leu Asn Thr Asp Ile Leu Arg Pro Val
                405                 410                 415
Ser Glu Pro Phe Ala Ala Asn Gly Gly Leu Lys Ile Leu Lys Gly Asn
            420                 425                 430
Leu Gly Arg Ala Val Ile Lys Ile Ser Ala Ile Lys Asp Glu His Arg
        435                 440                 445
Lys Val Lys Ala Arg Ala Ile Val Phe Lys Thr Gln Ser Glu Phe Leu
    450                 455                 460
Glu Arg Phe Lys Asn Lys Glu Leu Glu Arg Asp Phe Val Ala Val Leu
465                 470                 475                 480
Pro Phe Gln Gly Pro Lys Ser Asn Gly Met Pro Glu Leu His Lys Leu
                485                 490                 495
Thr Thr Asn Leu Gly Ala Leu Gln Asp Met Gly Tyr Lys Val Ala Leu
            500                 505                 510
Val Thr Asp Gly Arg Met Ser Gly Ala Ser Gly Lys Val Pro Ser Ala
        515                 520                 525
Ile His Leu Ser Pro Glu Gly Ala Leu Asn Gly Ala Ile Ile Lys Ile
    530                 535                 540
Lys Asp Gly Asp Leu Ile Glu Leu Asp Ala Pro Asn Asn Ala Leu Asn
545                 550                 555                 560
Val Leu Glu Lys Asp Phe Glu Lys Arg Gly Ile Asn Pro Leu Phe Leu
                565                 570                 575
Glu Thr Leu Glu Asn Leu Glu Lys Pro Thr Phe Gly Leu Gly Arg Glu
            580                 585                 590
Leu Phe Thr Ser Leu Arg Leu Asn Ala Asn Thr Ala Glu Glu Gly Gly
        595                 600                 605
Met Ser Phe Gly Ile Lys Val
    610                 615
```

(2) INFORMATION FOR SEQ ID NO:1740:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 214 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(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:1740

```
Lys Tyr Lys Gly Asp Lys Met Gln Asp Lys Ile Ile Glu Ile Leu Gln
1               5                  10                  15
Ile Ser Pro Ile Val Pro Val Val Val Val Glu Asn Ile Lys Asp Ala
            20                  25                  30
Val Pro Leu Ala Gln Ser Leu Ile Glu Gly Gly Ile Pro Ile Ile Glu
        35                  40                  45
Val Thr Leu Arg Ser Asn Cys Ala Leu Glu Ala Ile Glu Leu Ile Ala
    50                  55                  60
Lys Asn Val Pro Lys Met Arg Val Gly Ala Gly Thr Ile Leu Asn Leu
65                  70                  75                  80
Thr Gln Leu Glu Gln Ala Gln Asn Arg Gly Ala Glu Phe Leu Ile Ser
                85                  90                  95
Pro Gly Leu Thr Ile Lys Leu Leu Glu His Ala Lys Lys Lys Asp Met
            100                 105                 110
Pro Leu Ile Pro Gly Val Ser Ser Ser Ser Glu Val Met Gln Ala Leu
        115                 120                 125
Glu Leu Gly Tyr Asn Ala Leu Lys Phe Phe Pro Ala Glu Tyr Cys Gly
    130                 135                 140
Gly Val Lys Leu Leu Asn Ala Phe Asn Gly Pro Phe Lys Gly Val Lys
145                 150                 155                 160
Phe Cys Pro Thr Gly Gly Ile Ser Ala Asp Asn Met Arg Ser Tyr Leu
                165                 170                 175
Ala Leu Glu Asn Val Val Cys Val Gly Gly Ser Trp Leu Thr Pro Lys
            180                 185                 190
Asp Leu Ile Gln Asn Lys Glu Trp Asp Lys Ile Thr Glu Ile Cys Lys
        195                 200                 205
Arg Ala Leu Ala Leu Arg
    210
```

(2) INFORMATION FOR SEQ ID NO:1741:

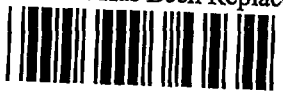
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1741

```
Asn Thr Ala Ile Val Ser Phe Leu Trp Phe Ala Tyr Val Ser Ile Gly
1               5                  10                  15
Leu Thr Asn Phe Val Ala Val Gly Tyr Met Val Ser Leu Leu Gly Ala
            20                  25                  30
```

```
Leu Lys Arg Thr Pro Cys Thr Asn Arg Phe Tyr Leu Lys Ala Leu Leu
        35                  40                  45
Phe Ala Ile Phe Tyr His Ala Val Asn Asn Phe Leu Thr Gln Cys Pro
    50                  55                  60
Pro His Gln Val Arg Glu Phe Phe Ser Ser Arg His Ala Gln Gly Trp
65                  70                  75                  80
Lys Arg Glu Thr Leu Pro Cys Ala Leu Ser Phe Gln Asn Ala Leu
                85                  90                  95
```

(2) INFORMATION FOR SEQ ID NO:1742:

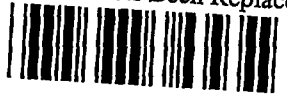
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 360 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1742

```
Lys Lys Thr Pro Pro Ile Leu Cys Arg Leu Leu Gly Phe Tyr Ile Leu
1               5                  10                  15
Lys Lys Leu Pro Gln Arg Cys Phe Met Pro Lys Thr Glu Thr Tyr Pro
            20                  25                  30
Arg Leu Leu Ala Asp Ile Gly Gly Thr Asn Ala Arg Phe Gly Leu Glu
        35                  40                  45
Val Ala Pro Arg Gln Ile Glu Cys Val Glu Val Leu Arg Cys Glu Asp
    50                  55                  60
Phe Glu Ser Leu Ser Asp Ala Val Arg Phe Tyr Leu Ser Lys Cys Lys
65                  70                  75                  80
Glu Ser Leu Lys Leu His Pro Ile Tyr Gly Ser Phe Ala Val Ala Thr
                85                  90                  95
Pro Ile Met Gly Asp Phe Val Gln Met Thr Asn Asn His Trp Thr Phe
            100                 105                 110
Ser Ile Glu Thr Thr Arg Gln Cys Leu Asn Leu Lys Lys Leu Leu Val
        115                 120                 125
Ile Asn Asp Phe Val Ala Gln Ala Tyr Ala Ile Ser Ala Met Gln Glu
    130                 135                 140
Asn Asp Leu Ala Gln Ile Gly Gly Ile Lys Cys Glu Ile Asn Ala Pro
145                 150                 155                 160
Lys Ala Ile Leu Gly Pro Gly Thr Gly Leu Gly Val Ser Thr Leu Ile
                165                 170                 175
Gln Asn Ser Asp Gly Ser Leu Lys Val Leu Pro Asp Glu Gly Gly His
            180                 185                 190
Val Ser Phe Ala Pro Phe Asp Asp Leu Glu Ile Leu Val Trp Gln Tyr
        195                 200                 205
Ala Arg Ser Lys Phe Asn His Val Ser Ala Glu Arg Phe Leu Ser Gly
    210                 215                 220
Ser Gly Leu Val Leu Ile Tyr Glu Ala Leu Ser Lys Arg Lys Gly Leu
225                 230                 235                 240
Glu Lys Val Ala Lys Leu Ser Lys Ala Glu Leu Thr Pro Gln Ile Ile
                245                 250                 255
Ser Glu Arg Ala Leu Asn Gly Asp Tyr Pro Ile Cys Arg Leu Thr Leu
            260                 265                 270
Asp Thr Phe Cys Ser Met Leu Gly Thr Leu Ala Ala Asp Val Ala Leu
```

```
        275                 280                 285
Thr Leu Gly Ala Arg Gly Gly Val Tyr Leu Cys Gly Gly Ile Ile Pro
    290                 295                 300
Arg Phe Ile Asp Tyr Phe Lys Thr Ser Pro Phe Arg Ala Arg Phe Glu
305                 310                 315                 320
Thr Lys Gly Arg Met Gly Ala Phe Leu Ala Ser Ile Pro Val His Val
                325                 330                 335
Val Met Lys Lys Thr Pro Gly Leu Asp Gly Ala Gly Ile Ala Leu Glu
            340                 345                 350
Asn Tyr Leu Leu His Asp Arg Ile
        355                 360
```

(2) INFORMATION FOR SEQ ID NO:1743:

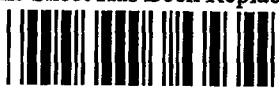
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1743

```
Ser Gln Gly Leu Ile Phe Asp Lys Lys Lys Gln Lys Phe Leu Lys Asp
1               5                   10                  15
Phe Lys Ala Gly Glu Leu Leu Tyr Gln Ser His Phe Lys Pro Leu Val
            20                  25                  30
Glu Phe Ile Ala Glu Glu Leu Leu Lys Asn Ser Arg Ala Lys Ile Ile
        35                  40                  45
Gln Ser Asn Cys Asn Lys Ala Leu Lys Val Val Glu Glu Leu Gln Asn
    50                  55                  60
Thr Ile Lys Thr Thr Ile Glu Lys Gln Ile Asn Pro Gly Met Lys Glu
65                  70                  75                  80
Thr Gln Asp Pro Gln Gln Glu Ala Arg Phe Asn Leu Asp Arg Ser Thr
                85                  90                  95
Asp Lys Phe Ile Ser Asp Leu Glu Lys Ser Ala Phe Ser Lys Ile Asn
            100                 105                 110
Gln Phe Glu Phe Asn Phe Arg Lys Glu Met His Glu Arg Ile Glu Arg
        115                 120                 125
Gly Ile Gly Asn Asn Glu Cys Lys Glu Ile Phe Gly Asn Glu Leu Lys
    130                 135                 140
Gln Arg Lys Thr Lys Leu Ile Glu Asp Ile Glu Arg Arg Phe Lys Glu
145                 150                 155                 160
Cys Glu Glu Gln Phe Arg Gly Ser Val Gly Lys Asn Ile Glu Gln Leu
                165                 170                 175
Glu Glu Arg Val Lys Asp Ser Leu Ala Ile Ile Lys Arg Ile Asn Asn
            180                 185                 190
Leu Gly Leu Asn Pro Asn Ser Asn Phe Asn Met Asp Ser Gly Ile Asp
        195                 200                 205
Thr Ile Gly Leu Phe Ser Ser Ile Gly Gly Leu Val Leu Leu Leu Leu
    210                 215                 220
Thr Pro Val Val Gly Glu Phe Ala Leu Ile Ala Gly Val Gly Leu Ala
225                 230                 235                 240
Leu Val Gly Val Gly Lys Ser Ile Trp Ser Phe Phe Asp Ser Asp Tyr
                245                 250                 255
```

```
Lys Lys Ser Gln Gln Arg Lys Glu Val Asp Lys Asn Leu His Gln Ile
            260                 265                 270
Cys Glu Lys Ile Val Gln Asp Val Lys Ser Arg Ile Glu Ser Tyr Lys
        275                 280                 285
Asn Gly Ala Leu Gly Met Ile Glu Glu Leu Asn Ala Gly Phe Asn Lys
    290                 295                 300
Leu Val Asp His Tyr Glu Arg Met Lys Arg Gln Leu Glu Glu Ala His
305                 310                 315                 320
Glu Lys Leu Gly Tyr Ile Tyr Asn Ser Ile His Leu Thr Ile Ser Asn
                325                 330                 335
Arg Arg Ile Gln
            340
```

(2) INFORMATION FOR SEQ ID NO:1744:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1744

```
Ser Ala Leu Trp His Lys Asp Pro Thr Thr Ile Lys Gln Phe Gly Leu
1               5                   10                  15
Glu Ala Leu Asp Phe Phe Lys Pro His Glu Ile Glu Leu Leu Ile Val
            20                  25                  30
Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu Met Gln Lys Tyr
        35                  40                  45
Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser Ile Leu Ala Ile
    50                  55                  60
Lys Arg Gln Val Glu Asp Lys Asn Ala Pro Ile Leu Val Leu Gly Thr
65                  70                  75                  80
Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala Leu Lys Gln Gln
                85                  90                  95
Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu Phe Val Pro Leu
            100                 105                 110
Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu Thr Cys Met His
        115                 120                 125
Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val Ile Ile Leu Gly
    130                 135                 140
Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu Gly Tyr Phe Met
145                 150                 155                 160
Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile His Ser Gly Asp
                165                 170                 175
Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu Lys Asn Asn Ala
            180                 185                 190
Cys Thr Phe Pro Lys Val Glu Phe His Ala Ser Gly Asp Val Ile Trp
        195                 200                 205
Leu Glu Arg Gln Ala Lys Glu Trp Leu Lys Leu
    210                 215
```

(2) INFORMATION FOR SEQ ID NO:1745:

(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:1745

```
Gly Ile Lys Leu Gly Gly Ile Asn Met Ala Gly Thr Gln Ala Ile Tyr
1               5                  10                  15
Glu Ser Ser Ser Ala Gly Phe Leu Ser Gln Val Ser Ser Ile Ile Ser
            20                  25                  30
Ser Thr Ser Gly Val Ala Gly Pro Phe Ala Gly Ile Val Ala Gly Ala
        35                  40                  45
Met Thr Ala Ala Ile Ile Pro Ile Val Val Gly Phe Thr Asn Pro Gln
    50                  55                  60
Met Thr Ala Ile Met Thr Gln Tyr Asn Gln Ser Ile Ala Glu Ala Val
65                  70                  75                  80
Ser Val Pro Met Lys Ala Ala Asn Gln Gln Tyr Ser Gln Leu Tyr Gln
                85                  90                  95
Gly Phe Asn Asp Gln Ser Met Ala Val Gly Thr Ile Ser
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:1746:

(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:1746

```
Phe Gln Phe Glu Arg Lys Arg Met Lys Phe Phe Thr Arg Ile Thr Asp
1               5                  10                  15
Ser Tyr Lys Lys Val Val Val Thr Leu Gly Leu Val Val Thr Thr Asn
            20                  25                  30
Pro Leu Met Ala Val Thr Ser Pro Ala Thr Gly Val Thr Glu Thr Lys
        35                  40                  45
Ser Leu Val Ile Gln Ile Ile Ser Val Leu Ala Ile Val Gly Gly Cys
    50                  55                  60
Ala Leu Gly Val Lys Gly Ile Ala Asp Ile Trp Lys Ile Ser Asp Asp
65                  70                  75                  80
```

This Sheet Has Been Replaced



```
Ile Lys Arg Gly Gln Ala Thr Val Phe Ala Tyr Ala Gln Pro Ile Ala
                85                  90                  95
Met Leu Ala Val Ala Gly Gly Ile Ile Tyr Leu Ser Thr Lys Phe Gly
            100                 105                 110
Phe Asn Ile Gly Glu Ser Gly Gly Ala Ser
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:1747:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 991 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1747

```
Ser Gly Ile Ser Ile Lys Arg Gly Val Phe Val Ala Ser Lys Gln Ala
1               5                   10                  15
Asp Glu Gln Lys Lys Leu Val Ile Glu Gln Glu Val Gln Lys Arg Gln
            20                  25                  30
Phe Gln Lys Ile Glu Glu Leu Lys Ala Asp Met Gln Lys Gly Val Asn
        35                  40                  45
Pro Phe Phe Lys Val Leu Phe Asp Gly Gly Asn Arg Leu Phe Gly Phe
    50                  55                  60
Pro Glu Thr Phe Ile Tyr Ser Ser Ile Phe Ile Leu Phe Val Thr Ile
65                  70                  75                  80
Val Leu Ser Val Ile Leu Phe Gln Ala Tyr Glu Pro Val Leu Ile Val
                85                  90                  95
Ala Ile Val Ile Val Leu Val Ala Leu Gly Phe Lys Lys Asp Tyr Arg
            100                 105                 110
Leu Tyr Gln Arg Met Glu Arg Ala Met Lys Phe Lys Lys Pro Phe Leu
        115                 120                 125
Phe Lys Gly Val Lys Asn Lys Ala Phe Met Ser Ile Phe Ser Met Lys
    130                 135                 140
Pro Ser Lys Glu Met Ala Asn Asp Ile His Leu Asn Pro Asn Arg Glu
145                 150                 155                 160
Asp Arg Leu Val Ser Ala Ala Asn Ser Tyr Leu Ala Asn Asn Tyr Glu
                165                 170                 175
Cys Phe Leu Asp Asp Gly Val Ile Leu Thr Asn Asn Tyr Ser Leu Leu
            180                 185                 190
Gly Thr Ile Lys Leu Gly Gly Ile Asp Phe Leu Thr Thr Ser Lys Lys
        195                 200                 205
Asp Leu Ile Glu Leu His Ala Ser Ile Tyr Ser Val Phe Arg Asn Phe
    210                 215                 220
Val Thr Pro Glu Phe Lys Phe Tyr Phe His Thr Val Lys Lys Lys Ile
225                 230                 235                 240
Val Ile Asp Glu Thr Asn Arg Asp Tyr Gly Leu Ile Phe Ser Asn Asp
                245                 250                 255
Phe Met Arg Ala Tyr Asn Glu Lys Gln Lys Arg Glu Ser Phe Tyr Asp
            260                 265                 270
Ile Ser Phe Tyr Leu Thr Ile Glu Gln Asp Leu Leu Asp Thr Leu Asn
        275                 280                 285
Glu Pro Val Met Asn Lys Lys His Phe Ala Asp Asn Asn Phe Glu Glu
```

This Sheet Has Been Replaced



```
    290                 295                 300
Phe Gln Arg Ile Ile Arg Ala Lys Leu Glu Asn Phe Lys Asp Arg Ile
305                 310                 315                 320
Glu Leu Ile Glu Glu Leu Leu Ser Lys Tyr His Pro Thr Arg Leu Lys
                325                 330                 335
Glu Tyr Thr Lys Asp Gly Ile Ile Tyr Ser Lys Gln Cys Glu Phe Tyr
            340                 345                 350
Asn Phe Leu Val Gly Met Asn Glu Ala Pro Phe Ile Cys Asn Arg Lys
        355                 360                 365
Asp Leu Tyr Leu Lys Glu Lys Met His Gly Gly Val Lys Glu Val Tyr
    370                 375                 380
Phe Ala Asn Lys His Gly Lys Ile Leu Asn Asp Asp Leu Ser Glu Lys
385                 390                 395                 400
Tyr Phe Ser Ala Ile Glu Ile Ser Glu Tyr Ala Pro Lys Ser Gln Ser
                405                 410                 415
Asp Leu Phe Asp Lys Ile Asn Ala Leu Asp Ser Glu Phe Ile Phe Met
            420                 425                 430
His Ala Tyr Ser Pro Lys Asn Ser Gln Val Leu Lys Asp Lys Leu Ala
        435                 440                 445
Phe Thr Ser Arg Arg Ile Ile Ile Ser Gly Gly Ser Lys Glu Gln Gly
    450                 455                 460
Met Thr Leu Gly Cys Leu Ser Glu Leu Val Gly Asn Gly Asp Ile Thr
465                 470                 475                 480
Leu Gly Ser Tyr Gly Asn Ser Leu Val Leu Phe Ala Asp Ser Phe Glu
                485                 490                 495
Lys Met Lys Gln Ser Val Lys Glu Cys Val Ser Ser Leu Asn Ala Lys
            500                 505                 510
Gly Phe Leu Ala Asn Ala Ala Thr Phe Ser Met Glu Asn Tyr Phe Phe
        515                 520                 525
Ala Lys His Cys Ser Phe Ile Thr Leu Pro Phe Ile Phe Asp Val Thr
    530                 535                 540
Ser Asn Asn Phe Ala Asp Phe Ile Ala Met Arg Ala Met Ser Phe Asp
545                 550                 555                 560
Gly Lys Glu Asp Asn Asn Ala Trp Gly Asn Ser Val Met Thr Leu Lys
                565                 570                 575
Ser Glu Ile Asn Ser Pro Phe Tyr Leu Asn Phe His Met Pro Thr Asp
            580                 585                 590
Phe Gly Ser Ala Ser Ala Gly His Thr Leu Ile Leu Gly Ser Thr Gly
        595                 600                 605
Ser Gly Lys Thr Val Phe Met Ser Met Thr Leu Asn Ala Met Gly Gln
    610                 615                 620
Phe Ala Tyr Asn Phe Pro Ala Asn Ile Ser Lys Asp Lys Gln Lys Leu
625                 630                 635                 640
Thr Met Val Tyr Met Asp Lys Asp Tyr Gly Ala Tyr Gly Asn Ile Val
                645                 650                 655
Ala Met Gly Gly Glu Tyr Val Lys Ile Glu Leu Gly Thr Asp Thr Gly
            660                 665                 670
Leu Asn Pro Phe Ala Trp Ala Ala Cys Val Gln Lys Thr Asn Ala Thr
        675                 680                 685
Met Glu Gln Lys Gln Thr Ala Ile Ser Val Val Lys Glu Leu Val Lys
    690                 695                 700
Asn Leu Ala Thr Lys Ser Asp Glu Lys Asp Glu Asn Gly Asn Ser Ile
705                 710                 715                 720
Ser Phe Ser Leu Ala Asp Ser Asn Thr Leu Ala Ala Ala Val Thr Asn
                725                 730                 735
Leu Ile Thr Gly Asp Met Asn Leu Asp Tyr Pro Ile Thr Gln Leu Ile
            740                 745                 750
Asn Ala Phe Gly Lys Asp His Asn Asp Pro Asn Gly Leu Val Ala Arg
        755                 760                 765
Leu Ala Pro Phe Cys Lys Ser Thr Asn Gly Glu Phe Gln Trp Leu Phe
    770                 775                 780
Asp Asn Lys Ala Thr Asp Arg Leu Asp Phe Ser Lys Thr Ile Ile Gly
785                 790                 795                 800
Val Asp Gly Ser Ser Phe Leu Asp Asn Asn Asp Val Ser Pro Phe Ile
                805                 810                 815
```

This Sheet Has Been Replaced



```
Cys Phe Tyr Leu Phe Ala Arg Ile Gln Glu Ala Met Asp Gly Arg Arg
            820                 825                 830
Phe Val Leu Asp Ile Asp Glu Ala Trp Lys Tyr Leu Gly Asp Pro Lys
        835                 840                 845
Val Ala Tyr Phe Val Arg Asp Met Leu Lys Thr Ala Arg Lys Arg Asn
    850                 855                 860
Ala Ile Val Arg Leu Ala Thr Gln Ser Ile Thr Asp Leu Leu Ala Cys
865                 870                 875                 880
Pro Ile Ala Asp Thr Ile Arg Glu Gln Cys Pro Thr Lys Ile Phe Leu
                885                 890                 895
Arg Asn Asp Gly Gly Asn Leu Ser Asp Tyr Gln Arg Leu Ala Asn Val
            900                 905                 910
Thr Glu Lys Glu Phe Glu Ile Ile Thr Lys Gly Leu Asp Arg Lys Ile
        915                 920                 925
Leu Tyr Lys Gln Asp Gly Ser Pro Ser Val Ile Ala Ser Phe Asn Leu
    930                 935                 940
Arg Gly Ile Pro Lys Glu Tyr Leu Lys Ile Leu Ser Thr Asp Thr Val
945                 950                 955                 960
Phe Val Lys Glu Ile Asp Lys Ile Ile Gln Asn His Ser Ile Ile Asp
                965                 970                 975
Lys Tyr Gln Ala Leu Arg Gln Met Tyr Gln Gln Ile Lys Glu Tyr
            980                 985                 990
```

(2) INFORMATION FOR SEQ ID NO:1748:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1183 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1748

```
Phe Leu Val Ala Leu Met Ile Pro Asn Leu Asp Ile Glu Gly Glu Thr
1               5                  10                  15
Met Thr Asn Glu Ala Ile Asn Gln Gln Pro Gln Thr Glu Ala Ala Phe
            20                  25                  30
Asn Pro Gln Gln Phe Ile Asn Asn Leu Gln Val Ala Phe Ile Lys Val
        35                  40                  45
Asp Asn Val Val Ala Ser Phe Asp Pro Asn Gln Lys Pro Ile Val Asp
    50                  55                  60
Lys Asn Asp Arg Asp Asn Arg Gln Ala Phe Glu Lys Ile Ser Gln Leu
65                  70                  75                  80
Arg Glu Glu Phe Ala Asn Lys Ala Ile Lys Asn Pro Thr Lys Lys Asn
                85                  90                  95
Gln Tyr Phe Ser Ser Phe Ile Ser Lys Ser Asn Asp Leu Ile Asp Lys
            100                 105                 110
Asp Asn Leu Ile Asp Thr Gly Ser Ser Ile Lys Ser Phe Gln Lys Phe
        115                 120                 125
Gly Thr Gln Arg Tyr Gln Ile Phe Met Asn Trp Val Ser His Gln Asn
    130                 135                 140
Asp Pro Ser Lys Ile Asn Thr Gln Lys Ile Arg Gly Phe Met Glu Asn
145                 150                 155                 160
Ile Ile Gln Pro Pro Ile Ser Asp Asp Lys Glu Lys Ala Glu Phe Leu
```

```
                165                 170                 175
Arg Ser Ala Lys Gln Ala Phe Ala Gly Ile Ile Ile Gly Asn Gln Ile
            180                 185                 190
Arg Ser Asp Gln Lys Phe Met Gly Val Phe Asp Glu Ser Leu Lys Glu
        195                 200                 205
Arg Gln Glu Ala Glu Lys Asn Gly Glu Pro Asn Gly Asp Pro Thr Gly
    210                 215                 220
Gly Asp Trp Leu Asp Ile Phe Leu Ser Phe Val Phe Asn Lys Lys Gln
225                 230                 235                 240
Ser Ser Asp Leu Lys Glu Thr Leu Asn Gln Glu Pro Val Pro His Val
                245                 250                 255
Gln Pro Asp Val Ala Thr Thr Thr Thr Asp Ile Gln Ser Leu Pro Pro
            260                 265                 270
Glu Ala Arg Asp Leu Leu Asp Glu Arg Gly Asn Phe Ser Lys Phe Thr
        275                 280                 285
Leu Gly Asp Met Asn Met Leu Asp Val Glu Gly Val Ala Asp Ile Asp
    290                 295                 300
Pro Asn Tyr Lys Phe Asn Gln Leu Leu Ile His Asn Asn Ala Leu Ser
305                 310                 315                 320
Ser Val Leu Met Gly Ser His Asn Gly Ile Glu Pro Glu Lys Val Ser
                325                 330                 335
Leu Leu Tyr Gly Asn Asn Gly Gly Pro Glu Ala Arg His Asp Trp Asn
            340                 345                 350
Ala Thr Val Gly Tyr Lys Asn Gln Arg Gly Asp Asn Val Ala Thr Leu
        355                 360                 365
Ile Asn Val His Met Lys Asn Gly Ser Gly Leu Val Ile Ala Gly Gly
    370                 375                 380
Glu Lys Gly Ile Asn Asn Pro Ser Phe Tyr Leu Tyr Lys Glu Asp Gln
385                 390                 395                 400
Leu Thr Gly Ser Gln Arg Ala Leu Ser Gln Glu Glu Ile Gln Asn Lys
                405                 410                 415
Val Asp Phe Met Glu Phe Leu Ala Gln Asn Asn Ala Lys Leu Asp Asn
            420                 425                 430
Leu Ser Lys Lys Glu Lys Glu Lys Phe Gln Asn Glu Ile Glu Asp Phe
        435                 440                 445
Gln Lys Asp Ser Lys Ala Tyr Leu Asp Ala Leu Gly Asn Asp His Ile
    450                 455                 460
Ala Phe Val Ser Lys Lys Asp Lys Lys His Leu Ala Leu Val Ala Glu
465                 470                 475                 480
Phe Gly Asn Gly Glu Leu Ser Tyr Thr Leu Lys Asp Tyr Gly Lys Lys
                485                 490                 495
Ala Asp Lys Ala Leu Asp Arg Glu Ala Lys Thr Thr Leu Gln Gly Ser
            500                 505                 510
Leu Lys His Asp Gly Val Met Phe Val Asp Tyr Ser Asn Phe Lys Tyr
        515                 520                 525
Thr Asn Ala Ser Lys Ser Pro Asp Lys Gly Val Gly Ala Thr Asn Gly
    530                 535                 540
Val Ser His Leu Glu Ala Gly Phe Ser Lys Val Ala Val Phe Asn Leu
545                 550                 555                 560
Pro Asn Leu Asn Asn Leu Ala Ile Thr Ser Val Val Arg Gln Asp Leu
                565                 570                 575
Glu Asp Lys Leu Ile Ala Lys Gly Leu Ser Pro Gln Glu Ala Asn Lys
            580                 585                 590
Leu Val Lys Asp Phe Leu Ser Ser Asn Lys Glu Leu Val Gly Lys Ala
        595                 600                 605
Leu Asn Phe Asn Lys Ala Val Ala Glu Ala Lys Asn Thr Gly Asn Tyr
    610                 615                 620
Asp Glu Val Lys Gln Ala Gln Lys Asp Leu Glu Lys Ser Leu Lys Lys
625                 630                 635                 640
Arg Glu Arg Leu Glu Lys Asp Val Ala Lys Asn Leu Glu Ser Lys Ser
                645                 650                 655
Gly Asn Lys Asn Lys Met Glu Ala Lys Ser Gln Ala Asn Ser Gln Lys
            660                 665                 670
Asp Glu Ile Phe Ala Leu Ile Asn Lys Glu Ala Asn Arg Asp Ala Arg
        675                 680                 685
```

This Sheet Has Been Replaced



```
Ala Ile Ala Tyr Ala Gln Asn Leu Lys Gly Ile Lys Arg Glu Leu Ser
    690                 695                 700
Asp Lys Leu Glu Asn Ile Asn Lys Asp Leu Lys Asp Phe Ser Lys Ser
705                 710                 715                 720
Phe Asp Glu Phe Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys Ala Glu
                725                 730                 735
Glu Thr Leu Lys Ala Leu Lys Gly Ser Val Lys Asp Leu Gly Ile Asn
            740                 745                 750
Pro Glu Trp Ile Ser Lys Val Glu Asn Leu Asn Ala Ala Leu Asn Glu
        755                 760                 765
Phe Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys Val Thr Gln Ala Lys
    770                 775                 780
Ser Asp Leu Glu Asn Ser Ile Lys Asp Val Ile Ile Asn Gln Lys Ile
785                 790                 795                 800
Thr Asp Lys Val Asp Asn Leu Asn Gln Ala Val Ser Val Ala Lys Ala
                805                 810                 815
Thr Gly Asp Phe Ser Gly Val Glu Gln Ala Leu Ala Asp Leu Lys Asn
            820                 825                 830
Phe Ser Lys Glu Gln Leu Ala Gln Gln Ala Gln Lys Asn Glu Asp Phe
        835                 840                 845
Asn Thr Gly Lys Asn Ser Ala Leu Tyr Gln Ser Val Lys Asn Gly Val
    850                 855                 860
Asn Gly Thr Leu Val Gly Asn Gly Leu Ser Lys Ala Glu Ala Thr Thr
865                 870                 875                 880
Leu Ser Lys Asn Phe Ser Asp Ile Lys Lys Glu Leu Asn Ala Lys Leu
                885                 890                 895
Gly Asn Phe Asn Asn Asn Asn Asn Asn Gly Leu Glu Asn Ser Thr Glu
            900                 905                 910
Pro Ile Tyr Thr Gln Val Ala Lys Lys Val Lys Ala Lys Ile Asp Arg
        915                 920                 925
Leu Asp Gln Ile Ala Ser Gly Leu Gly Asp Val Gly Gln Ala Ala Ser
    930                 935                 940
Phe Leu Leu Lys Arg His Asp Lys Val Asp Asp Leu Ser Lys Val Gly
945                 950                 955                 960
Leu Ser Ala Asn His Glu Pro Ile Tyr Ala Thr Ile Asp Asp Leu Gly
                965                 970                 975
Gly Pro Phe Pro Leu Lys Arg His Asp Lys Val Asp Asp Leu Ser Lys
            980                 985                 990
Val Gly Leu Ser Arg Glu Gln Lys Leu Thr Gln Lys Ile Asp Asn Leu
        995                 1000                1005
Asn Gln Ala Val Ser Glu Ala Lys Ala Ser His Phe Asp Asn Leu Asp
    1010                1015                1020
Gln Met Ile Asp Lys Leu Lys Asp Ser Thr Lys Lys Asn Val Val Asn
1025                1030                1035                1040
Leu Tyr Val Glu Ser Ala Lys Lys Val Pro Thr Ser Leu Ser Ala Lys
                1045                1050                1055
Leu Asp Asn Tyr Ala Thr Asn Ser His Thr Arg Ile Asn Ser Asn Val
            1060                1065                1070
Lys Asn Gly Thr Ile Asn Glu Lys Ala Thr Gly Met Leu Thr Gln Lys
        1075                1080                1085
Asn Ser Glu Trp Leu Lys Leu Val Asn Asp Lys Ile Val Ala His Asn
    1090                1095                1100
Val Gly Ser Ala Pro Leu Ser Ala Tyr Asp Lys Ile Gly Phe Asn Gln
1105                1110                1115                1120
Lys Asn Met Lys Asp Tyr Ser Asp Ser Phe Lys Phe Ser Thr Arg Leu
                1125                1130                1135
Ser Asn Ala Val Lys Asp Ile Lys Ser Gly Phe Val Gln Phe Leu Thr
            1140                1145                1150
Asn Ile Phe Ser Met Gly Ser Tyr Ser Leu Met Lys Ala Ser Val Glu
        1155                1160                1165
His Gly Val Lys Asn Thr Asn Thr Lys Gly Gly Phe Gln Lys Ser
    1170                1175                1180
```

(2) INFORMATION FOR SEQ ID NO:1749:

This Sheet Has Been Replaced



SUBSTITUTE SHEET (RULE 26)

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1749

```
Ala Leu Ser Leu Ala Ser Ile Leu Ala Arg Val Glu Glu Leu Ala Lys
1               5                  10                  15
Leu Ile Asn Asn Asn Asn Asn Asn Lys Lys Leu Arg Gly Phe Phe Leu
            20                  25                  30
Lys Val Leu Leu Ser Leu Val Val Phe Ser Ser Tyr Gly Ser Ala Asn
        35                  40                  45
Asp Asp Lys Glu Ala Lys Lys Glu Ala Leu Glu Lys Glu Lys Asn Thr
    50                  55                  60
Pro Asn Gly Leu Val Tyr Thr Asn Leu Asp Phe Asp Ser Phe Lys Ala
65                  70                  75                  80
Thr Ile Lys Asn Leu Lys Asp Lys Lys Val Thr Phe Lys Glu Val Asn
                85                  90                  95
Pro Asp Ile Ile Lys Asp Glu Val Phe Asp Phe Val Ile Val Asn Arg
            100                 105                 110
Val Leu Lys Lys Ile Lys Asp Leu Lys His Tyr Asp Pro Val Ile Glu
        115                 120                 125
Lys Ile Phe Asp Glu Lys Gly Lys Glu Met Gly Leu Asn Val Glu Leu
    130                 135                 140
Gln Ile Asn Pro Glu Val Lys Asp Phe Phe Thr Phe Lys Ser Ile Ser
145                 150                 155                 160
Thr Thr Asn Lys Gln Arg Cys Phe Leu Ser Leu His Gly Glu Thr Arg
                165                 170                 175
Glu Ile Leu Cys Asp Asp Lys Leu Tyr Asn Val Leu Leu Ala Val Phe
            180                 185                 190
Asn Ser Tyr Asp Pro Asn Asp Leu Leu Lys His Ile Ser Thr Ile Glu
        195                 200                 205
Ser Leu Lys Lys Ile Phe Tyr Thr Ile Thr Cys Glu Ala Val Tyr Leu
    210                 215                 220
```

(2) INFORMATION FOR SEQ ID NO:1750:

(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

This Sheet Has Been Replaced



SUBSTITUTE SHEET (RULE 26)

(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1750

```
Asn Asn Ala Lys Asn Lys Asn Lys Gly Val Lys Ser Met Lys Thr Asn
1               5                  10                  15
Phe Tyr Lys Ile Lys Leu Leu Phe Ala Trp Cys Leu Ile Ile Gly Met
            20                  25                  30
Phe Asn Ala Pro Leu Asn Ala Asp Gln Asn Thr Asp Ile Lys Asp Ile
        35                  40                  45
Ser Pro Glu Asp Met Ala Leu Asn Ser Val Gly Leu Val Ser Arg Asp
    50                  55                  60
Gln Leu Lys Ile Glu Ile Pro Lys Glu Thr Leu Glu Gln Lys Val Ala
65                  70                  75                  80
Ile Leu Asn Asp Tyr Asn Asp Lys Asn Val Asn Ile Lys Phe Asp Asp
                85                  90                  95
Ile Ser Leu Gly Ser Phe Gln Pro Asn Asp Asn Leu Gly Ile Asn Ala
            100                 105                 110
Met Trp Gly Ile Gln Asn Leu Leu Met Ser Gln Met Met Ser Asn Tyr
        115                 120                 125
Gly Pro Asn Asn Ser Phe Met Tyr Gly Tyr Ala Pro Thr Tyr Ser Asp
    130                 135                 140
Ser Ser Phe Leu Pro Pro Ile Leu Gly Tyr
145                 150
```

(2) INFORMATION FOR SEQ ID NO:1751:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 518 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

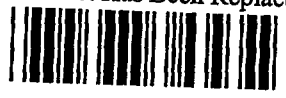
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...518

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1751

```
Pro Leu Val Lys Ile Arg Leu Phe Asp Phe Thr Ile Arg Leu Phe Lys
1               5                  10                  15
Pro Glu Phe His Ile Phe Asp Phe Leu Lys Gly Ile Arg Val Leu Met
            20                  25                  30
Ile Glu Trp Met Gln Asn His Arg Lys Tyr Leu Val Val Thr Ile Trp
        35                  40                  45
Ile Ser Thr Ile Ala Phe Ile Ala Ala Gly Met Ile Gly Trp Gly Gln
    50                  55                  60
Tyr Ser Phe Ser Leu Asp Ser Asp Ser Ala Ala Lys Val Gly Gln Ile
65                  70                  75                  80
Lys Ile Ser Gln Glu Glu Leu Ala Gln Glu Tyr Arg Arg Leu Lys Asp
                85                  90                  95
Ala Tyr Ala Glu Ser Ile Pro Asp Phe Lys Glu Leu Thr Glu Asp Gln
            100                 105                 110
Ile Lys Ala Met His Leu Glu Lys Ser Ala Leu Asp Ser Leu Ile Asn
        115                 120                 125
Gln Ala Leu Leu Arg Asn Phe Ala Leu Asp Leu Gly Leu Gly Ala Thr
    130                 135                 140
Lys Gln Glu Val Ala Lys Glu Ile Arg Lys Thr Asn Val Phe Gln Lys
```

```
145                 150                 155                 160
Asp Gly Val Phe Asp Glu Glu Leu Tyr Lys Asn Ile Leu Lys Gln Ser
                165                 170                 175
His Tyr Arg Pro Lys His Phe Glu Glu Ser Val Glu Arg Leu Leu Ile
            180                 185                 190
Leu Gln Lys Ile Ser Ala Leu Phe Pro Lys Thr Thr Thr Pro Leu Glu
        195                 200                 205
Gln Ser Ser Leu Ser Leu Trp Ala Lys Leu Gln Asp Lys Leu Asp Ile
    210                 215                 220
Leu Ile Leu Asn Pro Asn Asp Val Lys Ile Ser Leu Asn Glu Glu Glu
225                 230                 235                 240
Met Lys Lys Tyr Tyr Glu Asn His Arg Lys Asp Phe Lys Lys Pro Thr
                245                 250                 255
Ser Phe Lys Thr Arg Ser Leu Tyr Phe Asp Ala Ser Leu Glu Lys Thr
            260                 265                 270
Asp Leu Lys Glu Leu Glu Glu Tyr Tyr His Lys Asn Lys Val Ser Tyr
        275                 280                 285
Leu Asp Lys Glu Gly Lys Leu Gln Asp Phe Lys Ser Val Gln Glu Gln
    290                 295                 300
Val Lys His Asp Leu Asn Met Gln Lys Ala Asn Glu Lys Ala Leu Arg
305                 310                 315                 320
Ser Tyr Ile Ala Leu Lys Lys Gly Asn Ala Gln Asn Tyr Thr Thr Gln
                325                 330                 335
Asp Phe Glu Lys Asn Asn Ser Pro Tyr Thr Ala Glu Ile Thr Gln Lys
            340                 345                 350
Leu Thr Ala Leu Lys Pro Leu Glu Val Leu Lys Pro Glu Pro Phe Lys
        355                 360                 365
Asp Gly Phe Ile Val Val Gln Leu Val Ser Gln Ile Lys Asp Glu Leu
    370                 375                 380
Gln Asn Phe Asp Glu Ala Lys Ser Ala Leu Lys Thr Arg Leu Thr Gln
385                 390                 395                 400
Glu Lys Thr Leu Met Ala Leu Gln Thr Leu Ala Lys Glu Lys Leu Lys
                405                 410                 415
Asp Phe Lys Gly Lys Ser Val Gly Tyr Val Ser Pro Asn Phe Gly Gly
            420                 425                 430
Thr Ile Ser Glu Leu Asn Gln Glu Glu Ser Ala Lys Phe Ile Asn Thr
        435                 440                 445
Leu Phe Asn Arg Gln Glu Lys Lys Gly Phe Val Thr Ile Gly Asn Lys
    450                 455                 460
Val Val Leu Tyr Gln Ile Thr Glu Gln Asn Phe Asn His Pro Phe Ser
465                 470                 475                 480
Ala Glu Glu Asn Gln Tyr Met Gln Arg Leu Val Asn Asn Thr Lys Thr
                485                 490                 495
Asp Phe Phe Asp Lys Ala Leu Ile Glu Glu Leu Lys Lys Arg Tyr Lys
            500                 505                 510
Ile Val Lys Tyr Ile Gln
        515
```

(2) INFORMATION FOR SEQ ID NO:1752:

This Sheet Has Been Replaced



(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

SUBSTITUTE SHEET (RULE 26)

(B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1752

```
Lys Gly Lys Leu Gly Leu Phe Tyr Tyr Phe Ser Asp Leu Leu Glu Ser
1               5                  10                  15
Leu Ile Cys Phe Ser Asn Ser Cys Cys Lys Ala Cys Cys Cys Phe Ser
            20                  25                  30
Phe Phe Glu Arg Arg Arg Phe Phe Leu Gly Phe Phe Ser Phe Phe Glu
        35                  40                  45
Glu Val Ser Gly Ser Phe Glu Ala Val Ser Leu Ser Val Leu Ala Leu
    50                  55                  60
Val Ile Gly Ser Arg Ser Gly Leu Glu Glu Phe Cys Val Leu Glu Glu
65                  70                  75                  80
Leu Ile Asn Ser Gly Leu Ser Val Trp Leu Ser Ser Ser Pro Leu Leu
                85                  90                  95
Leu Phe Trp Asn Ala Ala Leu Val Ser Phe Ser Ala Cys Ser Ser Ile
            100                 105                 110
Phe Leu Arg Thr Ile Ala Ser Thr Phe Leu Ala Phe Ser Phe Trp Leu
        115                 120                 125
Thr Leu Thr Met Leu Ile Lys Tyr Leu Ile Tyr Pro Ser Tyr Met Ser
    130                 135                 140
Pro Asn Cys Ser Cys Lys Ala Pro Lys Ser Glu Pro Leu
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:1753:

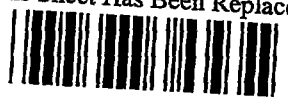
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 206 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1753

```
Gly Leu Leu Lys Pro Leu Glu Glu Thr Glu Ile Lys Ala Cys Asn Lys
1               5                  10                  15
Asp Ile Leu Pro Leu Lys Pro Tyr Glu Lys Ala Lys Leu Ile Ala Tyr
            20                  25                  30
Ile Pro Gln Val Glu Tyr Tyr Ala Phe Asn Phe Ser Val Leu Asp Phe
        35                  40                  45
Val Leu Met Gly Lys Ala Thr His Leu Asn Leu Phe Ala Met Pro Lys
    50                  55                  60
Ala Lys His Ile Lys Glu Ala Thr Ser Val Leu Glu Arg Leu Asp Leu
65                  70                  75                  80
Glu Ser Leu Lys Asp Gln Gly Ile Asn Asp Leu Ser Gly Gly Gln Arg
                85                  90                  95
Gln Met Val Leu Leu Ala Arg Ser Leu Leu Gln Arg Thr Pro Leu Leu
            100                 105                 110
Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Leu Lys Asn Gln Ala Leu
        115                 120                 125
Phe Phe Asp Ala Ile Lys Asp Glu Met Lys Lys Arg Glu Leu Ser Val
    130                 135                 140
Leu Val Asn Ile His Asp Pro Asn Leu Val Ala Arg His Ser Thr His
```

```
145                 150                 155                 160
Val Val Met Leu Lys Asp Lys Lys Leu Phe Leu Gln Ala Ser Thr Pro
                165                 170                 175
Ile Ala Met Thr Ser His Asn Leu Ser Ala Leu Tyr Asp Thr Pro Leu
            180                 185                 190
Glu Ala Ile Trp His Asp Asp Lys Leu Val Val Tyr Ala Leu
        195                 200                 205
```

(2) INFORMATION FOR SEQ ID NO:1754:

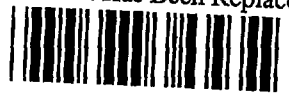
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1754

```
Lys Lys Lys Lys Asn Asp Glu Lys His Ile Ala Lys His Phe Val Ala
1               5                   10                  15
Val Ser Thr Asn Lys Glu Ala Val Gln Gln Phe Gly Ile Asp Glu His
            20                  25                  30
Asn Met Phe Gly Phe Trp Asp Phe Val Gly Gly Arg Tyr Ser Leu Trp
        35                  40                  45
Ser Ala Ile Gly Leu Ser Ile Met Ile Tyr Leu Gly Lys Lys Asn Phe
    50                  55                  60
Asn Ala Leu Leu Lys Gly Ala Tyr Leu Met Asp Glu His Phe Arg Asn
65                  70                  75                  80
Ala Pro Phe Glu Ser Asn Leu Pro Val Leu Met Gly Leu Ile Gly Val
                85                  90                  95
Trp Tyr Ile Asn Phe Phe Gln Ser Lys Gly His Leu Ile Ala Pro Tyr
            100                 105                 110
Asp
```

(2) INFORMATION FOR SEQ ID NO:1755:

(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:1755

```
His Asn Lys Thr Arg Met Lys Arg Ala Lys Arg Arg Lys Phe Ile Thr
1               5                  10                  15
Lys Phe Ser Arg Tyr Tyr Thr Pro Ser Val Leu Phe Ile Ala Leu Met
            20                  25                  30
Ile Ala Val Leu Pro Pro Leu Phe Ser Met Gly Ser Phe Asp Glu Trp
        35                  40                  45
Ile Tyr Arg Gly Leu Val Ala Leu Met Val Ser Cys Pro Cys Ala Leu
    50                  55                  60
Val Ile Ser Val Pro Leu Gly Tyr Phe Gly Gly Val Gly Ala Ala Ser
65                  70                  75                  80
Arg Lys Gly Ile Leu Met Lys Gly Val His Val Leu Glu Val Leu Thr
                85                  90                  95
Gln Thr Lys Ser Ile Ala Phe Asp Lys Thr Gly Thr Leu Thr Lys Gly
            100                 105                 110
Val Phe Lys Val Val Asp Ile Val Pro Gln Asn Gly His Ser Lys Glu
        115                 120                 125
Glu Val Cys Ile Thr Leu Leu Ala Arg Ser Phe Tyr Pro Arg Thr Arg
    130                 135                 140
Ser Leu Tyr Pro Phe Lys Lys His Ala Lys Lys Cys
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:1756:

(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

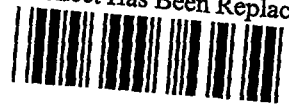
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1756

```
Arg Ser Thr Leu Ala Ser Ala Asp Val Gly Ile Gly Met Gly Lys Gly
1               5                  10                  15
Ser Glu Leu Ser Lys Gln Ser Ala Asp Ile Val Ile Thr Asn Asp Ser
            20                  25                  30
Leu Ser Ser Leu Val Lys Val Leu Ala Ile Ala Lys Lys Thr Lys Ser
        35                  40                  45
Ile Ile Trp Gln Asn Ile Leu Phe Ala Leu Gly Ile Lys Ala Val Phe
    50                  55                  60
Ile Val Leu Gly Leu Met Gly Val Ala Ser Leu Trp Glu Ala Val Phe
65                  70                  75                  80
Gly Asp Val Gly Val Thr Leu Leu Asp Leu Ala Asn Ser Met Arg Thr
                85                  90                  95
Met Arg Ala
```

(2) INFORMATION FOR SEQ ID NO:1757:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 amino acids
(B) TYPE: amino acid

This Sheet Has Been Replaced



(D) TOPOLOGY: linear

(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:1757

```
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
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
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1758:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 842 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1758

```
Phe Val Leu Asn Glu Glu Gln Asn Ser Leu Glu Glu Lys Gly Gly Glu
1               5                  10                  15
Asn Lys Asn Glu Lys Glu Thr Pro Leu Lys Gly Ile His Ser Lys Ile
            20                  25                  30
Pro Ser Leu Lys Gln Ala Leu Glu Gln Thr Ile Ser Lys Ile Lys Ser
        35                  40                  45
Ser Lys Glu Phe Phe Lys Gln Leu Leu His Asn Lys Lys Lys Leu Tyr
    50                  55                  60
Ile Ala Leu Gly Ile Leu Leu Ser Leu Ile Ala Leu Ile Val Ala Leu
65                  70                  75                  80
Ser Leu Leu Leu Gly His Lys Lys Glu Asn Lys Gln Thr Ser Leu Gln
                85                  90                  95
Thr Asn Thr Ala Thr Thr Asn Asn Glu Thr Pro Asn Asp Thr Asn Asn
            100                 105                 110
Ala Glu Ala Glu Gly Gln Ile Glu Asn Leu Asp Leu Pro Asp Leu Ile
        115                 120                 125
Gly Lys Asp Ser Leu Lys Arg Asn Asp Glu Ser Gln Val Asp Ala Met
    130                 135                 140
Met Gln Lys Ala Ser Leu Leu Tyr Glu Gln Gly Gln Lys Asp Glu Ala
145                 150                 155                 160
Leu His Leu Phe Asp Lys Ile Ala Ser Phe Ser Gln Gly Ile Ala Ser
                165                 170                 175
His Asn Leu Gly Val Ile Lys Phe Lys Glu Lys Asp Phe Asn Gly Ala
            180                 185                 190
Leu Asp Leu Phe Asp Ser Ser Ile Ala Ser Lys Glu Asn Ala Ser Val
        195                 200                 205
Ser Ala Ile Asp Ala Leu Val Thr Ala Tyr His Leu Gln Asp Ala Asp
    210                 215                 220
Leu Tyr Tyr His Tyr Leu Lys Ile Val Arg Asp Thr Leu Tyr Lys Asp
225                 230                 235                 240
Tyr Lys Lys Ser Phe Tyr Ser Tyr Ala Tyr Ala Leu Lys Ser Tyr Tyr
                245                 250                 255
Ala Gly Glu Tyr Phe Glu Ala Leu Ser Pro Leu Met His Pro Asn Ser
            260                 265                 270
Asn Ala Phe Leu Lys Pro Asn Ala Arg Leu Ala Ser Lys Leu Phe Leu
        275                 280                 285
Met Phe Lys Asp Glu Thr Asn Ala Tyr Lys Gln Leu Gln Lys Ser Ala
    290                 295                 300
Asn Ala Gln Asp Glu Leu Ala Leu Gly Leu Leu Gln Ala Arg Leu Gly
305                 310                 315                 320
Thr Tyr Lys Gln Ala Leu Glu His Leu Gln His Tyr Leu His Asn Tyr
                325                 330                 335
Pro Lys Asp Leu Asn Ala Leu Met Ala Leu Glu Leu Val Ser Leu Lys
            340                 345                 350
Met Gly Asp Thr Leu Lys Ala Ser Glu Ala Leu Lys Leu Ala Ser His
        355                 360                 365
Thr Gln Glu Asp Thr Leu Leu Ala Asn Ser Phe Tyr Pro Ile Lys Pro
```

```
    370                 375                 380
Thr Ile Asn Pro Met Phe Leu Asp Lys Glu Arg Ala Lys Glu Arg Phe
385                 390                 395                 400
Trp Asn Thr Gln Tyr Phe Glu Gly Lys Arg Asp Phe Ile Tyr Arg Leu
                405                 410                 415
Leu Phe Tyr Tyr Ala Pro Phe Lys Val Leu Asp Ser Lys Glu Thr Leu
            420                 425                 430
Gly Val Ile Glu Glu Gly Leu Phe Leu Leu Asp Ser Asp Thr Gln Lys
        435                 440                 445
Asp Leu Glu Gly Ala Ser Leu Ala Phe Lys Arg Gly Arg Leu Met Ala
    450                 455                 460
Ile Ala Asp Lys Asn Ala Leu Lys Gly Leu Lys Glu Leu Glu Lys Lys
465                 470                 475                 480
Arg Leu Lys Lys Ala Leu Ser Phe Phe Asp Leu Ser Leu Lys Asn Ser
                485                 490                 495
Pro Asn Asn Ala Leu Leu His Tyr Asn Val Gly Leu Ile Tyr Ala Gln
            500                 505                 510
Leu Glu Asn Tyr His Lys Ala Tyr Phe His Phe Leu Arg Ala Phe His
        515                 520                 525
Leu Asn Ser Ala Asp Tyr Leu Ser Ala Val Phe Ala Val Leu Ala Ser
    530                 535                 540
His Phe Thr His Glu Asp Thr Thr Glu Phe Leu Arg Glu Ile Thr Glu
545                 550                 555                 560
Asn Phe Tyr Ser His Asp Phe Ser Ser Pro Thr Gln Lys Ala Leu Leu
                565                 570                 575
Ser Ser Leu Ile Ala Tyr Leu Asn Tyr Arg Thr Asn Trp Asp Met Asp
            580                 585                 590
Trp Leu Lys Asn Ala Pro Lys Lys Leu Pro Phe Tyr Tyr Ala Leu Glu
        595                 600                 605
Ala Val Phe Ala Lys Glu Ser Lys Asp Lys Lys Leu Met Val Gln Ser
    610                 615                 620
Phe Gly Asn Leu Lys Lys Met Leu Pro Lys Asp Leu Ile Ser Asn Ile
625                 630                 635                 640
Phe Tyr Glu Ile Val Ser Tyr Tyr Asp Ala Ser Ile Arg His Thr Leu
                645                 650                 655
Ser Ile Tyr Thr Leu Leu Asp Ser His Lys Ile Ser Trp Asp Gln Thr
            660                 665                 670
Met Gln Gly Pro Ile Leu Gly Arg His Phe Tyr Thr Tyr Met Gly Phe
        675                 680                 685
Met Val Asn Asp Leu Asp His Gln Glu Arg Leu Leu Glu Gln Lys Ile
    690                 695                 700
Ala Ser Leu Glu Arg Gly Glu Ala Pro Asn Asp Trp Leu Glu Asn Leu
705                 710                 715                 720
Ala Leu Val Ser Leu Phe Gln Gly Gln Tyr Glu Lys Ala Ser Ala Leu
                725                 730                 735
Tyr Gln Asn Leu Ile Asp Gly Leu Lys Asp Asn Glu Ala Arg Leu Lys
            740                 745                 750
Ile Leu Ala Gly Leu Thr Tyr Ile Ala Gln Asn Asn Tyr Asn Asn Ala
        755                 760                 765
Ala Leu Trp Leu Glu Leu Gly Lys Leu Asp Asp Pro Asn Asn Glu Asn
    770                 775                 780
Ile Arg Tyr Ala Leu Gly Leu Leu Tyr Gln Arg Lys Gly Asp Leu Lys
785                 790                 795                 800
Ser Ala Leu Asn His Phe Leu Ala Ile Lys Thr Ser Asp Phe Ser Ser
                805                 810                 815
Pro Tyr Phe Asp Phe Glu Ile Asp Thr Asn Leu Leu Lys Glu Arg Leu
            820                 825                 830
Asn Gln Glu Glu Lys Gly Glu Phe Leu Glu
        835                 840
```

(2) INFORMATION FOR SEQ ID NO:1759:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 356 amino acids

This Sheet Has Been Replaced



SUBSTITUTE SHEET (RULE 26)

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1759

```
Lys Val Thr Thr Thr Met Ile Lys Ala Ile Ile Gly Lys Ile Ile Gly
1               5                  10                  15
Thr Arg Asn Asp Arg Trp Ile Lys Gln Tyr Lys Lys Lys Val Leu Ala
            20                  25                  30
Ile Asn Ala Leu Glu Pro Thr Tyr Glu Lys Met Ser Asp Val Glu Leu
        35                  40                  45
Gln Asn Ala Phe Glu Glu Leu Lys Lys Arg Val Arg Ser Val Glu Lys
    50                  55                  60
Asp Leu Gln Glu Lys Thr Leu Leu Glu Val Leu Pro Glu Ser Phe Ala
65                  70                  75                  80
Ile Thr Arg Glu Ala Ser Lys Arg Ile Leu Lys Met Arg His Phe Asp
                85                  90                  95
Val Gln Leu Ile Gly Gly Met Val Leu Asn Asp Gly Lys Ile Ala Glu
            100                 105                 110
Met Lys Thr Gly Glu Gly Lys Thr Leu Val Ala Thr Leu Ala Val Ala
        115                 120                 125
Leu Asn Ala Met Lys Gly Glu Ser Val Tyr Val Val Thr Val Asn Asp
    130                 135                 140
Tyr Leu Ala His Arg Asp Ser Lys Glu Met Glu Pro Leu Tyr Gln Phe
145                 150                 155                 160
Leu Gly Tyr Ser Val Gly Thr Ile Thr Ala Ser Val Arg Asp Asp Asp
                165                 170                 175
Glu Arg Leu Glu Ile Tyr Ser Lys Asp Ile Val Tyr Gly Thr Asn Asn
            180                 185                 190
Glu Phe Gly Phe Asp Tyr Leu Arg Asp Asn Met Lys Tyr Ser Leu Glu
        195                 200                 205
His Lys Val Gln Lys Ser His Ala Phe Ala Ile Val Asp Glu Val Asp
    210                 215                 220
Ser Ile Leu Ile Asp Glu Ala Arg Thr Pro Leu Ile Ile Ser Gly Pro
225                 230                 235                 240
Val Asp Arg Arg Met Glu Asn Tyr Asn Lys Ala Asp Glu Val Ala Lys
                245                 250                 255
Ser Met Gln Val Glu Val Asp Phe Thr Ile Asp Glu Lys Asn Arg Ala
            260                 265                 270
Ile Leu Ile Thr Glu Glu Gly Ile Lys Lys Ala Glu Asn Leu Phe Gly
        275                 280                 285
Val Asp Asn Leu Tyr Lys Ile Glu Asn Ala Ala Leu Ser His His Leu
    290                 295                 300
Asp Gln Ala Leu Lys Ala Asn Tyr Leu Phe Phe Ile Asp Lys Asp Tyr
305                 310                 315                 320
Ile Val Ala Asn Asn Glu Val Val Ile Val Asp Glu Phe Thr Gly Arg
                325                 330                 335
Leu Ser Glu Gly Arg Arg Phe Ser Glu Gly Leu His Gln Ala Leu Glu
            340                 345                 350
Ala Lys Glu Ala
        355
```

(2) INFORMATION FOR SEQ ID NO:1760:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1760

```
Lys Leu Phe Leu Lys Pro Leu Lys Glu Thr Ser Leu Ala Leu Val Gly
1               5                  10                  15
Val Ala Lys Asn Ile Lys Ile Val Ala Leu Lys Ala Gly Leu Lys Arg
            20                  25                  30
Ala Tyr Leu Pro Asn Arg Ser Leu Ile Phe Phe Leu Ile Lys Arg Tyr
        35                  40                  45
Leu Arg Phe Asp Lys Ser Gln Pro Phe Ile Ser Ile Thr Ala Leu Leu
    50                  55                  60
Ala Phe Phe Gly Val Ala Val Gly Val Met Val Leu Ile Val Ala Met
65                  70                  75                  80
Ala Ile Met Asn Gly Met Ser Lys Glu Phe Glu Lys Lys Leu Phe Val
                85                  90                  95
Met Asn Tyr Pro Leu Thr Leu Tyr Thr Thr Ser Pro Tyr Gly Ile Ser
            100                 105                 110
Glu Glu Val Val Gln Ala Leu Glu Lys Lys Phe Pro Asn Leu Leu Phe
        115                 120                 125
Ser Pro Tyr Leu Gln Thr Gln Ser Pro Ile Lys Ser Ala His Ser Met
    130                 135                 140
Asn Gly Gly Val Val Phe Gly Val Asp Phe Ser Lys Glu Arg His Ile
145                 150                 155                 160
Asn Glu Val Leu Asn Asp Ala Leu Lys Asn Ile Asn Glu Asn Asp Leu
                165                 170                 175
Phe Lys Asn Pro Phe Asn Leu Ile Val Gly Lys Ser Leu Arg Tyr Ser
            180                 185                 190
Leu Asn Leu Asp Leu Asn Gln Lys Ala Asp Leu Phe Phe Thr Glu Leu
        195                 200                 205
Glu Pro Thr Gly Leu Thr Leu Ser Pro Ile Met Lys Arg Phe Thr Ile
    210                 215                 220
Lys Gly Asp Phe Asp Ser Gly Leu Lys Ser Tyr Asp Met Ser Tyr Met
225                 230                 235                 240
Tyr Ala Ser Leu Gln Ala Ile Ser Ala Ile Arg Arg Leu Pro Leu Gly
                245                 250                 255
Leu Tyr Asp Gly Val His Val Tyr Ser Lys Thr Pro Met Lys Asp Ile
            260                 265                 270
Glu Lys Leu Arg Asn Ala Leu Lys Thr Ile Asn His His Gly Ile Gly
        275                 280                 285
Ile Glu Gly Trp Trp Gln Gln Asn Gly Asn Phe Phe Ser Ala Met Glu
    290                 295                 300
Leu Glu Lys Arg Ala Leu Phe Ile Val Leu Met Leu Ile Ile Leu Met
305                 310                 315                 320
Ala Ser Leu Asn Ile Ile Ser Ser Leu Leu Met Val Val Met Asn Arg
                325                 330                 335
Arg Lys Glu Ile Ala Leu Leu Phe Ser Met Gly Ser Ser Gln Lys Glu
            340                 345                 350
Ile Gln Lys Thr Phe Phe Tyr Leu Gly Asn Ile Ile Ser
        355                 360                 365
```

(2) INFORMATION FOR SEQ ID NO:1761:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1761

```
Arg Gly Val Ser Ile Lys Glu Glu Ser Gln Thr Leu Ala Asp Ile Thr
1               5                  10                  15
Phe Gln Asn Tyr Phe Arg Met Phe Ser Lys Leu Ser Gly Met Thr Gly
            20                  25                  30
Thr Ala Gln Thr Glu Ala Thr Glu Phe Leu Glu Ile Tyr Asn Leu Glu
        35                  40                  45
Val Val Ser Ile Pro Thr Asn Leu Ala Ile Lys Arg Lys Asp Leu Asn
    50                  55                  60
Asp Leu Ile Tyr Lys Ser Glu Lys Glu Lys Phe Asp Ala Val Ile Leu
65                  70                  75                  80
Lys Ile Lys Glu Leu His Asp Lys Gly Gln Pro Val Leu Val Gly Thr
                85                  90                  95
Ala Ser Ile Glu Lys Ser Glu Thr Leu His Ala Leu Leu Lys Lys Glu
            100                 105                 110
Arg Ile Pro His Thr Val Leu Asn Ala Lys Gln His Thr Lys Glu Ala
        115                 120                 125
Glu Ile Ile Lys Asp Ala Gly Leu Lys Gly Ala Val Thr Ile Ala Thr
    130                 135                 140
Asn Met Ala Gly Arg Gly Val Asp Ile Lys Leu Thr Asp Glu Val Lys
145                 150                 155                 160
Glu Leu Gly Gly Leu Tyr Ile Ile Gly Thr Glu Arg His Glu Ser Arg
                165                 170                 175
Arg Ile Asp Asn Gln Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp Pro
            180                 185                 190
Gly Val Ser Gln Phe Tyr Leu Ser Leu Glu Asp Asn Leu Leu Arg Ile
        195                 200                 205
Phe Gly Ser Asp Arg Thr Lys Gly Val Met Glu Lys Leu Gly Pro Lys
    210                 215                 220
Asp Gly Glu His Ile Glu Phe Lys Leu Val Thr Arg Ala Val Glu Asn
225                 230                 235                 240
Ala Gln Lys Lys Val Glu Asn Leu His Phe Asp Ser Arg Lys His Leu
                245                 250                 255
Leu Glu Tyr Asp Asp Val Ala Asn Glu Gln Arg Thr Ser Val Tyr Asn
            260                 265                 270
Leu Arg Asp Glu Leu Leu Asp Ile Asn Tyr Asp Ile Ser Ala Lys Ile
        275                 280                 285
Ala Glu Asn Arg Glu Tyr Ala Leu Asn Gln Ile Phe Ser Lys Leu Lys
    290                 295                 300
Ala Phe Asp His Gln Asn Leu Ser Glu Glu Glu Leu Leu Gly Leu Lys
305                 310                 315                 320
Asn Ile Leu Lys Glu Asp Phe Asn Ala Ser Val Glu Leu Glu Asp Leu
                325                 330                 335
Glu Lys Ala Ser Pro Ile Glu Ile Phe Val Ala Glu Lys Leu Lys Ser
```

340 345 350
Gly Leu

(2) INFORMATION FOR SEQ ID NO:1762:

(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:1762

```
Met Gln Lys Phe Phe Ser Arg Phe Arg Arg Trp Ala Leu Pro Phe Tyr
1               5                  10                  15
Phe Val Ser Ala Leu Ala Ala Ile Asp Ile Asp Glu Val Thr Glu Ala
            20                  25                  30
Gln Ala Asn Ser Ile Lys Leu Ser Asp Gln Leu Val Ser Leu Ser Asp
        35                  40                  45
Lys Leu Leu Glu Lys Ala Val Asp Arg Gly Arg Asn Thr Asp His Leu
    50                  55                  60
Lys Asp Leu Asn Asp Leu His Glu Lys Ile Lys His Leu Arg Leu Ile
65                  70                  75                  80
Leu Glu Pro Lys Pro Lys Gly Lys Glu Asp Ser Pro Asn Leu Gly Gly
                85                  90                  95
Asn Lys Asp Met Lys Thr Val Glu Ile Gly Ser
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:1763:

(i) SEQUENCE CHARACTERISTICS:
(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:1763

```
Lys Asn Gln Ile Leu Gln Ile Pro Leu Leu Pro Pro Pro Pro Asn Asn
1               5                  10                  15
Glu Glu Leu Leu Lys Ser Ile Thr Asp Leu Lys Asp Arg Leu Lys Lys
            20                  25                  30
```

This Sheet Has Been Replaced



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

(2) INFORMATION FOR SEQ ID NO:1764:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1764

```
Ala Leu Ser Asn Cys Leu Ser Leu Ser Val Arg Arg Trp Phe Ser Phe
1               5                   10                  15
Ser Lys Leu Val His Arg Phe Ser Arg Asn Pro Cys Ala Ser Cys Asn
            20                  25                  30
Arg Ala Arg Ser Cys Ser Arg Leu Ser Arg Ser Leu Val Ser Ala Val
        35                  40                  45
Thr Trp Trp Leu Ser Leu Ser Phe Ser Val Val Ser Ala Leu Phe Ser
    50                  55                  60
Leu Val Ser Ser Val Ile Leu Trp Val Ser Ser Val Phe Ser Leu Phe
65                  70                  75                  80
Ser Leu Ser Phe Ser Val Val Asn Ser Leu Phe Ser Ser Val Ser Arg
```

```
                85                  90                  95
Ser Leu Ala Ala Asn Lys Arg Val Phe Ser Leu Ala Lys Met Ser Phe
            100                 105                 110
Ser Val Phe Ser Ser Ala Phe Ser Leu Val Ser Leu Leu Leu Phe Cys
        115                 120                 125
His Asn
    130
```

(2) INFORMATION FOR SEQ ID NO:1765:

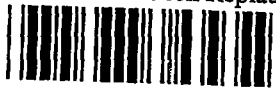
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...327

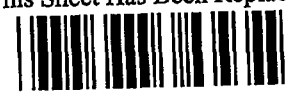
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1765

```
Met Gly Thr Leu Ile Glu Lys Trp Phe Gly Phe Ser Gln Ile Arg Glu
1               5                  10                  15
Glu Leu Glu Ala Arg Ile Ser Glu Leu Glu Asp Glu Asn Thr Glu Leu
            20                  25                  30
Leu Arg Glu Arg Glu Tyr Leu Ala Ala Glu Thr Ser Glu Leu Lys Asp
        35                  40                  45
Ala Asn Asp Gln Leu Arg Gln Lys Asn Asp Lys Leu Phe Ile Thr Lys
    50                  55                  60
Asp Lys Leu Thr Lys Glu Asn Thr Glu Leu Phe Ala Glu Asn Glu Ser
65                  70                  75                  80
Leu Ser Val Lys Ile Ser Gly Leu Glu His Ser Asn Asp Gln Leu Trp
                85                  90                  95
Gln Asn Asn Asn Lys Leu Thr Lys Glu Lys Ala Glu Leu Lys Thr Glu
            100                 105                 110
Lys Asp Ile Leu Ala Lys Glu Asn Thr Arg Leu Leu Ala Ala Arg Asp
        115                 120                 125
Arg Leu Thr Glu Glu Lys Arg Glu Leu Thr Thr Glu Lys Glu Arg Leu
    130                 135                 140
Lys Arg Glu Asn Thr Glu Leu Thr His Lys Ile Thr Glu Leu Thr Lys
145                 150                 155                 160
Glu Asn Lys Ala Leu Thr Thr Glu Asn Asp Lys Leu Asn His Gln Val
                165                 170                 175
Thr Ala Leu Thr Asn Glu Arg Asp Ser Leu Glu Gln Glu Arg Ala Arg
            180                 185                 190
Leu Gln Asp Ala His Gly Phe Leu Glu Lys Arg Cys Thr Asn Leu Glu
        195                 200                 205
Lys Glu Asn Gln Arg Leu Thr Asp Lys Leu Lys Gln Leu Glu Ser Ala
    210                 215                 220
Gln Lys Ser Leu Glu Asn Thr Asn Asn Gln Leu Arg Gln Ala Leu Glu
225                 230                 235                 240
Asn Ser Asn Val Gln Leu Ala Gln Ala Lys Glu Lys Ile Ala Ile Glu
                245                 250                 255
Lys Ser Glu Leu Glu Arg Glu Ile Ala Arg Leu Lys Ser Leu Glu Gly
            260                 265                 270
Met Glu Ala Lys Ser Asp Leu Asp Leu His Asn Arg Arg Leu Ala Ser
        275                 280                 285
```

```
Ala Asn Glu Asp Leu Lys Arg Gln Asn Arg Lys Leu Glu Glu Glu Asn
    290                 295                 300
Ile Ala Leu Lys Glu Arg Val Asp Gly Leu Asn Glu Gln Leu Ser Lys
305                 310                 315                 320
Leu Gln Pro Gln Lys Pro Gln
                325
```

(2) INFORMATION FOR SEQ ID NO:1766:

This Sheet Has Been Replaced



(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:1766

```
Phe Lys Thr Ile Glu Arg Asn Asp Phe Lys Leu Asn Gly Leu Thr Lys
1               5                  10                  15
Ile Leu Gln Asn Lys Gly Tyr Lys Met Lys Thr Ile Lys Asn Gly Ile
            20                  25                  30
Met Ile Gly Thr Leu Gly Ala Leu Leu Leu Ser Gly Cys Ser Ser Phe
        35                  40                  45
Asp Ala Gln Arg Phe Ala Cys Leu Pro Lys Asp His Ser Ser Lys Asp
    50                  55                  60
Ala Ser Thr Lys Lys Glu Ala Gln Tyr Ile Pro Lys Gly Phe Phe Asp
65                  70                  75                  80
Pro Tyr Ser Ser Asn Leu Asn His Trp Asp Ser Thr Phe
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:1767:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1767

```
Ser Leu Asn Lys Gly Leu Ala Leu Phe Leu Val Lys Lys Ile Gly Val
1               5                  10                  15
Val Ile Met Ile Leu Val Cys Phe Leu Ala Cys Ser Gln Glu Ser Phe
```

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

(2) INFORMATION FOR SEQ ID NO:1768:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

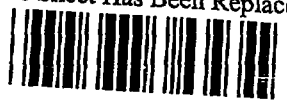
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1768

```
Ala Trp Leu Lys Ser Arg Val Leu Met Lys Arg Leu Ala Val Ala Leu
1               5                   10                  15
Ile Leu Val Leu Gly Val Val Trp Gly Lys Ser Leu Pro Lys Trp Ala
            20                  25                  30
Lys Asp Cys Ser Lys Glu Met Arg Ile Glu Lys Thr Gln Thr Lys Asp
        35                  40                  45
Glu Lys Ile Leu Val Cys Gly Met Ser Asp Ile Leu Leu Ser Asp Met
    50                  55                  60
```

```
Asp Tyr Ser Leu Ser Ser Ala Arg Gln Asn Ala Leu Glu Lys Val Met
65                  70                  75                  80
Glu Ala Phe Lys Gly Asp Arg Ile Glu Ile Lys Ala Gly Glu Leu Lys
                85                  90                  95
Ala Thr Phe Ile Asp Thr Asp Lys Val Tyr Val Leu Leu Arg Ile Thr
            100                 105                 110
Lys Lys His Val Ala Leu Met Asn Glu
        115                 120
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1769:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1769

```
Gly Leu Ile Met Lys Lys Ile Ile Leu Ala Cys Leu Val Ala Phe Val
1               5                   10                  15
Gly Ala Asn Leu Ser Ala Glu Pro Lys Trp Tyr Ser Lys Ala Tyr Asn
            20                  25                  30
Lys Thr Asn Ala Gln Lys Gly Tyr Leu Tyr Gly Ser Gly Ser Ala Thr
        35                  40                  45
Ser Lys Glu Ala Ser Lys Gln Lys Ala Leu Ala Asp Leu Val Ala Ser
    50                  55                  60
Ile Ser Val Val Val Asn Ser Gln Ile His Ile Gln Lys Ser Arg Val
65                  70                  75                  80
Asp Asn Lys Leu Lys Ser Ser Asp Ser Gln Thr Ile Asn Leu Lys Thr
                85                  90                  95
Asp Asp Leu Glu Leu Asn Asn Val Glu Ile Val Asn Gln Glu Ala Gln
            100                 105                 110
Lys Gly Ile Tyr Tyr Thr Arg Val Arg Ile Asn Gln Asn Leu Phe Leu
        115                 120                 125
Gln Gly Leu Arg Asp Lys Tyr Asn Ala Leu Tyr Gly Gln Phe Ser Thr
    130                 135                 140
Leu Met Pro Lys Val Cys Lys Gly Val Phe Tyr Lys Gln Ser Lys Ser
145                 150                 155                 160
Met Gly Asp Leu Leu Ala Lys Ala Ala Pro Met Glu Arg Ile Leu Lys
                165                 170                 175
Ala Tyr Ser Val Pro Val Ser Ser Leu Glu Asn Tyr Glu Lys Ile Tyr
            180                 185                 190
Tyr Gln Asn Ala Phe Lys Pro Lys Val Arg Ile Ala Phe Asp Asp Asn
        195                 200                 205
Ser Asp Thr Glu Ile Lys Asn Ala Leu Met Ser Ala Tyr Ala Arg Val
    210                 215                 220
Leu Thr Pro Ser Asp Glu Glu Lys Leu Tyr Gln Ile Lys Asn Glu Val
225                 230                 235                 240
Phe Thr Asp Ser Ala Asn Gly Ile Thr Arg Ile Arg Val Ile Ile Ser
                245                 250                 255
Ala Ser Asp Cys Gln Gly Thr Pro Val Leu Asn Arg Ser Leu Glu Val
            260                 265                 270
Asp Glu Lys Asn Lys Asn Phe Ala Ile Thr Arg Leu Gln Ser Leu Leu
```

```
        275                 280                 285
Tyr Lys Glu Leu Lys Gly Tyr Ala Asn Lys Glu Gly Gln Gly Asn Thr
    290                 295                 300
Gly Leu
305
```

(2) INFORMATION FOR SEQ ID NO:1770:

(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:1770

```
Pro Gln Arg Val Val Phe Arg Val Arg Phe Leu Leu Ala Ile Pro Gln
1               5                  10                  15
Ile Leu Val Gly Leu Arg Ile Ala Val Val Met Leu Val Ala Met Ala
            20                  25                  30
Gly Ile Gly Ala Leu Ile Gly Ala Gly Gly Leu Gly Gln Ala Ile Phe
        35                  40                  45
Arg Gly Leu Asn Thr Gln Asn Thr Thr Ile Leu Val Ala Gly Ser Phe
    50                  55                  60
Ile Ile Ala Leu Phe Ser Val Leu Ala Asp Gln Phe Val Ser Val Phe
65                  70                  75                  80
Gln His Glu Asn Ala Leu Gln Arg Leu Phe Ser Gln Asn Ala Thr Gln
                85                  90                  95
Lys Gln Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Phe Leu
            100                 105                 110
Leu Leu Ala Ser Ala Leu Trp Leu Ile Pro Arg Ser Ala Ile Glu Glu
        115                 120                 125
Lys Pro Leu Val Val Ala Thr Lys Pro Ser Ser Glu Gln Tyr Ile Leu
    130                 135                 140
Gly Glu Ile Leu Ser Leu Leu Leu Glu Lys His His Ile Pro Ile Lys
145                 150                 155                 160
Arg Ala Phe Gly Ile Gly Gly Gly Thr Met Asn Ile His Pro Ala Leu
                165                 170                 175
Ile Arg Gly Asp Phe Asp Leu Tyr Val Glu Tyr Thr Gly Thr Ala Trp
            180                 185                 190
Val Asn Thr Leu Lys Asn Pro Leu Thr Gln Lys Val Asp Phe Glu Thr
        195                 200                 205
Ile Lys Lys Arg Tyr Glu Lys Glu Phe Asn Leu Leu Trp Val Gly Leu
    210                 215                 220
Leu Gly Phe Asn Asn Thr Tyr Ser Leu Ala Ile Ser Lys Glu Asp Ala
225                 230                 235                 240
Gln Lys Tyr Ala Ile Glu Thr Phe Ser Asp Leu Ala Phe His Ser Pro
                245                 250                 255
Asn Phe Asp Phe Gly Ala Glu Phe Asp Phe Phe Glu Arg Glu Asp Ala
            260                 265                 270
Phe Lys Gly Leu Ile Lys Ala Tyr Arg Phe His Phe Arg Ser Leu His
        275                 280                 285
Glu Met Asp Ile Asn Leu Arg Tyr Lys Ser Phe Glu Ser His Lys Ile
    290                 295                 300
```

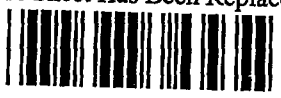
This Sheet Has Been Replaced



```
Asn Ala Leu Asp Val Phe Thr Thr Asp Ala Gln Ile Lys Glu Leu Asp
305                 310                 315                 320
Leu Lys Val Leu Lys Asp Asp Lys Gly Phe Phe Pro Asn Tyr Gln Ala
                325                 330                 335
Gly Ile Val
```

(2) INFORMATION FOR SEQ ID NO:1771:

This Sheet Has Been Replaced



(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:1771

```
Gly Ala Lys Met Lys Lys Ile Gly Leu Ser Leu Cys Leu Val Leu Ser
1               5                  10                  15
Leu Gly Phe Leu Lys Ala His Glu Val Ser Ala Glu Glu Ile Ala Asp
            20                  25                  30
Ile Phe Tyr Lys Leu Asn Ala Lys Glu Pro Lys Met Lys Ile Asn His
        35                  40                  45
Thr Lys Gly Phe Cys Ala Lys Gly Val Phe Leu Pro Asn Pro Gln Ala
    50                  55                  60
Arg Glu Asp Leu Glu Val Pro Leu Leu Asn Glu Lys Glu Ile Pro Ala
65                  70                  75                  80
Ser Val Arg Tyr Ser Leu Gly Gly Val Ala Met Asp Asp Lys Ser Lys
                85                  90                  95
Val Arg Gly Met Ala Leu Lys Leu Glu Asn Gln Asn Ala Ser Trp Thr
            100                 105                 110
Met Val Met Leu Asn Thr Glu Ile Asn Phe Ala Lys Asn Pro Glu Glu
        115                 120                 125
Phe Ala Gln Phe Phe Glu Met Arg Leu Pro Lys Asn Gly Gln Gly Arg
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:1772:

(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:1772

```
His Glu Phe Leu Ala Ile Asn Glu Leu Met Phe Asp Val Phe Leu Pro
1               5                  10                  15
Ser Arg Leu Lys Gln Lys Glu Leu Leu Glu Lys Ile Glu Val Ile Gln
            20                  25                  30
Lys Phe Phe Pro Asn Phe Pro Lys Glu Thr Leu Leu Asn Asn Tyr Gln
        35                  40                  45
Lys Glu Asn Ser Leu Tyr Asn His Asn Leu Ile Lys Val Val Gly Phe
    50                  55                  60
Ile Pro Tyr Ala Thr Met Gln Ser Leu Tyr Thr Lys Leu Ile Gln Thr
65                  70                  75                  80
Gln Gly Ile Phe Val Arg Pro Leu Asp Lys Arg Tyr Tyr Pro Asn Asn
                85                  90                  95
Ala Leu Ala Ser His Val Leu Gly Tyr Val Gly Val Ala Ser Leu Gln
            100                 105                 110
Asp Leu Lys Asp Asp Glu Glu Asn Gln Tyr Ser Gln Ile Val Gly Lys
        115                 120                 125
Thr Gly Ile Glu Lys Glu Tyr Asn Lys Phe Leu Gln Gly Lys Val Gly
    130                 135                 140
Tyr Lys Ile Ile His Val Asn Ala Leu Asn Gln Glu Leu Ala Thr Leu
145                 150                 155                 160
Glu Val Val Pro Pro Arg Ser Asn Asn His Ser Gln Leu Ser Leu Asp
                165                 170                 175
Lys Arg Phe Gln Lys Glu Ala His Lys Leu Phe Val Asn Lys Arg Gly
            180                 185                 190
Pro Ile Leu Val Met Asp Ala Glu Asn Gly Glu Leu Leu Val Ala Gly
        195                 200                 205
Ser Tyr Pro Glu Tyr Asn Leu Asn Asp Phe Val Gly Gly Ile Ser Gln
    210                 215                 220
Asp Lys Trp Gln Lys Leu Gln Asp Asp Ile Tyr Asn Pro Leu Leu Asn
225                 230                 235                 240
Arg Phe Ala Asn Ala Leu Tyr Pro Pro Gly Ser Val Val Lys Met Gly
                245                 250                 255
Val Gly Leu Ser Phe Leu Glu Asn Leu His Ile Thr Glu Asn Thr Thr
            260                 265                 270
Ile Pro Thr Pro Pro Phe Ile Glu Val Gly Lys Arg Lys Phe Arg Asp
        275                 280                 285
Trp Lys Lys Thr Gly His Gly Asn Ser Asn Leu Tyr Lys Ala Ile Arg
    290                 295                 300
Glu Ser Val Asp Val Tyr Phe Tyr Lys Phe Gly Leu Glu Ile Ser Ile
305                 310                 315                 320
Glu Lys Leu Ser Lys Thr Leu Arg Glu Val Gly Phe Gly Glu Lys Thr
                325                 330                 335
Gly Val Asp Leu Pro Asn Glu Phe Val Gly Ile Val Pro Asp Asn Leu
            340                 345                 350
Trp Lys Leu Lys Arg Phe Asn Gln Asp Trp Arg Val Gly Asp Thr Leu
        355                 360                 365
Ile Thr Ala Ile Gly Gln Gly Ser Phe Leu Ala Thr Pro Leu Gln Val
    370                 375                 380
Leu Ala Tyr Thr Gly Leu Ile Ala Thr Gly Lys Leu Ala Thr Pro His
385                 390                 395                 400
Phe Ala Ile His Asn Gln Gln Pro Leu Lys Asp Pro Leu Asn Ser Phe
                405                 410                 415
Gln Lys Lys Lys Leu Gln Ala Leu Arg Val Gly Met Tyr Glu Val Cys
            420                 425                 430
Asn His Lys Asp Gly Thr Ala Tyr His Ser Thr Arg Gly Ser Lys Val
        435                 440                 445
Thr Leu Ala Cys Lys Thr Gly Thr Ala Gln Val Val Glu Ile Ala Gln
    450                 455                 460
Asn Ile Val Asn Arg Met Lys Glu Lys Asp Met Glu Tyr Phe His Arg
465                 470                 475                 480
Ser His Ala Trp Ile Thr Ala Phe Leu Pro Tyr Glu Lys Pro Lys Tyr
                485                 490                 495
```

```
Ala Ile Thr Ile Leu Val Glu His Gly Glu Gly Gly Ser Lys Leu Gly
            500                 505                 510
Gly Leu Leu Val Lys Met Ser Asn Lys Leu Tyr Glu Leu Gly Tyr Leu
        515                 520                 525
```

(2) INFORMATION FOR SEQ ID NO:1773:

(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:1773

```
Ile Asn Phe Val Asn Lys Gly Val Phe Met Asn Ile Phe Lys Arg Ile
1               5                  10                  15
Ile Cys Val Thr Ala Ile Val Leu Gly Phe Phe Asn Leu Leu Asp Ala
            20                  25                  30
Lys His His Lys Glu Lys Lys Glu Asp His Lys Ile Thr Arg Glu Leu
        35                  40                  45
Lys Val Gly Ala Asn Pro Val Pro His Ala Gln Ile Leu Gln Ser Val
    50                  55                  60
Val Asp Asp Leu Lys Glu Lys Gly Ile Lys Leu Val Ile Val Ser Phe
65                  70                  75                  80
Thr Asp Tyr Val Leu Pro Asn Leu Ala Leu Asn Asp Gly Ser Leu Asp
                85                  90                  95
Ala Asn Tyr Phe Gln His Arg Pro Tyr Leu Asp Arg Phe Asn Leu Asp
            100                 105                 110
Arg Lys Met His Leu Val Gly Leu Ala Asn Ile His Val Glu Pro Leu
        115                 120                 125
Arg Phe Tyr Ser Gln Lys Ile Thr Asp Ile Lys Asn Leu Lys Lys Gly
    130                 135                 140
Ser Val Ile Ala Val Pro Asn Asp Pro Ala Asn Gln Gly Arg Ala Leu
145                 150                 155                 160
Ile Leu Leu His Lys Gln Gly Leu Ile Ala Leu Lys Asp Pro Ser Asn
                165                 170                 175
Leu Tyr Ala Thr Glu Phe Asp Ile Val Lys Asn Pro Tyr Asn Ile Lys
            180                 185                 190
Ile Lys Pro Leu Glu Ala Ala Leu Leu Pro Lys Val Leu Gly Asp Val
        195                 200                 205
Asp Gly Ala Ile Ile Thr Gly Asn Tyr Ala Leu Gln Ala Lys Leu Thr
    210                 215                 220
Gly Ala Leu Phe Ser Glu Asp Lys Asp Ser Pro Tyr Ala Asn Leu Val
225                 230                 235                 240
Ala Ser Arg Glu Asp Asn Ala Gln Asp Glu Ala Ile Lys Ala Leu Ile
                245                 250                 255
Glu Ala Leu Gln Ser Glu Lys Thr Arg Lys Phe Ile Leu Asp Thr Tyr
            260                 265                 270
Lys Gly Ala Ile Ile Pro Ala Phe
        275                 280
```

(2) INFORMATION FOR SEQ ID NO:1774:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1774

```
Met Met Ile Thr Lys Gln Ser Tyr Gln Arg Phe Ala Leu Met Arg Val
1               5                  10                  15
Phe Val Phe Ser Leu Ser Ala Phe Ile Phe Asn Thr Thr Glu Phe Val
            20                  25                  30
Pro Val Ala Leu Leu Ser Asp Ile Ala Lys Ser Phe Glu Met Glu Ser
        35                  40                  45
Ala Thr Val Gly Leu Met Ile Thr Ala Tyr Ala Trp Val Val Ser Leu
    50                  55                  60
Gly Ser Leu Pro Leu Met Leu Leu Ser Ala Lys Ile Glu Arg Lys Arg
65                  70                  75                  80
Leu Leu Leu Phe Leu Phe Ala Leu Phe Ile Phe Ser His Ile Leu Ser
                85                  90                  95
Ala Leu Ala Trp Asn Phe Trp Val Leu Leu Leu Ser Arg Met Gly Ile
            100                 105                 110
Ala Phe Ala His Ser Ile Phe Trp Ser Ile Thr Ala Ser Leu Val Ile
        115                 120                 125
Arg Val Ala Pro Arg Asn Lys Lys Gln Gln Ala Leu Gly Leu Leu Ala
    130                 135                 140
Leu Gly Ser Ser Leu Ala Met Ile Leu Gly Leu Pro Leu Gly Arg Ile
145                 150                 155                 160
Ile Gly Gln Ile Leu Asp Trp Arg Ser Thr Phe Gly Val Ile Gly Gly
                165                 170                 175
Val Ala Thr Leu Ile Met Leu Leu Met Trp Lys Leu Leu Pro His Leu
            180                 185                 190
Pro Ser Arg Asn Ala Gly Thr Leu Ala Ser Val Pro Ile Leu Met Lys
        195                 200                 205
Arg Pro Leu Leu Val Gly Ile Tyr Leu Leu Val Ile Met Val Ile Ser
    210                 215                 220
Gly His Phe Thr Thr Tyr Ser Tyr Ile Glu Pro Phe Ile Ile Gln Ile
225                 230                 235                 240
Ser Gln Phe Ser Pro Asp Ile Thr Thr Leu Met Leu Phe Val Phe Gly
                245                 250                 255
Leu Ala Asp Val Val Gly Ser Phe Leu Phe Gly Arg Leu Tyr Ala Lys
            260                 265                 270
Asn Ser Arg Lys Phe Ile Ala Phe Ala Met Val Leu Val Ile Cys Pro
        275                 280                 285
Gln Leu Leu Leu Phe Val Phe Lys Asn Leu Glu Trp Val Ile Phe Leu
    290                 295                 300
Gln Ile Phe Leu Trp Gly Ile Gly Ile Thr Ser Leu Thr Ile Thr Leu
305                 310                 315                 320
Gln Asn Glu Gly Ile His
                325
```

(2) INFORMATION FOR SEQ ID NO:1775:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1775

```
Lys Gly Ile Gln Lys Lys Gln Asn Leu Lys Glu Val Ala Leu Asp Ala
1               5                  10                  15
Phe Leu Pro Lys Ser Ile Asn Tyr Tyr His Phe Asn Gly Ser Leu Thr
            20                  25                  30
Ala Pro Pro Cys Thr Glu Gly Val Ala Trp Phe Val Ile Glu Glu Pro
        35                  40                  45
Leu Glu Val Ser Ala Lys Gln Leu Ala Glu Ile Lys Lys Arg Met Lys
    50                  55                  60
Asn Ser Pro Asn Gln Arg Pro Val Gln Pro Asp Tyr Asn Thr Val Ile
65                  70                  75                  80
Ile Lys Ser Ser Ala Glu Thr Arg
                85
```

(2) INFORMATION FOR SEQ ID NO:1776:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...150

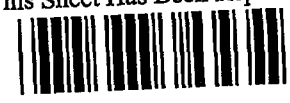
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1776

```
Arg Ile Ile Lys Met Lys Lys Thr Phe Leu Ile Ala Leu Ala Leu Thr
1               5                  10                  15
Ala Ser Leu Ile Gly Ala Glu Asn Thr Lys Trp Asp Tyr Lys Asn Lys
            20                  25                  30
Glu Asn Gly Pro His Arg Trp Asp Lys Leu His Lys Asp Phe Glu Val
        35                  40                  45
Cys Lys Ser Gly Lys Ser Gln Ser Pro Ile Asn Ile Glu His Tyr Tyr
    50                  55                  60
His Thr Gln Asp Lys Ala Asp Leu Gln Phe Lys Tyr Ala Ala Ser Lys
65                  70                  75                  80
Pro Lys Ala Val Phe Phe Thr His His Thr Leu Lys Ala Ser Phe Glu
                85                  90                  95
Pro Thr Asn His Ile Asn Tyr Arg Gly His Asp Tyr Val Leu Asp Asn
```

```
            100                 105                 110
Val His Phe His Ala Pro Met Glu Phe Leu Ile Asn Asn Lys Thr Arg
        115                 120                 125
Pro Leu Ser Ala His Phe Val His Lys Asp Ala Lys Gly Arg Leu Leu
    130                 135                 140
Val Leu Ala Ile Gly Phe
145                 150
```

(2) INFORMATION FOR SEQ ID NO:1777:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 383 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1777

```
Met Pro Val Ile Arg Val Leu Val Met Leu Ala Thr Met Met Met Lys
1               5                  10                  15
Leu Val Lys Thr Ala Lys Glu Lys Lys Val Phe Lys Asn Val Gly Ile
            20                  25                  30
Ser Ile Met Gly Ile Ala Phe Trp Glu Ala Ile Lys Asp Ser Ile Lys
        35                  40                  45
Lys Gln Ile Lys Lys Ser Asp Trp Ile Cys Gly Asn Val Lys Thr Ala
    50                  55                  60
Asp Asp Tyr Leu Lys Thr His Pro Asn Ser Trp Phe Asn Ser Ala Ile
65                  70                  75                  80
Gly Val Thr Ala Ile Thr Ala Met Leu Met Asn Val Cys Phe Ala Asp
                85                  90                  95
Asp Gln Ser Lys Lys Glu Val Ala Gln Ala Gln Lys Glu Ala Glu Asn
            100                 105                 110
Ala Arg Asp Arg Ala Asn Lys Ser Gly Ile Glu Leu Glu Gln Glu Glu
        115                 120                 125
Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Glu Gln Glu Lys Gln Lys
    130                 135                 140
Thr Glu Gln Glu Lys Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Glu
145                 150                 155                 160
Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln Ile Lys
                165                 170                 175
Val Glu Gln Glu Gln Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Asn
            180                 185                 190
Asn Thr Gln Lys Asp Leu Val Asn Lys Ala Glu Gln Asn Cys Gln Glu
        195                 200                 205
Asn His Asn Gln Phe Phe Ile Lys Lys Leu Gly Ile Lys Ala Gly Ile
    210                 215                 220
Ala Ile Glu Ile Glu Ala Glu Cys Lys Thr Pro Lys Pro Thr Lys Thr
225                 230                 235                 240
Asn Gln Thr Pro Ile Gln Pro Lys His Leu Pro Asn Ser Lys Gln Pro
                245                 250                 255
His Ser Gln Arg Gly Ser Lys Ala Gln Glu Leu Ile Ala Tyr Leu Gln
            260                 265                 270
Lys Glu Leu Glu Ser Leu Pro Tyr Ser Gln Lys Ala Ile Ala Lys Gln
        275                 280                 285
```

```
Val Asp Phe Tyr Arg Pro Ser Ser Ile Ala Tyr Leu Glu Leu Asp Pro
    290                 295                 300
Arg Asp Phe Asn Ala Thr Glu Glu Trp Gln Lys Glu Asn Leu Lys Ile
305                 310                 315                 320
Arg Ser Lys Ala Gln Ala Lys Met Leu Glu Met Arg Ser Leu Lys Pro
                325                 330                 335
Asp Pro Gln Ala His Leu Ser Thr Ser Gln Ser Leu Leu Leu Val Gln
            340                 345                 350
Lys Ile Phe Ala Asp Val Ser Lys Glu Ile Lys Val Val Ala Asn Thr
        355                 360                 365
Glu Lys Lys Val Glu Lys Ala Gly Tyr Gly Tyr Ser Lys Arg Met
    370                 375                 380
```

(2) INFORMATION FOR SEQ ID NO:1778:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 332 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

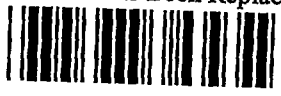
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1778

```
Asn Lys Arg Lys Asn Ile Lys Glu Val Tyr Ala Gly Glu Ile Cys Ala
1               5                  10                  15
Phe Val Gly Leu Lys Asp Thr Leu Thr Gly Asp Thr Leu Cys Asp Glu
            20                  25                  30
Lys Asn Ala Val Val Leu Glu Arg Met Glu Phe Pro Glu Pro Val Ile
        35                  40                  45
His Ile Ala Val Glu Pro Lys Thr Lys Ala Asp Gln Glu Lys Met Gly
    50                  55                  60
Val Ala Leu Gly Lys Leu Ala Glu Glu Asp Pro Ser Phe Arg Val Met
65                  70                  75                  80
Thr Gln Glu Glu Thr Gly Gln Thr Leu Ile Gly Gly Met Gly Glu Leu
                85                  90                  95
His Leu Glu Ile Ile Val Asp Arg Leu Lys Arg Glu Phe Lys Val Glu
            100                 105                 110
Ala Glu Ile Gly Gln Pro Gln Val Ala Phe Arg Glu Thr Ile Arg Ser
        115                 120                 125
Ser Val Ser Lys Glu His Lys Tyr Ala Lys Gln Ser Gly Gly Arg Gly
    130                 135                 140
Gln Tyr Gly His Val Phe Ile Lys Leu Glu Pro Lys Glu Pro Gly Ser
145                 150                 155                 160
Gly Tyr Glu Phe Val Asn Glu Ile Ser Gly Gly Val Ile Pro Lys Glu
                165                 170                 175
Tyr Ile Pro Ala Val Asp Lys Gly Ile Gln Glu Ala Met Gln Asn Gly
            180                 185                 190
Val Leu Ala Gly Tyr Pro Val Val Asp Phe Lys Val Thr Leu Tyr Asp
        195                 200                 205
Gly Ser Tyr His Asp Val Asp Ser Ser Glu Met Ala Phe Lys Ile Ala
    210                 215                 220
Gly Ser Met Ala Phe Lys Glu Ala Ser Arg Ala Ala Asn Pro Val Leu
225                 230                 235                 240
Leu Glu Pro Met Met Lys Val Glu Val Glu Val Pro Glu Glu Tyr Met
```

This Sheet Has Been Replaced



```
                245                 250                 255
Gly Asp Val Ile Gly Asp Leu Asn Arg Arg Arg Gly Gln Ile Asn Ser
            260                 265                 270
Met Asp Asp Arg Leu Gly Leu Lys Ile Val Asn Ala Phe Val Pro Leu
        275                 280                 285
Val Glu Met Phe Gly Tyr Ser Thr Asp Leu Arg Ser Ala Thr Gln Gly
    290                 295                 300
Arg Gly Thr Tyr Ser Met Glu Phe Asp His Tyr Gly Glu Val Pro Ser
305                 310                 315                 320
Asn Ile Ala Lys Glu Ile Val Glu Lys Arg Lys Gly
                325                 330
```

(2) INFORMATION FOR SEQ ID NO:1779:

This Sheet Has Been Replaced



(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:1779

```
Ser Lys Arg Ala Phe Ala Ser Ser Leu Val Ser Ser Lys Leu Phe Leu
1               5                  10                  15
Arg Asp Lys Glu Thr Arg Lys Arg Gly Leu Glu Thr Val Gly Gly Arg
            20                  25                  30
Ile Ala Pro Thr Lys Asn Pro Phe Ser Phe Lys Lys Tyr Trp Ala Phe
        35                  40                  45
Lys Arg Ala Gly Leu Phe Ser Asn Ser Arg Val Lys Asn Pro Val Gly
    50                  55                  60
Val Leu Thr Pro Lys Val Ser Lys Ile Ile Cys Trp Cys Leu Leu Ser
65                  70                  75                  80
Ser Phe Phe Asn Ser Cys Phe Cys Ala Ile Lys Tyr Ser Lys Trp Ala
                85                  90                  95
Lys Val Lys Ala Val Ser Asn Arg Leu Lys Ala Val Val
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:1780:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 438 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature

(B) LOCATION 1..:438

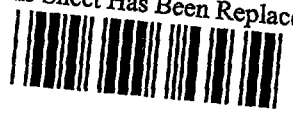
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1780

```
Ile Arg Asn Ala Thr Met Phe Gly Asn Lys Gln Leu Gln Leu Gln Ile
1               5                  10                  15
Ser Gln Lys Asp Ser Glu Ile Ala Glu Leu Lys Lys Glu Val Asn Leu
            20                  25                  30
Tyr Gln Ser Leu Leu Asn Leu Cys Leu His Glu Gly Phe Val Gly Ile
        35                  40                  45
Lys Asn Asn Lys Val Val Phe Lys Ser Gly Asn Leu Ala Ser Leu Asn
    50                  55                  60
Asn Leu Glu Glu Gln Ser Val His Phe Lys Glu Asn Ala Glu Ser Val
65                  70                  75                  80
Asn Leu Gln Gly Val Ser Tyr Ser Leu Lys Ser Gln Asn Ile Asp Gly
                85                  90                  95
Val Gln Tyr Phe Ser Leu Ala Lys Lys Thr Gly Gly Val Gly Glu Tyr
            100                 105                 110
His Lys Asn Asp Leu Phe Lys Thr Phe Cys Thr Ser Leu Lys Glu Gly
        115                 120                 125
Leu Glu Asn Ala Gln Glu Ser Met Gln Tyr Phe His Gln Glu Thr Gly
    130                 135                 140
Leu Leu Leu Asn Ala Ala Lys Asn Gly Glu Glu His Ser Asn Glu Gly
145                 150                 155                 160
Leu Ile Thr Val Asn Lys Thr Gly Gln Asp Ile Glu Ser Leu Tyr Glu
                165                 170                 175
Lys Met Gln Asn Ala Thr Ser Leu Ala Asp Ser Leu Asn Gln Arg Ser
            180                 185                 190
Asn Glu Ile Thr Gln Val Ile Ser Leu Ile Asp Asp Ile Ala Glu Gln
        195                 200                 205
Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile Glu Ala Ala Arg Ala Gly
    210                 215                 220
Glu His Gly Arg Gly Phe Ala Val Val Ala Asp Glu Val Arg Lys Leu
225                 230                 235                 240
Ala Glu Lys Thr Gln Lys Ala Thr Lys Glu Ile Ala Val Val Val Lys
                245                 250                 255
Ser Met Gln Gln Glu Ala Asn Asp Ile Gln Thr Asn Thr His Asp Ile
            260                 265                 270
Asn Ser Ile Val Gly Ser Ile Lys Gly Asp Val Glu Glu Leu Lys Ser
        275                 280                 285
Thr Val Lys Asn Asn Met Ile Val Ala Gln Ala Ala Lys Tyr Thr Ile
    290                 295                 300
Tyr Asn Ile Asn Asn Arg Val Phe Cys Gly Leu Ala Lys Leu Asp His
305                 310                 315                 320
Val Val Phe Lys Asn Asn Leu Tyr Gly Met Val Phe Gly Leu Asn Ser
                325                 330                 335
Phe Asp Ile Thr Ser His Lys Ser Cys Arg Leu Gly Lys Trp Tyr Tyr
            340                 345                 350
Glu Gly Ala Gly Lys Glu Asn Phe Ala Asn Thr Ser Gly Tyr Arg Ala
        355                 360                 365
Leu Glu Ser His His Ala Ser Val His Ala Glu Ala Asn Asp Leu Val
    370                 375                 380
Lys Ala Val Gln Glu Asp His Val Thr Asp Ser Lys Tyr Leu Glu His
385                 390                 395                 400
Lys Val His Leu Met Glu Asp Ser Ala Lys His Val Lys Glu Asn Ile
                405                 410                 415
Asp Lys Met Phe Tyr Glu Lys Gln Asp Glu Leu Asn Lys Ile Ile Glu
            420                 425                 430
Lys Ile Gln Lys Gly Glu
        435
```

(2) INFORMATION FOR SEQ ID NO:1781:

(i) SEQUENCE CHARACTERISTICS:

This Sheet Has Been Replaced



(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:1781

```
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 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:1782:

This Sheet Has Been Replaced



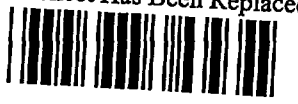
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 593 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



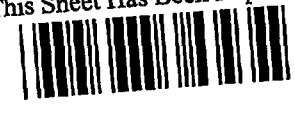
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1782

```
Ile Arg Thr Pro Met Asp Thr Ile Lys Ser Ile Pro Ile Arg Thr Phe
1               5                  10                  15
Ile Leu Leu Tyr Lys Ser Ser Pro Lys Cys Val Val Leu Ala Ser Ile
            20                  25                  30
Thr Val Leu Phe Val Gly Ile Leu Pro Ser Leu Asn Ile Leu Val Met
        35                  40                  45
Ile Lys Leu Ile Asp Ile Val Val Asn Leu Leu Gln Lys His Thr His
    50                  55                  60
Phe Glu Tyr Ser Leu Leu Leu Pro Thr Leu Leu Leu Trp Gly Ala Leu
65                  70                  75                  80
Leu Phe Leu Thr His Val Phe Ser Gly Ile Leu Ser Ser Leu Gln Thr
                85                  90                  95
Ile Ile Ala Glu Gln Phe Ser Ile Asn Ile Ile Thr Gln Leu Ala Asn
            100                 105                 110
Lys Leu Thr Gln Val Lys Asn Leu Asn Phe Phe Glu Asn Lys Asp His
        115                 120                 125
Thr Ile Lys Leu Asn Thr Ile His Asn Gly Leu His Ile Arg Pro Leu
    130                 135                 140
Asn Tyr Val Ser Asn Leu Phe Phe Asn Leu Gln Arg Ile Ile Gly Leu
145                 150                 155                 160
Ile Ser Leu Phe Gly Ile Leu Phe Ser Ile Ser Ile Tyr Leu Pro Phe
                165                 170                 175
Ile Met Ile Phe Ala Thr Val Pro Cys Ile Leu Ile Ser Asn His Ile
            180                 185                 190
Ala Lys Lys His Ser Ala Ser Ile Asp Lys Leu Gln Asp Gln Lys Glu
        195                 200                 205
Ser Met Gln Asn Tyr Leu Tyr Ser Gly Leu Asp Asn Gln Lys Asn Lys
    210                 215                 220
Asp Asn Leu Leu Phe Asn Phe Met Leu Asn Phe His His Lys Phe Ile
225                 230                 235                 240
Glu Thr Lys Glu Leu Tyr Leu Asn Asn Phe Val Lys Val Ala Gln Lys
                245                 250                 255
Asn Leu Ile Phe Thr Ile Tyr Ala Asp Val Leu Ile Thr Thr Leu Ser
            260                 265                 270
Ile Ala Leu Phe Phe Leu Met Val Phe Ile Ile Leu Ser Lys Leu Ile
        275                 280                 285
Gly Val Gly Ala Ile Ala Gly Tyr Ile Gln Ala Phe Ser Ser Thr Gln
    290                 295                 300
Gln Gln Leu Gln Asp Leu Ser Phe Tyr Gly Lys Trp Phe Phe Ala Ile
305                 310                 315                 320
Asn Lys Tyr Phe Glu Asn Tyr Phe Cys Ile Leu Asp Tyr Lys Ile Pro
                325                 330                 335
Lys Pro Glu Thr Gln Ile Lys Leu Glu Glu Lys Ile His Ser Ile Thr
            340                 345                 350
Phe Glu Asn Ile Ser Phe Ser Tyr Pro Asn Ser Lys Leu Ile Phe Glu
        355                 360                 365
Asn Phe Asn Leu Ser Leu His Ser Asn Lys Ile Tyr Ala Leu Val Gly
```

```
    370                 375                 380
Lys Asn Ala Ser Gly Lys Ser Thr Leu Ile Asn Leu Leu Leu Gly Phe
385                 390                 395                 400
Tyr Thr Pro Asn Ser Gly Gln Ile Ile Ile Asn Asn Lys Tyr Pro Leu
                405                 410                 415
Gln Asp Leu Glu Leu Asn Ser Tyr His Gln Gln Met Ser Ala Ile Phe
            420                 425                 430
Gln Asp Phe Ser Leu Tyr Ala Gly Tyr Ser Ile Asp Asp Asn Leu Phe
        435                 440                 445
Met Gln Asn Asn Ile Thr Lys Glu Gln Leu Lys Gln Lys Arg Glu Ile
    450                 455                 460
Leu Lys Ser Phe Asp Glu Asn Phe Gln Asn Cys Leu Asn Asp Cys Asn
465                 470                 475                 480
Asn Thr Leu Phe Gly Ala Gln Tyr Asn Gly Val Asp Phe Ser Leu Gly
                485                 490                 495
Gln Lys Gln Arg Ile Ala Thr Met Arg Ala Phe Leu Lys Pro Ser Asn
            500                 505                 510
Cys Ile Val Leu Asp Glu Pro Ser Ser Ala Ile Asp Pro Ile Met Glu
        515                 520                 525
Lys Glu Phe Leu Asp Phe Ile Phe Lys Lys Ser Gln Ser Lys Met Ala
    530                 535                 540
Leu Ile Ile Thr His Arg Met Asn Ser Val Lys Gln Ala Asn Glu Ile
545                 550                 555                 560
Ile Val Leu Asp Gln Gly Lys Leu Ile Glu Gln Gly Asn Phe Glu Thr
                565                 570                 575
Leu Met Lys Lys Gln Gly Leu Phe Cys Glu Leu Phe Leu Lys Gln Gln
            580                 585                 590
Tyr
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1783:

(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:1783

```
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:1784:

(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:1784

```
Gln Gly Val Thr Thr Met Ala Phe Gln Val Asn Thr Asn Ile Asn Ala
1               5                  10                  15
Met Asn Ala His Val Gln Ser Ala Leu Thr Gln Asn Ala Leu Lys Thr
            20                  25                  30
Ser Leu Glu Arg Leu Ser Ser Gly Leu Arg Ile Asn Lys Ala Ala Asp
        35                  40                  45
Asp Ala Ser Gly Met Thr Val Ala Asp Ser Leu Arg Ser Gln Ala Ser
    50                  55                  60
Ser Leu Gly Gln Ala Ile Pro Asn Thr Asn Asp Gly Met Gly Ile Ile
65                  70                  75                  80
Gln Val Ala Asp Lys Ala Met Asp Glu Gln Leu Lys Ile Leu Asp Thr
                85                  90                  95
Val Lys Val Lys Ala Thr Gln Ala Ala Gln Asp Gly Gln Thr Thr Glu
            100                 105                 110
Ser Arg Lys Ala Ile Gln Ser Asp Ile Val Arg Leu Ile Gln Gly Leu
        115                 120                 125
Asp Asn Ile Gly Asn Thr Thr Thr Tyr Asn Gly Pro Ser Val Ile Val
    130                 135                 140
Trp Ser Ile His
145
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1785:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...248

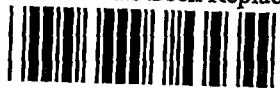
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1785

SUBSTITUTE SHEET (RULE 26)

```
Phe Lys Val Trp Ile Ile Ser Val Thr Gln Arg Leu Ile Thr Gly Gln
1               5                  10                  15
Ala Leu Leu Ser Gly Gln Phe Thr Asn Lys Glu Phe Gln Val Gly Ala
            20                  25                  30
Tyr Ser Asn Gln Ser Ile Lys Ala Ser Ile Gly Ser Thr Thr Ser Asp
        35                  40                  45
Lys Ile Gly Gln Val Arg Ile Ala Thr Gly Ala Leu Ile Thr Ala Ser
    50                  55                  60
Gly Asp Ile Ser Leu Thr Phe Lys Gln Val Asp Gly Val Asn Asp Val
65                  70                  75                  80
Thr Leu Glu Ser Val Lys Val Ser Ser Ser Ala Gly Thr Gly Ile Gly
                85                  90                  95
Val Leu Ala Glu Val Ile Asn Lys Asn Ser Asn Arg Thr Gly Val Lys
            100                 105                 110
Ala Tyr Ala Ser Val Ile Thr Thr Ser Asp Val Ala Val Gln Ser Gly
        115                 120                 125
Ser Leu Ser Asn Leu Thr Leu Asn Gly Ile His Leu Gly Asn Ile Ala
    130                 135                 140
Asp Ile Lys Lys Asn Asp Ser Asp Gly Arg Leu Val Thr Ala Ile Asn
145                 150                 155                 160
Ala Val Thr Ser Glu Thr Gly Val Glu Ala Tyr Thr Asp Gln Lys Gly
                165                 170                 175
Arg Leu Asn Leu Arg Ser Ile Asp Gly Arg Gly Ile Glu Ile Lys Ile
            180                 185                 190
Asp Ser Val Ser Asn Gly Pro Ser Ala Leu Thr Lys Arg Trp Ser Lys
        195                 200                 205
Ser Gly Gln Asp Glu Thr Lys Gly Ser Thr Asn Tyr Gly Arg Tyr Ser
    210                 215                 220
Arg Thr Arg Leu Asp Val Arg Ala Ser Met Ser Ile Arg Tyr Leu Asn
225                 230                 235                 240
His Ala Cys Leu Leu Gln Ser Tyr
                245
```

(2) INFORMATION FOR SEQ ID NO:1786:

This Sheet Has Been Replaced



(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:1786

```
Ser Pro Leu Trp Leu Lys Thr Arg Phe Pro Asn Ile Trp Leu Ala Lys
1               5                  10                  15
Ile Leu Tyr Met Ala Ile Leu Leu Cys Ala Ile Ala His Ser Val Gly
            20                  25                  30
Leu Ile Leu Arg Trp Tyr Val Ser Gly His Ser Pro Trp Ser Asn Ala
        35                  40                  45
Tyr Glu Ser Met Leu Tyr Ile Ala Trp Ala Ser Val Ile Ala Gly Phe
    50                  55                  60
Val Leu Arg Ser Lys Leu Ala Leu Ser Ala Ser Ser Phe Leu Ala Gly
65                  70                  75                  80
```

```
Ile Ala Leu Phe Val Ala His Leu Gly Phe Met Asp Pro Gln Ile Gly
                85                  90                  95
Pro Leu Val Pro Val Leu Lys Ser Tyr Trp Leu Asn Ile His Val Ser
            100                 105                 110
Val Ile Thr Ala Ser Tyr Gly Phe Leu Gly Leu Cys Phe Val Leu Gly
        115                 120                 125
Ile Leu
    130
```

(2) INFORMATION FOR SEQ ID NO:1787:

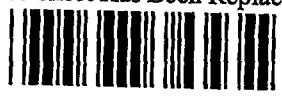
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



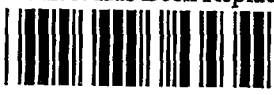
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1787

```
Lys Arg Leu Glu Met Gly Leu Ser Val Gly Ile Val Gly Leu Pro Asn
1               5                  10                  15
Val Gly Lys Ser Ser Thr Phe Asn Ala Leu Thr Lys Thr Gln Asn Ala
            20                  25                  30
Gln Ser Ala Asn Tyr Pro Phe Cys Thr Ile Glu Pro Asn Lys Ala Ile
        35                  40                  45
Val Asn Val Pro Asp Arg Arg Leu Asp Ala Leu Ala Gln Ile Val Lys
    50                  55                  60
Pro Glu Arg Ile Leu His Ser Val Val Glu Phe Val Asp Ile Ala Gly
65                  70                  75                  80
Leu Ile Lys Gly Ala Ser Lys Gly Glu Gly Leu Gly Asn Gln Phe Leu
                85                  90                  95
Ala Asn Ile Lys Glu Cys Glu Val Ile Leu Gln Val Val Arg Cys Phe
            100                 105                 110
Glu Asp Asp Asn Ile Thr His Val Asn Asp Lys Ile Asp Pro Leu Asn
        115                 120                 125
Asp Ile Glu Thr Ile Glu Leu Glu Leu Ile Leu Ala Asp Ile Ala Thr
    130                 135                 140
Leu Asp Lys Arg Ile Asp Arg Leu Gln Lys Ala Leu Lys Ser Ser Lys
145                 150                 155                 160
Asp Ala Lys Asn Leu Leu Glu Cys Ala Leu Ser Leu Lys Thr His Leu
                165                 170                 175
Glu Glu Leu Lys Pro Ala Lys Thr Phe Pro Leu Asn Thr Ser Glu Ala
            180                 185                 190
Phe Leu Glu Leu Asp Lys Glu Leu Arg Phe Leu Ser His Lys Lys Met
        195                 200                 205
Ile Tyr Val Ala Asn Val Gly Glu Glu Asp Leu Asn Ile Leu Asn Glu
    210                 215                 220
His Ala Lys Lys Val Glu Asn His Ala Lys Val Gln Asn Ser Glu Phe
225                 230                 235                 240
Val Ala Leu Cys Ala Lys Leu Glu Glu Glu Met Val Ser Met Ser Gly
                245                 250                 255
Asp Glu Val Lys Glu Phe Leu Gln Ser Leu Gly Val Glu Glu Ser Gly
            260                 265                 270
Leu Glu Lys Thr Ile Arg Leu Ser Phe Lys Glu Leu Gly Leu Ile Asn
```

```
        275                 280                 285
Tyr Phe Thr Ala Gly Val Lys Glu Val Arg Ser Trp Thr Ile Lys Lys
    290                 295                 300
Gly Ser Ser Ala Pro Val Ala Ala Gly Val Ile His Lys Asp Phe Glu
305                 310                 315                 320
Lys Gly Phe Ile Arg Ala Glu Thr Ile Ser Tyr Asp Asp Phe Ile Ala
                325                 330                 335
Tyr Lys Gly Glu Ala Gly Ala Lys Glu Lys Gly Ala Leu Arg Ile Glu
            340                 345                 350
Gly Lys Asp Tyr Ile Val Gln Asp Gly Asp Val Leu His Phe Arg Phe
        355                 360                 365
Asn Val
    370
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1788:

(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:1788

```
Arg Asn Lys Thr Met Gln Ala Leu Lys Ser Leu Leu Glu Val Ile Thr
1               5                  10                  15
Lys Leu Gln Asn Leu Gly Gly Tyr Leu Met His Ile Ala Ile Phe Ile
            20                  25                  30
Ile Phe Ile Trp Ile Gly Gly Leu Lys Phe Val Pro Tyr Glu Ala Glu
        35                  40                  45
Gly Ile Ala Pro Phe Val Ala Asn Ser Pro Phe Phe Ser Phe Met Tyr
    50                  55                  60
Lys Phe Glu Lys Pro Ala Tyr Lys Gln His Lys Met Ser Glu Ser Gln
65                  70                  75                  80
Ser Met Gln Glu Glu Met Gln Asp Asn Pro Lys Ile Val Glu Asn Lys
                85                  90                  95
Glu Trp His Lys Glu Asn Arg Thr Tyr Leu Val Ala Glu Gly Leu Gly
            100                 105                 110
Ile Thr Ile Met Ile Leu Gly Ile Leu Val Leu Leu Gly Leu Trp Met
        115                 120                 125
Pro Leu Met Gly Val Val Gly Gly Phe Leu Ser Leu Glu
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:1789:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...77

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1789

```
Arg Ser Pro Pro Tyr Ser Phe Leu Phe Thr Thr Pro Glu Val Phe Val
1               5                  10                  15
Asn Gln His Phe Pro Trp Leu Ser Gly Ala Gly Arg Leu Val Val Lys
            20                  25                  30
Asp Leu Ala Leu Phe Ala Gly Gly Leu Phe Val Ala Gly Phe Asp Ala
        35                  40                  45
Lys Arg Tyr Leu Glu Gly Lys Gly Phe Cys Leu Met Asp Arg Ser Ser
    50                  55                  60
Val Gly Ile Lys Thr Lys Cys Ser Ser Gly Cys Cys Ser
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:1790:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1790

```
Trp Cys Phe Thr Asn Ile Gln Glu Ile Gly Asn Asp Phe Leu Ile Pro
1               5                  10                  15
Gln Ser Phe Lys Lys Lys Asp Phe Ser Asn Leu Ala Gln Gln Val Cys
            20                  25                  30
His Arg His Glu Gly Phe Gly Ala Asp Gly Leu Val Val Val Leu Pro
        35                  40                  45
Ser Lys Asp Tyr Asp Tyr Glu Trp Asp Phe Tyr Asn Ser Asp Gly Ser
    50                  55                  60
Lys Ala Gly Met Cys Gly Asn Ala Ser Arg Cys Val Gly Leu Phe Ala
65                  70                  75                  80
Tyr Gln His Ala Ile Ala Pro Lys Glu His Val Phe Leu Ala Gly Lys
                85                  90                  95
Arg Glu Ile Ser Ile Arg Ile Glu Glu Pro Asn Ile Val Glu Ser Asn
            100                 105                 110
Leu Gly Asn Tyr Gln Ile Leu Asp Thr Ile Pro Asn Leu Arg Cys Lys
        115                 120                 125
Lys Phe Phe Thr Asn Asn Ser Val Leu Glu Asn Ile Pro Met Phe Tyr
    130                 135                 140
Leu Ile Asn Thr Gly Val Pro His Leu Val Gly Phe Val Lys Asn Lys
145                 150                 155                 160
Gly Leu Leu Asn Ser Leu Asn Thr Leu Glu Leu Arg Ala Leu Arg His
                165                 170                 175
Glu Phe Asn Ala Asn Ile Asn Ile Ala Phe Ile Glu Asn Lys Glu Thr
```

```
            180                 185                 190
Ile Phe Leu Gln Thr Tyr Glu Arg Gly Val Glu Asp Phe Thr Leu Ala
        195                 200                 205
Cys Gly Thr Gly Met Ala Ala Val Phe Ile Ala Ala Arg Leu Phe His
    210                 215                 220
Asn Thr Pro Lys Lys Ala Thr Leu Ile Pro Lys Ser Asn Glu Phe Leu
225                 230                 235                 240
Glu Leu Ser Leu Lys Asn Asp Gly Ile Phe Tyr Lys Gly Val Ala Arg
                245                 250                 255
Tyr Ile Gly Met Ser Val Leu Gly Met Gly Val Phe Lys Asn Gly Cys
            260                 265                 270
Phe
```

(2) INFORMATION FOR SEQ ID NO:1791:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1791

```
Phe Leu Val Gln Phe Asn Gly Asp Asn Cys Met Lys Ala Gln Tyr Phe
1               5                  10                  15
Phe Trp Ile Leu Phe Leu Ile Gly Phe Tyr Trp Met Leu Tyr Leu Tyr
            20                  25                  30
Gln Asp Phe Leu Met Asp Ala Leu Ile Ala Gly Leu Leu Cys Val Gly
        35                  40                  45
Leu Phe Gln Val Lys Val Phe Leu Asn Lys Arg Phe Ser Asn Val Ile
    50                  55                  60
Ser Ser Phe Leu Cys Val Leu Val Leu Ala Ser Val Val Ile Val Pro
65                  70                  75                  80
Leu Tyr Phe Ile Val Tyr Lys Gly Ser Asn Val Ile Phe Glu Ile Asn
                85                  90                  95
Phe Glu Lys Leu Ser Ala Leu Ile Lys Trp Leu Lys Gly Thr Ile Thr
            100                 105                 110
Glu Asn Leu Ser His Phe Pro Ala Ile His Asp Gly Val Ser Lys Phe
        115                 120                 125
Leu Glu Asn Phe Ser Ala Ala Ser Ile Thr Gly Tyr Leu Leu Lys Val
    130                 135                 140
Ser Ser Tyr Ile Gly Lys Tyr Ser Leu Lys Leu Val Thr Asp Ala Leu
145                 150                 155                 160
Phe Ile Leu Gly Leu Leu Phe Phe Phe Phe Tyr Tyr Gly Glu Lys Phe
                165                 170                 175
Tyr Arg Tyr Phe Leu Gly Val Leu Pro Leu Glu Met Asn Gln Ser Lys
            180                 185                 190
Lys Ile Phe Glu Glu Val Ala Gly Ile Leu Arg Ile Val Leu Leu Thr
        195                 200                 205
Ser Leu Ile Thr Val Ile Leu Glu Gly Val Ala Phe Gly Thr Met Ile
    210                 215                 220
Ile Trp Phe Gly His Asp Gly Trp Ser Leu Gly Ile Leu Tyr Gly Leu
225                 230                 235                 240
```

```
Ala Ser Leu Val Pro Ala Val Gly Gly Ala Leu Ile Trp Ile Pro Ile
                245                 250                 255
Ala Ile Tyr Glu Leu Tyr His Gly His Val Asn Glu Ala Ile Phe Ile
            260                 265                 270
Val Leu Tyr Ser Ile Leu Leu Ile Gly Val Leu Ile Asp Ser Val Ile
        275                 280                 285
Lys Pro Ile Leu Ile Val Phe Ile Lys Lys Arg Ile Phe Lys Thr Thr
    290                 295                 300
Leu Lys Ile Asn Glu Ile Leu Ile Phe Phe Ser Met Ile Ala Gly Ile
305                 310                 315                 320
Ser Gln Phe Gly Phe Trp Gly Ile Ile Val Gly Pro Thr Ile Thr Ala
                325                 330                 335
Phe Phe Ile Ala Leu Leu Arg Leu Tyr Glu Asn Tyr Phe Ile Gln Lys
            340                 345                 350
Glu Gln Lys Thr Cys Glu Cys
        355
```

(2) INFORMATION FOR SEQ ID NO:1792:

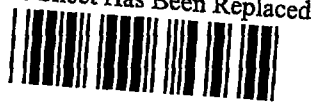
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 215 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1792

```
Arg Leu Asn Met Asn Tyr Lys Val Ala Ser Ala Arg Asn Ile Ala Thr
1               5                  10                  15
Leu Leu Phe Leu Phe Phe Ser Gln Ser Glu Ala Phe Asp Leu Gly Lys
            20                  25                  30
Ile Ala Lys Ile Lys Ala Gly Ala Glu Ser Phe Ser Lys Val Gly Phe
        35                  40                  45
Asn Asn Lys Pro Ile Asn Thr Asn Lys Gly Ile Tyr Pro Thr Glu Thr
    50                  55                  60
Phe Met Thr Ile Met Ala Tyr Met Gln Val Asp Phe Thr Glu Leu Leu
65                  70                  75                  80
Pro Lys Ser Ala Thr Ala Asn Gly His His Leu Asp Gly Ser Leu Gly
                85                  90                  95
Gly Trp Gly Gly Ala Val Ile Tyr Asp Ser Thr Lys Asp Phe Ile Asn
            100                 105                 110
Glu Val Thr Gly Lys Pro Tyr Gly Ala Met Thr Trp Asn Tyr Val Gly
        115                 120                 125
Tyr Trp Gly Gly Leu Val Gly Gln Lys Pro Trp Ala Ser Cys Gly Leu
    130                 135                 140
Ala Thr Gly Asn Leu Thr Gln Gly Gln Tyr Asp Lys Met Thr Gln Ala
145                 150                 155                 160
Glu Met Thr Gln Leu Ser Asn Gln Glu Ala Leu Ala Ala Ser Thr Cys
                165                 170                 175
Ala Lys Thr Tyr Ala Asp His Thr Arg Asn Tyr Val Ile Tyr Asn Ala
            180                 185                 190
Tyr Leu Arg Tyr Asn Tyr Lys Asp Ile Phe Glu Ile Arg Gly Gly Arg
        195                 200                 205
Tyr Glu Ser Gln Arg Ile Ile
```

210 215

(2) INFORMATION FOR SEQ ID NO:1793:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1793

```
Ile Phe Tyr Pro Asn Gly Tyr Asn Asn Arg Met Gly Phe Leu Lys Val
1               5                  10                  15
Leu Lys His Asp Ala Leu Gly Gln Val Gly Asn Ile Val Ile Gly Asn
            20                  25                  30
Phe Leu Ile Thr Leu Thr Val Leu Ala Val Cys Phe Ser Ser Gln Ser
        35                  40                  45
Ala Glu Glu Thr Thr Met Leu Thr Leu Ser Tyr Thr Leu Phe Phe Ile
    50                  55                  60
Leu Gly Ala Phe Leu Leu Val Ala Ile Ser Val Gly Ala Ile Lys Asn
65                  70                  75                  80
Leu Asn Ala Leu Phe Ser Lys Arg Gly Val Leu Ser Phe Ser Leu Pro
                85                  90                  95
Ile Ser Leu Glu Ser Leu Leu Leu Pro Lys Ile Leu Leu Pro Met Val
            100                 105                 110
Phe Phe Ile Phe Ser Leu Phe Trp Phe Val Ala Ser Val Arg Leu Gly
        115                 120                 125
Tyr Tyr Leu Phe Asn Ala Gln Ser Ser Val Leu Phe Ile Leu His Thr
    130                 135                 140
Ala Leu Lys Thr Phe Ala Leu Lys Pro Thr Lys Thr Ile Gly Val Ala
145                 150                 155                 160
Leu Phe Leu Gly Leu Val Leu Met Lys Phe Leu Phe Val Leu Ser Val
                165                 170                 175
Leu Asn Ala Thr Arg Ile Lys Lys Ala Arg Phe Leu Leu Gly Gly Leu
            180                 185                 190
Leu Phe Ile Leu Val Gly Val Val Leu Glu Leu Ala Phe Asn Ser Leu
        195                 200                 205
Leu Pro Leu Met Ser Ser Ser Leu Ser Ile Asn Glu Gly Phe Tyr Tyr
    210                 215                 220
Phe Leu Gln Gln Gln Glu Leu Gln Glu Asn Lys Tyr Tyr Leu Leu Trp
225                 230                 235                 240
Gly Val Asp Phe Leu Lys Ile Leu Leu Leu Tyr Gly Val Ile Arg Tyr
                245                 250                 255
Leu Leu Thr His Lys Leu Glu Leu Asp
            260                 265
```

(2) INFORMATION FOR SEQ ID NO:1794:

(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:1794

```
His Met Lys Gly Leu Trp Leu Val Ile Ser Leu Val Phe Val Gly Phe
1               5                  10                  15
Leu Trp Ala Asn Glu Ser Tyr Val Phe Asn Asn Ser Lys Gly Arg Leu
            20                  25                  30
Thr Glu Lys Ser Val Ala Phe Ile Glu Gly Val Ser Lys Glu Leu Tyr
        35                  40                  45
Leu Lys Thr Gly Val Arg Phe Ala Ile Asp Met Thr Asp Phe Glu Lys
    50                  55                  60
Asn Pro Ile Ala Leu Ala Asn Lys Lys Glu Arg Gln Ser Tyr Gln Glu
65                  70                  75                  80
Gly Phe Leu Lys Gln Leu Lys Pro Pro Phe Val Val Phe Phe Phe Tyr
                85                  90                  95
His Asp Ala Gln Lys Ile Glu Leu Val Ala Asn Pro Lys Asp Leu Leu
            100                 105                 110
Asp Thr Asp Lys Ile Phe Phe Glu Lys Ile Ala Pro Leu Leu Pro Thr
        115                 120                 125
Asn Ala Lys Glu Tyr Thr Pro Gln Arg Ile Ser Ala Met Leu Ile Asn
    130                 135                 140
Gly Tyr Ser Val Ala Val Asp Ala Leu Ala Glu Lys Tyr His Val Asn
145                 150                 155                 160
Ile Thr Gln Asn Phe Ser Ala Pro Lys Gly Val Thr Phe Val Lys Val
                165                 170                 175
Val Ile Tyr Ile Leu Leu Leu Thr Leu Leu Gly Ala Phe Leu Gly Leu
            180                 185                 190
Tyr Phe Phe Lys Lys Ser
        195
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1795:

(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:1795

```
Glu Gly Lys Ser Met Lys Glu Lys Asn Phe Trp Pro Leu Gly Ile Met
1               5                  10                  15
Ser Val Leu Ile Phe Gly Leu Gly Ile Val Val Phe Leu Val Val Phe
```

```
            20                  25                  30
Ala Leu Lys Asn Ser Pro Lys Asn Asp Leu Val Tyr Phe Lys Gly His
        35                  40                  45
Asn Glu Val Asp Leu Asn Phe Asn Ala Met Leu Lys Thr Tyr Glu Asn
    50                  55                  60
Phe Lys Ser Asn Tyr Arg Phe Ser Val Gly Leu Lys Pro Leu Thr Glu
65                  70                  75                  80
Ser Pro Lys Thr Pro Ile Leu Pro Tyr Phe Ser Lys Gly Thr His Gly
                85                  90                  95
Asp Lys Lys Ile Gln Glu Asn Leu Leu Asn Asn Ala Leu Ile Leu Glu
            100                 105                 110
Lys Ser Asn Thr Leu Tyr Ala Gln Leu Gln Pro Leu Lys Pro Ala Leu
        115                 120                 125
Asp Ser Pro Asn Ile Gln Val Tyr Leu Ala Phe Tyr Pro Ser Gln Ser
    130                 135                 140
Gln Pro Arg Leu Leu Gly Thr Leu Asp Cys Lys Asn Ala Cys Glu Pro
145                 150                 155                 160
Leu Lys Phe Asp Leu Leu Glu Gly Asp Lys Val Gly Arg Tyr Lys Ile
                165                 170                 175
Leu Phe Lys Phe Val Phe Lys Asn Lys Glu Glu Leu Ile Leu Glu Gln
            180                 185                 190
Leu Ala Phe Phe Lys
        195
```

(2) INFORMATION FOR SEQ ID NO:1796:

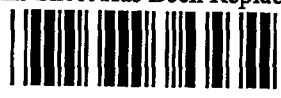
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1796

```
Ala Asn Gln Phe Ala Leu Gln Phe Ser Phe Ser Asn Phe Lys His Gly
1               5                   10                  15
Asp Phe Thr Thr Arg Asp Phe Met Leu Tyr Ser Leu Leu Tyr Gly Tyr
            20                  25                  30
Phe Asn Ile Asn Leu Phe Gln Tyr Leu Thr Phe Arg Ala Gly Leu Gly
        35                  40                  45
Phe Phe Ile Ala Phe Phe Leu Thr Leu Phe Leu Met Pro Lys Phe Ile
    50                  55                  60
Leu Trp Ala Lys Ala Lys Lys Ala Asn Gln Pro Ile Ser Ser Phe Val
65                  70                  75                  80
Pro Ser His Gln Asn Lys Lys Asp Thr Pro Thr Met Gly Gly Ile Val
                85                  90                  95
Phe Val Phe Ala Thr Ile Val Ala Ser Val Leu Cys Ala Ser Leu Ser
            100                 105                 110
Asn Leu Tyr Val Leu Leu Gly Ile Ile Val Leu Val Gly Phe Ser Phe
        115                 120                 125
Val Gly Phe Arg Asp Asp Tyr Thr Lys Ile Asn Gln Gln Asn Asn Ala
    130                 135                 140
Gly Met Ser Ala Lys Met Lys Phe Gly Met Leu Phe Ile Leu Ser Leu
145                 150                 155                 160
```

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

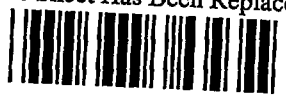
(2) INFORMATION FOR SEQ ID NO:1797:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1797

```
Ala Arg Phe Ile Lys Ile Phe Gly Met Gly Lys Phe Ser Lys Leu Gly
1               5                  10                  15
Phe Ile Leu Ala Thr Leu Gly Ser Ser Ile Gly Leu Gly His Ile Trp
            20                  25                  30
Arg Phe Pro Tyr Met Val Gly His Asn Gly Gly Ser Ala Phe Val Leu
        35                  40                  45
Leu Tyr Leu Ala Leu Thr Leu Ser Leu Gly Ile Ala Met Leu Leu Val
    50                  55                  60
Glu Met Leu Ile Gly Asn Leu Gly Lys Lys Asp Val Val Ser Asn Tyr
65                  70                  75                  80
Gln Ile Leu Asp Pro Lys Arg Lys Lys Tyr Tyr Pro Phe Thr Ser Phe
                85                  90                  95
Phe Ile Leu Gly Gly Pro Leu Ile Leu Ser Phe Tyr Ala Val Val Leu
            100                 105                 110
Gly Trp Val Leu Tyr Tyr Leu Phe Val Val Thr Phe Asp Leu Pro Lys
```

```
        115                 120                 125
Asp Leu Glu Gln Ala Lys Met Gln Phe Ser Met Leu Gln Asn Gly Ser
    130                 135                 140
Leu Ile Trp Pro Val Ile Gly Phe Ser Ala Cys Leu Leu Pro Thr Ile
145                 150                 155                 160
Trp Phe Val Ser Arg Gly Ile Glu Glu Gly Ile Glu Lys Leu Asn Val
                165                 170                 175
Val Leu Met Pro Leu Leu Phe Val Ile Phe Ile Gly Leu Leu Ile Tyr
            180                 185                 190
Ala Met Thr Leu Glu Ser Met Pro Lys Ala Leu Arg Phe Leu Phe Asn
        195                 200                 205
Phe Glu Ile Gln Lys Ile Asp Phe Lys Val Val Met Asp Ala Leu Gly
    210                 215                 220
Gln Met Phe Phe Ser Leu Ser Leu Gly Val Gly Thr Ile Ile Thr Tyr
225                 230                 235                 240
Ser Ala Phe Thr Pro Lys Lys Glu Asn Leu Leu Lys Ser Ser Leu Phe
                245                 250                 255
Ile Val Leu Pro Gly Ile Leu Ile Ser Leu Ile Ala Gly Val Met Ile
            260                 265                 270
Phe Thr Phe Val Phe Glu Tyr His Ala Asp Val Ser Gln Gly Pro Gly
        275                 280                 285
Leu Val Phe Ile Ser Leu Pro Leu Thr Phe Ala Lys Met Gly Ser
    290                 295                 300
```

(2) INFORMATION FOR SEQ ID NO:1798:

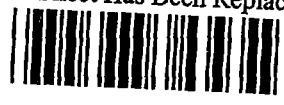
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1798

```
Arg Cys Val Lys Met Lys Ile Ser Leu Leu Gly His Gly Lys Thr Thr
1               5                  10                  15
Leu Ala Leu Gly Arg Phe Phe Lys Lys Asn His Asn Glu Val Lys Phe
            20                  25                  30
Phe Asp Asp Lys Phe Pro Ala Phe Phe Lys Asp Ser Glu Gly Phe Leu
        35                  40                  45
Cys Tyr Pro Ser Lys Asp Phe Asn Pro Asn Asp Ser Gln Leu Glu Ile
    50                  55                  60
Val Ser Pro Gly Ile Ser Phe Thr His Pro Leu Val Met Lys Ala Lys
65                  70                  75                  80
His Leu Met Ser Glu Tyr Asp Tyr Ile Asp Ser Leu Phe Asp His Ser
                85                  90                  95
Phe Thr Pro Thr Met Ile Ser Ile Ser Gly Thr Asn Gly Lys Thr Thr
            100                 105                 110
Thr Thr Glu Met Leu Thr Thr Leu Leu Glu Asp Phe Lys Ala Val Ser
        115                 120                 125
Gly Gly Asn Ile Gly Thr Pro Leu Ile Glu Leu Phe Glu Lys Arg Ser
    130                 135                 140
Pro Leu Trp Val Leu Glu Thr Ser Ser Phe Ser Leu His Tyr Thr Asn
145                 150                 155                 160
```

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

(2) INFORMATION FOR SEQ ID NO:1799:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1799

```
Asp Met Gly Asn His Phe Ser Lys Leu Gly Phe Val Leu Ala Ala Leu
1               5                   10                  15
Gly Ser Ala Ile Gly Leu Gly His Ile Trp Arg Phe Pro Tyr Met Thr
            20                  25                  30
Gly Val Ser Gly Gly Gly Ala Phe Val Leu Leu Phe Leu Phe Leu Ser
        35                  40                  45
Leu Ser Val Gly Ala Ala Met Phe Ile Ala Glu Met Leu Leu Gly Gln
    50                  55                  60
Ser Thr Gln Lys Asn Val Thr Glu Ala Phe Lys Glu Leu Asp Ile Asn
```

```
65                  70                  75                  80
Pro Lys Lys Arg Trp Lys Tyr Ala Gly Ile Met Leu Ile Ser Gly Pro
                85                  90                  95
Leu Ile Leu Thr Phe Tyr Gly Thr Ile Leu Gly Trp Val Leu Tyr Tyr
            100                 105                 110
Leu Val Ser Ile Ser Phe Asn Leu Pro Ser Ser Ile Gln Glu Ser Glu
        115                 120                 125
Gln Ile Phe Thr Gln Thr Leu Gln Ser Ile Gly Leu Gln Ser Ile Gly
    130                 135                 140
Leu Phe Ser Val Leu Phe Ile Thr Gly Trp Ile Val Ser Arg Gly Ile
145                 150                 155                 160
Lys Glu Gly Ile Glu Lys Leu Asn Leu Val Leu Met Pro Leu Leu Phe
                165                 170                 175
Ala Thr Phe Phe Gly Leu Leu Phe Tyr Ala Met Ser Met Asp Ser Phe
            180                 185                 190
Ser Lys Ala Phe His Phe Met Phe Asp Phe Lys Pro Lys Asp Leu Thr
        195                 200                 205
Ser Gln Val Phe Thr Tyr Ser Leu Gly Gln Val Phe Phe Ser Leu Ser
    210                 215                 220
Ile Gly Leu Gly Ile Asn Ile Thr Tyr Ala Ala Val Thr Asp Lys Thr
225                 230                 235                 240
Gln Asn Leu Leu Lys Ser Thr Ile Trp Val Val Leu Ser Gly Ile Leu
                245                 250                 255
Ile Ser Leu Val Gly Arg Ala Tyr Asp Phe His Phe Cys Val
            260                 265                 270
```

(2) INFORMATION FOR SEQ ID NO:1800:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1800

```
Cys Leu Thr Arg His Arg Val Asn Leu His Phe Phe Thr Gly Gly Phe
1               5                   10                  15
Trp Pro Asn Gly Ser Asp Arg Arg Ser Cys Phe Asn Ser Phe Leu Ala
            20                  25                  30
Arg Ala Arg Phe Cys Trp His His Phe Tyr Gly Gly Phe Ile Arg Ala
        35                  40                  45
Lys Arg Asp Val Ser Tyr Arg Lys Val Ser Ile Leu Ser Phe
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:1801:

(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

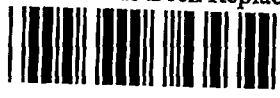
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1801

```
Phe Leu Leu Trp Ala Gly Leu Met Ile Phe Thr Phe Val Phe Glu Tyr
1               5                  10                  15
Gly Ala Asn Val Ser Gln Gly Thr Gly Leu Ile Phe Thr Ser Leu Pro
            20                  25                  30
Val Val Phe Gly Gln Met Gly Ala Ile Gly Val Leu Val Ser Ile Leu
        35                  40                  45
Phe Leu Leu Ala Leu Ala Phe Ala Gly Ile Thr Ser Thr Val Ala Leu
    50                  55                  60
Leu Glu Pro Ser Val Met Tyr Leu Thr Glu Lys Tyr Gln Tyr Ser Arg
65                  70                  75                  80
Phe Lys Val Thr Trp Gly Leu Val Ala Leu Ile Phe Val Val Gly Val
                85                  90                  95
Val Leu Ile Phe Ser Leu His Lys Asp Tyr Lys Asp Tyr Leu Thr Phe
            100                 105                 110
Phe Glu Lys Ser Leu Phe Asp Trp Leu Asp Phe Ala Ser Ser Thr Ile
        115                 120                 125
Ile Met Pro Leu Gly Gly Met Ala Thr Phe Ile Phe Met Gly Trp Val
    130                 135                 140
Leu Lys Lys Glu Lys Leu Arg Leu Leu Ser Ala His Phe Leu Gly Pro
145                 150                 155                 160
Lys Leu Phe Ala Thr Trp Tyr Phe Leu Leu Lys Tyr Ile Thr Pro Leu
                165                 170                 175
Ile Val Phe Ser Ile Trp Leu Ser Lys Ile Tyr
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:1802:

This Sheet Has Been Replaced



(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

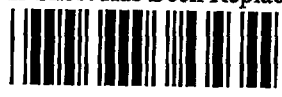
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1802

```
Glu Ser Phe Met Gly Cys Ser Phe Ile Phe Lys Lys Val Arg Val Tyr
1               5                  10                  15
Ser Lys Met Leu Val Ala Leu Gly Leu Ser Ser Val Leu Ile Gly Cys
            20                  25                  30
Ala Met Asn Pro Ser Ala Glu Thr Lys Lys Pro Asn Asp Ala Lys Asn
        35                  40                  45
Gln Gln Pro Val Gln Thr His Glu Arg Met Thr Thr Ser Ser Glu His
```

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

(2) INFORMATION FOR SEQ ID NO:1803:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...351

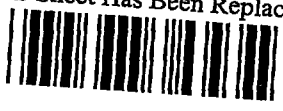
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1803

```
Glu Leu Val Leu Phe Glu Lys Leu Lys Phe Phe Lys Ile Lys Lys Asp
1               5                  10                  15
Asp Glu Asn Gln Pro Glu Val Asn Leu Asn Ser Glu Ile Tyr Glu Gln
            20                  25                  30
Phe Lys Val Phe Arg Leu Pro Leu Ile Leu Ile Gln Leu Leu Val Leu
        35                  40                  45
Leu Gly Thr Leu Gly Tyr Phe Ala Leu Glu Asn Tyr Ser Leu Met Gln
    50                  55                  60
Ala Phe Phe Gln Thr Thr Tyr Thr Met Thr Ala Thr Gly Phe Gly Ala
65                  70                  75                  80
Leu Asn Glu Ser Gln Phe Gly Pro Ile Ser Ile Phe Leu Thr Ser Ile
                85                  90                  95
Leu Met Phe Cys Gly Thr Gly Ile Ile Ala Phe Ser Val Ala Ile Leu
            100                 105                 110
```

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

(2) INFORMATION FOR SEQ ID NO:1804:

This Sheet Has Been Replaced



(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:1804

```
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:1805:

(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:1805

```
Ile Met Ala Cys Lys Phe Cys Pro Lys Ile Arg Lys Thr Asp Trp Ile
1               5                  10                  15
Phe Ile Leu Ile Ala Ala Leu Gly Phe Tyr Ser Val Asn Lys Leu Gly
            20                  25                  30
Tyr Ala Pro Lys Phe Asn Thr Pro Thr Pro Lys Ser Ser Arg Pro Leu
        35                  40                  45
Ser Arg Pro Ile Glu Lys Pro Asn Asn Met Thr Glu Glu Glu Arg Lys
    50                  55                  60
Lys Arg Phe Ile Glu Leu Gln Lys Ala Cys Leu Leu His Lys Asp Lys
65                  70                  75                  80
Lys Ala Cys Glu Glu Val Phe
                85
```

This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:1806:

(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:1806

```
Arg Ala Ile Thr Thr Asn Gln Phe Val Gly Thr Asn Met Phe Phe Lys
1               5                  10                  15
Thr Tyr Gln Lys Leu Leu Gly Ala Ser Cys Leu Ala Leu Tyr Leu Val
            20                  25                  30
Gly Cys Gly Asn Gly Gly Gly Gly Glu Ser Pro Val Glu Met Ile Ala
        35                  40                  45
Asn Ser Glu Gly Thr Phe Gln Ile Asp Ser Lys Ala Asp Ser Ile Thr
    50                  55                  60
```

```
Ile Gln Gly Val Lys Leu Asn Arg Gly Asn Cys Ala Val Asn Phe Val
65                  70                  75                  80
Pro Val Ser Glu Thr Phe Gln Met Gly Val Leu Ser Gln Val Thr Pro
                85                  90                  95
Ile Ser Ile Gln Asp Phe Lys Asp Met Ala Ser Thr Tyr Lys Ile Phe
            100                 105                 110
Asp Gln Lys Lys Gly Leu Ala Asn Ile Ala Asn Lys Ile Ser Gln Leu
        115                 120                 125
Glu Gln Lys Gly Val Met Met Glu Pro Gln Thr Leu Asn Phe Gly Glu
    130                 135                 140
Ser Leu Lys Gly Ile Ser Gln Gly Cys Asn Ile Ile Glu Ala Glu Ile
145                 150                 155                 160
Gln Thr Asp Lys Gly Ala Trp Thr Phe Asn Phe Asp Lys
                165                 170
```

(2) INFORMATION FOR SEQ ID NO:1807:

(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:1807

```
Ile Ser Asn Met Glu Asn Thr Pro Lys Asp Arg Ala Arg Ile Leu Ile
1               5                  10                  15
Glu Glu Leu Lys Ile Leu Gln Gly Val Ile Asn Arg Met Ala Gln Asn
            20                  25                  30
Ser Leu Glu Cys Lys Lys Trp Thr Leu Ala Leu Ala Val Gly Val Leu
        35                  40                  45
Ser Leu Lys Ile Glu Ala Ile Ser Asn Phe Tyr Gly Leu Cys Val Leu
    50                  55                  60
Gly Val Leu Leu Ala Cys Phe Tyr Leu Leu Asp Ala Tyr Tyr Leu Met
65                  70                  75                  80
Gln Glu Arg Leu Phe Arg Glu Gln Tyr Gln Trp Leu Ile Lys Asn Arg
                85                  90                  95
Leu Lys Thr Asp Glu Arg Leu Phe Glu Val Phe Pro Ile His Gln Thr
            100                 105                 110
Cys Gln Ser Thr Gln Phe Leu Ser Ala Met Arg Ser Phe Ser Leu Phe
        115                 120                 125
Pro Tyr Trp Ala Leu Gly Leu Cys Leu Val Gly Tyr Gly Phe Cys Cys
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:1808:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1808

```
Pro Leu Lys Ser Lys Ala Ser Lys Leu Leu Gly Ala Asn Ile Val Tyr
1               5                  10                  15
Lys Ile His Cys Leu Val Lys Gly Val Thr Leu Glu Gln Gln Asn Lys
            20                  25                  30
Leu Leu Lys Thr Ile Glu Pro Phe Lys Lys Phe Ala Ser Leu Glu Phe
        35                  40                  45
Ile Asp Ile Asn Ser Leu Asp Tyr Ser Ile Glu Ser Tyr Leu Asn Glu
    50                  55                  60
Ser Cys Ser Lys Arg Tyr Gly Gly Leu Leu Val Leu Cys Arg Leu Leu
65                  70                  75                  80
Leu Ala Ser Leu Phe Pro Asn Tyr Ser Lys Ile Ile Ser Ile Asp Val
                85                  90                  95
Asp Thr Val Phe Leu Gly Asp Val Ala Ser Ala Tyr Phe Ala Leu Asp
            100                 105                 110
Asn Glu Pro Thr Lys Leu Leu Gly Met Val Arg Asp Thr Phe Ser His
        115                 120                 125
Leu Pro Phe Glu Ala Phe Cys Asp Phe Cys Glu Arg Thr Cys Lys Asn
    130                 135                 140
Phe Lys Ile Asp Leu Leu Arg Phe Ser Gln Asn Glu Leu Lys Arg Ile
145                 150                 155                 160
His Gln Gly Phe Asn Met Gly Phe Leu Val Ala Asn Leu Asp Leu Trp
                165                 170                 175
Arg Glu Asn Gly Phe Glu Lys Ile Ala Leu Glu Phe Leu Lys Thr Arg
            180                 185                 190
Gly Lys Asp Leu Phe Tyr Pro Glu Gln Cys Leu Ile Asn Met Val Phe
        195                 200                 205
Leu Glu Arg Ile Leu Glu Leu Pro Ile His Tyr Asn Cys Tyr Ser Asp
    210                 215                 220
Phe Phe Lys Glu His Tyr Pro Lys Ser Ile Ile Met Leu His Phe Ile
225                 230                 235                 240
Lys Tyr Lys Pro Trp Arg Ser Val Ser Ser Leu Asn Gly Arg Leu Ile
                245                 250                 255
Cys Tyr Glu Ala Glu Ala Ser Phe Trp Leu Ala Asn Leu Phe Cys Thr
            260                 265                 270
Pro Phe Lys Asn Asp Phe Phe Lys Glu Arg Leu Glu Met Ala Lys Asp
        275                 280                 285
Gln Gln Met Gln Ser Phe Lys Thr His Ile Arg Ser Lys Thr Ile Arg
    290                 295                 300
Asp Tyr Phe Tyr Phe Arg Ile Lys Asn Ile Leu Lys Lys Val Phe Glu
305                 310                 315                 320
Leu Ser
```

(2) INFORMATION FOR SEQ ID NO:1809:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 566 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1809

```
Lys Lys Phe Ser Asn Ser Leu Lys Gly Gln Lys Lys Thr Met Lys Phe
1               5                  10                  15
Leu Lys Phe Phe Ala Ser Ser Val Thr Leu Asp Glu Lys Phe Leu Met
            20                  25                  30
Phe Leu Leu Cys Asn Ala Leu Ser Asn Ala Tyr Lys Asn Ser Asp Leu
        35                  40                  45
Phe Ser Phe Ser Lys Gly Phe Leu Gly Ala Phe Leu Ile Gly Phe Val
    50                  55                  60
Val Tyr Tyr Gly Cys Ala Leu Ile Pro Lys Lys Arg Leu Lys Tyr Ser
65                  70                  75                  80
Leu Glu Trp Leu Phe Ile Gly Ser Gly Ile Ile Phe Ser Val Ala Glu
                85                  90                  95
Ile Phe Thr Leu Phe Met Phe Lys Met Pro Phe Ser Lys Gly Leu Ile
            100                 105                 110
Asp Thr Leu Leu Ala Thr Asn Ser Ser Glu Thr Met Ala Phe Ile Lys
        115                 120                 125
Ser Tyr Lys Asn Tyr Leu Leu Tyr Tyr Ala Leu Ile Leu Ile Ala Leu
    130                 135                 140
Leu Ile Ala Ile Lys Ile Ile Arg Phe Arg Ala Leu Val Pro Gly Val
145                 150                 155                 160
Ile Ala Ser Val Leu Gly Leu Ser Ile Leu Thr Ile Gly Ser Val Arg
                165                 170                 175
Asn Ile Lys His Leu Thr Lys Asn Asp Ala Ile Leu Lys Arg Ser Leu
            180                 185                 190
Phe Ser Leu Ser Leu Ala Arg Gly Phe Tyr Ser Ala Tyr Leu Ser Leu
        195                 200                 205
Phe Asp Arg Gln Gln Ala Ile Lys Phe Tyr Ser Phe Leu Asn Asn Leu
    210                 215                 220
Tyr Leu Pro Ser Asp Tyr Leu Ser Ser Thr Gly Asp Ile Ser Asn Val
225                 230                 235                 240
Val Leu Val Ile Gly Glu Ser Ala Ser Arg Asn Phe Met Gln Leu Tyr
                245                 250                 255
Gly Tyr Ser Val Pro Asn Asn Pro Leu Cys Glu Arg Thr Arg Gln Ala
            260                 265                 270
Arg Glu Arg Glu Arg Glu Ser Asn Asn Leu Phe Val Phe Ser Asp Thr
        275                 280                 285
Ile Ser Lys Glu Ala His Thr Ser Asp Val Phe Glu Ser Leu Leu Asn
    290                 295                 300
Tyr Ser Asp Ala Glu Thr Thr Lys Pro Trp Tyr His Tyr His Asn Met
305                 310                 315                 320
Ile Asp Ile Phe Lys Arg Ser His Tyr Glu Thr Phe Trp Leu Glu Lys
                325                 330                 335
Gln Ile Val Asp Glu Trp Gly Ile Thr Gln Asn Leu Val Ser Asn Arg
            340                 345                 350
Ser Lys Asn Arg Tyr Tyr Ile Leu Gly Asn Tyr Gly Ala Tyr Asp Glu
        355                 360                 365
Glu Leu Val Lys Phe Tyr Ser Lys Asn Val Gln Pro Gln Leu Lys Ser
    370                 375                 380
Lys Asn Phe Ile Val Phe His Leu Leu Gly Ser His Ser Trp Tyr Ala
385                 390                 395                 400
Asp Arg Phe Pro Lys Ser Phe Ala Lys Phe Lys Pro Ser Asp Leu Ser
                405                 410                 415
Phe Ser Asn Leu His Ala Ser Ser Asp Arg Asp Lys Gln Ile Val Ala
            420                 425                 430
Asp Tyr Val Asn Ser Leu Tyr Tyr Asn Asp Phe Val Leu Asn Gly Ile
```

```
        435                 440                 445
Phe Asn Leu Phe Lys Asp Lys Asp Ala Ile Val Phe Tyr Leu Ser Asp
    450                 455                 460
His Ala Gln Asp Ile Phe Glu Ser Gly Pro Thr Tyr Gly His Ser Cys
465                 470                 475                 480
Ser Lys Ala Gly Leu Glu Ile Pro Phe Met Ile Tyr Val Ser Asp Ile
                485                 490                 495
Phe Lys Glu Lys His Pro Glu Lys Val Lys Leu Ile Lys Asn Ala Leu
            500                 505                 510
Asn Lys Pro Phe Met Ser Asp Asp Leu Ile His Ser Leu Leu Pro Leu
        515                 520                 525
Val Gly Ile His Thr Lys Asp Glu Ile Glu Ser Lys Asn Leu Phe Ser
    530                 535                 540
Pro Gln Phe Asp Ala Gln Arg Lys Arg Ala Val Cys Tyr Gly Ser Met
545                 550                 555                 560
Asn Tyr Asp Arg Thr Lys
                565
```

(2) INFORMATION FOR SEQ ID NO:1810:

(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:1810

```
Lys Ser Phe Met Pro Pro Thr Arg Pro Gln Ala Ser Ile Leu Arg Leu
1               5                  10                  15
Thr Leu Lys Asn Pro Leu Ser Met Leu Ser Arg Tyr Ser Leu Cys Leu
            20                  25                  30
Leu Lys Lys Thr Arg Leu Gln Thr Thr Ser Asn Ser Ala Pro Lys Ala
        35                  40                  45
Cys Leu Ile Ala Gly Leu Leu Lys Lys Ser Lys Pro Phe Ile Leu Asn
    50                  55                  60
Thr Leu Lys Ile Arg Ser Leu Leu Lys Pro
65                  70
```

(2) INFORMATION FOR SEQ ID NO:1811:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1811

```
Thr Ser Ala Ser Arg Val Ala Lys Asp Ile Ile Ser Glu Ser Gln Asn
1               5                  10                  15
Leu Cys Ala Arg Lys Phe Arg Arg Leu Tyr Ala Leu Leu Lys Glu Asn
            20                  25                  30
Glu Met Leu Ile Arg Ile Gly Ser Tyr Gln Met Gly Asn Asp Lys Glu
        35                  40                  45
Leu Asp Glu Ala Ile Lys Lys Lys Ala Leu Met Glu Gln Phe Leu Val
    50                  55                  60
Gln Asp Glu Asn Ala Leu Gln Pro Phe Glu Gln Ser Phe Gln Gln Leu
65                  70                  75                  80
Glu Glu Ile Leu Arg
                85
```

(2) INFORMATION FOR SEQ ID NO:1812:

(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:1812

```
Asp Lys Arg Asn Ile Met Glu Ser Gln Leu Met Lys Leu Ala Ile Glu
1               5                  10                  15
Thr Tyr Lys Ile Thr Leu Met Ile Ser Leu Pro Val Leu Leu Ala Gly
            20                  25                  30
Leu Val Val Gly Leu Leu Val Ser Ile Phe Gln Ala Thr Thr Gln Ile
        35                  40                  45
Asn Glu Met Thr Leu Ser Phe Val Pro Lys Ile Leu Ala Val Ile Gly
    50                  55                  60
Val Leu Ile Leu Thr Met Pro Trp Met Thr Asn Met Leu Leu Asp Tyr
65                  70                  75                  80
Thr Lys Thr Leu Ile Lys Leu Ile Pro Lys Ile Ile Gly
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:1813:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1813

```
Lys Met Leu Glu Thr Thr Ile Asp Phe Ser Arg Tyr Ser Ser Val Lys
1               5                  10                  15
Ile Gly Ala Pro Leu Lys Val Ser Val Leu Glu Asn Asp Asn Glu Ile
            20                  25                  30
Ser Gln Glu His Gln Ile Ile Gly Leu Ala Asn Asn Leu Leu Ile Ala
        35                  40                  45
Pro Asp Val Lys Asn Leu Ala Leu Leu Gly Lys Asn Tyr Asp Tyr Ile
    50                  55                  60
Cys Asp Lys Gly Glu Trp Val Glu Val Gly Gly Ala Ala Asn Ala Ser
65                  70                  75                  80
Lys Ile Phe Asn Tyr Phe Arg Ala Asn Asp Leu Glu Gly Leu Glu Phe
                85                  90                  95
Leu Gly Gln Leu Pro Gly Thr Leu Gly Ala Leu Val Lys Met Asn Ala
            100                 105                 110
Gly Met Lys Glu Phe Glu Ile Lys Asn Val Leu Glu Ser Ala Cys Val
        115                 120                 125
Asn Gly Glu Trp Leu Glu Lys Glu Ala Leu Gly Leu Asp Tyr Arg Ser
    130                 135                 140
Ser Gly Phe Asn Gly Val Val Leu Arg Ala Arg Phe Lys Lys Thr His
145                 150                 155                 160
Gly Phe Arg Glu Gly Val Leu Lys Ala Cys Lys Ser Met Arg Lys Ser
                165                 170                 175
His Pro Lys Leu Pro Asn Phe Gly Ser Cys Phe Lys Asn Pro Pro Asn
            180                 185                 190
Asp Tyr Ala Gly Gln Ala Phe Arg Gly Arg Gly Leu Lys Gly Leu Leu
        195                 200                 205
Ser Lys Lys Ser Gly Ala Leu Pro Lys Gln His Ala Asn Phe Leu Val
    210                 215                 220
Asn Leu Gly Gly Ala Glu Phe Glu Glu Ala Leu Asp Leu Ile Glu Leu
225                 230                 235                 240
Ala Lys Thr Arg Val Leu Gln Glu Tyr Gly Ile His Leu Glu Glu Glu
                245                 250                 255
Val Lys Ile Leu Arg
            260
```

(2) INFORMATION FOR SEQ ID NO:1814:

(i) SEQUENCE CHARACTERISTICS:
(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:1814

This Sheet Has Been Replaced



```
Leu Asn Ser Glu His Pro Leu Phe Asp Trp Ala Ser Lys Gln Thr Tyr
1               5                  10                  15
Ile Gln Met Ala Asn Met Met Met Ala Ala Ala Met Leu Gly Ile Asp
            20                  25                  30
Ser Cys Pro Ile Glu Gly Tyr Asp Gln Glu Lys Val Ala Ala Tyr Leu
        35                  40                  45
Glu Glu Lys Gly Tyr Leu Asn Thr Ala Glu Phe Gly Val Ser Val Met
    50                  55                  60
Ala Ser Phe Gly Tyr Arg Asn Gln Glu Ile Thr Pro Lys Thr Arg Trp
65                  70                  75                  80
Lys Thr Glu Val Ile Tyr Glu Val Ile Glu
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:1815:

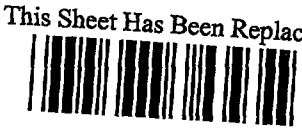
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1815

```
Lys Glu Ile Thr Met Arg Lys Leu Phe Ile Pro Leu Leu Leu Phe Ser
1               5                  10                  15
Ala Leu Glu Ala Asn Glu Lys Asn Gly Phe Phe Ile Glu Ala Gly Phe
            20                  25                  30
Glu Thr Gly Leu Leu Glu Gly Thr Gln Thr Gln Glu Lys Arg His Thr
        35                  40                  45
Thr Thr Lys Asn Thr Tyr Ala Thr Tyr Asn Tyr Leu Pro Thr Asp Thr
    50                  55                  60
Ile Leu Lys Arg Ala Ala Asn Leu Phe Thr Asn Ala Glu Ala Ile Ser
65                  70                  75                  80
Lys Leu Lys Phe Ser Ser Leu Ser Pro Val Arg Val Leu Tyr Met Tyr
                85                  90                  95
Asn Gly Gln Leu Thr Ile Glu Asn Phe Leu Pro Tyr Asn Leu Asn Asn
            100                 105                 110
Val Lys Leu Ser Phe Thr Asp Ala Gln Gly Asn Val Ile Asp Leu Gly
        115                 120                 125
Val Ile Glu Thr Ile Pro Lys His Ser Lys Ile Val Leu Pro Gly Glu
    130                 135                 140
Ala Phe Asp Ser Leu Lys Ile Asp Pro Tyr Thr Leu Phe Leu Pro Lys
145                 150                 155                 160
Ile Glu Ala Thr Ser Thr Ser Ile Ser Asp Ala Asn Thr Gln Arg Val
                165                 170                 175
Phe Glu Thr Leu Asn Lys Ile Lys Thr Asn Leu Val Val Asn Tyr Arg
            180                 185                 190
Asn Glu Asn Lys Phe Lys Asp His Glu Asn His Trp Glu Ala Phe Thr
        195                 200                 205
Pro Gln Thr Ala Glu Glu Phe Thr Asn Leu Met Leu Asn Met Ile Ala
    210                 215                 220
Val Leu Asp Ser Gln Ser Trp Gly Asp Ala Ile Leu Asn Ala Pro Phe
225                 230                 235                 240
Glu Phe Thr Asn Ser Pro Thr Asp Cys Asp Asn Asp Pro Ser Lys Cys
```

```
                245                 250                 255
Val Asn Pro Gly Thr Asn Gly Leu Val Asn Ser Lys Val Asp Gln Lys
            260                 265                 270
Tyr Val Leu Asn Lys Gln Asp Ile Val Asn Lys Phe Lys Asn Lys Ala
        275                 280                 285
Asp Leu Asp Val Ile Val Leu Lys Asp Ser Gly Val Val Gly Leu Gly
    290                 295                 300
Ser Asp Ile Thr Pro Ser Asn Asn Asp Asp Gly Lys His Tyr Gly Gln
305                 310                 315                 320
Leu Gly Val Val Ala Ser Ala Leu Asp Pro Lys Lys Leu Phe Gly Asn
                325                 330                 335
Asp Leu Lys Thr Ile Asn Leu Glu Asp Leu Arg Thr Ile Leu His Glu
            340                 345                 350
Phe Ser His Thr Lys Gly Tyr Gly His Asn Gly Asn Met Thr Tyr Gln
        355                 360                 365
Arg Val Pro Val Thr Lys Asp Val Lys
    370                 375
```

(2) INFORMATION FOR SEQ ID NO:1816:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1816

```
Ile Met Gly Val Gly Glu Lys Glu Glu Lys Lys Glu Ser Gln Lys Val
1               5                   10                  15
Ala Val Ile Thr Gly Ala Ser Ser Gly Ile Gly Leu Glu Cys Val Leu
            20                  25                  30
Met Leu Leu Asn Gln Gly Tyr Lys Val Tyr Ala Leu Ser Arg His Ala
        35                  40                  45
Thr Leu Cys Val Ala Leu Asn His Ala Leu Cys Glu Cys Val Asp Ile
    50                  55                  60
Asp Val Ser Asp Ser Asn Ala Leu Lys Glu Val Phe Leu Asn Ile Ser
65                  70                  75                  80
Ala Lys Glu Asp His Cys Asp Val Leu Ile Asn Ser Ala Gly Tyr Gly
                85                  90                  95
Val Phe Gly Ser Val Glu Asp Thr Pro Ile Glu Glu Val Lys Lys Gln
            100                 105                 110
Phe Ser Val Asn Phe Phe Ala Leu Cys Glu Val Val Gln Leu Cys Leu
        115                 120                 125
Pro Leu Leu Lys Asn Lys Pro Tyr Ser Lys Ile Phe Asn Leu Ser Ser
    130                 135                 140
Ile Ala Gly Arg Val Ser Met Leu Phe Leu Gly His Tyr Ser Ala Ser
145                 150                 155                 160
Lys His Ala Leu Glu Ala Tyr Ser Asp Ala Leu Arg Leu Glu Leu Lys
                165                 170                 175
Pro Phe Asn Val Gln Val Cys Leu Ile Glu Pro Gly Pro Val Lys Ser
            180                 185                 190
Asn Trp Glu Lys Thr Ala Phe Glu Asn Asp Glu Arg Lys Asp Ser Val
        195                 200                 205
```

Tyr Ala Leu Glu Val Asn Ala Ala
210 215

(2) INFORMATION FOR SEQ ID NO:1817:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1817

```
Asp Ser Asn Arg Ser Ala Phe Ile Cys His Asn Leu Ala Met Val Leu
1               5                  10                  15
Met Ile Phe Thr Ser Ile Leu Lys Ile Ala Leu Lys Val Leu Ser Glu
            20                  25                  30
Arg Lys Lys Asn Arg Tyr Gly Phe Pro Arg Ile Phe Asp Val Ala Asp
        35                  40                  45
Ile Glu Gln Glu Glu Arg Glu Val Ile Glu Trp Arg Glu Lys Lys Lys
    50                  55                  60
Ala Ser Lys Gln Ser Tyr Lys Gln Asn Leu Gln Ile Asn Lys Ile Ala
65                  70                  75                  80
Asn Asp Leu Lys Arg Asp Lys Ile Val Asp Lys Arg Thr Ile Leu Ser
                85                  90                  95
Val Ile Asp Ala Asp Ile Glu Arg Gly Phe Ile Pro Pro Lys Asp Leu
            100                 105                 110
Leu Lys Gln Leu Glu Lys Ile Ser Ala Ser Leu Ser Lys Asp Ile Val
        115                 120                 125
Ile Thr Ile Lys Gln Val Glu Lys Leu Glu Leu Asn Tyr Ala Leu Ile
    130                 135                 140
Asp Asn Ile Gln His Asn Thr Leu Asp Asp Thr Leu Asp Phe Thr Phe
145                 150                 155                 160
Ile Val Gly Asp Ser Leu Ser Val Gln Ser Leu Tyr Val Thr Phe Asn
                165                 170                 175
Leu Val Ile Asp Ile Asp Arg Pro Met Ser Glu Gln Phe Leu Asn His
            180                 185                 190
Ile Gly Lys Leu Gly Ser Phe Glu Ser Arg Glu Gln Ala Leu Glu Trp
        195                 200                 205
Val Arg Leu Ser Gln Thr Lys Leu Ile Ile Glu Thr Pro Lys Glu Ala
    210                 215                 220
Leu Lys Asn Ala Glu Leu Ser Gln Ile Glu Glu Ile Leu Thr Gly Cys
225                 230                 235                 240
Ile Phe Asn Gly Ala Tyr Arg Leu Gln Asn Asp Leu Lys Lys Gly Arg
                245                 250                 255
```

(2) INFORMATION FOR SEQ ID NO:1818:

(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:1818

```
Gly Asn Ala Arg Thr Cys Ile Val Ile Cys Trp Asp Cys Leu Asn Gln
1               5                  10                  15
Gln Trp Asp Cys Gly Leu Thr Lys Val Asp Pro Lys Ser Thr Ala Val
            20                  25                  30
Met Asn Phe Phe Val Gly Gly Leu Ser Ile Val Cys Asn Val Val Val
        35                  40                  45
Ile Thr Tyr Ser Ala Leu His Pro Thr Ala Pro Val Glu Gly Ala Glu
    50                  55                  60
Asp Ile Val Gln Val Ser His His Leu Thr Ser Phe Tyr Gly Pro Ala
65                  70                  75                  80
Thr Gly Leu Leu Phe Gly Phe Thr Tyr Leu Tyr Ala Ala Ile Asn His
                85                  90                  95
Thr Phe Gly Leu Asp Trp Arg Pro Tyr Ser Trp Tyr Ser Leu Phe Val
            100                 105                 110
Ala Ile Asn Thr Val Pro Ala Ala Ile Leu Ser His Tyr Ser Asp Met
        115                 120                 125
Leu Asp Asp His Lys Val Leu Gly Ile Thr Glu Gly Asp Trp Trp Ala
    130                 135                 140
Ile Ile Trp Leu Ala Trp Gly Val Leu Trp Leu Thr Ala Phe Ile Glu
145                 150                 155                 160
Asn Ile Leu Lys Ile Pro Leu Gly Lys Phe Thr Pro Trp Leu Ala Ile
                165                 170                 175
Ile Glu Gly Ile Leu Thr Ala Trp Ile Pro Ala Trp Leu Leu Phe Ile
            180                 185                 190
Gln His Trp Val
        195
```

(2) INFORMATION FOR SEQ ID NO:1819:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 640 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...640

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1819

```
Ser Ile Cys His Glu Tyr Leu Lys Val Asn Leu Gln Glu Lys Leu Ala
1               5                  10                  15
Gly Phe Arg Asp Phe Val His Tyr Asn Glu Asn Ala Lys Asp Ser Leu
            20                  25                  30
```

Pro Leu Lys Ala Leu Phe Leu Ser Gly Val Asp Ala Leu Ser Lys Asp
35 40 45
Ala Leu Tyr Tyr Leu Glu Lys Ile Met Arg Phe Gly Ser Lys Asn Gly
50 55 60
Val Leu Ser Phe Val Asn Leu Glu Ser Glu Lys Asn Asn Gln Ser Ala
65 70 75 80
Glu Asp Leu Lys Arg Tyr Ala Glu Phe Phe Lys Asp Arg Thr Ser Phe
85 90 95
Glu Gly Leu Lys Tyr Leu Asn Val Glu Ile Ile Ser Asp Gln Gly Ile
100 105 110
Lys Ser Gln His Met Gln Asp Phe Ala Asp Lys Ile Lys Ala Tyr Tyr
115 120 125
Lys Gln Lys Lys Glu Val Lys Arg Glu Leu Lys Asp Leu Gln Arg Asp
130 135 140
Lys Glu Phe Trp Thr Lys Ser Ser Gln His Glu Val Ser Val Pro Val
145 150 155 160
Gly Trp Asp Ile Asn His Lys Glu Val Cys Phe Lys Ile Gly Asn Glu
165 170 175
Gln Asn His Thr Leu Ile Cys Asp His Ser Gly Ser Gly Lys Ser Asn
180 185 190
Phe Leu His Val Leu Ile Gln Asn Leu Ala Phe Tyr Tyr Asp Pro Asp
195 200 205
Glu Val Gln Leu Phe Leu Leu Asp Tyr Lys Glu Gly Val Glu Phe Asn
210 215 220
Ala Tyr Val Ala Asp Pro Ala Leu Glu His Ala Arg Leu Val Ser Val
225 230 235 240
Ala Ser Ser Ile Ser Tyr Gly Ile Thr Phe Leu Lys Trp Leu Cys Asp
245 250 255
Glu Met Gln Lys Arg Ala Asp Arg Phe Lys Gln Phe Asn Val Lys Asp
260 265 270
Leu Ser Asp Tyr Arg Lys His Glu Lys Met Pro Arg Leu Ile Val Val
275 280 285
Ile Asp Glu Phe Gln Val Leu Phe Ser Asp Asn Lys Ser Thr Lys Ala
290 295 300
Val Glu Gly His Leu Asn Thr Leu Leu Lys Lys Gly Arg Ser Tyr Gly
305 310 315 320
Val His Leu Val Leu Ala Thr Gln Thr Met Arg Gly Thr Asp Ile Asn
325 330 335
Pro Ser Phe Lys Ala Gln Ile Ala Asn Arg Ile Ala Leu Pro Met Asp
340 345 350
Ala Glu Asp Ser Ser Ser Val Leu Gly Asp Asp Ala Ala Cys Glu Ile
355 360 365
Gln Asn Pro Glu Gly Ile Phe Asn Asn Asn Gly Gly Asn Arg Lys Tyr
370 375 380
His Thr Lys Met Ser Val Pro Lys Ala Pro Asp Asp Phe Lys Ser Phe
385 390 395 400
Leu Thr Lys Ile His Ala Glu Phe Asn Gln Arg Asn Leu Ala Pro Ile
405 410 415
Asp Arg Lys Ile Tyr Asn Gly Glu Thr Pro Leu Lys Met Pro Asp Thr
420 425 430
Leu Lys Ala Asn Glu Met Arg Leu His Leu Gly Lys Lys Val Asp Tyr
435 440 445
Glu Gln Lys Asp Leu Ile Val Glu Phe Glu Ser Asn Glu Ser His Leu
450 455 460
Leu Val Val Ile Gln Asp Leu Asn Ala Arg Ile Ala Leu Met Lys Leu
465 470 475 480
Leu Phe Gln Asn Val Lys Ser Ala Asn Lys Glu Leu Val Phe Cys Asn
485 490 495
Lys Glu Lys Arg Leu Ile Arg Ser Phe Asp Ala Gln Lys Glu Tyr Gly
500 505 510
Ile Thr Pro Val Glu Asn Ile Leu Ser Val Leu Asp Thr Ala Met Asn
515 520 525
Pro Asn Ser Ala Leu Val Ile Asp Asn Leu Asn Glu Ala Lys Glu Leu
530 535 540
His Asp Lys Val Gly Ala Glu Lys Leu Lys Ser Phe Leu Glu Lys Ala

```
545                 550                 555                 560
Ile Asp Asn Glu Gln Tyr Cys Val Ile Phe Ala His Asp Phe Arg Gln
                565                 570                 575
Ile Lys Thr Asn Tyr His Phe Asp Lys Leu Lys Glu Leu Leu Asn Asn
            580                 585                 590
His Phe Lys Gln Cys Leu Ala Phe Arg Cys Asn Gly Glu Asn Leu Asn
        595                 600                 605
Ala Ile Lys Ser Asp Leu Pro Pro Pro Ser Lys Leu Asn Val Leu Leu
    610                 615                 620
Ile Glu Leu Ser Lys Asp Ser Val Thr Glu Phe Arg Pro Phe Ser Leu
625                 630                 635                 640
```

(2) INFORMATION FOR SEQ ID NO:1820:

(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:1820

```
Arg Pro Asn Leu Ser Ser Gln Phe Leu Tyr Thr Glu Met Leu Ser Leu
1               5                   10                  15
Lys Leu Thr Tyr Glu Ser Thr Leu Gln Gln Asp Leu Lys Lys Ile Leu
            20                  25                  30
Gly Ile Glu Glu Val Ile Met Leu Ser Thr Ser Pro Met Glu Leu Arg
        35                  40                  45
Leu Ala Asn Gln Lys Leu Gly Asn Arg Phe Ile Lys Thr Leu Gln Ala
    50                  55                  60
Met Asn Glu Leu Asp Met Gly Ala Phe Phe Asn Ala Tyr Ala Gln Thr
65                  70                  75                  80
Thr Gln Arg Ser His Pro Cys His
                85
```

(2) INFORMATION FOR SEQ ID NO:1821:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...223

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1821

```
Glu Lys Ser Thr Ser Asn Leu Lys Lys Pro Ser Val Trp Arg Ser Lys
1               5                  10                  15
Leu Ile Cys Lys Ile Ala Thr His Lys Ala Arg Ser Ile Gly Leu Cys
            20                  25                  30
Val Lys Pro Lys Ser Met Lys Glu Lys Leu Arg Gly Ala Met Val Asn
        35                  40                  45
Ile Leu Arg Ile Lys Met Ile Glu Ile Ser Glu Trp Leu Gln Lys Leu
    50                  55                  60
Asp Asp Ala Leu Asp Lys Val Val Ala Lys Lys Glu Pro Glu Ser Phe
65                  70                  75                  80
Leu Lys Pro Ile Ile Ser Pro Ile Glu Asp Tyr Gln Lys Ser Val Arg
                85                  90                  95
Gln Ile Gln Ala Gln Phe Thr Asp Ala Pro Lys Phe Asn Glu Glu Gly
            100                 105                 110
Ala Tyr Pro Gln Phe Leu Ser Cys Gly Leu Leu Gln Val Arg Gly Lys
        115                 120                 125
Asn Gly Ala Asn Met Glu Phe Leu Leu Pro Lys Val Tyr Pro Phe Pro
    130                 135                 140
Pro Lys Ser Leu Tyr Ile Glu His Glu Lys Asp Gly Gln Phe Leu Arg
145                 150                 155                 160
Glu Met Leu Met Arg Leu Leu Ser Ser Ala Pro Leu Val Gln Leu Glu
                165                 170                 175
Val Ile Leu Ile Asp Ala Leu Ser Leu Gly Gly Ile Phe Asn Leu Ala
            180                 185                 190
Arg Arg Leu Leu Asp Lys Asn Asn Asp Phe Ile Tyr Gln Gln Arg Ile
        195                 200                 205
Leu Thr Glu Ser Lys Glu Ile Glu Glu Ala Leu Lys His Leu Pro
    210                 215                 220
```

(2) INFORMATION FOR SEQ ID NO:1822:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1822

```
Thr Trp Val His Phe Leu Thr Leu Thr Leu Lys Gln Pro Lys Asp Pro
1               5                  10                  15
Thr His Ala Thr Ser Tyr Gly Val Phe Ala Ala Ser Leu Asn Met Glu
            20                  25                  30
Leu Lys Lys Ala Leu Arg His Tyr Leu Tyr Ala Gln Thr Ser Asn Met
        35                  40                  45
Val Ile Asn Cys Val Lys Ser Val Pro Leu Ser Gln Asn Asp Gly Gln
    50                  55                  60
Lys Ile Leu Leu Ser Leu Gln Ser Pro Phe Asn Gln Leu Ile Glu Lys
65                  70                  75                  80
Thr Leu Glu Leu Asp Glu Ser His Leu Cys Ala Ala Ser Val Gln Asn
                85                  90                  95
Asp Ile Lys Ala Met Gln His Glu Ser Leu Tyr Ser Arg Leu Tyr Met
```

100 105 110

Ser

(2) INFORMATION FOR SEQ ID NO:1823:

(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:1823

```
Arg Ala Ser Met Lys Asn Phe Ser Pro Leu Tyr Cys Leu Lys Lys Leu
1               5                  10                  15
Lys Lys Arg His Leu Ile Ala Leu Ser Leu Pro Leu Leu Ser Tyr Ala
            20                  25                  30
Asn Gly Phe Lys Ile Gln Glu Gln Ser Leu Asn Gly Thr Ala Leu Gly
        35                  40                  45
Ser Ala Tyr Val Ala Gly Ala Arg Gly Ala Asp Ala Ser Phe Tyr Asn
    50                  55                  60
Pro Ala Asn Met Gly Phe Thr Asn Asp Trp Gly Glu Asn Arg Ser Glu
65                  70                  75                  80
Phe Glu Met Thr Thr Thr Val Ile Asn Ile Pro Ala Phe Ser Phe Lys
                85                  90                  95
Val Pro Thr Thr Asn Gln Gly Leu Tyr Ser Val Thr Ser Leu Glu Ile
            100                 105                 110
Asp Lys Ser Gln Gln Asn Ile Leu Gly Ile Ile Asn Thr Ile Gly Leu
        115                 120                 125
Gly Asn Ile Leu Lys Ala Leu Gly Asn Thr Ala Ala Thr Asn Gly Leu
    130                 135                 140
Ser Gln Gly Ile Asn Arg Val Gln Gly Val Met Asn
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:1824:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1824

```
Ala Asp Arg Glu Asp Lys Leu Ser His Ser Ile Ile Met Arg Tyr Phe
1               5                  10                  15
Arg Ser Ala Phe Leu Leu Phe Phe Met Thr Leu Phe Phe Val Ser Cys
            20                  25                  30
Ser Lys His Pro Phe Ser Lys Gln Thr Pro Lys Thr Lys Glu Arg Ile
        35                  40                  45
Arg Gln Glu Glu Ala Asn Lys Lys Arg Glu Glu Thr Leu Asn Ala Leu
    50                  55                  60
Arg Gln Phe Arg Leu Ile Tyr Ile Asn Thr Pro Val Phe Arg Phe Tyr
65                  70                  75                  80
Asp Tyr Gly Thr Ile Lys Thr Asp Lys Asp His Asn Thr Glu Val Thr
                85                  90                  95
Leu Tyr Lys Leu Ser Gln Lys Val Gly Asp Ile Tyr Met Thr Lys Arg
            100                 105                 110
Ser Ile Cys Phe Ser Gln Lys Cys Ser Ala Lys Trp Ile Ala Ala Arg
        115                 120                 125
Asp Leu Phe Gly Lys Val Ser Tyr Gly Asp Leu Phe Asp Asp Ile Val
    130                 135                 140
Leu Gly Arg Asp Ile Phe Lys Gly Leu Gly Lys Arg His Leu Thr Pro
145                 150                 155                 160
Glu Tyr Val Ile Gln Arg Phe Gln Lys Ser Gly Glu Ile Ile Leu Tyr
                165                 170                 175
Glu Arg Lys Asn Gly Leu Ile Ser Phe Gln Asn Leu Thr Gln Lys Ile
            180                 185                 190
Ala Ile Arg Ile Glu Pro Tyr Glu Pro Ser Leu Gln Asp Leu Glu Asp
        195                 200                 205
Asn Glu Asn Ala Asp Ser Glu Leu Gln
    210                 215
```

(2) INFORMATION FOR SEQ ID NO:1825:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 236 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

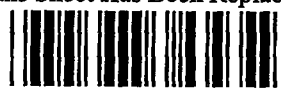
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...236

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1825

```
Glu Ile Ala Glu Ile Val Ser Gln Trp Thr His Ile Pro Phe Gln Lys
1               5                  10                  15
Met Phe Gln Ser Glu Lys Asn Arg Val Leu Asn Ile Glu Ser Glu Leu
            20                  25                  30
Gln Lys Arg Val Val Gly Gln Glu Lys Ala Leu Lys Ala Ile Ala Lys
        35                  40                  45
Ala Ile Lys Arg Asn Lys Ala Gly Leu Ser Asp Ser Asn Lys Pro Ile
    50                  55                  60
Gly Ser Phe Leu Phe Leu Gly Pro Thr Gly Val Gly Lys Thr Glu Ser
65                  70                  75                  80
Ala Lys Ala Leu Ala Gln Phe Leu Phe Asp Ser Asp Lys Asn Leu Ile
                85                  90                  95
Arg Ile Asp Met Ser Glu Tyr Met Glu Lys His Ala Ile Ser Arg Leu
```

```
            100                 105                 110
Ile Gly Ala Ala Pro Gly Tyr Val Gly Tyr Glu Glu Gly Gly Gln Leu
        115                 120                 125
Thr Glu Ala Val Arg Arg Lys Pro Tyr Ser Val Val Leu Leu Asp Glu
    130                 135                 140
Val Glu Lys Ala His Pro Asp Val Phe Asn Phe Leu Leu Gln Val Phe
145                 150                 155                 160
Asp Glu Gly His Leu Thr Asp Ser Lys Gly Val Arg Val Asp Phe Lys
                165                 170                 175
Asn Thr Ile Leu Ile Leu Thr Ser Asn Val Ala Ser Gly Ala Leu Leu
            180                 185                 190
Glu Glu Asp Leu Ser Glu Ala Asp Lys Gln Lys Ala Ile Lys Glu Ser
        195                 200                 205
Leu Arg Gln Phe Phe Lys Pro Glu Phe Leu Asn Arg Leu Asp Glu Ile
    210                 215                 220
Ile Ser Phe Asn Ala Leu Asp Ser His Ala Ile Ile
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:1826:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1826

```
Val Arg Phe Cys Tyr Ser Lys Lys Tyr Lys Lys Thr Ile Ile Leu Lys
1               5                  10                  15
Lys Asp Trp Met Met Phe Asp Asn Thr Leu Ile Asn Leu Phe Glu Thr
            20                  25                  30
Ala Pro Leu Leu Thr Ser Leu Leu Ala Gly Ile Leu Thr Phe Leu Ser
        35                  40                  45
Pro Cys Val Leu Pro Leu Ile Pro Ala Tyr Met Ser Tyr Ile Ser Gln
    50                  55                  60
Ile Ser Leu Glu Asp Ile Lys Asp Gly Lys Ala Lys Arg Val Ser Val
65                  70                  75                  80
Phe Leu Lys Ser Leu Met Phe Val Val Gly Phe Ser Leu Val Phe Leu
                85                  90                  95
Gly Val Gly Met Ser Met Ala Lys Leu Ile His Ser Phe Ser Phe Ser
            100                 105                 110
Trp Val Asn Tyr Ile Ala Gly Gly Ile Val Ile Leu Phe Gly Leu His
        115                 120                 125
Phe Leu Gly Val Phe Arg Phe Ala Leu Leu Tyr Lys Thr Gln Ser Ala
    130                 135                 140
Gly Leu Ala Ser Lys Ser Asn Ser Met Gln Arg Phe Tyr Pro Phe Leu
145                 150                 155                 160
Leu Gly Met Ser Phe Ala Leu Gly Trp Thr Pro Cys Ile Gly Pro Ile
                165                 170                 175
Phe Thr Ser Ile Val Ile Met Ser Ala Ser Lys Asp Ala Tyr Gly Leu
            180                 185                 190
Met Leu Met Val Val Phe Val Met Gly Leu Ala Ile Pro Phe Val Leu
        195                 200                 205
```

```
Val Ala Leu Met Leu Glu Arg Ala Leu Leu Phe Leu Lys Ser Leu Arg
    210                 215                 220
Lys Tyr Asn Arg Ala Ile Glu Ile Val Ser Gly Leu Val Leu Ile Leu
225                 230                 235                 240
Met Gly Ile Leu Ile Met Thr Asn Ser Leu Glu Ser Leu Thr Asn Phe
                245                 250                 255
Leu Gln Asn
```

(2) INFORMATION FOR SEQ ID NO:1827:

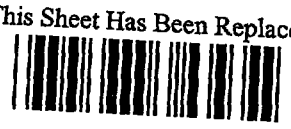
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1827

```
Ile Gly Gly Ala His Ala Phe Leu Tyr Tyr Leu Thr Phe Leu Phe Ile
1               5                  10                  15
Val Gly Phe Gly Val Phe Val Tyr Ser Ile Asp Pro Gln Ala Tyr Ala
            20                  25                  30
Phe Asn Leu Gly Ser Tyr Ser Phe Asn Leu Pro Ile Ala Val Trp Leu
        35                  40                  45
Met Gly Val Leu Gly Met Phe Ala Phe Phe Ser Trp Val Phe Leu Phe
    50                  55                  60
Lys His Asn Leu Ser His Lys Ile Arg Leu Tyr His Glu Lys Lys Asp
65                  70                  75                  80
Phe Asp Lys Leu Leu Lys Gln Ile Leu Ser Gln Asp Thr Gln Lys Thr
                85                  90                  95
Phe Leu Lys Thr Lys Phe Lys Ser Asp Leu Ala Lys Asn Leu Ser Gln
            100                 105                 110
Ile Leu Ala Arg Tyr Asp Leu Lys Ala Asp Leu Asn Thr Pro Asn Ser
        115                 120                 125
Gly Cys Glu Lys Val Asp Asn Leu Phe Lys His Tyr His Asn Ile Glu
    130                 135                 140
Asn Asn Thr Leu Glu Pro Lys Asp His Ala Lys His Ser Leu Ala Tyr
145                 150                 155                 160
Glu His Ala Tyr Phe Ser Lys Arg Leu Lys Ala Phe Ile His Asn Asp
                165                 170                 175
Leu Lys Asn Ala Phe Glu Val Leu Thr Asn Ala Gln Ile Pro Leu Glu
            180                 185                 190
Leu Arg Arg Tyr Ala Leu
        195
```

(2) INFORMATION FOR SEQ ID NO:1828:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1828

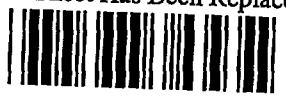
```
Gln Asp Lys Gly Leu Leu Leu Ser Val Ala Leu Pro Asn Ser Asn Asn
1               5                  10                  15
Ala Ser Gln Asn Asn Ile Leu Ser Leu Ser Val Leu His Asn Gln Ile
            20                  25                  30
Lys Met Ser Tyr Gly Asn Lys Val Met Asp Phe Thr Pro Pro 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:1829:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

This Sheet Has Been Replaced



(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:1829

```
Thr Ile Leu Cys Pro Gly Ala Lys Ser Tyr Lys Tyr Trp Glu Gly Met
1               5                  10                  15
Gly Met Ser His Ile Ile Lys Ser Ile Glu Ala Leu Asp Asp Tyr Thr
            20                  25                  30
Ile Arg Phe Thr Leu Asn Gly Pro Glu Ala Pro Phe Leu Ala Asn Leu
        35                  40                  45
Gly Met Asp Phe Leu Ser Ile Leu Ser Lys Asp Tyr Ala Asp Tyr Leu
    50                  55                  60
Ala Gln Asn Asn Lys Lys Asp Glu Leu Ala Lys Lys Pro Val Gly Thr
65                  70                  75                  80
Gly Pro Phe Lys Phe Phe Leu Trp Asn Lys Asp Glu Lys Ile Ile Leu
                85                  90                  95
Val Lys Asn Gln Asp Tyr Trp Gly Leu Lys Ala Tyr Leu Asp Lys Val
            100                 105                 110
Val Val Arg Thr Ile His Asn Phe Ser Thr Arg Ala Leu Ala Leu Arg
        115                 120                 125
Thr Gly Glu Ile Met Leu Met Thr Gly His Asn Leu Asn Glu Val Glu
    130                 135                 140
Gln Leu Glu Lys Leu His Asn Ile Val Val Asp Arg Ser Pro Gly Leu
145                 150                 155                 160
Ile Ala Asn Trp Leu Ser Leu Asn Thr Gln Lys Lys Tyr Phe Asn Asn
                165                 170                 175
Pro Leu Val Arg Leu Ala Ile Asn His Ala Ile Asn Val Asp Asp Tyr
            180                 185                 190
Ile Lys Val Ile Tyr Glu Gly Phe Ala Gln Lys Met Val Asn Pro Phe
        195                 200                 205
Pro Pro Thr Ile Trp Gly Tyr Asn Tyr Asn Ile Lys Pro Tyr Glu Tyr
    210                 215                 220
Asp Leu Lys Lys Ala Lys Glu Leu Leu Lys Gln Ala Gly Tyr Pro Asn
225                 230                 235                 240
Gly Phe Lys Thr Asn Ile Cys Thr Ser Leu Leu
                245                 250
```

(2) INFORMATION FOR SEQ ID NO:1830:

(i) SEQUENCE CHARACTERISTICS:

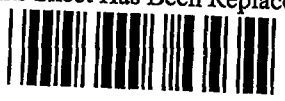
(A) LENGTH: 879 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1830

```
Ile His Ile Lys Arg Ile Phe Leu Leu Lys Asn Thr Pro Phe Asn Pro
1               5                  10                  15
Pro Leu Phe Leu His Ile Ala Pro Leu Lys Pro Phe Met Ile Ile Ile
            20                  25                  30
Asn Leu Phe Trp Asn Thr Phe Ser Leu Phe Val Lys Lys Thr Asn Lys
        35                  40                  45
Asp Leu Ile Met Arg Val Thr Phe Gly Ser Lys Tyr Asn Gln Met Asn
    50                  55                  60
His Tyr Gln Asn Ala Leu Gln Asn Lys Ile Asn Asp Ala Asn Thr Gln
65                  70                  75                  80
Ile Ala Ser Gly Leu Lys Ile Arg Tyr Gly Tyr Gln Asn Ser Asp Ile
                85                  90                  95
Asn Asn Gln Asn Leu Lys Phe Gln Tyr Glu Glu Asn Thr Leu Asp Gln
            100                 105                 110
Gly Ile Asp Val Ala Gln Asn Ala Tyr Thr Ser Thr Leu Asn Thr Asp
        115                 120                 125
Lys Ala Leu Gln Glu Phe Ser Lys Thr Met Glu Ala Phe Lys Thr Lys
    130                 135                 140
Leu Ile Gln Ser Ala Asn Asp Val His Ser Glu Thr Ser Arg Ala Ala
145                 150                 155                 160
Ile Ala Asn Asp Leu Glu Arg Leu Lys Glu His Met Ile Asn Val Ala
                165                 170                 175
Asn Thr Ser Ile Gly Gly Glu Phe Leu Phe Gly Gly Ser Lys Val Asp
            180                 185                 190
Arg Pro Pro Ile Asp Ser Asn Gly Lys Tyr His Gly Asn Gly Glu Asp
        195                 200                 205
Leu Asn Ala Leu Ile Ser Ser Asp Asn Leu Val Pro Tyr Asn Ile Ser
    210                 215                 220
Gly Gln Asp Leu Phe Leu Gly Thr Asp Lys Asp Lys His Lys Leu Ile
225                 230                 235                 240
Thr Thr Asn Ile Lys Leu Leu Asn Gln Asn Lys Leu His Pro Asp Val
                245                 250                 255
Met Asp Ala Leu Glu His Ser Ser Leu Pro Glu Glu Val Phe Ile Lys
            260                 265                 270
Pro Ser Asp Thr Leu Arg Glu Leu Ile Gly Asp Asn Asp Lys Asn Pro
        275                 280                 285
Thr Asn Asp Pro Lys Glu Phe Phe Tyr Leu Gln Gly Ile Arg Pro Asp
    290                 295                 300
Gly Ser Ser Phe Lys Glu Lys Phe Ala Leu Asp Lys Ala Tyr Gln Asn
305                 310                 315                 320
Gln Glu Ser Ala Thr Lys Val Ser Asp Leu Leu Asp Lys Ile Gly His
                325                 330                 335
Ala Tyr Gly Asn Thr Ser Gln Asn Lys Val Val Asp Val Ser Leu Asn
            340                 345                 350
Asn Trp Gly Gln Ile Glu Ile Lys Asn Leu Thr Pro Gly Ser Glu Asn
        355                 360                 365
Leu Asp Phe His Leu Ile Ser Ser Asp Gly Asp Phe Asp Asp Leu Asp
    370                 375                 380
```

Ala Leu Arg Ser Ser Gly Lys Arg Val Thr Glu Tyr Val Lys Ser Ala
385 390 395 400
Phe Val Thr Asp Arg Ser Leu Ser Gln Val Lys Ala Val Pro Asn Met
405 410 415
Tyr Asn Pro Lys Val Leu Glu Ile Pro Ser Val Phe Val Thr Lys Asp
420 425 430
Asn Val Leu Ala Asn Lys Asn Thr Lys Leu Ser Glu Ile Phe Gly Asp
435 440 445
Lys Val Glu Thr Leu Lys Ile Asn Ala Ser Arg Leu Gly Asp Glu Ser
450 455 460
Ala Ile Lys Ile Pro Asn Leu Pro Ile Asn Leu Asp Ile Pro Ile Leu
465 470 475 480
Leu Asp Val Lys Asn Ser Thr Ile Lys Asp Leu Lys Asp Ala Ile Lys
485 490 495
Glu Arg Phe Asn Asn Glu Val Asp Val Glu Ile Glu Thr Asn Gly Arg
500 505 510
Leu Arg Ile Ile Asp Asn Ser Ser Lys Glu Ser Pro Ile Ser Phe Ala
515 520 525
Leu Ser Thr Leu Asp Gln Lys Gly Leu Glu Val Ala Gly Ile Pro Thr
530 535 540
Asn Asn Ala Ser Glu Tyr Gln Lys Thr Tyr Phe Asn Lys Glu Gly Ala
545 550 555 560
Lys Leu Glu Ser Asn Val Ala Gln Thr Ala Gln Asn Asp Ala Ala Asn
565 570 575
Gly Ser Thr Lys Leu Ser Glu Val Ser Lys Gly Ser Leu Glu Asn Ser
580 585 590
Val Phe Asn Met Lys Leu Asn Asp Val Asn Gly Ser Phe Leu Glu Ala
595 600 605
Gln Ile Asn Leu Asp Asn Asn Gly Ala Phe Leu Ser Leu Pro Asn Gly
610 615 620
Val Lys Ile Pro Leu Tyr Asp Pro Thr Thr Ala Asp Ile Gln Ala Ser
625 630 635 640
Lys Pro Asn Glu Val Thr Tyr Arg Gln Leu Met Asp Ala Met Ser Ile
645 650 655
Ala Leu Asn Tyr Ser Asn Thr Asp Pro Ala Ile Tyr Gln Gln Ile Ser
660 665 670
Asp Asn Pro Thr Ser Lys Glu Ser Lys Glu Arg Phe Ile Glu Leu Leu
675 680 685
Lys Gln Ala Lys Asp Asn Leu Ser Ile Asn Leu Asn Glu Glu Gly Lys
690 695 700
Val Ile Ile Gln Asp Asn Met His Ser Asn Thr Lys Met Gln Phe Met
705 710 715 720
Leu Phe Asp Lys Asp Ala Asn Asp Phe Ser Gln Asn Ala Leu His Ser
725 730 735
Asp Lys Pro Ser Leu Lys Leu Asn Ala Asn Asn Ala Leu Ile Ile Asp
740 745 750
Lys Pro Ser Val Asn Phe Phe Asp Gln Leu Glu Asn Ile Ile Thr Ser
755 760 765
Val Arg Lys Gly Ile Tyr Arg Pro Asp Ala Leu Gly Asp Thr Tyr Ser
770 775 780
Ser Asp Met Arg Asn Leu Gly Ile Gln Asn Gly Ile Thr Leu Ile Asp
785 790 795 800
His Leu Ser Asp His Ile Glu Lys Met Ile Ala Lys Asn Gly Ala His
805 810 815
Gly Lys Ala Phe Glu Asn Ile Ile Arg Arg Asn Glu Val Leu Lys Thr
820 825 830
Gln Val Gln Ser Ile Arg Gly Glu Thr Thr Gly Thr Asp Met Ala Glu
835 840 845
Thr Tyr Asn Lys Phe Ser Asn Leu Thr Asn Asn Tyr Asn Ala Val Leu
850 855 860
Ala Ser Thr Asn Lys Ile Asn Asn Leu Ser Leu Thr Lys Tyr Leu
865 870 875

(2) INFORMATION FOR SEQ ID NO:1831:

This Sheet Has Been Replaced

SUBSTITUTE SHEET (RULE 26)

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 181 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1831

```
Arg Ile Asp Gln Ile Lys Ile Met Lys Leu Val Ser Leu Ile Val Ala
1               5                  10                  15
Leu Val Phe Cys Cys Phe Leu Gly Ala Val Glu Leu Pro Gly Val Tyr
            20                  25                  30
Gln Thr Gln Glu Phe Leu Tyr Met Lys Ser Ser Phe Val Glu Phe Phe
        35                  40                  45
Glu His Asn Gly Lys Phe Tyr Ala Tyr Gly Ile Ser Asp Val Asp Gly
    50                  55                  60
Ser Lys Ala Lys Lys Asp Lys Leu Asn Pro Asn Pro Lys Leu Arg Asn
65                  70                  75                  80
Arg Ser Asp Lys Gly Val Val Phe Leu Ser Asp Leu Ile Lys Val Gly
                85                  90                  95
Glu Gln Ser Tyr Lys Gly Gly Lys Ala Tyr Asn Phe Tyr Asp Gly Lys
            100                 105                 110
Thr Tyr His Val Arg Val Thr Gln Asn Ser Asn Gly Asp Leu Glu Phe
        115                 120                 125
Thr Ser Ser Tyr Asp Lys Trp Gly Tyr Val Gly Asn Thr Phe Thr Leu
    130                 135                 140
Lys Arg Val Arg Gly Ala Glu Ile Ser Ile Leu Lys Leu Lys Arg Phe
145                 150                 155                 160
Asn Leu Met Arg Ser Phe Tyr Arg Gln Thr His Leu Phe Ser Ile Gly
                165                 170                 175
Lys Ala Tyr Ala Thr
            180
```

(2) INFORMATION FOR SEQ ID NO:1832:

(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:1832

This Sheet Has Been Replaced



```
Lys Asp Leu Ser Lys Met Phe Val Val Phe Ile Glu Gly Phe Gly Leu
1               5                  10                  15
Ala Ile Ser Leu Cys Ala Ala Val Gly Ala Gln Ser Leu Phe Ile Val
            20                  25                  30
Glu Arg Gly Met Ala Arg Asn Tyr Val Phe Leu Ile Cys Ala Leu Cys
        35                  40                  45
Phe Met Cys Asp Ile Val Leu Met Ser Met Gly Val Phe Gly Val Gly
    50                  55                  60
Ala Tyr Phe Ala Lys Asn Leu Tyr Leu Ser Leu Phe Leu Asn Leu Phe
65                  70                  75                  80
Gly Ala Val Phe Thr Gly Phe Tyr Ala Phe Leu Ala Leu Lys Thr Leu
                85                  90                  95
Phe Gln Thr Phe Lys Lys Lys Gln Val Gln Thr Pro Lys Lys Leu Ser
            100                 105                 110
Leu Lys Lys Thr Leu Leu Phe Thr Leu Gly Val Thr Leu Leu Asn Pro
        115                 120                 125
Gln Val Tyr Leu Glu Met Val Phe Leu Ile Gly Ala Ser Ala Met Ser
    130                 135                 140
Phe Asn Leu Val Gln Lys Phe Val Phe Leu Ala Gly Thr Leu Ser Ala
145                 150                 155                 160
Ala Phe Ser Trp Leu Leu Leu Leu Cys Thr Met Ser Leu Arg Tyr Gly
                165                 170                 175
Ser Lys Leu Leu Asn Asn Gln Lys Ile Phe Met Gly Val Asn Leu Phe
            180                 185                 190
Val Thr Ala Ile Met Gly Thr Leu Ser Val Thr Leu Phe Arg Asp Phe
        195                 200                 205
Leu Ala Leu Leu Ser Lys Thr
    210                 215
```

(2) INFORMATION FOR SEQ ID NO:1833:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...240

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1833

```
Met Asp Ile Leu Lys Ala Glu His Leu Asn Lys Gln Ile Lys Lys Thr
1               5                  10                  15
Lys Ile Val Ser Asp Val Ser Leu Glu Val Lys Ser Gly Glu Val Val
            20                  25                  30
Gly Leu Leu Gly Pro Asn Gly Ala Gly Lys Thr Thr Thr Phe Tyr Met
        35                  40                  45
Ile Cys Gly Leu Leu Glu Pro Ser Gly Gly Ser Val Tyr Leu Asn Asp
    50                  55                  60
Val Asp Leu Ala Lys Tyr Pro Leu His Lys Arg Ser Asn Leu Gly Ile
65                  70                  75                  80
Gly Tyr Leu Pro Gln Glu Ser Ser Ile Phe Lys Glu Leu Ser Val Glu
                85                  90                  95
Glu Asn Leu Ala Leu Ala Gly Glu Ser Thr Phe Lys Asn Ser Lys Glu
            100                 105                 110
Ser Glu Glu Lys Met Glu Ser Leu Leu Asp Ala Phe Asn Ile Gln Ala
```

```
        115                 120                 125
Ile Arg Glu Arg Lys Gly Met Ser Leu Ser Gly Gly Glu Arg Arg Arg
    130                 135                 140
Val Glu Ile Ala Arg Ala Leu Met Lys Asn Pro Lys Phe Val Leu Leu
145                 150                 155                 160
Asp Glu Pro Phe Ala Gly Val Asp Pro Ile Ala Val Ile Asp Ile Gln
                165                 170                 175
Arg Ile Ile Glu Ser Leu Ile Gly Leu Asn Ile Gly Val Leu Ile Thr
            180                 185                 190
Asp His Asn Val Arg Glu Thr Leu Ser Val Cys His Arg Ala Tyr Val
        195                 200                 205
Ile Lys Ser Gly Thr Leu Leu Ala Ser Gly Asn Ala Asn Glu Ile Tyr
    210                 215                 220
Glu Asn Ala Leu Val Arg Lys Tyr Tyr Leu Gly Glu Asn Phe Lys Val
225                 230                 235                 240
```

(2) INFORMATION FOR SEQ ID NO:1834:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1834

```
Asn Thr Gly Leu Trp His Ser Trp Gly Leu Ala Pro Ala Leu Leu Glu
1               5                   10                  15
Thr Gln Leu Pro Lys His Ala His Gln Phe Phe Gln Ile Phe Phe Phe
            20                  25                  30
Pro Lys Lys Pro Phe Lys Gln Met Ile Val Ile Val Glu Leu Leu Val
        35                  40                  45
Asn Phe Ile Phe Asn Leu Phe His Ala Ile His Val Gly Val Lys Met
    50                  55                  60
Ile Asp Asn Ile Lys Leu Pro Leu Arg Arg Ile Lys Met Arg Ala Leu
65                  70                  75                  80
```

(2) INFORMATION FOR SEQ ID NO:1835:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 548 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

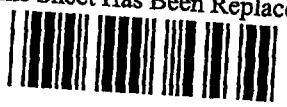
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature

This Sheet Has Been Replaced



(B) LOCATION 1...548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1835

```
Ile Asp Leu Gly Val Ile Glu Thr Ile Pro Lys His Ser Lys Ile Val
1               5                  10                  15
Leu Pro Gly Glu Ala Phe Asp Ser Leu Lys Glu Ala Phe Asp Lys Ile
            20                  25                  30
Asp Pro Tyr Thr Phe Phe Phe Pro Lys Phe Glu Ala Thr Ser Thr Ser
        35                  40                  45
Ile Ser Asp Thr Asn Thr Gln Arg Val Phe Glu Thr Leu Asn Asn Ile
    50                  55                  60
Lys Thr Asn Leu Ile Met Lys Tyr Ser Asn Glu Asn Pro Asn Asn Phe
65                  70                  75                  80
Asn Thr Cys Pro Tyr Asn Asn Asn Gly Asn Thr Lys Asn Asp Cys Trp
                85                  90                  95
Gln Asn Phe Thr Pro Gln Thr Ala Glu Glu Phe Thr Asn Leu Met Leu
            100                 105                 110
Asn Met Ile Ala Val Leu Asp Ser Gln Ser Trp Gly Asp Ala Ile Leu
        115                 120                 125
Asn Ala Pro Phe Glu Phe Thr Asn Ser Ser Thr Asp Cys Asp Ser Asp
    130                 135                 140
Pro Ser Lys Cys Val Asn Pro Gly Val Asn Gly Arg Val Asp Thr Lys
145                 150                 155                 160
Val Asp Gln Gln Tyr Ile Leu Asn Lys Gln Gly Ile Ile Asn Asn Phe
                165                 170                 175
Arg Lys Lys Ile Glu Ile Asp Ala Val Val Leu Lys Asn Ser Gly Val
            180                 185                 190
Val Gly Leu Ala Asn Gly Tyr Gly Asn Asp Gly Glu Tyr Gly Thr Leu
        195                 200                 205
Gly Val Glu Ala Tyr Ala Leu Asp Pro Lys Lys Leu Phe Gly Asn Asp
    210                 215                 220
Leu Lys Thr Ile Asn Leu Glu Asp Leu Arg Thr Ile Leu His Glu Phe
225                 230                 235                 240
Ser His Thr Lys Gly Tyr Gly His Asn Gly Asn Met Thr Tyr Gln Arg
                245                 250                 255
Val Pro Val Thr Lys Asp Gly Gln Val Glu Lys Asp Ser Asn Gly Lys
            260                 265                 270
Pro Lys Asp Ser Asp Gly Leu Pro Tyr Asn Val Cys Ser Leu Tyr Gly
        275                 280                 285
Gly Phe Asn Gln Pro Ala Phe Pro Ser Asn Tyr Pro Asn Ser Ile Tyr
    290                 295                 300
His Asn Cys Ala Asp Val Pro Ala Gly Phe Leu Gly Val Thr Ala Ala
305                 310                 315                 320
Val Trp Gln Gln Leu Ile Asn Gln Asn Ala Leu Pro Ile Asn Tyr Ala
                325                 330                 335
Asn Leu Gly Ser Gln Thr Asn Tyr Asn Leu Asn Ala Ser Leu Asn Thr
            340                 345                 350
Gln Asp Leu Ala Asn Ser Met Leu Ser Thr Ile Gln Lys Thr Phe Val
        355                 360                 365
Thr Ser Ser Val Thr Asn His His Phe Ser Asn Ala Ser Gln Ser Phe
    370                 375                 380
Arg Ser Pro Ile Leu Gly Val Asn Ala Lys Ile Gly Tyr Gln Asn Tyr
385                 390                 395                 400
Phe Asn Asp Phe Ile Gly Leu Ala Tyr Tyr Gly Ile Ile Lys Tyr Asn
                405                 410                 415
Tyr Ala Lys Ala Val Asn Gln Lys Val Gln Gln Leu Ser Tyr Gly Gly
            420                 425                 430
Gly Ile Asp Leu Leu Leu Asp Phe Ile Thr Thr Tyr Ser Asn Lys Asn
        435                 440                 445
Ser Pro Thr Gly Ile Gln Thr Lys Arg Asn Phe Ser Ser Ser Phe Gly
    450                 455                 460
Ile Phe Gly Gly Leu Arg Gly Leu Tyr Asn Ser Tyr Tyr Val Leu Asn
465                 470                 475                 480
Lys Val Lys Gly Ser Gly Asn Leu Asp Val Ala Thr Gly Leu Asn Tyr
```

```
                485                 490                 495
Arg Tyr Lys His Ser Lys Tyr Ser Val Gly Ile Ser Ile Pro Leu Ile
            500                 505                 510
Gln Arg Lys Ala Ser Val Val Ser Ser Gly Gly Asp Tyr Thr Asn Ser
        515                 520                 525
Phe Val Phe Asn Glu Gly Ala Ser His Phe Lys Val Phe Phe Asn Tyr
    530                 535                 540
Gly Trp Val Phe
545
```

(2) INFORMATION FOR SEQ ID NO:1836:

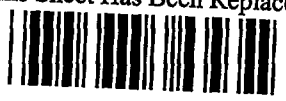
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1836

```
Asp His Ser Phe Asn Ile Gln Asn Ser Ile Lys Arg Lys Val Met Tyr
1               5                  10                  15
Ala Ala His Pro Ile Lys Pro Ile Lys Ala Pro Lys Leu Lys Ser Gln
            20                  25                  30
Phe Leu Arg Arg Val Phe Val Gly Ala Ser Ile Arg Arg Trp Asn Asp
        35                  40                  45
Gln Ala Cys Pro Leu Glu Phe Val Glu Leu Asp Lys Gln Ala His Lys
    50                  55                  60
Ala Met Ile Ala Tyr Leu Leu Ala Lys Asp Leu Lys Asp Arg Gly Lys
65                  70                  75                  80
Asp Leu Asp Leu Asp Leu Leu Ile Lys Tyr Phe Cys Phe Glu Phe Leu
                85                  90                  95
Glu Arg Leu Val Leu Thr Asp Ile Lys Pro Pro Ile Phe Tyr Ala Leu
            100                 105                 110
Gln Gln Thr His Ser Lys Glu Leu Ala Ser Tyr Val Ala Gln Ser Leu
        115                 120                 125
Gln Asp Glu Ile Ser Ala Tyr Phe Ser Leu Glu Glu Leu Lys Glu Tyr
    130                 135                 140
Leu Ser His Arg Pro Gln Ile Leu Glu Thr Gln Ile Leu Glu Ser Ala
145                 150                 155                 160
His Phe Tyr Ala Ser Lys Trp Glu Phe Asp Ile Ile Tyr His Phe Asn
                165                 170                 175
Pro Asn Met Tyr Gly Val Lys Glu Ile Lys Asp Lys Ile Asp Lys Gln
            180                 185                 190
Leu His Asn Asn Asp His Leu Phe Glu Gly Leu Phe Gly Glu Lys Glu
        195                 200                 205
Asp Leu Lys Lys Leu Val Ser Met Phe Gly Gln Leu Arg Phe Gln Lys
    210                 215                 220
Arg Trp Ser Gln Thr Pro Arg Val Pro Gln Thr Ser Val Leu Gly His
225                 230                 235                 240
Thr Leu Cys Val Ala Ile Met Gly Tyr Leu Leu Ser Phe Asp Leu Lys
                245                 250                 255
Ala Cys Lys Ser Met Arg Ile Asn His Phe Leu Gly Gly Leu Phe His
            260                 265                 270
```

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

(2) INFORMATION FOR SEQ ID NO:1837:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1837

```
Asn Ile Thr Ile Lys Asp Arg Thr Met Lys Thr Asn Gly His Phe Lys
1               5                  10                  15
Asp Phe Ala Trp Lys Lys Cys Phe Leu Gly Ala Ser Val Val Ala Leu
            20                  25                  30
Leu Val Gly Cys Ser Pro His Ile Ile Glu Thr Asn Glu Val Ala Leu
        35                  40                  45
Lys Leu Asn Tyr His Pro Ala Ser Glu Lys Val Gln Ala Leu Asp Glu
    50                  55                  60
Lys Ile Leu Leu Leu Arg Pro Ala Phe Gln Tyr Ser Asp Asn Ile Ala
65                  70                  75                  80
Lys Glu Tyr Glu Asn Lys Phe Lys Asn Gln Thr Thr Leu Lys Val Glu
                85                  90                  95
Glu Ile Leu Gln Asn Gln Gly Tyr Lys Val Ile Asn Val Asp Ser Ser
            100                 105                 110
Asp Lys Asp Asp Phe Ser Phe Ala Gln Lys Lys Glu Gly Tyr Leu Ala
        115                 120                 125
Val Ala Met Asn Gly Glu Ile Val Leu Arg Pro Asp Pro Lys Arg Thr
    130                 135                 140
Ile Gln Lys Lys Ser Glu Pro Gly Leu Leu Phe Ser Thr Gly Leu Asp
145                 150                 155                 160
Lys Met Glu Arg Val Leu Ile Pro Ala Gly Phe Val Lys Val Thr Ile
                165                 170                 175
Leu Lys Pro Met Ser Gly Glu Ser Leu Asp Ser Phe Thr Met Asp Leu
```

```
          180                 185                 190
Ser Glu Leu Asp Ile Gln Glu Lys Phe Leu Lys Thr Thr His Ser Ser
      195                 200                 205
His Ser Gly Gly Leu Val Ser Thr Met Val Lys Gly Thr Asp Asn Ser
  210                 215                 220
Asn Asp Ala Ile Lys Ser Ala Leu Asn Lys Ile Phe Ala Ser Ile Met
225                 230                 235                 240
Gln Glu Met Asp Lys Lys Leu Thr Gln Arg Asn Leu Glu Ser Tyr Gln
                245                 250                 255
Lys Asp Ala Lys Glu Leu Lys Asn Lys Arg Asn Arg
            260                 265
```

(2) INFORMATION FOR SEQ ID NO:1838:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1838

```
Ser Asn Phe Lys Lys Gly Phe Phe Met Phe Lys Ser Arg Leu Asn Ser
1               5                  10                  15
Trp Ile Leu Leu Gly Ile Leu Gly Val Leu Val Val Val Phe Trp Asp
            20                  25                  30
Val Ile Lys Tyr Lys Ile Glu Asp Leu Gln His Asp His Tyr Leu Ser
        35                  40                  45
Gln Val Lys Glu Arg Glu Glu Tyr Tyr Lys Asn His Ile Glu Glu Ala
    50                  55                  60
Leu Lys Lys Asp Ser Glu Cys Phe Glu Lys Gly Gly Asp Lys Val Asp
65                  70                  75                  80
Cys Ser Ala Ala Met Arg Ile Ala Ala Gly Glu Arg Asn Arg Arg Met
                85                  90                  95
Leu Glu Ile Lys
            100
```

(2) INFORMATION FOR SEQ ID NO:1839:

(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:1839

```
Lys Leu Phe Leu Val Ile Ile Phe Gln Lys Thr Leu Arg Glu Ile Met
1               5                  10                  15
Gln Asp Leu Gln His Phe Lys Asn Asp Ile Thr Leu Ile Leu Ser Lys
            20                  25                  30
Asp Arg Leu Asp Thr Tyr Asp Ser Leu Glu Gln Tyr Lys Glu Asn Leu
        35                  40                  45
Lys Leu Ile Ala Phe Ile Thr Pro Lys Ile Ser Asn Leu Glu Ile Tyr
    50                  55                  60
Leu Arg Asn Ala Leu Asp Tyr Cys Leu Thr Gln Met Lys Gly Ser Glu
65                  70                  75                  80
Trp Val Phe Asn Glu Ser Val Leu Thr Pro Leu Ile Lys Glu Leu Lys
                85                  90                  95
Glu Lys Lys Lys Glu Ile Thr His Ser Leu Ile Leu Ser Lys Met Ser
            100                 105                 110
Leu Gly Ala Val Ile Arg Leu Ile Phe Cys Tyr Lys Leu Glu Gly Val
        115                 120                 125
Ile Leu Asp Leu Lys Arg Ile Asn Phe Lys Ser Tyr Tyr Pro Asn Asn
    130                 135                 140
Lys Asn Ala Leu Phe Ile Asn Asn Lys Lys Asn Pro Leu Ser Ser Ala
145                 150                 155                 160
Ser Lys Val His Ile Ala Leu Asn Leu Leu Trp Thr Ile Arg Asn Arg
                165                 170                 175
Ala Tyr His Trp Glu Asn Leu Leu Lys Ile Gln Pro Asn Lys Arg Pro
            180                 185                 190
Arg Ile Thr Thr Tyr Phe Ile Gly Leu Lys Asp Asn Asp Arg Ala Arg
        195                 200                 205
Ile Pro Met Asn Ile Ser Val Glu Pro Ser Lys Ile Val Leu Phe Leu
    210                 215                 220
Asp Asp Leu Ile Lys Ser Ile Gly Asn Lys Asp Leu Glu Asp Leu Ser
225                 230                 235                 240
Ser Leu
```

(2) INFORMATION FOR SEQ ID NO:1840:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 467 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1840

```
Gly Met Lys Ala Leu Lys Thr Phe Leu Lys Lys Ser Leu Ile Leu Leu
1               5                  10                  15
Leu Ala Ile Ala Leu Asn His Leu Asn Ala Val Ala Met Ile Val Asp
            20                  25                  30
Asn Pro Thr Gln Asn Ala Trp Asn Gly Ala Lys Arg Ala Trp Asp Glu
        35                  40                  45
Ser Lys Trp Ala Lys His Leu Ala Thr Ile Thr Glu Arg Ile Lys Leu
```

```
    50                  55                  60
Ala Gln Asp Thr Leu Asp Arg Ala Asn Gln Thr Leu Asn Ser Ile Asn
65                  70                  75                  80
Lys Val Asn Asp Val Leu Asn Lys Thr Asn Gln Phe Leu Thr Gly Ser
                85                  90                  95
Ile Leu Ser Ile Pro Asn Pro Met Gln Tyr Val Glu Lys Ile Gln Ser
            100                 105                 110
Phe Ala Lys Gln Val Gln Ala Asn Thr Glu Arg Ile Lys Glu Asn Ala
        115                 120                 125
Gln Asn Tyr Asp Ile Arg Asn Gln Ile Ala Ala Lys Arg Ile Ser Glu
    130                 135                 140
Lys Cys Pro Glu Leu Asn Trp Asp Val Ser Gln Asp Ala Ser Pro Thr
145                 150                 155                 160
Glu Lys Asn Leu His Gln Phe Phe Thr Ser Lys Gly Lys Glu Ser Ala
                165                 170                 175
Asn Thr Lys Ala Leu Lys Asp Phe Ala Asn Ala Ile Gly Asn Thr Gln
            180                 185                 190
Ile Ser Thr Ala Asn Asp Leu Gly Ala Gly Leu Arg Gly Arg Ala Leu
        195                 200                 205
Leu Glu Tyr Ile Cys Ile Gln Lys Gly Asn Leu Glu Ala Ala Lys Lys
    210                 215                 220
Ile Gln Leu Leu Asp Ser Gln Met Thr Leu Ala Leu Leu Asn Asn Asp
225                 230                 235                 240
Tyr Thr Ala Tyr Glu Lys Leu Arg Ala Glu Lys Glu Glu Leu Lys Arg
                245                 250                 255
Gln Ile Ala Ser Asn Val Tyr Ala Lys Val Lys Gln Leu Val Val Ala
            260                 265                 270
Ser Gln Asp Arg Ala Phe Ser Gln Met Asp Asn Glu Leu Gly Val Lys
        275                 280                 285
Thr Phe Gly Phe Asn Asp Glu Asn Val Lys Lys Gly Tyr Cys Lys Lys
    290                 295                 300
Glu Asn Arg Asn Gly Lys Ser Glu Cys Ile Pro Asn Met Leu Asn Val
305                 310                 315                 320
Asn Arg Leu Lys Ala Gln Phe Asp Glu Leu Asn Leu Asp Tyr Ser Arg
                325                 330                 335
Asp Ile Ala Gly Lys Lys Gly Glu Ala Ala Ala Lys Val Phe Asn Asp
            340                 345                 350
Tyr Lys His Arg Phe Gln Gln Leu Ser Val Glu Thr Ala Leu Glu Ile
        355                 360                 365
Ala Gln Asn Leu Ser Phe Met Asn Lys Thr Leu Gly Leu Met Val Gln
    370                 375                 380
Met Gln Ser Tyr Ala Phe Lys Gln Gln Met Gly Tyr Phe Glu Asp Ile
385                 390                 395                 400
Ile Pro Ala Asp Ala Leu Lys Asp Asp Lys Glu His Gln Glu Asn Leu
                405                 410                 415
Glu Gln Lys Gln Gln Glu Ile Glu Lys Val Tyr Arg Ala Lys Leu Asp
            420                 425                 430
Ala Tyr Gly Phe Pro Asn Gly Ser Val Gly Lys Ala Ser Gly Val Asn
        435                 440                 445
Ser Asn Ser Asn Asn Glu Ala Pro Ser Ser Asp Asn Ile Gln Ser Phe
    450                 455                 460
Asn Pro Tyr
465
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1841:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 424 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1841

```
Arg Leu Asn Asn Met Ala Ala Pro Leu Leu Ala Leu Pro Phe Leu Ser
1               5                  10                  15
Asn Pro Leu Val Leu Gly Ala Leu Ala Val Ile Gly Val Gly Ala Tyr
            20                  25                  30
Leu Tyr Pro Asn Lys Gln Asp Ser Leu Val Val Gln Ala Asp Gly Leu
        35                  40                  45
Tyr Ser Glu Ile Leu Gly Phe Phe Ile Ser Phe Ser Ser Lys Ile Leu
    50                  55                  60
Lys Gly Ile Gly Glu Pro Leu Ala Asn Val Ile Gln Pro Phe Gly Met
65                  70                  75                  80
Val Leu Gly Met Leu Leu Ile Leu Leu Tyr Ser Phe Lys Arg Tyr Gln
                85                  90                  95
Asn Asn Asp Leu Phe Glu Ile Lys Thr Phe Leu Met Leu Phe Val Phe
            100                 105                 110
Val Gly Tyr Leu Ser Leu Tyr His Tyr Ala Phe Lys Ser Asp Gly Ser
        115                 120                 125
Ser Ser Gly Asn Gly Arg Ser Ser Phe Ala Phe Gln Asn His Val Thr
    130                 135                 140
Glu Ile Phe Asp Thr Pro Ala Asn Leu Leu Asn Ala Gly Ile Ser Asn
145                 150                 155                 160
Val Val Lys Glu Tyr Gln Thr Asn Ser Ala Arg Glu His Lys Asn Ile
                165                 170                 175
Asp Thr His His Ser Ile Thr Asn Ala Asn Ile Ser Phe His Val Arg
            180                 185                 190
Gln Ile Leu Thr Ser Leu Asn Lys Leu Tyr Glu Asp Phe Lys Ile Asn
        195                 200                 205
Asn Gly Leu Ser Leu Lys Thr Leu Ile Ala Ala Val Leu Leu Leu Val
    210                 215                 220
Ile Leu Gly Leu Glu Leu Phe Leu Leu Phe Lys Val Phe Cys Tyr Val
225                 230                 235                 240
Phe Met Thr Tyr Leu Glu Lys Ile Ile Tyr Leu Ser Leu Val Ile Phe
                245                 250                 255
Met Leu Leu Leu Gly Phe Phe Gln Gln Thr Arg Gly Phe Leu Val Ser
            260                 265                 270
Tyr Val Lys Lys Ile Ile Ser Leu Thr Phe Tyr Met Pro Leu Leu Leu
        275                 280                 285
Leu Leu Val Leu Phe Asn Ser Phe Ala Leu Gln Tyr Ala Ile Lys Val
    290                 295                 300
Gly Gly Ser Asn Glu Ile Val Ala Lys Phe Gly Ile Ile Val Ala Ile
305                 310                 315                 320
Gly Ile Ser Leu Thr Phe Ile Gln Lys Val Pro Glu Met Ile Asn Ala
                325                 330                 335
Ile Phe Gly Thr Gln Gly Gly Leu Thr Asp Ala Lys Ser Phe Ile Tyr
            340                 345                 350
Gln Gly Val Gln Met Ala Ser Ala Gly Ala Gly Ala Ile Ala Gly Ser
        355                 360                 365
Leu Lys Ser Val Gly Arg Ser Ala Phe Gly Arg Thr Leu Glu Ala Tyr
    370                 375                 380
Lys Asp Ala Lys Ser Thr Ile Asn Ser Thr Thr Ala Asn Met Arg Asp
385                 390                 395                 400
Met Pro Gly His Pro Gly Val Arg Val Gly Val Glu Thr Ile Glu Leu
                405                 410                 415
Pro Lys Ser His Arg Ala Ser Lys
            420
```

This Sheet Has Been Replaced

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:1842:

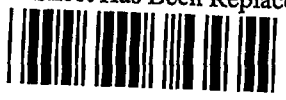
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 384 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1842

```
Lys Asn Arg Tyr Leu Lys Arg Gly Arg Asn Ala Ile Leu Glu Pro Ser
1               5                  10                  15
Arg Asn Arg Leu Lys His Ala Ala Phe Phe Val Gly Leu Phe Ile Val
            20                  25                  30
Leu Phe Leu Ile Ile Met Lys His Gln Thr Ser Pro Tyr Ala Phe Thr
        35                  40                  45
His Asn Gln Ala Leu Val Thr Gln Thr Pro Pro Tyr Phe Thr Gln Leu
    50                  55                  60
Thr Ile Pro Lys Pro Asn Asp Ala Leu Ser Ala His Ala Ser Ser Leu
65                  70                  75                  80
Ile Ser Leu Pro Asn Asp Asn Leu Leu Ser Ala Tyr Phe Ser Gly Thr
                85                  90                  95
Lys Glu Gly Ala Arg Asp Val Lys Ile Ser Ala Asn Leu Phe Asp Ser
            100                 105                 110
Lys Thr Asn Arg Trp Ser Glu Ala Phe Ile Leu Leu Thr Lys Glu Glu
        115                 120                 125
Leu Ser His His Ser His Glu Tyr Ile Lys Lys Leu Gly Asn Pro Leu
    130                 135                 140
Leu Phe Leu His Asp Asn Lys Ile Leu Leu Phe Val Val Gly Val Ser
145                 150                 155                 160
Met Gly Gly Trp Ala Thr Ser Lys Ile Tyr Gln Phe Glu Ser Ala Leu
                165                 170                 175
Glu Pro Ile His Phe Lys Phe Ala Arg Lys Leu Ser Leu Ser Pro Phe
            180                 185                 190
Leu Asn Leu Ser His Leu Val Arg Asn Lys Pro Leu Asn Thr Thr Asp
        195                 200                 205
Gly Gly Phe Met Leu Pro Leu Tyr His Glu Leu Ala Thr Gln Tyr Pro
    210                 215                 220
Leu Leu Leu Lys Phe Asp Gln Gln Asn Asn Pro Arg Glu Leu Leu Arg
225                 230                 235                 240
Pro Asn Thr Leu Asn His Gln Leu Gln Pro Ser Leu Thr Pro Phe Lys
                245                 250                 255
Asp Cys Ala Val Met Ala Phe Arg Asn His Ser Phe Lys Asp Ser Leu
            260                 265                 270
Met Leu Glu Thr Cys Lys Thr Pro Thr Asp Trp Gln Lys Pro Ile Ser
        275                 280                 285
Thr Asn Leu Lys Asn Leu Asp Asp Ser Leu Asn Leu Leu Asn Leu Asn
    290                 295                 300
Gly Ile Leu Tyr Leu Ile His Asn Pro Ser Asp Leu Ser Leu Arg Arg
305                 310                 315                 320
Lys Glu Leu Trp Leu Ser Lys Leu Glu Asn Ser Asn Ser Phe Lys Thr
                325                 330                 335
Leu Lys Val Leu Asp Lys Ala Asn Glu Val Ser Tyr Pro Ser Tyr Ser
            340                 345                 350
```

```
Leu Asn Pro His Phe Ile Asp Ile Val Tyr Thr Tyr Asn Arg Ser His
        355                 360                 365
Ile Lys His Ile Arg Phe Asn Met Ala Tyr Leu Asn Ser Leu Leu Lys
    370                 375                 380
```

(2) INFORMATION FOR SEQ ID NO:1843:

(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:1843

```
Leu Val Met Phe Ile Ser Ser Ser Tyr Thr Leu Ser Phe Val Trp Leu
1               5                  10                  15
Phe Leu Ile Phe Phe Phe Phe Lys Asn Lys Pro Leu Gly Leu Arg Phe
            20                  25                  30
Ser Leu Ser Leu Ile Ser Val Ile Leu Ser Asn Ile Ala Leu Lys Asp
        35                  40                  45
Ser Leu Ser Leu Asn Glu Phe Leu Ser Ser Phe Thr Ala Pro Leu Ser
    50                  55                  60
Pro Phe Ser Cys Leu Leu Ile Leu Ala Tyr Ala Ser Phe Ser Cys His
65                  70                  75                  80
Ile Leu Lys Lys Pro Pro Leu Glu Thr Leu Gln Ser Tyr Ser Val Met
                85                  90                  95
Leu Phe Phe Asn Leu Leu Leu Leu Thr Asp Ile Leu Gly Phe Leu Pro
            100                 105                 110
Phe Ser Ile Tyr His His Phe Met Ala Ser Leu Ile Phe Ser Ala Leu
        115                 120                 125
Phe Cys Ser Ser Leu Phe Leu Ser Ser Pro Leu Leu Gly Val Ile Ala
    130                 135                 140
Leu Val Ala Leu Ser Ser Ser Leu Leu Met Arg Ser Asn Phe Gln Ile
145                 150                 155                 160
Leu Asp Ser Leu Leu Asp Phe Pro Leu Phe Leu Phe Val Phe Phe Lys
                165                 170                 175
Thr Leu Tyr Leu Ala Lys Lys Arg Leu
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:1844:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 982 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1844

```
Lys Arg Ile Leu Met Lys Lys Arg Lys His Val Ser Lys Lys Val Phe
1               5                  10                  15
Asn Val Ile Ile Leu Phe Val Ala Val Phe Thr Leu Leu Val Val Ile
            20                  25                  30
His Lys Thr Leu Ser Asn Gly Ile His Ile Gln Asn Leu Lys Ile Gly
        35                  40                  45
Lys Leu Gly Ile Ser Glu Leu Tyr Leu Lys Leu Asn Asn Lys Leu Ser
    50                  55                  60
Leu Glu Val Glu Arg Val Asp Leu Ser Ser Phe Phe His Gln Lys Pro
65                  70                  75                  80
Thr Lys Lys Arg Leu Glu Val Ser Asp Leu Ile Lys Asn Ile Arg Tyr
                85                  90                  95
Gly Ile Trp Ala Val Ser Tyr Phe Glu Lys Leu Lys Val Lys Glu Ile
            100                 105                 110
Ile Leu Asp Asp Lys Asn Lys Ala Asn Ile Phe Phe Asp Gly Asn Lys
        115                 120                 125
Tyr Glu Leu Glu Phe Pro Gly Ile Lys Gly Glu Phe Ser Leu Glu Asp
    130                 135                 140
Asp Lys Asn Ile Lys Leu Lys Ile Ile Asn Leu Leu Phe Lys Asp Val
145                 150                 155                 160
Lys Val Gln Val Asp Gly Asn Ala His Tyr Ser Pro Lys Ala Arg Lys
                165                 170                 175
Met Ala Phe Asn Leu Ile Val Lys Pro Leu Val Glu Pro Ser Ala Ala
            180                 185                 190
Ile Tyr Leu Gln Gly Leu Thr Asp Leu Lys Thr Ile Glu Leu Lys Ile
        195                 200                 205
Asn Thr Ser Pro Met Lys Ser Leu Ala Phe Leu Lys Pro Leu Phe Gln
    210                 215                 220
Arg Gln Ser Gln Lys Asn Leu Lys Thr Trp Ile Phe Asp Lys Ile Gln
225                 230                 235                 240
Phe Ala Ser Phe Lys Ile Asp Asn Ala Leu Ile Lys Ala Asn Phe Thr
                245                 250                 255
Pro Ser Glu Phe Ile Pro Ser Leu Leu Glu Asn Ser Val Val Lys Ala
            260                 265                 270
Thr Leu Ile Lys Pro Ser Val Val Phe Asn Asp Gly Leu Ser Pro Ile
        275                 280                 285
Lys Met Asp Lys Thr Glu Leu Ile Phe Lys Asn Lys Gln Leu Leu Ile
    290                 295                 300
Gln Pro Gln Lys Ile Thr Tyr Glu Thr Met Glu Leu Thr Gly Ser Tyr
305                 310                 315                 320
Ala Thr Phe Ser Asn Leu Leu Glu Ala Pro Lys Leu Glu Val Phe Leu
                325                 330                 335
Lys Thr Thr Pro Asn Tyr Tyr Gly Asp Ser Ile Lys Asp Leu Leu Ser
            340                 345                 350
Ala Tyr Lys Val Val Leu Pro Leu Asp Lys Ile Ser Met Pro Ser Ser
        355                 360                 365
Ala Asp Leu Lys Leu Thr Leu Gln Phe Leu Lys Asn Thr Ala Pro Leu
    370                 375                 380
Phe Ser Val Gln Gly Ser Val Asn Leu Gln Glu Gly Thr Phe Ser Leu
385                 390                 395                 400
Tyr Asn Ile Pro Leu Tyr Thr Gln Ser Ala Gln Ile Asn Leu Asp Ile
                405                 410                 415
Ala Gln Glu Tyr Gln Tyr Ile Tyr Ile Asp Thr Ile His Thr Arg Tyr
            420                 425                 430
Ala Asn Met Leu Asp Leu Asp Ala Lys Ile Ala Leu Asp Leu Gly Gln
        435                 440                 445
Lys Asn Leu Ser Leu Asp Ser Leu Val His Lys Ile Gln Val Asn Thr
    450                 455                 460
```

This Sheet Has Been Replaced

SUBSTITUTE SHEET (RULE 26)



Asn Asn Asn Ile Asn Met Arg Ser Tyr Asp Pro Asn Asn Thr Gln Glu
465 470 475 480
Asp Pro Gln Thr Asn Phe Thr Leu Asp Leu Lys Ser Leu His Ser Ile
485 490 495
Ile Gln Glu Gly Glu Asn Ser Glu Val Phe Arg Arg Lys Ile Ile Asp
500 505 510
Thr Ile Lys Ala Gln Ser Glu Asp Lys Phe Thr Lys Asp Val Phe Tyr
515 520 525
Ala Thr Gly Asp Thr Leu Lys Ser Leu Ser Leu Ser Phe Asp Phe Ser
530 535 540
Asn Pro Asp His Ile Gln Trp Ser Val Pro Gln Leu Leu Leu Glu Gly
545 550 555 560
Glu Phe Lys Asp Asn Ala Tyr Thr Phe Lys Ile Lys Asp Leu Lys Lys
565 570 575
Ile Lys Pro Tyr Ser Pro Ile Met Asp Tyr Ile Ala Leu Lys Asp Gly
580 585 590
Ser Leu Glu Val Ser Thr Ser Asp Phe Val Asn Ile Asp Phe Phe Ala
595 600 605
Lys Asp Leu Lys Ile Asn Leu Pro Ile Tyr Arg Ser Asp Gly Ser His
610 615 620
Phe Asp Ser Phe Ser Leu Phe Gly Ser Ile Asn Lys Asp Glu Ile Ser
625 630 635 640
Val Tyr Thr Pro Ser Lys Ser Ile Ser Ile Lys Val Lys Gly Asp Gln
645 650 655
Lys Asp Ile Thr Leu Asn Asn Ile Asp Leu Ser Ile Asp Asp Phe Leu
660 665 670
Asp Ser Lys Met Pro Ala Ile Ala Gly Leu Phe Ser Lys Glu Arg Lys
675 680 685
Glu Lys Pro Ser Ser Lys Glu Ile Gln Asp Glu Asp Val Phe Ile Ser
690 695 700
Ala Lys Gln Arg Tyr Glu Lys Ala His Lys Ile Ile Pro Ile Ser Thr
705 710 715 720
Arg Ile His Ala Lys Asp Val Val Leu Ile Tyr Lys Lys Met Pro Phe
725 730 735
Pro Leu Glu Asn Leu Asp Ile Val Ala Gln Asp Asp Arg Val Lys Ile
740 745 750
Asp Gly Asn Tyr Lys Asn Ala Met Ile Met Ala Asp Leu Val His Gly
755 760 765
Ala Leu Tyr Leu Lys Ala His Asn Phe Ser Gly Asp Tyr Ile Asn Thr
770 775 780
Ile Leu Gln Lys Asp Phe Val Glu Gly Gly Leu Phe Thr Leu Ile Gly
785 790 795 800
Ala Leu Glu Asp Gln Val Phe Asn Gly Glu Leu Lys Phe Gln Asn Thr
805 810 815
Ser Leu Lys Asn Phe Ala Leu Met Gln Asn Met Val Asn Leu Ile Asn
820 825 830
Thr Ile Pro Ser Leu Ile Val Phe Arg Asn Pro His Leu Gly Ala Asn
835 840 845
Gly Tyr Gln Ile Lys Thr Gly Ser Val Val Phe Gly Ile Thr Lys Glu
850 855 860
Tyr Leu Gly Leu Glu Lys Ile Asp Leu Val Gly Lys Thr Leu Asp Ile
865 870 875 880
Ala Gly Asn Gly Ile Ile Glu Leu Asp Lys Asn Lys Leu Asp Leu Asn
885 890 895
Leu Glu Val Ser Thr Ile Lys Ala Leu Ser Asn Val Leu Asn Lys Ile
900 905 910
Pro Ile Val Gly Tyr Leu Val Leu Gly Lys Gly Gly Lys Ile Thr Thr
915 920 925
Asn Val Asn Val Lys Gly Thr Leu Asp Lys Pro Lys Thr Gln Val Thr
930 935 940
Leu Ala Ser Asp Ile Ile Gln Ala Pro Phe Lys Ile Leu Arg Arg Ile
945 950 955 960
Phe Thr Pro Ile Asp Ile Ile Val Asp Glu Val Lys Lys Asn Ile Asp
965 970 975
Ser Lys Arg Lys Leu Lys

This Sheet Has Been Replaced

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:1845:

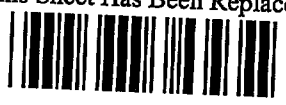
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1845

```
Arg Pro Phe Arg Ser Leu Ile Arg Ile Thr His Ala Pro Lys Leu Lys
1               5                  10                  15
Pro Ser Phe Ala Leu Glu Cys Val Ile Thr Trp Glu Ala Ile Asn Ser
            20                  25                  30
Met Glu Ile Thr Leu Phe Asp Pro Ile Asp Ala His Leu His Val Arg
        35                  40                  45
Glu Asn Ala Leu Leu Lys Ala Val Leu Glu Tyr Ser Ser Glu Pro Phe
    50                  55                  60
Ser Ala Ala Val Ile Met Pro Asn Leu Ser Lys Pro Leu Ile Asp Thr
65                  70                  75                  80
Pro Ile Thr Leu Glu Tyr Glu Glu Glu Ile Leu Lys Asn Ser Ser Asn
                85                  90                  95
Phe Lys Pro Leu Met Ser Leu Tyr Phe Asn Asp Gly Leu Thr Leu Glu
            100                 105                 110
Glu Leu Gln Arg Ala Lys Asn Lys Gly Ile Lys Phe Leu Lys Leu Tyr
        115                 120                 125
Pro Lys Gly Met Thr Thr Asn Ala Gln Asn Gly Thr Ser Asp Leu Leu
    130                 135                 140
Gly Glu Lys Thr Leu Glu Val Leu Glu Asn Ala Gln Lys Leu Gly Phe
145                 150                 155                 160
Ile Leu Cys Val His Ala Glu Gln Ala Gly Phe Cys Leu Asp Lys Glu
                165                 170                 175
Phe Leu Cys His Ser Val Leu Glu Thr Phe Ala Leu Ser Phe Pro Lys
            180                 185                 190
Leu Lys Ile Ile Ile Glu His Leu Ser Asp Trp Arg Ser Ile Ala Leu
        195                 200                 205
Ile Glu Lys His Asp Asn Leu Tyr Ala Thr Leu Thr Leu His His Ile
    210                 215                 220
Ser Met Thr Leu Asp Asp Leu Leu Gly Gly Ser Leu Asp Pro His Cys
225                 230                 235                 240
Phe Cys Lys Pro Leu Ile Lys Thr Lys Lys Asp Gln Glu Arg Leu Leu
                245                 250                 255
Ser Leu Ala Leu Lys Ala His Pro Lys Ile Ser Phe Gly Ser Asp Ser
            260                 265                 270
Ala Pro His Phe Ile Ser Lys Lys His Ser Ala Asn Ile Pro Ala Gly
        275                 280                 285
Ile Phe Ser Ala Pro Ile Leu Leu Pro Ala Leu Cys Glu Leu Phe Glu
    290                 295                 300
Lys His Asn Ala Leu Glu Asn Leu Gln Ala Phe Ile Ser Asp Asn Ala
305                 310                 315                 320
Lys Lys Ile Tyr Ala Leu Asp Asn Leu Pro Ser Lys Lys Ala His Leu
                325                 330                 335
```

```
Ser Lys Lys Pro Phe Ile Val Pro Thr His Thr Leu Cys Leu Asn Glu
            340                 345                 350
Lys Ile Ala Ile Leu Arg Gly Gly Glu Thr Leu Ser Trp Asn Leu Gln
        355                 360                 365
Glu Ile Ala
    370
```

(2) INFORMATION FOR SEQ ID NO:1846:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1846

```
Glu Ile Tyr Met Pro Glu Asn Ser Lys Leu Gln Pro Ala Lys Leu Gly
1               5                  10                  15
Lys Asn Phe Asp Pro Val Asp His Ser Asn Arg Asn Phe Phe Phe Ser
            20                  25                  30
Leu Ile Leu Ser Val Leu Leu His Trp Leu Ile Tyr Phe Leu Phe Glu
        35                  40                  45
His Arg Glu Asp Phe Phe Pro Ser Lys Pro Lys Leu Val Lys Leu Asn
    50                  55                  60
Pro Glu Asn Leu Leu Val Leu Lys Arg Gly His Ser Gln Asp Pro Ser
65                  70                  75                  80
Lys Asn Asn Pro Gly Ala Pro Lys Pro Thr Leu Ala Gly Pro Gln Lys
                85                  90                  95
Pro Pro Thr Pro Pro Thr Pro Pro Thr Pro Pro Thr Pro Pro Lys Pro
            100                 105                 110
Ile Glu Lys Pro Lys Pro Glu Pro Lys Pro Lys Pro Lys Pro Glu Pro
        115                 120                 125
Lys Lys Pro Asn His Lys His Lys Ala Leu Lys Lys Val Glu Lys Val
    130                 135                 140
Glu Glu Lys Lys Val Val Glu Glu Lys Lys Glu Glu Lys Lys Val Val
145                 150                 155                 160
Glu Gln Lys Val Glu Gln Lys Lys Ile Glu Glu Lys Lys Pro Val Lys
                165                 170                 175
Lys Glu Phe Asp Pro Asn Gln Leu Ser Phe Leu Pro Lys Glu Val Ala
            180                 185                 190
Pro Pro Arg Gln Glu Asn Asn Lys Gly Leu Asp Asn Gln Thr Arg Arg
        195                 200                 205
Asp Ile Asp Glu Leu Tyr Gly Glu Glu Phe Gly Asp Leu Gly Thr Ala
    210                 215                 220
Arg Lys Arg Phe His Gln Glu
225                 230
```

(2) INFORMATION FOR SEQ ID NO:1847:

(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:1847

```
Ser Arg Tyr His Pro Arg Gly Phe Ser Gln Leu Pro Lys Leu Lys Leu
1               5                  10                  15
Ile Cys Ile Thr Ala Thr Gly Thr Asp Asn Val Asp Ile Lys Ser Ala
            20                  25                  30
Lys Ala Leu Gly Ile Glu Val Lys Asn Val Ser Ala Tyr Ser Thr Glu
        35                  40                  45
Ser Val Ala Gln His Thr Leu Ala Cys Ala Leu Ser Leu Leu Gly Arg
    50                  55                  60
Ile Asn Asp Tyr Asp Arg Tyr Cys Lys Ser Gly Glu Tyr Ser Gln Ser
65                  70                  75                  80
Asp Ile Phe Thr His Ile Ser Asp Ile Lys Met Gly Leu Ile Lys Gly
                85                  90                  95
Gly Gln Trp Gly Val Ile Gly Leu Gly Asn Ile Gly Lys Arg Val Ala
            100                 105                 110
Lys Leu Ala Gln Ala Phe Gly Ala Lys Val Val Tyr Phe Ser Pro Lys
        115                 120                 125
Asp Lys Lys Glu Glu Tyr Glu Arg Leu Ser Leu Glu Glu Leu Leu Lys
    130                 135                 140
Thr Ser Gly Ile Ile Ser Ile His Ala Pro Leu Asn Glu Ser Thr Arg
145                 150                 155                 160
Asp Leu Ile Ala Leu Lys Glu Leu Gln Ser Leu Lys Asp Gly Ala Ile
                165                 170                 175
Leu Ile Asn Val Gly Arg Gly Gly Ile Val Asn Glu Lys Asp Leu Ala
            180                 185                 190
Leu Ile Leu Glu Thr Lys Asp Leu Tyr Tyr Ala Ser Asp Val
        195                 200                 205
```

(2) INFORMATION FOR SEQ ID NO:1848:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1848

```
Ile Leu Glu Asn Leu Arg Ile Tyr Ala Arg Leu Leu Glu Met Ile Leu
1               5                  10                  15
```

```
Lys Asn Leu Ile Leu Leu Phe Leu Ala Lys Arg Lys Leu Ile Phe Ile
            20                  25                  30
Glu Ala Asn Phe Tyr Thr Ile Ser Gly Ser Lys Leu Asn Glu Val Ala
        35                  40                  45
Arg Ser Tyr Gln Asp Leu Ala Leu Lys Phe Glu Ala Phe Pro Asn Tyr
    50                  55                  60
Glu Phe Ile Trp Ile Thr Asp Gly Ile Gly Trp Leu Asp Ala Lys Ser
65                  70                  75                  80
Lys Leu Gln Glu Ala Tyr Lys Ser Val Glu Ile Tyr Asn Leu Ser Tyr
                85                  90                  95
Val Asn Asp Phe Ile Ser Lys Val Gln Lys
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:1849:

(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:1849

```
Cys Val Met Leu Met Ala Ile Phe Thr Pro Tyr Ile Leu Ile Leu Lys
1               5                   10                  15
Met Met Lys Lys Ser Met Ser Leu Phe Ala Asn Met Gly Leu Glu Gln
            20                  25                  30
Ile Phe Cys Asn Arg Asp Ile Lys Asp Leu Asn Asp Phe Val Phe Gly
        35                  40                  45
Ile Glu Val Gly Leu Asp Ser Asn Ala Arg Lys Asn Arg Ser Arg Lys
    50                  55                  60
Ala Met Glu Asn His Leu Ile Gly Leu Phe Val Gln Ala Gln Leu Asn
65                  70                  75                  80
Phe Lys Glu Gln Val Asp Ile Arg Glu Phe Glu Asp Leu Arg Gln Ala
                85                  90                  95
Phe Gly Asn Asp Thr Lys Lys Phe Asp Phe Val Ile Phe Ser Lys Glu
            100                 105                 110
Lys Thr Tyr Phe His Arg Ser
        115
```

(2) INFORMATION FOR SEQ ID NO:1850:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1850

```
Leu Val Ile Asn Ser Lys Thr Gly Leu Leu Thr Ile Lys Gly Glu Asp
1               5                  10                  15
Ala Leu Gly Lys Ala Ser Leu Lys Asp Leu Gly Leu Ser Ala Gly Met
            20                  25                  30
Val Gln Ser Tyr Glu Ala Ser Gln Asp Thr Leu Phe Met Ser Lys Asn
        35                  40                  45
Leu Gln Lys Ala Ser Asp Ser Gln Phe Thr Tyr Asn Gly Val Ser Ile
    50                  55                  60
Thr Arg Pro Thr Asn Glu Val Asn Asp Val Ile Ser Gly Val Asn Ile
65                  70                  75                  80
Thr Leu Glu Gln Thr Thr Glu Pro Asn Lys Pro Ala Ile Ile Ser Val
                85                  90                  95
Ser Arg Asp Asn Gln Ala Ile Ile Asp Ser Leu Lys Glu Phe Val Lys
            100                 105                 110
Ala Tyr Asn Glu Leu Ile Pro Lys Leu Asp Glu Asp Thr Arg Tyr Asp
        115                 120                 125
Ala Asp Thr Lys Ile Ala Gly Ile Phe Asn Gly Val Gly Asp Ile Arg
    130                 135                 140
Ala Ile Arg Ser Ser Leu Asn Asn Val Phe Ser Tyr Ser Val His Thr
145                 150                 155                 160
Asp Asn Gly Val Glu Ser Leu Met Lys Tyr Gly Leu Ser Leu Asp Asp
                165                 170                 175
Lys Gly Val Met Ser Leu Asp Glu Ala Lys Leu Ser Ser Ala Leu Asn
            180                 185                 190
Ser Asn Pro Lys Ala Thr Gln Asp Phe Phe Tyr Gly Ser Asp Ser Lys
        195                 200                 205
Asp Met Gly Gly Arg Glu Ile His Gln Glu Gly Ile Phe Ser Lys Phe
    210                 215                 220
Asn Gln Val Ile Ala Asn Leu Ile Asp Gly Gly Asn Ala Lys Leu Lys
225                 230                 235                 240
Ile Tyr Glu Asp Ser Leu Asp Arg Asp Ala Lys Ser Leu Thr Lys Asp
                245                 250                 255
Lys Glu Asn Ala Gln Glu Leu Leu Lys Thr Arg Tyr Asn Ile Met Ala
            260                 265                 270
Glu Arg Phe Ala Ala Tyr Asp Ser Gln Ile Ser Lys Ala Asn Gln Lys
        275                 280                 285
Phe Asn Ser Val Gln Met Met Ile Asp Gln Ala Ala Ala Lys Lys Asn
    290                 295                 300
```

(2) INFORMATION FOR SEQ ID NO:1851:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1851

```
Arg Asn Ile Met Gln Tyr Ala Asn Ala Tyr Gln Ala Tyr Gln His Asn
1               5                  10                  15
Arg Val Ser Val Glu Ser Pro Ala Lys Leu Ile Glu Met Leu Tyr Glu
            20                  25                  30
Gly Ile Leu Arg Phe Ser Ser Gln Ala Lys Arg Cys Ile Glu Asn Glu
        35                  40                  45
Asp Ile Glu Lys Lys Ile Tyr Tyr Ile Asn Arg Val Thr Asp Ile Phe
    50                  55                  60
Thr Glu Leu Leu Asn Ile Leu Asp Tyr Glu Lys Gly Gly Lys Val Ala
65                  70                  75                  80
Val Tyr Leu Thr Gly Leu Tyr Thr His Gln Ile Lys Val Leu Thr Gln
                85                  90                  95
Ala Asn Val Glu Asn Asp Ala Ser Lys Ile Asp Leu Val Leu Asn Val
            100                 105                 110
Ala Arg Gly Leu Leu Glu Ala Trp Arg Glu Ile His Ser Asp Glu Leu
        115                 120                 125
Ala
```

(2) INFORMATION FOR SEQ ID NO:1852:

(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:1852

```
Phe Asp Asp Leu Tyr Gly Ser Asn Ser Leu Pro Phe Tyr Pro Arg Val
1               5                  10                  15
Thr Pro Val Lys Phe Pro Thr Phe Lys Trp Ala Leu Leu Lys Ala Leu
            20                  25                  30
Ile Lys Asp Asp Phe Pro Thr Leu Gly Trp Pro Thr Arg Ala Thr Met
        35                  40                  45
Ile Ser Phe Ile Gly Phe Glu Cys Ser Ala Leu Lys Val Phe Leu Ile
    50                  55                  60
Phe Gly Tyr Ile Val Phe Lys Ser Trp His Tyr Ser Ala Ile Arg Leu
65                  70                  75                  80
Ile Val Ile
```

(2) INFORMATION FOR SEQ ID NO:1853:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 220 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1853

```
Lys Arg Asp Lys Asn Val Lys Met Arg Lys Gly Arg Val Met Leu Cys
1               5                  10                  15
Val Phe Asp Ile Glu Thr Ile Pro Asn Ile Ser Leu Cys Lys Glu His
            20                  25                  30
Phe Gln Leu Lys Glu Asp Asp Ala Leu Lys Ile Cys Glu Trp Ser Phe
        35                  40                  45
Glu Lys Gln Lys Glu Lys Ser Gly Ser Glu Phe Leu Pro Leu Tyr Leu
    50                  55                  60
His Glu Ile Ile Ser Ile Ala Ala Val Ile Gly Asp Asp Tyr Gly Gln
65                  70                  75                  80
Phe Ile Lys Val Gly Asn Phe Gly Gln Lys His Glu Asn Lys Glu Asp
                85                  90                  95
Phe Ala Ser Glu Lys Glu Leu Leu Glu Asp Phe Phe Lys Tyr Phe Asn
            100                 105                 110
Glu Lys Gln Pro Arg Leu Ile Ser Phe Asn Gly Arg Gly Phe Asp Ile
        115                 120                 125
Pro Leu Leu Thr Leu Lys Ala Leu Lys Tyr Asn Leu Thr Leu Asp Ala
    130                 135                 140
Phe Tyr Ser Gln Glu Asn Lys Trp Glu Asn Tyr Arg Ala Arg Tyr Ser
145                 150                 155                 160
Glu Gln Phe His Leu Asp Leu Met Asp Ser Leu Ser His Tyr Gly Ser
                165                 170                 175
Val Arg Gly Leu Asn Leu Asn Gly Val Cys Ser Met Thr Asn Ile Pro
            180                 185                 190
Gly Lys Phe Asp Val Ser Gly Asp Leu Val His Ala Ile Tyr Tyr Asn
        195                 200                 205
Pro His Leu Arg Pro Lys Gly Gly Lys Arg His Tyr
    210                 215                 220
```

(2) INFORMATION FOR SEQ ID NO:1854:

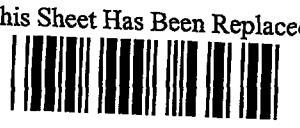
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1854

```
Arg Phe Lys Ala Arg Ile Val Arg Phe Phe Ile Phe Leu Ile Leu Ile
1               5                  10                  15
Cys Pro Leu Ile Cys Pro Leu Met Ser Ala Asp Ser Ala Leu Pro Ser
            20                  25                  30
```

```
Val Asn Leu Ser Leu Asn Ala Pro Ser Asp Pro Lys Gln Leu Val Thr
        35                  40                  45
Thr Leu Asn Val Ile Ala Leu Leu Thr Leu Leu Val Leu Ala Pro Ser
    50                  55                  60
Leu Ile Leu Val Met Thr Ser Phe Thr Arg Leu Ile Val Val Phe Ser
65                  70                  75                  80
Phe Leu Arg Thr Ala Leu Gly Thr Gln Gln Thr Pro Pro Thr Gln Ile
                85                  90                  95
Leu Val Ser Leu Ser Leu Ile Leu Thr Phe Phe Ile Met Glu Pro Ser
            100                 105                 110
Leu Lys Lys Ala Tyr Asp Thr Gly Ile Lys Pro Tyr Met Asp Lys Lys
        115                 120                 125
Ile Ser Tyr Thr Glu Ala Phe Glu Lys Ser Thr Leu Pro Phe Lys Glu
    130                 135                 140
Phe Met Leu Lys Asn Thr Arg Glu Lys Asp Leu Ala Leu Phe Phe Arg
145                 150                 155                 160
Ile Arg Asn Leu Pro Asn Pro Lys Thr Pro Asp Asp Val Ser Leu Ser
                165                 170                 175
Val Leu Ile Pro Ala Phe Met Ile Ser Glu Leu Lys Thr Ala Phe Gln
            180                 185                 190
Ile Gly Phe Leu Leu Tyr Leu Pro Phe Leu Val Ile Asp Met Val Ile
        195                 200                 205
Ser Ser Ile Leu Met Ala Met Gly Met Met Met Leu Pro Pro Val Met
    210                 215                 220
Ile Ser Leu Pro Phe Lys Ile Leu Val Phe Ile Leu Val Asp Gly Phe
225                 230                 235                 240
Asn Leu Leu Thr Glu Asn Leu Val Ala Ser Phe Lys Met Val
                245                 250
```

(2) INFORMATION FOR SEQ ID NO:1855:

(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

This Sheet Has Been Replaced



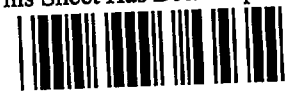
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1855

```
Lys Trp Gly Ile Leu Pro Gly Leu Pro Val Asp Lys Met Glu Val Ser
1               5                   10                  15
Leu Ile His Lys Asp His Gln Ile Thr Ile Ile Asp Leu Pro Gly Thr
            20                  25                  30
Tyr Ala Leu Asn Asp Phe Thr Thr Glu Glu Lys Val Thr Lys Asp Phe
        35                  40                  45
Leu Glu Lys Gly Gln Tyr Asn Leu Ile Leu Asn Val Val Asp Ser Thr
    50                  55                  60
Asn Leu Glu Arg Asn Leu Ala Leu Ser Ala Gln Leu Leu Asp Thr Asn
65                  70                  75                  80
Lys Lys Met Leu Leu Ala Leu Asn Met Trp Asp Glu Ala Lys Lys Glu
                85                  90                  95
Gly Ile Asn Ile Asn Thr Glu Lys Leu Ser Gln Glu Leu Gly Val Val
            100                 105                 110
Cys Val Pro Thr Ser Ala Arg Ser Lys Glu Asp Arg Leu Asn Thr Glu
```

```
        115                 120                 125
Leu Leu Leu Asp Glu Ile Val Arg Leu Tyr Ser Gln Asn Thr Thr Asn
    130                 135                 140
Asn Glu Asn Ile Lys Val Pro Ser Gln Ser Phe Lys Glu Ser Leu Lys
145                 150                 155                 160
Tyr Ser Gln Ser Ala Gln Arg Ile Ala Lys Ser Val Ile Ser Glu Asn
                165                 170                 175
Lys Gln Asn Ala Ser Phe Glu His Thr Tyr Lys Ile Asp Lys Ile Leu
            180                 185                 190
Met His Gln Arg Tyr Gly Ile Phe Ile Phe Leu Gly Phe Met Phe Ile
        195                 200                 205
Ile Phe Ser Leu Ser Phe Leu Ile Gly Gly Gly Val Gln Lys Ala Leu
    210                 215                 220
Glu Glu Gly Phe Lys Ile Leu Ser Asp Ser Ile Lys Glu Asn Val Ala
225                 230                 235                 240
Asn Glu Asp Leu Ala Ser Leu Val Gly Asp Gly Ile Ile Gly Gly Val
                245                 250                 255
Gly Ala Thr Val Ser Phe Leu Pro Leu Ile Val Val Leu Tyr Phe Gly
            260                 265                 270
Ile Ser Leu Leu Glu Thr Thr Gly Tyr Met Ser Arg Val Ala Phe Leu
        275                 280                 285
Leu Asp Gly Ile Leu His Lys Phe Gly Leu His Gly Lys Ser Phe Ile
    290                 295                 300
Pro Leu Ile Thr Gly Phe Gly Cys Ser Val Pro Ala Tyr Met Ala Thr
305                 310                 315                 320
Arg Thr Leu Gln Asn Tyr Asn Glu Arg Leu Ile Thr Leu Phe Val Ile
                325                 330                 335
Gly Phe Met Ser Cys Ser Ala Arg Leu Pro Ile Tyr Val Leu Phe Val
            340                 345                 350
Gly Ser Phe Phe Pro Ser Ser Ser Ala Gly Phe Val Leu Phe Cys Ile
        355                 360                 365
Tyr Ile Leu Gly Ala Val Val Ala Leu Val Met Ala Lys Leu Leu Lys
    370                 375                 380
Leu Ser Val Phe Lys Gly Gln Thr Glu Ser Phe Ile Met Glu Met Pro
385                 390                 395                 400
Lys Tyr Arg Phe Pro Ser Trp Arg Met Val Tyr Phe Ser Ile Tyr Thr
                405                 410                 415
Lys Ser Leu Ser Tyr Leu Lys Lys Ala Gly Thr Tyr Ile Leu Val Gly
            420                 425                 430
Ala Ile Leu Ile Trp Phe Met Ser Gln Tyr Pro Lys Asn Asp Ala Ala
        435                 440                 445
Met Lys Thr Tyr Lys Gln Glu Ser Leu Leu Val Gln Lys Asn Ala Asn
    450                 455                 460
Leu Ser Ser Glu Ala Lys Glu Glu Lys Leu Lys Glu Leu Lys Thr Glu
465                 470                 475                 480
Leu Asp Lys Lys Asn Leu Lys Asn Ser Val Val Gly Arg Gly Gly Ala
                485                 490                 495
Tyr Leu Glu Lys Val Phe Asn Pro Met Asp Phe Asp Trp Arg Leu Ser
            500                 505                 510
Val Ser Leu Val Thr Gly Phe Met Ala Lys Glu Val Val Val Ser Thr
        515                 520                 525
Leu Gly Val Leu Phe Ser Leu Gly Asp Gln Asn Glu Lys Ser Asp Ala
    530                 535                 540
Phe Arg Glu Ile Ile Arg Lys Glu Val Ser Val Pro Ser Gly Ile Ala
545                 550                 555                 560
Phe Ile Val Phe Val Met Phe Tyr Ile Pro Cys Phe Ala Ala Thr Ile
                565                 570                 575
Thr Phe Gly Arg Glu Ala Gly Gly Ile Lys Phe Val Ala Tyr Leu Phe
            580                 585                 590
Ile Phe Thr Thr Val Val Ala Tyr Ala Phe Ser Leu Ile Ala Phe Tyr
        595                 600                 605
Ala Thr Gln Ile Leu Val
    610
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1856:

(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:1856

```
Met Lys Arg Ile Leu Val Ser Leu Ala Val Leu Ser His Ser Ala His
1               5                  10                  15
Ala Val Lys Thr His Asn Leu Glu Arg Val Glu Ala Ser Gly Val Ala
            20                  25                  30
Asn Asp Lys Glu Ala Pro Leu Ser Trp Arg Ser Lys Glu Val Arg Asn
        35                  40                  45
Tyr Met Gly Ser Arg Thr Val Ile Ser Asn Lys Gln Leu Thr Lys Ser
    50                  55                  60
Ala Asn Gln Ser Ile Glu Glu Ala Leu Gln Asn Val Pro Gly Val His
65                  70                  75                  80
Ile Arg Asn Ser Thr Gly Ile Gly Ala Val Pro Ser Ile Ser Ile Arg
                85                  90                  95
Gly Phe Gly Ala Gly Gly Pro Gly His Ser Asn Thr Gly Met Ile Leu
            100                 105                 110
Val Asn Gly Ile Pro Ile Tyr Val Ala Pro Tyr Val Glu Ile Gly Thr
        115                 120                 125
Val Ile Phe Pro Val Thr Phe Gln Ser Val Asp Arg Ile Ser Val Thr
    130                 135                 140
Lys Gly Gly Glu Ser Val Arg Tyr Gly Pro Asn Ala Phe Gly Gly Val
145                 150                 155                 160
Ile Asn Ile Ile Thr Lys Gly Ile Pro Thr Asn Trp Glu Ser Gln Val
                165                 170                 175
Ser Glu Arg Thr Thr Phe Trp Gly Lys Ser Glu Asn Gly Gly Phe Phe
            180                 185                 190
Asn Gln Asn Ser Lys Asn Ile Asp Lys Ser Leu Val Asn Asn Met Leu
        195                 200                 205
Phe Asn Thr Tyr Leu Arg Thr Gly Gly Met Met Asn Lys His Phe Gly
    210                 215                 220
Ile Gln Ala Gln Val Asn Trp Leu Lys Gly Gln Gly Phe Arg Tyr Asn
225                 230                 235                 240
Ser Pro Thr Asp Ile Gln Asn Tyr Met Leu Asp Ser Leu Tyr Gln Ile
                245                 250                 255
Asn Asp Ser Asn Lys Ile Thr Ala Phe Phe Gln Tyr Tyr Ser Tyr Phe
            260                 265                 270
Leu Thr Asp Pro Gly Ser Leu Gly Ile Ala Ala Tyr Asn Gln Asn Arg
        275                 280                 285
Phe Gln Asn Asn Arg Pro Asn Asn Asp Lys Ser Gly Arg Ala Lys Arg
    290                 295                 300
Trp Gly Ala Val Tyr Gln Asn Phe Phe Gly Asp Thr Asp Arg Val Gly
305                 310                 315                 320
Gly Gly Phe His Phe
                325
```

(2) INFORMATION FOR SEQ ID NO:1857:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 797 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1857

```
Arg Leu Lys Pro Asn Val Ile Glu Arg Arg Met Leu Glu Lys Leu Leu
1               5                  10                  15
Ser Ala Ile Lys Gln Lys Val Ser Asn Tyr Phe Leu Gly Val Leu Pro
            20                  25                  30
Lys Ser Tyr Ser Met Ser Glu Glu Asn Asn Ile Leu Gly Leu Tyr Asp
        35                  40                  45
Glu His Phe Leu Leu Thr Lys Asn Glu Asn Leu Val Gly Ile Leu Arg
    50                  55                  60
Leu Glu Gly Val Ser Tyr Thr His Leu Ser Thr Glu Gln Leu Gln Asp
65                  70                  75                  80
Leu Phe Thr Glu Arg Gln Met Ala Leu Asp Ser Leu Glu Lys Val Val
                85                  90                  95
Ala Arg Leu Val Val Lys Arg Arg Lys Ile Asp Tyr Lys Gln Ser Ile
            100                 105                 110
Gln Ser Asp Ser Gln Tyr Leu Gln Ala Ile Leu Asn Gln Phe Glu Asn
        115                 120                 125
Lys Glu Val Tyr Glu Asn Gln Tyr Phe Leu Val Leu Glu Ser Thr His
    130                 135                 140
Ser Leu His Gly Val Leu Glu His Lys Lys Lys Ser Phe Met His Ala
145                 150                 155                 160
Asn Arg Glu Asn Phe Lys Asp Ile Leu Ser Tyr Lys Ala His Phe Leu
                165                 170                 175
Gln Glu Thr Leu Lys Ser Leu Glu Ile Gln Leu Lys Asn Tyr Ala Pro
            180                 185                 190
Lys Leu Leu Asn Ser Lys Glu Val Leu Asn Phe Tyr Ala Glu Tyr Ile
        195                 200                 205
Asn Gly Phe Glu Leu Pro Leu Lys Pro Leu Val Gly Gly Tyr Leu Ser
    210                 215                 220
Asp Ser Tyr Ile Ala Ser Ser Ile Thr Phe Glu Lys Asp Tyr Phe Ile
225                 230                 235                 240
Gln Glu Ser Phe Asn Gln Lys Thr Tyr Asn Arg Leu Ile Gly Ile Lys
                245                 250                 255
Ala Tyr Glu Ser Glu Arg Ile Thr Ser Ile Ala Val Gly Ala Leu Leu
            260                 265                 270
Tyr Gln Glu Thr Pro Leu Asp Ile Ile Phe Ser Ile Glu Pro Met Ser
        275                 280                 285
Val Asn Lys Thr Leu Ser Phe Leu Lys Glu Arg Ala Lys Phe Ser Met
    290                 295                 300
Ser Asn Leu Val Lys Asn Glu Leu Leu Glu Tyr Gln Glu Leu Val Lys
305                 310                 315                 320
Thr Lys Arg Leu Ser Met Gln Lys Phe Ala Leu Asn Val Leu Ile Lys
                325                 330                 335
Ala Pro Ser Leu Glu Asp Leu Asp Ala Gln Thr Ser Leu Ile Leu Gly
            340                 345                 350
Leu Leu Phe Lys Glu Asn Leu Val Gly Val Ile Glu Thr Phe Gly Leu
        355                 360                 365
```

Lys Gly Gly Tyr Phe Ser Phe Phe Pro Glu Arg Ile His Leu Asn His
370 375 380
Arg Leu Arg Phe Leu Thr Ser Lys Ala Leu Ala Cys Leu Met Val Phe
385 390 395 400
Glu Arg Gln Asn Leu Gly Phe Lys Ala Asn Ser Trp Gly Asn Ser Pro
405 410 415
Leu Ser Val Phe Lys Asn Leu Asp Tyr Ser Pro Phe Leu Phe Asn Phe
420 425 430
His Asn Gln Glu Val Ser His Asn Asn Ala Lys Glu Ile Ala Arg Val
435 440 445
Asn Gly His Thr Leu Val Ile Gly Ala Thr Gly Ser Gly Lys Ser Thr
450 455 460
Leu Ile Ser Tyr Leu Met Met Ser Ala Leu Lys Tyr Gln Asn Met Arg
465 470 475 480
Leu Leu Ala Phe Asp Arg Met Gln Gly Leu Tyr Ser Phe Thr Glu Phe
485 490 495
Phe Lys Gly His Tyr His Asp Gly Gln Ser Phe Ser Ile Asn Pro Phe
500 505 510
Cys Leu Glu Pro Asn Leu Gln Asn Leu Glu Phe Leu Gln Ser Phe Phe
515 520 525
Leu Ser Met Leu Asp Leu Ala Pro Ser Arg Asp Lys Glu Ala Leu Glu
530 535 540
Asp Met Asn Ala Ile Ser Gly Ala Ile Lys Ser Leu Tyr Glu Thr Leu
545 550 555 560
Tyr Pro Lys Asp Phe Ser Leu Leu Asp Phe Lys Glu Thr Leu Lys Arg
565 570 575
Thr Ser Ser Asn Gln Leu Gly Leu Ser Leu Glu Pro Tyr Leu Asn Asn
580 585 590
Pro Leu Phe Asn Ala Leu Asn Asp Ala Phe Asn Ser Asn Ala Phe Leu
595 600 605
Asn Val Ile Asn Leu Asp Ala Ile Thr Gln Asn Pro Lys Asp Leu Gly
610 615 620
Leu Leu Ala Tyr Tyr Leu Phe Tyr Lys Ile Leu Glu Glu Ser Arg Lys
625 630 635 640
Asn Asp Ser Gly Phe Leu Val Phe Leu Asp Glu Phe Lys Ser Tyr Val
645 650 655
Glu Asn Asp Leu Leu Asn Thr Lys Ile Asn Ala Leu Ile Thr Gln Ala
660 665 670
Arg Lys Ala Asn Gly Val Val Val Leu Ala Leu Gln Asp Ile Tyr Gln
675 680 685
Leu Ser Gly Val Lys Asn Ala His Ser Phe Leu Ser Asn Met Gly Thr
690 695 700
Leu Ile Leu Tyr Pro Gln Lys Asn Ala Arg Glu Leu Lys His Asn Phe
705 710 715 720
Asn Val Pro Leu Ser Glu Thr Glu Ile Ser Phe Leu Glu Asn Thr Pro
725 730 735
Leu Tyr Ala Arg Gln Val Leu Val Lys Asn Leu Gly Asn Gly Ser Ser
740 745 750
Asn Met Ile Asp Val Ser Leu Glu Gly Leu Gly Cys Tyr Leu Lys Ile
755 760 765
Phe Asn Ser Asp Ser Ser His Val Asn Lys Val Lys Ala Leu Gln Lys
770 775 780
Asp Tyr Pro Thr Glu Trp Arg Glu Lys Leu Leu Lys Ser
785 790 795

(2) INFORMATION FOR SEQ ID NO:1858:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 529 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced

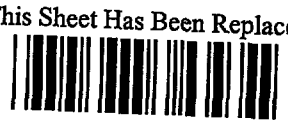


(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...529

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1858

```
Lys Met Ile Leu Lys Ser Ser Ile Asp Arg Leu Leu Gln Thr Ile Asp
1               5                  10                  15
Ile Val Glu Val Ile Ser Ser Tyr Val Asp Leu Arg Lys Ser Gly Ser
            20                  25                  30
Asn Tyr Met Ala Cys Cys Pro Phe His Glu Glu Arg Ser Ala Ser Phe
        35                  40                  45
Ser Val Asn Gln Val Lys Gly Phe Tyr Tyr Cys Phe Gly Cys Gly Ala
    50                  55                  60
Ser Gly Asp Ser Ile Lys Phe Val Met Ala Phe Glu Lys Leu Ser Phe
65                  70                  75                  80
Val Glu Ala Leu Glu Lys Leu Ala His Arg Phe Asn Ile Ala Leu Glu
                85                  90                  95
Tyr Asp Lys Gly Val Tyr Tyr Asp His Lys Glu Asp Tyr His Leu Leu
            100                 105                 110
Glu Met Val Ser Ser Leu Tyr Gln Glu Glu Leu Phe Asn Ala Pro Phe
        115                 120                 125
Phe Leu Asn Tyr Leu Gln Lys Arg Gly Leu Ser Met Glu Ser Ile Lys
    130                 135                 140
Ala Phe Lys Leu Gly Leu Cys Thr Asn Lys Ile Asp Tyr Gly Ile Glu
145                 150                 155                 160
Asn Lys Gly Leu Asn Lys Asp Lys Leu Ile Glu Leu Gly Val Leu Gly
                165                 170                 175
Lys Ser Asp Lys Glu Asp Lys Thr Tyr Leu Arg Phe Leu Asp Arg Ile
            180                 185                 190
Met Phe Pro Ile Tyr Ser Pro Ser Ala Gln Val Val Gly Phe Gly Gly
        195                 200                 205
Arg Thr Leu Lys Glu Lys Ala Ala Lys Tyr Ile Asn Ser Pro Gln Asn
    210                 215                 220
Lys Leu Phe Asp Lys Ser Ser Leu Leu Tyr Gly Tyr His Leu Ala Lys
225                 230                 235                 240
Glu His Ile Tyr Lys Gln Lys Gln Val Ile Val Thr Glu Gly Tyr Leu
                245                 250                 255
Asp Val Ile Leu Leu His Gln Ala Gly Phe Lys Asn Ala Ile Ala Thr
            260                 265                 270
Leu Gly Thr Ala Leu Thr Pro Ser His Leu Pro Leu Leu Lys Lys Gly
        275                 280                 285
Asp Pro Glu Ile Leu Leu Ser Tyr Asp Gly Asp Lys Ala Gly Arg Asn
    290                 295                 300
Ala Ala Tyr Lys Ala Ser Leu Met Leu Ala Lys Glu Gln Arg Lys Gly
305                 310                 315                 320
Gly Val Ile Leu Phe Glu Asn Asn Leu Asp Pro Ala Asp Met Ile Ala
                325                 330                 335
Asn His Gln Ile Glu Thr Leu Lys Asn Trp Leu Ser Arg Pro Ile Ala
            340                 345                 350
Phe Ile Glu Phe Val Leu Arg His Met Ala Gly Ser Tyr Leu Leu Asp
        355                 360                 365
Asp Pro Leu Glu Lys Asp Lys Ala Leu Lys Glu Met Leu Gly Phe Leu
    370                 375                 380
Lys Asn Phe Ser Leu Leu Leu Gln Asn Glu Tyr Lys Pro Leu Ile Ala
385                 390                 395                 400
Thr Leu Leu Gln Ala Pro Leu His Val Leu Gly Ile Arg Glu Pro Val
                405                 410                 415
Ser Phe Gln Pro Phe Tyr Pro Lys Thr Glu Lys Pro Asn Arg Pro Gln
            420                 425                 430
```

```
Lys Phe Ala His Val Ser Ser Met Pro Ser Leu Glu Phe Leu Glu
        435                 440                 445
Leu Val Ile Arg Tyr Leu Leu Glu Asp Arg Ser Leu Leu Asp Leu Ala
    450                 455                 460
Val Gly Tyr Ile His Ser Gly Val Phe Leu His Lys Lys Gln Glu Phe
465                 470                 475                 480
Asp Ala Leu Cys Gln Glu Lys Leu Asp Asp Pro Lys Leu Val Ala Leu
                485                 490                 495
Leu Leu Asp Ala Asn Leu Pro Leu Lys Lys Gly Gly Phe Glu Lys Glu
            500                 505                 510
Leu Arg Leu Leu Ile Leu Arg Tyr Phe Glu Pro Pro Thr Gln Arg Asn
        515                 520                 525
Pro
```

(2) INFORMATION FOR SEQ ID NO:1859:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 430 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1859

```
Leu Arg Gly His Arg Arg Thr Tyr Ile Gly Ser Met Pro Gly Arg Ile
1               5                  10                  15
Val Gln Gly Leu Ile Glu Ala Lys Lys Met Asn Pro Val Met Val Leu
            20                  25                  30
Asp Glu Ile Asp Lys Val Asp Arg Ser Val Arg Gly Asp Pro Ala Ser
        35                  40                  45
Ala Leu Leu Glu Ile Leu Asp Pro Glu Gln Asn Ile Ala Phe Arg Asp
    50                  55                  60
His Tyr Ala Asn Phe Ser Ile Asp Leu Ser Gln Val Ile Phe Ile Ala
65                  70                  75                  80
Thr Ala Asn Asn Ile Asp Arg Ile Pro Ala Pro Leu Arg Asp Arg Met
                85                  90                  95
Glu Phe Ile Ser Val Ser Ser Tyr Thr Pro Ser Glu Lys Glu Glu Ile
            100                 105                 110
Ala Lys Asn Tyr Leu Ile Pro Gln Glu Leu Glu Lys His Ala Leu Lys
        115                 120                 125
Pro Ser Glu Val Asp Ile Ser His Glu Cys Leu Lys Leu Ile Ile Glu
    130                 135                 140
Lys Tyr Thr Arg Glu Ala Gly Val Arg Asp Leu Arg Arg Gln Ile Ala
145                 150                 155                 160
Thr Ile Met Arg Lys Ala Ala Leu Lys Tyr Leu Glu Asp Asn Pro His
                165                 170                 175
Lys Lys Gly Arg Thr Lys Lys Ser Glu Asp Lys Asp Lys Lys Gly Gly
            180                 185                 190
Asn Glu Glu Asn Glu Lys Arg Gly Glu Ser Lys Asp Phe Cys Val Ser
        195                 200                 205
Ile Thr Pro Asp Asn Leu Lys Glu Tyr Leu Glu Arg Met Val Phe Glu
    210                 215                 220
Ile Asp Pro Ile Asp Glu Glu Asn Lys Ile Gly Ile Val Asn Gly Leu
```

```
225                 230                 235                 240
Ala Trp Thr Pro Val Gly Gly Asp Val Leu Lys Ile Glu Ala Val Lys
                245                 250                 255
Ile Arg Gly Lys Gly Glu Leu Lys Leu Thr Gly Ser Leu Gly Asp Val
            260                 265                 270
Met Lys Glu Ser Ala Ile Ile Ala Phe Ser Val Val Lys Val Leu Leu
        275                 280                 285
Asp Asn Glu Thr Leu Lys Val Pro Lys Ile Pro Ser Glu Thr Asp Ala
    290                 295                 300
Glu Asn Lys Lys Lys Lys Lys Val Leu Lys Val Tyr Asn Ala Tyr Asp
305                 310                 315                 320
Leu His Leu His Val Pro Glu Gly Ala Thr Pro Lys Asp Gly Pro Ser
                325                 330                 335
Ala Gly Ile Ala Met Ala Ser Val Met Ala Ser Ile Leu Cys Asp Arg
            340                 345                 350
Ala Ile Arg Ser Glu Val Ala Met Thr Gly Glu Leu Thr Leu Ser Gly
        355                 360                 365
Glu Val Leu Pro Ile Gly Gly Leu Lys Glu Lys Leu Ile Ala Ala Phe
    370                 375                 380
Lys Ala Gly Ile Lys Thr Ala Leu Ile Pro Val Lys Asn Tyr Glu Arg
385                 390                 395                 400
Asp Leu Asp Glu Ile Pro Thr Glu Val Arg Glu Asn Leu Asn Ile Val
                405                 410                 415
Ala Val Lys Asn Ile Ala Glu Val Leu Glu Lys Thr Leu Leu
            420                 425                 430
```

(2) INFORMATION FOR SEQ ID NO:1860:

(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:1860

```
Lys Arg Tyr Arg Lys Thr Ala Leu Leu Arg Leu Asp Asn Gly Asp Lys
1               5                  10                  15
Leu Ser Leu Met Arg Glu Phe Phe Lys Ser Val Arg Gly Phe Leu Asn
            20                  25                  30
Leu Leu Arg Met Ile Phe Pro Glu Arg Phe Gln Asn Ala Phe Leu Gly
        35                  40                  45
Leu Ser Glu Leu Phe Tyr Tyr Ala Ser Ser Leu Ser Phe Tyr Thr Ile
    50                  55                  60
Leu Ser Leu Ser Pro Ile Leu Leu Phe Val Phe Ser Leu Phe Val Ser
65                  70                  75                  80
His Tyr Leu Gln Ala His Ser Gly Glu Met Glu Ala Leu Ile Phe Pro
                85                  90                  95
Asn Ala Pro Lys Leu Ile Gly Ala Ile Lys Asp Phe Leu Glu Asn Phe
            100                 105                 110
Lys Lys Thr Asp Met Thr Leu Gly Thr Leu Glu Glu Val Ser Ile Val
        115                 120                 125
Val Ala Leu Val Leu Phe Cys Glu Asn Tyr Arg Ser Ile Ala Ser Lys
    130                 135                 140
```

This Sheet Has Been Replaced



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

(2) INFORMATION FOR SEQ ID NO:1861:

This Sheet Has Been Replaced



(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:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1861

```
Val Gly Val Val Met Ile Lys Lys Thr Leu Ala Ser Val Leu Leu Gly
1               5                  10                  15
Leu Ser Leu Met Ser Val Leu Asn Ala Lys Glu Cys Val Ser Pro Ile
            20                  25                  30
Thr Arg Ser Val Lys Tyr His Gln Gln Ser Ala Glu Ile Arg Ala Leu
        35                  40                  45
Gln Leu Gln Ser Tyr Lys Met Ala Lys Met Ala Leu Asp Asn Asn Leu
    50                  55                  60
Lys Leu Val Lys Asp Lys Lys Pro Ala Val Ile Leu Asp Leu Asp Glu
65                  70                  75                  80
Thr Val Leu Asn Thr Phe Asp Tyr Ala Gly Tyr Leu Val Lys Asn Cys
                85                  90                  95
Ile Lys Tyr Thr Pro Glu Thr Trp Asp Lys Phe Glu Lys Glu Gly Ser
            100                 105                 110
Leu Thr Leu Ile Pro Gly Ala Leu Asp Phe Leu Glu Tyr Ala Asn Ser
        115                 120                 125
Lys Gly Val Lys Ile Phe Tyr Ile Ser Asn Arg Thr Gln Lys Asn Lys
    130                 135                 140
Ala Phe Thr Leu Lys Thr Leu Lys Ser Phe Lys Leu Pro Gln Val Ser
145                 150                 155                 160
Glu Glu Ser Val Leu Leu Lys Glu Lys Gly Lys Pro Lys Ala Val Arg
                165                 170                 175
Arg Glu Leu Val Ala Lys Asp Tyr Ala Ile Val Leu Gln Val Gly Asp
            180                 185                 190
Thr Leu His Asp Phe Asp Ala Ile Phe Ala Lys Asp Ala Lys Asn Ser
        195                 200                 205
Gln Glu Gln Gln Ala Lys Val Leu Gln Asn Ala Gln Lys Phe Gly Thr
```

```
    210                 215                 220
Glu Trp Ile Ile Leu Pro Asn Ser Leu Tyr Gly Thr Trp Glu Asp Gly
225                 230                 235                 240
Pro Ile Lys Ala Trp Gln Asn Lys Lys
                245
```

(2) INFORMATION FOR SEQ ID NO:1862:

This Sheet Has Been Replaced



(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:1862

```
His Asp Lys Lys Phe Asp Leu Leu Gly Gly Val Met Asp Phe Val Gly
1               5                  10                  15
Phe Glu Asp Leu Lys Cys Lys Asp Lys Glu Asn Ser Gln Lys Val Phe
            20                  25                  30
Val Ile Arg Asn Asp Lys Leu Gly Asp Phe Ile Leu Val Ile Pro Ala
        35                  40                  45
Leu Ile Ala Leu Lys His Ala Phe Leu Glu Lys Gly Val Glu Val Tyr
    50                  55                  60
Leu Gly Val Val Val Pro Ser Tyr Thr Thr Pro Ile Ala Leu Glu Phe
65                  70                  75                  80
Pro Phe Ile Asp Glu Val Ile Ile Glu Asp Asn His Leu Ala Thr Thr
                85                  90                  95
Pro Lys Asn Arg Ser Thr Asp Ala Leu Ile Phe Leu Phe Ser Asn Phe
            100                 105                 110
Lys Asn Ala Lys Leu Ala Phe Ser Leu Arg Lys Ser Ile Pro Tyr Ile
        115                 120                 125
Leu Ala Pro Lys Thr Lys Ile Tyr Ser Trp Leu Tyr Gln Lys Arg Val
    130                 135                 140
Arg Gln Asn Arg Ser Leu Cys Leu Lys Thr Glu Tyr Glu Tyr Asn Leu
145                 150                 155                 160
Asp Leu Ile His Ala Phe Cys Lys Asp Tyr Asp Leu Pro Asn Ala Gln
                165                 170                 175
Leu Lys Lys Ile Ala Trp Lys Leu Lys Asp Lys Ser Lys Glu Arg Ser
            180                 185                 190
Ile Ile Ala Ser Lys Leu Asn Ala Asn Val Asp Leu Leu Trp Ile Gly
        195                 200                 205
Val His Met His Ser Gly Gly Ser Ser Pro Val Leu Pro Ala Ser His
    210                 215                 220
Phe Ile Glu Leu Ile Ala Ile Leu His Glu Lys Leu Ser Cys Glu Ile
225                 230                 235                 240
Ile Leu Ile Cys Gly Pro Gly Glu Arg Lys Ala Thr Glu Glu Leu Leu
                245                 250                 255
Lys Glu Val Pro Phe Ala His Leu Tyr Asp Thr Ser His Ser Leu Val
            260                 265                 270
Asp Leu Ala Lys Leu Cys Ala Asn Leu Ser Val Cys Ile Gly Asn Ala
        275                 280                 285
Ser Gly Pro Leu His Val Asn Ala Leu Phe Asp Asn Gln Ser Ile Gly
    290                 295                 300
```

```
Phe Tyr Pro Asn Glu Leu Thr Ala Ser Ile Ala Arg Trp Arg Pro Phe
305                 310                 315                 320
Asn Glu Gln Phe Leu Gly Ile Thr Pro Pro Asn Gly Ser Asn Asp Met
                325                 330                 335
Gly Leu Ile Asp Ile Gln Lys Glu Ser Glu Lys Ile Met Gly Phe Ile
            340                 345                 350
Thr Lys Asn Leu Ser His His Met Gln Glu Arg
        355                 360
```

(2) INFORMATION FOR SEQ ID NO:1863:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 662 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1863

```
Gly Asn Thr Ile Ile Lys Met Gln Lys Ser Leu Ile Thr Thr Pro Ile
1               5                   10                  15
Tyr Tyr Val Asn Asp Ile Pro His Ile Gly His Ala Tyr Thr Thr Leu
            20                  25                  30
Ile Ala Asp Thr Leu Lys Lys Tyr Tyr Thr Leu Gln Gly Glu Glu Val
        35                  40                  45
Phe Phe Leu Thr Gly Thr Asp Glu His Gly Gln Lys Ile Glu Gln Ser
    50                  55                  60
Ala Arg Leu Arg Asn Gln Ser Pro Lys Ala Tyr Ala Asp Ser Ile Ser
65                  70                  75                  80
Ala Ile Phe Lys Asn Gln Trp Asp Phe Phe Asn Leu Asp Tyr Asp Gly
                85                  90                  95
Phe Ile Arg Thr Thr Asp Ser Glu His Gln Lys Cys Val Gln Asn Ala
            100                 105                 110
Phe Glu Ile Met Phe Glu Lys Gly Asp Ile Tyr Lys Gly Thr Tyr Ser
        115                 120                 125
Gly Tyr Tyr Cys Val Ser Cys Glu Ser Tyr Cys Ala Val Ser Lys Val
    130                 135                 140
Asp Asn Thr Asp Ser Lys Val Leu Cys Pro Asp Cys Leu Arg Glu Thr
145                 150                 155                 160
Thr Leu Leu Glu Glu Glu Ser Tyr Phe Phe Lys Leu Ser Ala Tyr Glu
                165                 170                 175
Lys Pro Leu Leu Glu Phe Tyr Ala Lys Asn Pro Glu Ala Ile Leu Pro
            180                 185                 190
Ile Tyr Arg Lys Asn Glu Val Thr Ser Phe Ile Glu Gln Gly Leu Leu
        195                 200                 205
Asp Leu Ser Ile Thr Arg Thr Ser Phe Glu Trp Gly Ile Pro Leu Pro
    210                 215                 220
Lys Lys Met Asn Asp Pro Lys His Val Val Tyr Val Trp Leu Asp Ala
225                 230                 235                 240
Leu Leu Asn Tyr Ala Ser Ala Leu Gly Tyr Leu Asn Gly Leu Asp Asn
                245                 250                 255
Lys Met Ala His Phe Glu Arg Ala Arg His Ile Val Gly Lys Asp Ile
            260                 265                 270
Leu Arg Phe His Ala Ile Tyr Trp Pro Ala Phe Leu Met Ser Leu Asn
```

```
        275                 280                 285
Leu Pro Leu Phe Lys Gln Leu Cys Val His Gly Trp Trp Thr Ile Glu
    290                 295                 300
Gly Val Lys Met Ser Lys Ser Leu Gly Asn Val Leu Asp Ala Gln Lys
305                 310                 315                 320
Leu Ala Met Glu Tyr Gly Ile Glu Glu Leu Arg Tyr Phe Leu Leu Arg
                325                 330                 335
Glu Val Pro Phe Gly Gln Asp Gly Asp Phe Ser Lys Lys Ala Leu Val
            340                 345                 350
Glu Arg Ile Asn Ala Asn Leu Asn Asn Asp Leu Gly Asn Leu Leu Asn
        355                 360                 365
Arg Leu Leu Gly Met Ala Lys Lys Tyr Phe Asn Tyr Ser Leu Lys Ser
    370                 375                 380
Thr Lys Ile Thr Ala Tyr Tyr Pro Lys Glu Leu Glu Lys Ala His Gln
385                 390                 395                 400
Ile Leu Asp Asn Ala Asn Ser Phe Val Pro Lys Met Gln Leu His Lys
                405                 410                 415
Ala Leu Glu Glu Leu Phe Asn Ile Tyr Asp Phe Leu Asn Lys Leu Ile
            420                 425                 430
Ala Lys Glu Glu Pro Trp Val Leu His Lys Asn Asn Glu Ser Glu Lys
        435                 440                 445
Leu Glu Ala Leu Leu Ser Leu Ile Ala Asn Thr Leu Leu Gln Ser Ser
    450                 455                 460
Phe Leu Leu Tyr Ala Phe Met Pro Lys Ser Ala Met Lys Leu Ala Ser
465                 470                 475                 480
Ala Phe Arg Val Glu Ile Thr Pro Asn Asn Tyr Glu Arg Phe Phe Lys
                485                 490                 495
Ala Lys Lys Leu Gln Asp Met Val Leu Gln Asp Thr Glu Pro Leu Phe
            500                 505                 510
Ser Lys Ile Glu Lys Ile Glu Lys Ile Glu Lys Ile Glu Lys Ile Glu
        515                 520                 525
Lys Ile Glu Lys Gly Glu Glu Ala Leu Ala Glu Lys Ala Glu Lys Lys
    530                 535                 540
Glu Lys Glu Lys Ala Pro Pro Thr Gln Glu Asn Tyr Ile Ser Ile Glu
545                 550                 555                 560
Asp Phe Lys Lys Val Glu Ile Lys Val Gly Leu Ile Lys Glu Ala Gln
                565                 570                 575
Arg Ile Glu Lys Ser Asn Lys Leu Leu Arg Leu Lys Val Asp Leu Gly
            580                 585                 590
Glu Asn Arg Leu Arg Gln Ile Ile Ser Gly Ile Ala Leu Asp Tyr Glu
        595                 600                 605
Pro Glu Ser Leu Val Gly Gln Met Val Cys Val Val Ala Asn Leu Lys
    610                 615                 620
Pro Ala Lys Leu Met Gly Glu Met Ser Glu Gly Met Ile Leu Ala Val
625                 630                 635                 640
Arg Asp Asn Asp Asn Leu Ala Leu Ile Ser Pro Thr Arg Glu Lys Ile
                645                 650                 655
Ala Gly Ser Leu Ile Ser
            660
```

(2) INFORMATION FOR SEQ ID NO:1864:

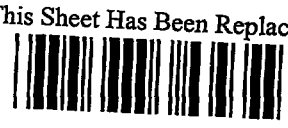
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 342 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1864

```
Gly Arg Met Met Lys Ile Val Ile Asp Leu Met Gly Ala Asp His Gly
1               5                  10                  15
Val Leu Pro Ile Ile Glu Gly Val Ser Arg Ala Leu Glu Asn Lys Ser
            20                  25                  30
Phe Ser Val Val Leu Val Gly Asp Lys Asp Lys Ala Thr Pro Phe Ile
        35                  40                  45
Ser Lys Glu Leu Ala Ser Lys Val Glu Met Ile His Thr Gln Asp Tyr
    50                  55                  60
Ile Lys Met Glu Glu Ala Ala Thr Glu Ala Ile Lys Arg Lys Glu Ser
65                  70                  75                  80
Ser Ile Tyr Leu Gly Met Asp Ile Leu Lys Asn Gly Ala Asp Ala Leu
                85                  90                  95
Ile Ser Ala Gly His Ser Gly Ala Thr Met Gly Leu Ala Thr Leu Arg
            100                 105                 110
Leu Gly Arg Ile Lys Gly Val Glu Arg Pro Ala Ile Cys Thr Leu Met
        115                 120                 125
Pro Ser Val Gly Lys Arg Pro Ser Val Leu Leu Asp Ala Gly Ala Asn
    130                 135                 140
Thr Asp Cys Lys Pro Glu Tyr Leu Ile Asp Phe Ala Leu Met Gly Tyr
145                 150                 155                 160
Glu Tyr Ala Lys Ser Val Leu His Tyr Asp Ser Pro Lys Val Gly Leu
                165                 170                 175
Leu Ser Asn Gly Glu Glu Asp Ile Lys Gly Asn Thr Leu Val Lys Glu
            180                 185                 190
Thr His Lys Met Leu Lys Ala Tyr Asp Phe Phe Tyr Gly Asn Val Glu
        195                 200                 205
Gly Ser Asp Ile Phe Lys Gly Val Val Asp Val Val Val Cys Asp Gly
    210                 215                 220
Phe Met Gly Asn Val Val Leu Lys Thr Thr Glu Gly Val Ala Ser Ala
225                 230                 235                 240
Ile Gly Ser Ile Phe Lys Asp Glu Ile Lys Ser Ser Phe Lys Ser Lys
                245                 250                 255
Met Gly Ala Leu Met Leu Lys Asn Ala Phe Gly Ile Leu Lys Gln Lys
            260                 265                 270
Thr Asp Tyr Ala Glu Tyr Gly Gly Ala Pro Leu Leu Gly Val Asn Lys
        275                 280                 285
Ser Val Ile Ile Ser His Gly Lys Ser Asn Ala Arg Ala Val Glu Cys
    290                 295                 300
Ala Ile Tyr Gln Ala Ile Ser Ala Val Glu Ser Gln Val Cys Leu Arg
305                 310                 315                 320
Ile Thr Gln Ala Phe Glu Ser Leu Lys Ser Gln Ser Phe Glu Ser Gln
                325                 330                 335
Ser Asp Gln Gln Asp Ala
            340
```

(2) INFORMATION FOR SEQ ID NO:1865:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1865

```
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 Glu Ile Lys Ala Phe Phe Lys Arg
                245                 250
```

(2) INFORMATION FOR SEQ ID NO:1866:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1866

```
Ser Thr Ile His Lys Glu Phe Lys Leu Lys Gln Arg Thr Leu Ser Ile
1               5                  10                  15
Ile Lys Pro Asp Ala Leu Lys Lys Lys Val Val Gly Lys Thr Ile Asp
            20                  25                  30
```

```
Arg Phe Glu Ser Asn Gly Leu Glu Val Val Ala Met Lys Arg Leu His
        35                  40                  45
Leu Ser Val Lys Asp Ala Glu Asn Phe Tyr Ala Ile Leu Arg Glu Arg
    50                  55                  60
Pro Phe Phe Lys Asp Leu Ile Glu Phe Met Val Ser Gly Pro Val Val
65                  70                  75                  80
Val Met Val Leu Glu Gly Lys Asp Ala Val Ala Lys Asn Arg Glu Leu
                85                  90                  95
Met Gly Ala Thr Asp Pro Lys Leu Ala Gln Lys Gly Thr Ile Arg Ala
            100                 105                 110
Asp Phe Ala Glu Ser Ile Asp Ala Asn Ala Val His Gly Ser Asp Ser
        115                 120                 125
Leu Glu Asn Ala His Asn Glu Ile Ala Phe Phe Phe Ala Ala Arg Glu
    130                 135                 140
Phe
145
```

(2) INFORMATION FOR SEQ ID NO:1867:

(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

This Sheet Has Been Replaced

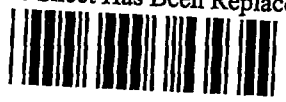


(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1867

```
Gly Arg Gly Gly Ile Tyr Ile Glu His Gly Arg Val Lys Met Val Ala
1               5                   10                  15
Leu Ser Asn Ala Leu Ser Arg Val Phe Gly Ser Val Ala Gly Tyr Lys
            20                  25                  30
Phe Pro Ser Phe Ile Gln Lys Ser Ile Asn Ala Leu Tyr Val Lys Ile
        35                  40                  45
Phe Lys Ile Asp Leu Ser Glu Phe Glu Pro Leu Glu Asn Tyr Lys Ser
    50                  55                  60
Leu Asn Ala Leu Phe Met Arg Ser Leu Lys Lys Glu Arg Pro Phe Asp
65                  70                  75                  80
Lys Ala Pro Asn Ile Cys Ile Ala Pro Cys Asp Ala Leu Ile Thr Glu
                85                  90                  95
Cys Ala Phe Leu Asp Asn Asp Ser Ala Leu Gln Ile Lys Gly Met Pro
            100                 105                 110
Tyr Lys Ala His Glu Leu Val Gly Glu Ile Asn Pro Leu Ser Pro Ser
        115                 120                 125
Phe Phe Tyr Val Asn Phe Tyr Leu Ser Pro Lys Asp Tyr His His Tyr
    130                 135                 140
His Ala Pro Cys Asp Leu Glu Ile Leu Glu Ala Arg Tyr Phe Ala Gly
145                 150                 155                 160
Lys Leu Leu Pro Val Asn Lys Pro Ser Leu His Lys Asn Lys Asn Leu
                165                 170                 175
Phe Val Gly Asn Glu Arg Val Ala Leu Val Ala Lys Asp Asp Ser Arg
            180                 185                 190
Gln
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1868:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1868

```
Asn His Asn Lys Gly Ala Glu Ile Ser Leu Trp Gly Leu Thr Arg Leu
1               5                  10                  15
Val Asp Arg Asp Ile Asp Lys Asp Asn Pro Arg Thr Lys Asn Arg Pro
            20                  25                  30
Ser Val Asp Gly Arg Ile Ser Val Lys Gly Met Val Ile Phe Ser Val
        35                  40                  45
Ser Asn Ala Ile Leu Phe Val Gly Trp Ser Asn Phe Ile Asn Pro Leu
    50                  55                  60
Ala Phe Lys Leu Ser Leu Pro Phe Leu Ile Ile Leu Gly Gly Tyr Ser
65                  70                  75                  80
Tyr Phe Lys Arg Phe Ser Ser Leu Ala His Phe Val Val Gly Leu Ala
                85                  90                  95
Leu Gly Leu Ala Pro Ile Ala Gly Ser Val Ala Val Leu Gly Asp Ile
            100                 105                 110
Pro Leu Trp Asn Val Phe Leu Ala Leu Gly Val Met Leu Trp Val Ala
        115                 120                 125
Gly Phe Asp Leu Leu Tyr Ser Leu Gln Asp Met Glu Phe Asp Lys Glu
    130                 135                 140
Arg Gly Leu Phe Ser Ile Pro Ser Gln Leu Gly Glu Lys Trp Cys Leu
145                 150                 155                 160
Asn Leu Ser Arg Leu Ser His Leu Val Ala Leu Ile Cys Trp Leu Cys
                165                 170                 175
Phe Val Lys Cys Tyr His Gly Gly Leu Phe Ala Tyr Leu Gly Leu Gly
            180                 185                 190
Val Ser Ala Leu Ile Leu Leu Tyr Glu Gln Ile Leu Val Ala Arg Asp
        195                 200                 205
Tyr Lys Asn Ile Pro Lys Ala Phe Phe Val Ser Asn Gly Tyr Leu Gly
    210                 215                 220
Val Val Phe Phe Ile Phe Ile Val Leu Asp Val Gly Phe Lys His Ala
225                 230                 235                 240
```

(2) INFORMATION FOR SEQ ID NO:1869:

(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:

This Sheet Has Been Replaced



(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1869

```
Val Met Ala Ile Trp Gly Trp Cys Phe Leu Phe Leu Ser Ser Leu Met
1               5                  10                  15
Trp Gly Ser Ser Met His Glu Leu Val Leu Arg Ser Gln Ala Leu Gly
            20                  25                  30
Phe Glu Thr Arg Leu Val Gln Cys Asp Leu Ser Phe Ser Tyr Glu Arg
        35                  40                  45
Phe Ile Ser Lys Thr Lys Arg Ser Leu Ala Val Leu Glu Glu Phe Asp
    50                  55                  60
Trp Leu Asn Ser Gly Phe Asp Phe Ser Arg Leu Asn Val Glu Asn Asp
65                  70                  75                  80
Thr Leu Glu Leu Leu Lys Ala Leu Tyr Phe Lys Leu Glu Lys Leu Glu
                85                  90                  95
Ser Leu Leu Leu Lys Glu Asn Leu Leu Glu Leu Glu Gln Lys Asp Arg
            100                 105                 110
Ile Ile Ala Leu Gly His Gly Leu Val Cys Leu Lys Lys Gln Ser Leu
        115                 120                 125
Ile Ala Pro Gln Thr Tyr Tyr Gly Arg Cys Val Leu Glu Gly Lys Ile
    130                 135                 140
Leu Ala Phe Phe Gly Val Ala Arg Asp Lys Asp Phe Leu Glu Ile Thr
145                 150                 155                 160
Arg Met His Ala Leu Asp Ile Lys Arg Tyr Asp Ser Phe Ile Val Asp
                165                 170                 175
Ser Glu Arg Lys Gly Leu Lys Leu
            180
```

(2) INFORMATION FOR SEQ ID NO:1870:

(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

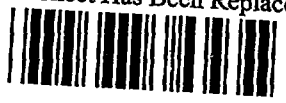
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1870

```
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
    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:1871:

This Sheet Has Been Replaced



(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:1871

Glu Pro Ile Lys Ser Asp Lys Glu Ala Phe Asp Leu Val Met Gln Asn
1 5 10 15
Arg Ser His Glu Ile Gln Gly Val Ser His Ile Lys Asn Asn Tyr Lys
20 25 30
Phe Phe Thr Lys Glu Leu Asp Asn Tyr Ile Ser Lys Gly Tyr Arg Ile
35 40 45
Glu Glu Ile Tyr Gly Ala Phe Leu Trp Leu Lys Ile Val Ala Ile Gly
50 55 60
Leu Glu Leu Gly Glu Asp Asp Pro Gln Val Val Phe Glu Ser Ile Asn
65 70 75 80
Ala Thr Gly Val Gln Leu Lys Gly Leu Asp Leu Ile Arg Asn Tyr Leu
85 90 95
Met Met Gly Glu Asn Ser Asp Asn Gln Asn Arg Leu Tyr Asn Thr Tyr
100 105 110
Trp Val Pro Leu Glu Asn Trp Leu Gly Glu Lys Asp Leu Asn Asp Phe
115 120 125
Ile Lys Thr Tyr Leu Arg Ile Tyr Phe Glu Asp Arg Val Lys Glu Gly
130 135 140
Glu Arg Glu Val Tyr Tyr Ala Leu Lys Ala His His Arg Asp Asn Phe
145 150 155 160
Pro Asn Asn Ile Gln Gly Leu Met Ser Asp Met Arg Glu Tyr Gly Arg
165 170 175
Ile Phe Gln Ile Phe Leu Asp Arg Asp His Tyr Phe Leu His Arg Gly
180 185 190
Asp Pro Gln Gln Leu Ala Asn Leu Arg Leu Arg Val Lys Asp Leu Val
195 200 205
Lys Ile Lys Phe Gly Val Ala Lys Pro Phe Val Leu Arg Cys Ala Arg
210 215 220
Asp Phe Glu Glu Gly Lys Leu Asp Tyr Glu Asn Phe His Glu Ile Leu
225 230 235 240
Gln Ile Leu Ile Ser Tyr Phe Val Arg Arg Ser Val Cys Gly Asp Ser
245 250 255
Thr Pro Thr Leu Thr Arg Val Leu Tyr Ser Leu Tyr Arg Gln Leu Gly
260 265 270
Glu Asp Val Ser Ala Asp Ala Leu Lys Arg Tyr Leu Gly Lys Ser Val
275 280 285
Gly Gln Met Ala Phe Pro Asn Asp Asp Lys Ile Lys Ala Ala Phe Leu
290 295 300

```
Val Arg Asn Ala Tyr Ala Ala Asn Gln Val Cys Lys Phe Ile Leu Leu
305                 310                 315                 320
Glu Ile Glu Lys Leu Ala Thr Leu Asn Arg Gln Lys Lys Arg Ile
                325                 330                 335
```

(2) INFORMATION FOR SEQ ID NO:1872:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...94

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1872

```
Phe Tyr Val Ser Ile Ile Lys Cys Thr Pro Leu Leu Val Gln Ile Val
1               5                   10                  15
Ile Val Phe Tyr Gly Leu Pro Ala Leu Gly Val Tyr Met Asp Pro Ile
            20                  25                  30
Pro Ala Gly Ile Ile Ala Phe Ser Phe Asn Val Gly Ala Tyr Ala Ser
        35                  40                  45
Glu Thr Leu Arg Ala Ser Phe Leu Ser Val Pro Lys Asp Gln Trp Asp
    50                  55                  60
Ser Ser Leu Ser Leu Gly Leu Asn Tyr Leu Gln Thr Phe Trp His Val
65                  70                  75                  80
Ile Phe Phe Gln Ala Leu Lys Val Ala Thr Ala Lys Pro Lys
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:1873:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 461 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1873

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

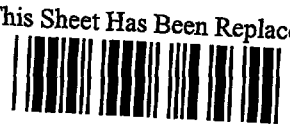
This Sheet Has Been Replaced



```
        35                  40                  45
Ile Trp Ser Glu Ile Asn Thr Tyr Gly Ile Phe Ala Ala Gly Tyr Leu
    50                  55                  60
Ala Arg Pro Leu Gly Gly Ile Val Met Ala His Phe Gly Asp Lys Phe
65                  70                  75                  80
Gly Arg Lys Asn Met Phe Met Leu Ser Ile Leu Leu Met Val Ile Pro
                85                  90                  95
Thr Phe Ala Leu Ala Leu Met Pro Thr Phe Asn Asp Leu Val Gly Phe
            100                 105                 110
Gly Val Asp Ser Met Gly Leu Thr Pro Lys Asn Ala His Tyr Leu Gly
        115                 120                 125
Tyr Ile Ala Pro Val Phe Leu Val Leu Val Arg Ile Cys Gln Gly Val
    130                 135                 140
Ala Val Gly Gly Glu Leu Pro Gly Ala Trp Val Phe Val His Glu His
145                 150                 155                 160
Ala Pro Gln Gly Gln Lys Asn Thr Tyr Ile Gly Phe Leu Thr Ala Ser
                165                 170                 175
Val Val Ser Gly Ile Leu Leu Gly Ser Leu Val Tyr Ile Gly Ile Tyr
            180                 185                 190
Met Val Phe Asp Lys Pro Val Val Glu Asp Trp Ala Trp Arg Val Ala
        195                 200                 205
Phe Gly Leu Gly Gly Ile Phe Gly Ile Ile Ser Val Tyr Leu Arg Arg
    210                 215                 220
Phe Leu Glu Glu Thr Pro Val Phe Gln Gln Met Lys Gln Asp Asp Ala
225                 230                 235                 240
Leu Val Lys Phe Pro Leu Lys Glu Val Phe Lys Asn Ser Leu Phe Gly
                245                 250                 255
Ile Ser Ile Ser Met Leu Ile Thr Trp Val Leu Thr Ala Cys Ile Leu
            260                 265                 270
Ile Phe Ile Leu Phe Val Pro Asn Phe Thr Leu Thr His Pro Asn Phe
        275                 280                 285
His Phe Thr Pro Phe Glu Lys Thr Tyr Phe Gln Ile Leu Gly Leu Val
    290                 295                 300
Gly Ile Val Ser Ser Ile Ile Phe Thr Gly Phe Leu Ala Asp Lys Ile
305                 310                 315                 320
Lys Pro His Lys Val Cys Met Ala Phe Ser Ala Ala Phe Gly Phe Phe
                325                 330                 335
Gly Phe Leu Phe Phe Lys Glu Phe Tyr Ser Asn Ala Pro Ser Leu Val
            340                 345                 350
Asn Thr Ile Ile Leu Tyr Phe Leu Ala Cys Phe Cys Ala Gly Ile Met
        355                 360                 365
Asn Phe Cys Pro Ile Phe Met Ser Asp Val Phe Ser Ala Arg Ile Arg
    370                 375                 380
Phe Ser Gly Ile Ser Phe Ala Tyr Asn Ile Ala Tyr Ala Ile Thr Ala
385                 390                 395                 400
Gly Phe Thr Pro Gln Leu Ser Ser Trp Leu Asn Ala Lys Ala Ile Ala
                405                 410                 415
Val Pro Glu Ser Leu Gln Ser Tyr Gly Leu Ser Phe Tyr Ile Leu Ile
            420                 425                 430
Val Ser Leu Ile Ala Phe Ile Thr Ser Leu Leu Met Ala Pro Ile Tyr
        435                 440                 445
His Lys Ser Asn Thr Gln His Glu Val Ser Pro Thr Ala
    450                 455                 460
```

(2) INFORMATION FOR SEQ ID NO:1874:

This Sheet Has Been Replaced

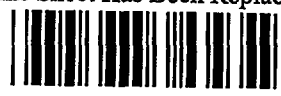


(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 507 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1874

```
Lys Ser Leu Lys Lys Lys Cys Arg Ser Phe Leu Gln Glu Tyr Glu Val
1               5                  10                  15
Tyr Ser Leu Asp Leu Ala Leu Met Val Ala Gly Ala Lys Tyr Arg Gly
            20                  25                  30
Asp Phe Glu Lys Arg Leu Lys Lys Thr Leu Lys Glu Ile Gln Gln Asn
        35                  40                  45
Gly Arg Ile Ile Leu Phe Ile Asp Glu Ile His Thr Leu Leu Gly Ala
    50                  55                  60
Gly Ser Ser Asn Ala Gly Ser Leu Asp Ala Ala Asn Ile Leu Lys Pro
65                  70                  75                  80
Val Leu Thr Asp Gly Ser Leu Lys Cys Leu Gly Ala Thr Thr Phe Glu
                85                  90                  95
Glu Tyr Arg Ser Val Phe Glu Lys Asp Lys Ala Phe Asn Arg Arg Phe
            100                 105                 110
Ser Ile Val Asn Val Glu Glu Pro Ser Lys Glu Ala Cys Tyr Leu Ile
        115                 120                 125
Leu Lys Asn Ile Ala Pro Leu Tyr Glu Glu His His Gln Val Arg Tyr
    130                 135                 140
Asn Glu Ser Val Phe Lys Ala Cys Val Asp Leu Thr Ser Tyr Tyr Met
145                 150                 155                 160
His Asp Lys Phe Leu Pro Asp Lys Ala Ile Glu Leu Leu Asp Glu Val
                165                 170                 175
Gly Ser Arg Lys Lys Ile Asn Pro Lys Lys Gly Lys Lys Ile Ser Val
            180                 185                 190
Asp Asp Val Gln Glu Thr Leu Ala Leu Lys Leu Lys Ile Pro Lys Met
        195                 200                 205
Arg Leu Asn Ser Asp Lys Lys Ala Leu Leu Arg Asn Leu Glu Lys Ser
    210                 215                 220
Leu Lys Asn Lys Ile Phe Ala Gln Thr Glu Ala Ile Asn Leu Val Ser
225                 230                 235                 240
Asn Ala Ile Lys Ile Gln His Cys Gly Leu Ser Ala Lys Asn Lys Pro
                245                 250                 255
Val Gly Ser Phe Leu Phe Val Gly Pro Ser Gly Val Gly Lys Thr Glu
            260                 265                 270
Leu Ala Lys Glu Leu Ala Leu Asn Leu Asn Leu His Phe Glu Arg Phe
        275                 280                 285
Asp Met Ser Glu Tyr Lys Glu Ala His Ser Val Ala Lys Leu Ile Gly
    290                 295                 300
Ser Pro Ser Gly Tyr Val Gly Phe Glu Gln Gly Gly Leu Leu Val Asn
305                 310                 315                 320
Ala Ile Lys Lys His Pro His Cys Leu Leu Leu Leu Asp Glu Ile Glu
                325                 330                 335
Lys Ala His Pro Asn Val Tyr Asp Leu Leu Leu Gln Val Met Asp Asn
            340                 345                 350
Ala Thr Leu Ser Asp Asn Leu Gly Asn Lys Ala Ser Phe Lys His Val
        355                 360                 365
Ile Leu Ile Met Thr Ser Asn Val Gly Ser Lys Asp Lys Asp Thr Leu
    370                 375                 380
Gly Phe Phe Ser Thr Lys Asn Ala Lys Tyr Asp Arg Ala Val Lys Glu
385                 390                 395                 400
Leu Leu Thr Pro Glu Leu Arg Ser Arg Ile Asp Ala Ile Val Pro Phe
                405                 410                 415
Asn Ala Leu Ser Leu Glu Asp Phe Glu Arg Ile Val Ser Val Glu Leu
            420                 425                 430
Asp Gly Leu Lys Ala Leu Ala Ile Glu Gln Gly Val Ile Leu Lys Phe
```

```
        435                 440                 445
His Lys Glu Val Val Lys Cys Ile Ala Gln Lys Ser Tyr Gln Arg Ser
    450                 455                 460
Phe Gly Ala Arg Glu Ile Lys Lys Ile Ile Gln Arg Glu Ile Asn Pro
465                 470                 475                 480
Gln Leu Ser Asp Ile Val Leu Lys Gln Ser Leu Lys Lys Pro Thr Arg
                485                 490                 495
Ser Leu Arg Met Lys Ser Thr Phe His Lys Val
            500                 505
```

(2) INFORMATION FOR SEQ ID NO:1875:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1875

```
Gly Ile Lys Leu Ile Lys Phe Val Arg Asn Val Val Leu Phe Ile Leu
1               5                  10                  15
Thr Ala Ile Phe Leu Ala Phe Met Leu Leu Val Ser Tyr Cys Met Pro
            20                  25                  30
His Tyr Ser Val Ala Val Ile Ser Gly Val Glu Val Lys Arg Met Asn
        35                  40                  45
Glu Asn Glu Asn Thr Pro Asn Asn Lys Glu Val Lys Thr Leu Ala Arg
    50                  55                  60
Asp Val Tyr Phe Val Gln Thr Tyr Asp Pro Lys Asp Gln Lys Ser Val
65                  70                  75                  80
Thr Val Tyr Arg Asn Glu Asp Thr Arg Phe Gly Phe Pro Phe Tyr Phe
                85                  90                  95
Lys Phe Asn Ser Ala Asp Ile Ser Ala Leu Ala Gln Ser Leu Val Asn
            100                 105                 110
Gln Gln Val Glu Val Gln Tyr Tyr Gly Trp Arg Ile Asn Leu Phe Asn
        115                 120                 125
Met Phe Pro Asn Val Ile Phe Leu Lys Pro Leu Lys Glu Ser Asp Glu
    130                 135                 140
Met Ser Lys Pro Val Phe Ser Trp Ile Leu Tyr Ala Leu Leu Leu Val
145                 150                 155                 160
Gly Phe Phe Ile Ser Ala Arg Ser Val Cys Thr Leu Phe Lys Gly Lys
                165                 170                 175
Ala His
```

(2) INFORMATION FOR SEQ ID NO:1876:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 638 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

This Sheet Has Been Replaced



(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1876

```
Ala Arg Leu Leu Leu Tyr Asn Leu Lys Asn Phe Ile Lys Gly Lys Ser
1               5                  10                  15
Ser Met Ser Asn Gln Glu Tyr Thr Phe Gln Thr Glu Ile Asn Gln Leu
            20                  25                  30
Leu Asp Leu Met Ile His Ser Leu Tyr Ser Asn Lys Glu Ile Phe Leu
        35                  40                  45
Arg Glu Leu Ile Ser Asn Ala Ser Asp Ala Leu Asp Lys Leu Asn Tyr
    50                  55                  60
Leu Met Leu Thr Asp Glu Lys Leu Lys Gly Leu Asn Thr Thr Pro Ser
65                  70                  75                  80
Ile His Leu Ser Phe Asp Ser Gln Lys Lys Thr Leu Thr Ile Lys Asp
                85                  90                  95
Asn Gly Ile Gly Met Asp Lys Ser Asp Leu Ile Glu His Leu Gly Thr
            100                 105                 110
Ile Ala Lys Ser Gly Thr Lys Ser Phe Leu Ser Ala Leu Ser Gly Asp
        115                 120                 125
Lys Lys Lys Asp Ser Ala Leu Ile Gly Gln Phe Gly Val Gly Phe Tyr
    130                 135                 140
Ser Ala Phe Met Val Ala Ser Lys Ile Val Val Gln Thr Lys Lys Val
145                 150                 155                 160
Thr Ser His Gln Ala Tyr Ala Trp Val Ser Asp Gly Lys Gly Lys Phe
                165                 170                 175
Glu Ile Ser Glu Cys Val Lys Glu Glu Gln Gly Thr Glu Ile Thr Leu
            180                 185                 190
Phe Leu Lys Glu Glu Asp Ser His Phe Ala Ser Arg Trp Glu Ile Asp
        195                 200                 205
Ser Val Val Lys Lys Tyr Ser Glu His Ile Pro Phe Pro Ile Phe Leu
    210                 215                 220
Thr Tyr Thr Asp Thr Lys Phe Glu Gly Glu Gly Asp Asn Lys Lys Glu
225                 230                 235                 240
Val Lys Glu Glu Lys Cys Asp Gln Ile Asn Gln Ala Ser Ala Leu Trp
                245                 250                 255
Lys Met Asn Lys Ser Glu Leu Lys Glu Lys Asp Tyr Lys Asp Phe Tyr
            260                 265                 270
Gln Ser Phe Ala His Asp Asn Ser Glu Pro Leu Ser Tyr Ile His Asn
        275                 280                 285
Lys Val Glu Gly Ser Leu Glu Tyr Thr Thr Leu Phe Tyr Ile Pro Ser
    290                 295                 300
Lys Ala Pro Phe Asp Leu Phe Arg Val Asp Tyr Lys Ser Gly Val Lys
305                 310                 315                 320
Leu Tyr Val Lys Arg Val Phe Ile Thr Asp Asp Asp Lys Glu Leu Leu
                325                 330                 335
Pro Ser Tyr Leu Arg Phe Val Lys Gly Val Ile Asp Ser Glu Asp Leu
            340                 345                 350
Pro Leu Asn Val Ser Arg Glu Ile Leu Gln Gln Asn Lys Ile Leu Ala
        355                 360                 365
Asn Ile Arg Ser Ala Ser Val Lys Lys Ile Leu Ser Glu Ile Glu Arg
    370                 375                 380
Leu Ser Lys Asp Asn Lys Asn Tyr His Lys Phe Tyr Glu Pro Phe Gly
385                 390                 395                 400
Lys Val Leu Lys Glu Gly Leu Tyr Gly Asp Phe Glu Asn Lys Glu Lys
                405                 410                 415
Leu Leu Glu Leu Leu Arg Phe Tyr Ser Lys Asp Lys Gly Glu Trp Ile
```

```
            420                 425                 430
Ser Leu Lys Glu Tyr Lys Glu Asn Leu Lys Glu Asn Gln Lys Ser Ile
        435                 440                 445
Tyr Tyr Leu Leu Gly Glu Asn Leu Asp Leu Leu Lys Ala Ser Pro Leu
    450                 455                 460
Leu Glu Lys Tyr Ala Gln Lys Gly Tyr Asp Val Leu Leu Leu Ser Asp
465                 470                 475                 480
Glu Ile Asp Ala Phe Val Met Pro Gly Val Asn Glu Tyr Asp Lys Thr
                485                 490                 495
Pro Phe Arg Asp Ala Ser His Ser Glu Ser Leu Lys Glu Leu Gly Leu
            500                 505                 510
Ala Glu Ile His Asp Glu Val Lys Asp Gln Phe Lys Asp Leu Ile Lys
        515                 520                 525
Ala Phe Glu Glu Asn Leu Lys Asp Glu Ile Lys Gly Val Glu Leu Ser
    530                 535                 540
Gly His Leu Thr Ser Ala Val Ala Leu Ile Gly Asp Glu Pro Asn Ala
545                 550                 555                 560
Met Met Ala Asn Trp Met Arg Gln Met Gly Gln Ser Val Pro Glu Ser
                565                 570                 575
Lys Lys Thr Leu Glu Leu Asn Pro Asn His Ala Ile Leu Gln Lys Leu
            580                 585                 590
Leu Lys Cys Glu Asp Lys Glu Gln Leu Ser Ala Phe Ile Trp Leu Leu
        595                 600                 605
Tyr Asp Gly Ala Lys Leu Leu Glu Lys Gly Ala Leu Lys Asp Ala Lys
    610                 615                 620
Ser Phe Asn Glu Arg Leu Asn Ser Val Leu Leu Lys Ala Leu
625                 630                 635
```

(2) INFORMATION FOR SEQ ID NO:1877:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 425 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1877

```
Lys Gln Phe Gly Arg Arg Val Phe Thr Gln Ile Pro Lys Met Val Gln
1               5                  10                  15
Phe Gln Asn Thr Leu Ile Lys Phe His Ala Leu Ser Phe Lys Asn Ala
            20                  25                  30
Asn Leu Ile Tyr Asn Ala Lys Leu Asn Lys Thr Cys Tyr Lys Glu Asn
        35                  40                  45
Ser Asn Thr Ile Ile Leu Arg Ile Lys Met Leu Thr Gln Glu Asp Val
    50                  55                  60
Leu Asn Ala Leu Lys Thr Ile Ile Tyr Pro Asn Phe Glu Lys Asp Ile
65                  70                  75                  80
Val Ser Phe Gly Phe Val Lys Asn Ile Thr Leu His Asp Asn Gln Leu
                85                  90                  95
Gly Leu Leu Ile Glu Ile Pro Ser Ser Ser Glu Glu Thr Ser Ala Ile
            100                 105                 110
Leu Arg Glu Asn Ile Ser Lys Ala Met Gln Glu Lys Gly Val Lys Ala
        115                 120                 125
```

This Sheet Has Been Replaced



```
Leu Asn Leu Asp Ile Lys Thr Pro Pro Lys Pro Gln Ala Pro Lys Pro
    130                 135                 140
Thr Thr Lys Asn Leu Ala Lys Asn Ile Lys His Val Val Met Ile Ser
145                 150                 155                 160
Ser Gly Lys Gly Gly Val Gly Lys Ser Thr Thr Ser Val Asn Leu Ser
                165                 170                 175
Ile Ala Leu Ala Asn Leu Asn Gln Lys Val Gly Leu Leu Asp Ala Asp
            180                 185                 190
Val Tyr Gly Pro Asn Ile Pro Arg Met Met Gly Leu Gln Asn Ala Asp
        195                 200                 205
Val Ile Met Asp Pro Ser Gly Lys Lys Leu Ile Pro Leu Lys Ala Phe
    210                 215                 220
Gly Val Ser Val Met Ser Met Gly Leu Leu Tyr Asp Glu Gly Gln Ser
225                 230                 235                 240
Leu Ile Trp Arg Gly Pro Met Leu Met Arg Ala Ile Glu Gln Met Leu
                245                 250                 255
Ser Asp Ile Ile Trp Gly Asp Leu Asp Val Leu Val Val Asp Met Pro
            260                 265                 270
Pro Gly Thr Gly Asp Ala Gln Leu Thr Leu Ala Gln Ala Val Pro Leu
        275                 280                 285
Ser Ala Gly Ile Thr Val Thr Thr Pro Gln Ile Val Ser Leu Asp Asp
    290                 295                 300
Ala Lys Arg Ser Leu Asp Met Phe Lys Lys Leu His Ile Pro Ile Ala
305                 310                 315                 320
Gly Ile Val Glu Asn Met Gly Ser Phe Val Cys Glu His Cys Lys Lys
                325                 330                 335
Glu Ser Glu Ile Phe Gly Ser Asn Ser Met Ser Gly Leu Leu Glu Ala
            340                 345                 350
Tyr Asn Thr Gln Ile Leu Ala Lys Leu Pro Leu Glu Pro Lys Val Arg
        355                 360                 365
Leu Gly Gly Asp Lys Gly Glu Pro Ile Val Ile Ser His Pro Thr Ser
    370                 375                 380
Val Ser Ala Lys Ile Phe Glu Lys Met Ala Lys Asp Leu Ser Ala Phe
385                 390                 395                 400
Leu Asp Lys Val Glu Arg Glu Lys Leu Ala Asp Asn Lys Asp Ile Gln
                405                 410                 415
Pro Thr Gln Thr His Ala Tyr Ser His
            420                 425
```

(2) INFORMATION FOR SEQ ID NO:1878:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 443 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1878

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

```
        35                  40                  45
Thr Thr Thr Gly Ala Leu Gln Val Asp Ser Ser Leu Leu Pro Lys Gly
    50                  55                  60
Ile Glu Asn His Lys Leu Gly Phe Gly Val Gly Gly Glu Ile Gly Ala
65                  70                  75                  80
Leu Ala Tyr Asp Ser Thr Lys Phe Leu Ile Asp Glu Ala Asn Pro Lys
                85                  90                  95
Ala Gly Phe Gln Pro Ala Asn Trp Tyr Tyr Met Gly Arg Trp Glu Gly
            100                 105                 110
Tyr Leu Met Gln His Ser Gln Asn Trp Thr Arg Glu Gln Lys Ala Gln
        115                 120                 125
Asn Ala Arg Pro Tyr Val Leu Tyr Asn Leu Tyr Leu Asp Tyr Gln Tyr
    130                 135                 140
Lys Asp Ile Phe Gly Ile Lys Leu Gly Arg Tyr Pro Ser Lys Ala Leu
145                 150                 155                 160
Phe Leu Ser Gly Phe Asn Gln Gly Phe Glu Ile Phe Tyr Arg Trp Lys
                165                 170                 175
Lys Phe Lys Ile Val Trp Phe Ser Thr Phe Gly Arg Ala Leu Ala Asn
            180                 185                 190
Glu Gln Tyr Ile Arg Asp Phe Tyr Ala Pro Val Asn Tyr Lys Gln Lys
        195                 200                 205
Ile Asn Tyr Gly Met His Asn Phe Asn Leu Val Tyr Glu Asn Lys Tyr
    210                 215                 220
Ile Arg Ile Ala Pro Phe Ile Trp Phe Tyr Pro Lys Asn Phe Asn Ala
225                 230                 235                 240
Pro Gly Phe Glu Ile Thr His Asp Thr Lys Ser Tyr Trp Lys Ser Leu
                245                 250                 255
Trp Arg Ile Gln Thr Thr Phe Tyr Ala Trp Phe Pro Leu Tyr Ser Asp
            260                 265                 270
Tyr Leu Ser Lys Asp Tyr Tyr Arg Ala Ala Leu Val Gly Lys Lys Ser
        275                 280                 285
Ala Ala Leu Phe Val Phe Gln Arg Val Asn Phe Arg Ser Tyr Arg Phe
    290                 295                 300
Gly Trp Ser Val Tyr Lys Asn Phe Gly Asn Ala Ser Val Gln Leu Gly
305                 310                 315                 320
Trp Asn Gly Ser Pro Ile Asp Pro Phe Tyr Asp Thr Lys Asp Asp Thr
                325                 330                 335
Pro Tyr Glu Asp Ala Tyr Ser Asn Phe Tyr Asn Ala Asn Ser Ile Thr
            340                 345                 350
Ile Asn Ala Phe Ile Gly Lys Ser Ile Lys Asn Leu Leu Val Gln Leu
        355                 360                 365
Tyr Gly Lys Leu Thr Tyr Ser Pro Arg Ala Asp Ala Gln Ser Leu Gly
    370                 375                 380
Val Thr Phe Lys Tyr Asn Leu Lys Lys His Ile Tyr Phe Met Leu Met
385                 390                 395                 400
Val Asn Gly Tyr Gln Ile Thr Met His Lys Gly Tyr Lys Val Gly Phe
                405                 410                 415
Phe Thr Ser Gly Tyr Asn Pro Asp Phe Ala Gln Thr Ile Gln Asn Arg
            420                 425                 430
Ser Tyr Leu Met Ser Ser Met Ser Tyr Arg Phe
        435                 440
```

(2) INFORMATION FOR SEQ ID NO:1879:

(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:

This Sheet Has Been Replaced



(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1879

```
Tyr Pro Thr Asn Thr Ile Ile Glu Arg Ile Leu Met Phe Lys Lys Met
1               5                  10                  15
Cys Leu Ser Leu Leu Met Ile Ser Gly Val Cys Val Gly Ala Lys Asp
            20                  25                  30
Leu Asp Phe Lys Leu Asp Tyr Arg Ala Thr Gly Gly Lys Phe Met Gly
        35                  40                  45
Lys Met Thr Asp Ser Ser Leu Leu Ser Ile Thr Ser Met Asn Asp Glu
    50                  55                  60
Pro Val Val Ile Lys Asn Leu Ile Val Asn Arg Gly Asn Ser Val Glu
65                  70                  75                  80
Ala Thr Lys Lys Val Glu Pro Lys Phe Gly Asp Lys Phe Lys Lys Glu
                85                  90                  95
Lys Leu Phe Asp His Glu Leu Lys Tyr Ser Gln Gln Ile Phe Tyr Arg
            100                 105                 110
Leu Asp Cys Lys Pro Asn Gln Leu Leu Glu Val Lys Ile Ile Thr Asp
        115                 120                 125
Lys Gly Glu Tyr Tyr His Lys Phe Ser Lys
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:1880:

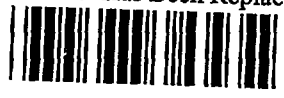
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 391 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



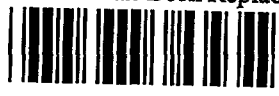
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1880

```
Arg Ile Gly Met Asp Ala Leu Glu Ile Thr Gln Lys Leu Ile Ser Tyr
1               5                  10                  15
Pro Thr Ile Thr Pro Lys Glu Cys Gly Ile Phe Glu Tyr Ile Lys Ser
            20                  25                  30
Leu Phe Pro Ala Phe Lys Thr Leu Glu Cys Glu Lys Asn Gly Val Lys
        35                  40                  45
Asn Leu Phe Leu Tyr Arg Ile Phe Asn Pro Leu Lys Lys His Ala Glu
    50                  55                  60
Lys Glu His Ala Lys Glu Lys His Val Lys Glu Asn Val Lys Pro Leu
65                  70                  75                  80
His Phe Cys Phe Ala Gly His Ile Asp Val Val Pro Pro Gly Asn Asn
                85                  90                  95
Trp Gln Ser Asp Pro Phe Lys Pro Ile Ile Lys Glu Gly Phe Leu Tyr
            100                 105                 110
Gly Arg Gly Ala Gln Asp Met Lys Gly Gly Val Gly Ala Phe Leu Ser
        115                 120                 125
Ala Ser Leu Asn Phe Asn Pro Lys Thr Pro Phe Leu Leu Ser Ile Leu
```

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

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1881:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 928 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1881

```
Thr Ser Leu Asp His Lys Ile Thr Asp Phe Ser Cys Val Asp Leu Arg
1               5                   10                  15
Ile Gln Ser Lys Glu Val Ser His Asn Leu Lys Glu Leu Ser Lys Thr
            20                  25                  30
Leu Ile Ser Tyr Pro Phe Glu Lys His Val Glu Ala Leu Gly Glu Gln
        35                  40                  45
Cys Ser Asn Phe Val Ser Ile Pro Ile Asn Asn Asp Asp Tyr Ser Asn
    50                  55                  60
Ile Cys Thr Phe Val Ser Asp Phe Ile Asn Leu Ile Ala Ser Tyr Asn
65                  70                  75                  80
```

Leu Leu Glu Ser Phe Leu Asp Phe Tyr Lys Asp Lys Leu Lys Leu Ser
85 90 95
Glu Leu Val Thr Glu Tyr Ala Asn Val Thr Asn Asn Leu Leu Phe Lys
100 105 110
Lys Leu Ile Lys His Leu Ser Gly Asn Asn Gln Leu Val Lys Asn Phe
115 120 125
Tyr Gln Cys Ile Arg Glu Ile Ile Lys Tyr Asn Ala Pro Asn Lys Glu
130 135 140
Tyr Lys Pro Asn Gln Phe Phe Ile Ile Gly Lys Gly Lys Gln Lys Gln
145 150 155 160
Leu Ala Lys Ile Tyr Ser His Leu Lys Glu Leu Ser Ala Ser Glu Ile
165 170 175
Lys Pro Gln Asp Met Glu Asp Ile Leu Lys Lys Leu Glu Glu Leu Asp
180 185 190
Lys Ile Phe Lys Thr Thr Asp Phe Thr Lys Phe Thr Pro Lys Thr Glu
195 200 205
Ile Lys Asp Ile Ile Lys Glu Ile Asp Glu Lys Tyr Pro Ile Asn Glu
210 215 220
Asn Phe Lys Arg Gln Phe Asn Glu Phe Glu Ser Asn Ile Glu Lys His
225 230 235 240
Asp Glu Ile Lys Lys Asp Phe Glu Arg Asn Lys Glu Ser Leu Ile Arg
245 250 255
Glu Ile Glu Asn His Cys Lys Asn Glu Cys Asn Ser Glu Glu Glu Pro
260 265 270
Glu Tyr Lys Ile Asn Asp Leu Leu Lys Asn Ile Gln Gln Ile Cys Lys
275 280 285
Asn Tyr Ile Glu Ser His Ala Val Asn Asp Val Ser Lys Asp Ile Lys
290 295 300
Ser Met Met Cys Gln Phe Tyr Leu Lys Gln Ile Asp Leu Leu Val Asn
305 310 315 320
Ser Glu Ile Val Arg Tyr Arg Tyr Ser Asn Leu Phe Glu Pro Ile Gln
325 330 335
Arg Ser Leu Trp Glu Ser Ile Lys Ile Leu Asp Asn Glu Ser Gly Ile
340 345 350
Tyr Leu Phe Pro Lys Asn Ile Gly Glu Ile Lys Asp Lys Phe Glu Ala
355 360 365
Asn Lys Glu Lys Phe Lys Gln Ser Lys Asn Val Ser Glu Phe Ala Glu
370 375 380
Tyr Cys Arg Glu Cys Asn Pro Tyr Thr Ala Phe Asn Phe His Leu Asn
385 390 395 400
Ile Asn Asn Gly Leu Ser His Gln Phe Glu Lys Phe Val Pro Ile Met
405 410 415
Lys Glu Tyr Lys Glu Pro Lys Ile Thr Asp Asn Asp Leu Glu Ala Ile
420 425 430
Ser Thr Lys Glu Thr Gly Leu Ala Ser Gln Leu Ser Gly His Trp Phe
435 440 445
Phe Gln Leu Ser Leu Phe Asn Lys Thr Asn Phe Asn Pro Asn Lys Ile
450 455 460
Trp Ile Pro Leu Glu Phe Asn Lys Arg Ser Lys Ile Lys Phe Asp Lys
465 470 475 480
Asp Leu Glu Ile Tyr Phe Asp Ser His Glu Ser Phe Asn Ile Ser Lys
485 490 495
Lys Tyr Leu Gln Glu Ile Asp Gln Glu Ser Leu Lys Lys Ile Lys Gln
500 505 510
Ser Lys Asp Phe Phe Ser Ile Gln Lys Ile Glu Ser Lys His Asp Asn
515 520 525
Asn Asp Ile Leu Gln Leu Glu Phe Phe Glu Asn Asp Thr Ser Phe Leu
530 535 540
Phe Ala Lys Gly Ser Phe Ala Glu Ile Leu Glu Tyr Asn Met Gln Leu
545 550 555 560
Lys Ile Asp Ser Leu Ile Thr Lys Glu Phe Asn Lys Leu Leu Ala Ile
565 570 575
Val Gln Asp Ser Pro Gln Asp Ser Tyr Gln Leu Lys Ile Arg Val Arg
580 585 590
His Asn Asn Lys Leu Pro Arg Glu Lys Tyr Thr Glu His Glu Ile Lys

595 600 605
Leu Glu Val Tyr Asp Cys Arg Lys Ser His Asp His Asn Glu Pro Ile
610 615 620
Ile Leu Ser Gln Gln Ser Thr Gly Phe Gln Trp Ala Phe Asn Phe Met
625 630 635 640
Phe Gly Phe Leu Tyr Asn Val Gly Ser His Phe Ser Phe Asn His Asn
645 650 655
Ile Ile Tyr Val Met Asp Glu Pro Ala Thr His Leu Ser Val Pro Ala
660 665 670
Arg Lys Glu Phe Arg Lys Phe Leu Lys Glu Tyr Ala His Lys Asn His
675 680 685
Val Thr Phe Val Leu Ala Thr His Asp Pro Phe Leu Val Asp Thr Asp
690 695 700
His Leu Asp Glu Ile Arg Ile Val Glu Lys Glu Thr Glu Gly Ser Val
705 710 715 720
Ile Lys Asn His Phe Asn Tyr Pro Leu Asn Asn Ala Ser Lys Asp Ser
725 730 735
Asp Ala Leu Asp Lys Ile Lys Arg Ser Leu Gly Val Gly Gln His Val
740 745 750
Phe His Asn Pro Gln Lys His Arg Ile Ile Phe Val Glu Gly Ile Thr
755 760 765
Asp Tyr Cys Tyr Leu Ser Ala Phe Lys Leu Tyr Leu Arg Tyr Lys Glu
770 775 780
Tyr Lys Asp Asn Pro Ile Pro Phe Thr Phe Leu Pro Ile Ser Gly Leu
785 790 795 800
Lys Asn Asp Ser Asn Asp Met Lys Glu Thr Ile Glu Lys Leu Cys Glu
805 810 815
Leu Asp Asn His Pro Ile Val Leu Thr Asp Asp Asp Arg Lys Cys Val
820 825 830
Phe Asn Gln Gln Ala Thr Ser Glu Arg Phe Lys Arg Ala Asn Glu Glu
835 840 845
Met His Asp Pro Ile Thr Ile Leu Gln Leu Ser Asp Cys Asp Arg His
850 855 860
Phe Lys Gln Ile Glu Asp Cys Phe Ser Ala Asn Asp Arg Asn Lys Tyr
865 870 875 880
Ala Lys Asn Lys Gln Met Glu Leu Ser Met Ala Phe Lys Thr Arg Leu
885 890 895
Leu Tyr Gly Gly Glu Asp Ala Ile Glu Lys Gln Thr Lys Arg Asn Phe
900 905 910
Leu Lys Leu Phe Lys Trp Ile Ala Trp Ala Thr Asn Leu Ile Lys Asn
915 920 925

(2) INFORMATION FOR SEQ ID NO:1882:

(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:1882

Gln Ala Leu Gly Ile Asn Met Cys Ser Lys Lys Ile Arg Asn Leu Ile
1 5 10 15

This Sheet Has Been Replaced



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

(2) INFORMATION FOR SEQ ID NO:1883:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1883

```
Arg Phe Phe Arg Lys His Arg Val Ile Ser Met Lys Glu Ile Val Thr
1               5                   10                  15
Ile Glu Asn Val Ser Phe Asn Tyr His Asn Arg Ala Ile Phe Lys Asp
            20                  25                  30
Phe Asn Leu Ser Ile Gln Glu Gly Asp Phe Leu Cys Val Leu Gly Glu
        35                  40                  45
Ser Gly Ser Gly Lys Ser Thr Leu Leu Gly Leu Ile Leu Gly Leu Leu
```

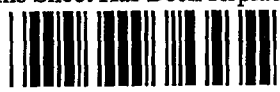
This Sheet Has Been Replaced



```
    50                  55                  60
Lys Pro Ser Leu Gly Ser Val Lys Ile Phe Asn Glu Thr Leu Ser Asn
65                  70                  75                  80
Asn Ala Phe Leu Arg Gln Lys Ile Gly Tyr Ile Ala Gln Gly Asn Ser
                85                  90                  95
Leu Phe Pro His Leu Asn Ala Leu Gln Asn Met Thr Phe Cys Leu Asn
            100                 105                 110
Leu Gln Gly Ile Asn Lys Gln Ala Ala Gln Lys Glu Ala Lys Ala Leu
        115                 120                 125
Ala Leu Lys Met Gly Leu Asp Glu Ser Leu Met Asp Lys Phe Pro Asn
    130                 135                 140
Glu Leu Ser Gly Gly Gln Ala Gln Arg Val Gly Ile Ile Arg Gly Ile
145                 150                 155                 160
Ile His Arg Pro Glu Leu Ile Leu Leu Asp Glu Pro Phe Ser Ala Leu
                165                 170                 175
Asp Ser Leu Asn Arg Lys Asn Leu Gln Asp Leu Ile Lys Glu Ile His
            180                 185                 190
Gln Asn Ser Cys Ala Thr Phe Ile Met Val Thr His Asp Glu Asn Glu
        195                 200                 205
Ala Gln Lys Leu Ala Thr Lys Thr Leu Glu Ile Lys Ala Leu Lys Gln
    210                 215                 220
Glu Gln
225
```

(2) INFORMATION FOR SEQ ID NO:1884:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 594 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1884

```
Met Ala Asp Leu Leu Ser Ser Leu Lys Asn Leu Ser Ser Ser Ser Gly
1               5                   10                  15
Val Tyr Gln Tyr Phe Asp Lys Asn Arg Gln Leu Leu Tyr Ile Gly Lys
            20                  25                  30
Ala Lys Asn Leu Lys Lys Arg Ile Lys Ser Tyr Phe Ser Val Arg Asn
        35                  40                  45
Asn Glu Ile Thr Pro Asn Pro Arg Thr Ser Leu Arg Val Gln Met Met
    50                  55                  60
Val Lys Gln Ile Ala Phe Leu Glu Thr Ile Leu Val Glu Asn Glu Gln
65                  70                  75                  80
Asp Ala Leu Ile Leu Glu Asn Ser Leu Ile Lys Gln Leu Lys Pro Lys
                85                  90                  95
Tyr Asn Ile Leu Leu Arg Asp Asp Lys Thr Tyr Pro Tyr Ile Tyr Met
            100                 105                 110
Asp Phe Ser Ile Asp Phe Pro Ile Pro Leu Ile Thr Arg Lys Ile Leu
        115                 120                 125
Lys Gln Pro Gly Val Lys Tyr Phe Gly Pro Phe Thr Ser Gly Ala Lys
    130                 135                 140
Asp Ile Leu Asp Ser Leu Tyr Glu Leu Leu Pro Leu Val Gln Lys Lys
145                 150                 155                 160
```

```
Asn Cys Ile Lys Asp Lys Lys Ala Cys Met Phe Tyr Gln Ile Glu Arg
                165                 170                 175
Cys Lys Ala Pro Cys Glu Asp Lys Ile Thr Lys Glu Glu Tyr Leu Lys
            180                 185                 190
Ile Ala Lys Glu Cys Leu Glu Met Ile Glu Asn Lys Asp Arg Leu Ile
        195                 200                 205
Lys Glu Leu Glu Leu Lys Met Glu Arg Leu Ser Ser Asn Leu Arg Phe
    210                 215                 220
Glu Glu Ala Leu Ile Tyr Arg Asp Arg Ile Ala Lys Ile Gln Lys Ile
225                 230                 235                 240
Ala Pro Phe Thr Cys Met Asp Leu Ala Lys Leu Tyr Asp Leu Asp Ile
                245                 250                 255
Phe Ala Phe Tyr Gly Gly Asn Asn Lys Ala Val Leu Val Lys Met Phe
            260                 265                 270
Met Arg Gly Gly Lys Ile Ile Ser Ser Ala Phe Glu Lys Ile His Ser
        275                 280                 285
Leu Asn Gly Phe Asp Thr Asp Glu Ala Met Lys Gln Ala Ile Ile Asn
    290                 295                 300
His Tyr Gln Ser His Leu Pro Leu Met Pro Glu Gln Ile Leu Leu Ser
305                 310                 315                 320
Ala Cys Ser Asn Glu Thr Leu Lys Glu Leu Gln Glu Phe Ile Ser His
                325                 330                 335
Gln Tyr Ser Lys Lys Ile Ala Leu Ser Ile Pro Lys Lys Gly Asp Lys
            340                 345                 350
Leu Ala Leu Ile Glu Ile Ala Met Lys Asn Ala Gln Glu Ile Phe Ser
        355                 360                 365
Gln Glu Lys Thr Ser Asn Glu Asp Arg Ile Leu Glu Glu Ala Arg Ser
    370                 375                 380
Leu Phe Asn Leu Glu Cys Val Pro Tyr Arg Val Glu Ile Phe Asp Thr
385                 390                 395                 400
Ser His His Ser Asn Ser Gln Cys Val Gly Gly Met Val Val Tyr Glu
                405                 410                 415
Asn Asn Ala Phe Gln Lys Asp Ser Tyr Arg Arg Tyr His Leu Lys Gly
            420                 425                 430
Ser Asn Glu Tyr Asp Gln Met Ser Glu Leu Leu Thr Arg Arg Ala Leu
        435                 440                 445
Asp Phe Ala Lys Glu Pro Pro Pro Asn Leu Trp Val Ile Asp Gly Gly
    450                 455                 460
Arg Ala Gln Leu Asn Ile Ala Leu Glu Ile Leu Lys Ser Ser Gly Ser
465                 470                 475                 480
Phe Val Glu Val Ile Ala Ile Ser Lys Glu Lys Arg Asp Ser Lys Ala
                485                 490                 495
Tyr Arg Ser Lys Gly Gly Ala Lys Asp Ile Ile His Thr Ile Ser His
            500                 505                 510
Thr Phe Lys Leu Leu Pro Ser Asp Lys Arg Leu Gln Trp Val Gln Lys
        515                 520                 525
Leu Arg Asp Glu Ser His Arg Tyr Ala Ile Asn Phe His Arg Ser Thr
    530                 535                 540
Lys Leu Lys Asn Met Lys Gln Ile Ala Leu Leu Lys Glu Lys Gly Ile
545                 550                 555                 560
Gly Glu Ala Ser Val Lys Lys Leu Leu Asp Tyr Phe Gly Ser Phe Glu
                565                 570                 575
Ala Ile Glu Lys Ala Ser Asp Gln Glu Lys Asn Ala Val Leu Lys Lys
            580                 585                 590
Arg Lys
```

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1885:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 424 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1885

```
Arg Lys Asn Met Lys Lys Arg Leu Asn Ile Gly Leu Val Gly Leu Gly
1               5                  10                  15
Cys Val Gly Ser Thr Val Ala Lys Ile Leu Gln Glu Asn Gln Glu Ile
            20                  25                  30
Ile Lys Asp Arg Ala Gly Val Glu Ile Lys Ile Lys Lys Ala Val Val
        35                  40                  45
Arg Asp Val Lys Lys His Lys Gly Tyr Ala Phe Glu Ile Ser Asp Asp
    50                  55                  60
Leu Glu Ser Val Ile Glu Asp Lys Gly Ile Asp Ile Val Val Glu Leu
65                  70                  75                  80
Met Gly Gly Val Glu Ala Pro Tyr Leu Leu Ala Lys Lys Thr Leu Ala
                85                  90                  95
Lys Gln Lys Ala Phe Val Thr Ala Asn Lys Ala Met Leu Ala Tyr His
            100                 105                 110
Arg Tyr Glu Leu Glu Gln Ile Ala Lys Asn Thr Pro Ile Gly Phe Glu
        115                 120                 125
Ala Ser Val Cys Gly Gly Ile Pro Ile Ile Lys Ala Leu Lys Asp Gly
    130                 135                 140
Leu Ser Ala Asn His Ile Leu Ser Phe Lys Gly Ile Leu Asn Gly Thr
145                 150                 155                 160
Ser Asn Tyr Ile Leu Ser Gln Met Phe Lys Asn Gln Ala Ser Phe Lys
                165                 170                 175
Asp Ala Leu Lys Asp Ala Gln His Leu Gly Tyr Ala Glu Leu Asn Pro
            180                 185                 190
Glu Phe Asp Ile Lys Gly Ile Asp Ala Ala His Lys Leu Leu Ile Leu
        195                 200                 205
Ala Ser Leu Ala Tyr Gly Ile Asp Ala Lys Leu Glu Glu Ile Leu Ile
    210                 215                 220
Glu Gly Ile Glu Lys Ile Glu Pro Asp Asp Met Glu Phe Ala Lys Glu
225                 230                 235                 240
Phe Gly Tyr Ser Ile Lys Leu Leu Gly Ile Ala Lys Lys His Gln Asp
                245                 250                 255
Cys Ile Glu Leu Arg Val His Pro Ser Met Ile Lys Asn Glu Cys Met
            260                 265                 270
Leu Ser Lys Val Asp Gly Val Met Asn Ala Ile Ser Val Ile Gly Asp
        275                 280                 285
Lys Val Gly Glu Thr Leu Tyr Tyr Gly Ala Gly Ala Gly Gly Glu Pro
    290                 295                 300
Thr Ala Ser Ala Val Ile Ser Asp Ile Ile Glu Ile Ala Arg Lys Lys
305                 310                 315                 320
Ser Ser Leu Met Leu Gly Phe Glu Thr Pro Gln Lys Leu Pro Leu Lys
                325                 330                 335
Pro Lys Glu Glu Ile Gln Cys Ala Tyr Tyr Ala Arg Leu Leu Val Ser
            340                 345                 350
Asp Glu Lys Gly Val Phe Ser Gln Ile Ser Ala Ile Leu Ala Gln Asn
        355                 360                 365
Asp Ile Ser Leu Asn Asn Val Leu Gln Lys Glu Ile Pro Gln Ser Asn
    370                 375                 380
Lys Ala Lys Ile Leu Phe Ser Thr His Thr Thr Asn Glu Lys Ser Met
385                 390                 395                 400
Leu Asn Ala Leu Lys Glu Leu Glu Asn Leu Gln Ser Val Leu Asp Thr
                405                 410                 415
```

This Sheet Has Been Replaced

SUBSTITUTE SHEET (RULE 26)

Pro Lys Met Ile Arg Leu Glu Asn
420

(2) INFORMATION FOR SEQ ID NO:1886:

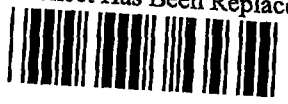
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1886

```
Ser Arg Phe Lys Arg Ala Ile Glu Gln Ala Phe Arg Leu Val Ala Met
1               5                  10                  15
Ile Asp Cys Ala Ile Ile Gly Gly Gly Pro Ala Gly Leu Ser Ala Gly
            20                  25                  30
Leu Tyr Ala Thr Arg Gly Gly Val Lys Asn Ala Val Leu Phe Glu Lys
        35                  40                  45
Gly Met Pro Gly Gly Gln Ile Thr Gly Ser Ser Glu Ile Glu Asn Tyr
    50                  55                  60
Pro Gly Val Lys Glu Val Val Ser Gly Leu Asp Phe Met Gln Pro Trp
65                  70                  75                  80
Gln Glu Gln Cys Phe Arg Phe Gly Leu Lys His Glu Met Thr Ala Ile
                85                  90                  95
Gln Arg Val Ser Lys Lys Gly Ser His Phe Val Ile Leu Ala Glu Asp
            100                 105                 110
Gly Lys Thr Phe Glu Ala Lys Ser Val Ile Ile Ala Thr Gly Gly Ser
        115                 120                 125
Pro Lys Arg Thr Gly Ile Lys Gly Glu Ser Glu Tyr Trp Gly Lys Gly
    130                 135                 140
Val Ser Thr Cys Ala Thr Cys Asp Gly Phe Phe Tyr Lys Asn Lys Glu
145                 150                 155                 160
Val Ala Val Leu Gly Gly Gly Asp Thr Ala Val Glu Glu Ala Ile Tyr
                165                 170                 175
Leu Ala Asn Ile Cys Lys Lys Val Tyr Leu Ile His Arg Arg Asp Gly
            180                 185                 190
Phe Arg Cys Ala Pro Ile Thr Leu Glu His Ala Lys Asn Asn Ser Lys
        195                 200                 205
Ile Glu Phe Leu Thr Pro Tyr Val Val Glu Glu Ile Lys Gly Asp Ala
    210                 215                 220
Ser Gly Val Ser Ser Leu Ser Ile Lys Asn Thr Ala Thr Asn Glu Lys
225                 230                 235                 240
Arg Glu Leu Val Val Pro Gly Leu Phe Ile Phe Val Gly Tyr Asp Val
                245                 250                 255
Asn Asn Ala Val Leu Lys Gln Glu Asp Asn Ser Met Leu Cys Glu Cys
            260                 265                 270
Asp Glu Tyr Gly Ser Ile Val Val Asp Phe Ser Met Lys Thr Asn Val
        275                 280                 285
Gln Gly Leu Phe Ala Ala Gly Asp Ile Arg Ile Phe Ala Pro Lys Gln
    290                 295                 300
Val Val Cys Ala Ala Ser Asp Gly Ala Thr Ala Ala Leu Ser Val Ile
305                 310                 315                 320
Ser Tyr Leu Glu His His
```

(2) INFORMATION FOR SEQ ID NO:1887:

(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:1887

```
Lys Leu Trp Glu Phe Ser Leu Arg Val Phe Ile Ile Ser Leu Asn Gln
1               5                  10                  15
Lys Val Cys Asp Lys Phe Gly Leu Val Phe Arg Asp Thr Thr Thr Leu
            20                  25                  30
Leu Asn Asn Ile Asn Ala Thr His His Gln Ala Gln Ile Phe Asp Ala
        35                  40                  45
Ile Tyr Ser Lys Thr Phe Glu Gly Gly Leu His Pro Leu Val Lys Lys
    50                  55                  60
His Leu His Pro Tyr Phe Ile Thr Gln Asn Ile Lys Asp Met Gly Ile
65                  70                  75                  80
Ala Thr Ser Leu Ile Ser Glu Val Ser Lys Phe Tyr Tyr Ala Leu Lys
                85                  90                  95
Tyr His Ala Lys Phe Met Ser Leu Gly Glu Leu Gly Cys Tyr Ala Ser
            100                 105                 110
His Tyr Ser Leu Trp Gln Lys Cys Ile Glu Leu Asn Glu Ala Ile Cys
        115                 120                 125
Ile Leu Glu Asp Asp Ile Thr Leu Lys Glu Asp Phe Lys Glu Gly Leu
    130                 135                 140
Asp Phe Leu Glu Lys His Ile Gln Glu Leu Gly Tyr Ala Arg Leu Met
145                 150                 155                 160
His Leu Leu Tyr Asp Ala Ser Val Lys Ser Glu Pro Leu Asn His Glu
                165                 170                 175
Asn Gln Glu Ile Gln Glu Arg Val Gly Ile Ile Lys Ala Tyr Ser His
            180                 185                 190
Gly Val Gly Thr Gln Gly Tyr Val Ile Thr Pro Lys Ile Ala Lys Val
        195                 200                 205
Phe Leu Lys His Ser Arg Lys Trp Val Val Pro Val Asp Thr Ile Met
    210                 215                 220
Asp Ala Thr Phe Ile His Gly Val Lys Asn Leu Val Leu Gln Pro Phe
225                 230                 235                 240
Val Ile Ala Asp Asp Glu Gln Ile Ser Thr Ile Ala Arg Lys Glu Glu
                245                 250                 255
Pro Tyr Ser Pro Lys Ile Ala Leu Met Arg Glu Leu His Phe Lys Phe
            260                 265                 270
Leu Lys Trp Trp Gln Phe Val
        275
```

(2) INFORMATION FOR SEQ ID NO:1888:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 236 amino acids

This Sheet Has Been Replaced



(B) TYPE: amino acid
(D) TOPOLOGY: linear

(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:1888

```
Gly Asp Phe Ile Ile Ser Asn Ile Ser Ile His Pro Lys Thr Met Phe
1               5                  10                  15
Lys Asn Ala Leu Asn Ile Gln Asp Phe Ser Phe Lys Asn His Thr Ser
            20                  25                  30
Thr Ala Ile Ile Gly Thr Asn Gly Ala Gly Lys Ser Thr Leu Ile Asn
        35                  40                  45
Thr Ile Leu Gly Ile Arg Ser Asp Tyr Asn Phe Lys Ala Gln Asn Asn
    50                  55                  60
Asn Ile Pro Tyr His Asp Asn Val Ile Pro Gln Arg Lys Gln Leu Gly
65                  70                  75                  80
Val Val Ser Asn Leu Phe Asn Tyr Pro Pro Gly Leu Asn Ala Asn Asp
                85                  90                  95
Leu Phe Lys Phe Tyr Gln Phe Phe His Lys Asn Cys Thr Leu Asp Leu
            100                 105                 110
Phe Glu Lys Asn Leu Leu Asn Lys Thr Tyr Glu His Leu Ser Asp Gly
        115                 120                 125
Gln Lys Gln Arg Leu Lys Ile Asp Leu Ala Leu Ser His His Pro Gln
    130                 135                 140
Leu Val Ile Met Asp Glu Pro Glu Thr Ser Leu Glu Gln Asn Ala Leu
145                 150                 155                 160
Ile Arg Leu Ser Asn Leu Ile Ser Leu Arg Asn Thr Gln Gln Leu Thr
                165                 170                 175
Ser Ile Ile Ala Thr His Asp Pro Ile Val Leu Asp Ser Cys Glu Trp
            180                 185                 190
Val Leu Leu Leu Lys Asn Gly Asn Ile Ala Gln Tyr Lys Pro Leu Asn
        195                 200                 205
Ser Ile Leu Lys Ser Val Ala Lys Thr Phe Asn Phe Lys Glu Lys Pro
    210                 215                 220
Thr Thr Lys Asp Leu Leu Ala Leu Leu Lys Asp Ile
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:1889:

(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:1889

```
Ile Tyr Ser His Leu Ala Pro Ile Met His Tyr Gln Leu Thr Ser Phe
1               5                  10                  15
Asn Ile Ile Gln Asp Leu Phe Ile Thr Cys His Val Leu Arg Ile Lys
            20                  25                  30
Met Arg Val Phe Val Cys Phe Leu Gly Val Phe Val Ser Asn Gly Leu
        35                  40                  45
Ala Arg Phe Gly Tyr Val Val Leu Ile Pro Leu Leu Ile Leu Ser Gly
    50                  55                  60
Ser Leu Thr Pro His Gln Ser Phe Gln Leu Gly Ile Ala Val Leu Met
65                  70                  75                  80
Gly Tyr Val Phe Gly Ser Phe Leu Ile Gln Phe Leu Ser Pro Leu Met
                85                  90                  95
Ser Leu Glu Ser Ile Ala Lys Ile Ser Phe Lys Leu Ile Thr Leu Ser
            100                 105                 110
Phe
```

(2) INFORMATION FOR SEQ ID NO:1890:

(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:1890

```
Ser Met Gly Gly Phe Thr Ser Ile Trp His Trp Val Ile Val Leu Leu
1               5                  10                  15
Val Ile Val Leu Leu Phe Gly Ala Lys Lys Ile Pro Glu Leu Ala Lys
            20                  25                  30
Gly Leu Gly Ser Gly Ile Lys Asn Phe Lys Lys Ala Val Lys Asp Asp
        35                  40                  45
Glu Glu Glu Ala Lys Asn Glu Leu Lys Thr Leu Asp Ala Gln Ala Thr
    50                  55                  60
Gln Thr Lys Val His Glu Thr Ser Glu Ile Lys Ser Lys Gln Glu Ser
65                  70                  75                  80
```

(2) INFORMATION FOR SEQ ID NO:1891:

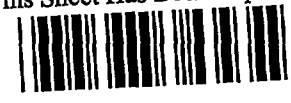
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 267 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

This Sheet Has Been Replaced



(A) ORGANISM: Helicobacter pylori

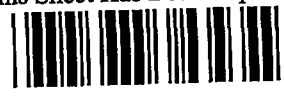
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1891

```
Arg Lys Thr Asn His Lys Arg Leu Ile Ser Val Thr Lys Gly Tyr Leu
1               5                  10                  15
Met Gly Ala Ile Leu Ser Ile Leu Lys Leu Glu Ile Lys Ser Tyr Leu
            20                  25                  30
Thr Asn Thr Ser Ala Leu Phe Trp Thr Phe Ile Tyr Pro Ile Leu Met
        35                  40                  45
Leu Leu Leu Leu Ile Phe Val Phe Ser Lys Asn Thr Thr Glu Ile Phe
    50                  55                  60
Tyr Phe Asn Asn Ile Ile Gly Leu Met Gly Leu Leu Ile Ile Ser Ser
65                  70                  75                  80
Ala Ile Phe Gly Leu Thr Gln Ala Ile Thr Ser Ser Arg Ser His Asn
                85                  90                  95
Ile Phe Leu Phe Tyr Met Leu Ser Pro Ala Thr Phe Lys Gln Ile Thr
            100                 105                 110
Leu Ala Leu Ile Ala Ser Arg Leu Ile Val Val Ile Leu Tyr Ala Phe
        115                 120                 125
Ile Phe Ile Val Leu Ser Phe Tyr Ala Leu Asn Ile Ile Thr Ile Leu
    130                 135                 140
Asn Phe Lys Ala Leu Ile Leu Gly Phe Ile Ser Ile Phe Ser Ser Ala
145                 150                 155                 160
Leu Phe Cys Phe Cys Leu Ala Ile Phe Val Ala Arg Ile Phe Gln Asn
                165                 170                 175
Glu Gln Ser Ile Leu Gly Phe Cys Asn Ile Ile Asn Leu Tyr Ala Leu
            180                 185                 190
Met Ser Cys Asn Val Phe Val Pro Leu Glu Tyr Leu Pro Asn Ile Gly
        195                 200                 205
Gln Leu Phe Ile Lys Thr Ser Ile Phe Tyr Tyr Leu Asn Gln Leu Leu
    210                 215                 220
Ile Lys Ala Phe Gln Gly Ile Asp Thr Ile Leu Val Leu Ala Thr Ser
225                 230                 235                 240
Thr Phe Phe Ile Ile Gly Gly Ile Ile Leu Phe Leu Leu Ser Ala Asn
                245                 250                 255
Arg Met Leu Leu Thr Pro Lys Glu Arg Met Arg
            260                 265
```

(2) INFORMATION FOR SEQ ID NO:1892:

This Sheet Has Been Replaced



(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:1892

```
Arg Lys Gln Glu Met Lys Lys Leu Leu Leu Leu Leu Glu His Lys Ile
```

```
1               5                   10                  15
Val Lys Ile Gly Leu Ile Ile Val Ile Val Leu Val Gly Phe Phe Leu
            20                  25                  30
Phe Tyr Glu Gln Glu Ile Lys Glu Lys Ala Val Asn Val Ser Gln Gly
        35                  40                  45
Lys Phe Pro Thr Ser Ser Tyr Leu Phe Gln Ala Tyr Glu Gly Ile Lys
    50                  55                  60
Asn Lys Ile Asp Thr Ile Asn Gln Val Lys Pro Asn Asp Glu Thr Lys
65                  70                  75                  80
Ser Val Asn Glu Asn Ile Glu Lys Thr Gln Lys Asp Leu Asp Asp Phe
                85                  90                  95
Asn Ala Leu Val Gln Lys Leu Pro Asn Leu Pro Lys Asp Phe Asn Lys
            100                 105                 110
Thr Leu Ile Lys Pro Gln Ser Pro Phe Phe Asn Tyr Asn Thr Ala Asn
        115                 120                 125
Glu Asp Glu Lys Asn Arg Leu Val Ile Leu Ala Ser Arg Ile Ser Ser
    130                 135                 140
Gln Lys Glu Thr Gln Pro Pro Ile Ser Ile Lys Asn Ser Val Ser His
145                 150                 155                 160
Ile Lys Ser Lys Glu Lys Arg Glu Leu Glu Lys Glu Trp Ala Lys Pro
                165                 170                 175
Ser Val Ser Phe Gly Ser Phe Ser Leu Leu Ser Ser Ser Ser Ser Phe
            180                 185                 190
Ser Ser Phe Glu Val Ser Phe Leu Ser Arg Gly Ile Gly Leu Asp Cys
        195                 200                 205
Glu Lys Leu Lys Ser Phe Leu Lys Ala Phe Ser Ser Ser Leu Phe Ser
    210                 215                 220
Leu Leu Ser Ser Leu Phe Cys His Pro Leu Ser Leu Phe Cys Ser Leu
225                 230                 235                 240
Ile Gly Leu Ile Phe Cys Phe Ser Lys Phe Ser Arg Glu Leu Val Asn
                245                 250                 255
Ala Ser Asn Asn Ser Leu Glu Phe Ser Ser Leu Ser Arg Leu Gly Ser
            260                 265                 270
```

(2) INFORMATION FOR SEQ ID NO:1893:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 338 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(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:1893

```
Lys Ile Phe Lys Lys Ala Leu Arg His Lys Met Glu Lys Val Cys Val
1               5                   10                  15
Ser Ala Trp Gly Leu Pro Lys Ile Leu Glu Glu Arg Leu Lys Glu Lys
            20                  25                  30
Tyr Gly Asp Asp Trp Glu Lys His Val Lys Ala Lys Ala Ile Asn Glu
        35                  40                  45
Glu Glu Leu Glu Glu Gln Val Lys Ala Lys Ala Lys Glu Gln Gln Lys
    50                  55                  60
Thr Gln Arg Glu Lys Thr Leu Asn Gly Phe Leu Lys Lys Val Gly Leu
65                  70                  75                  80
```

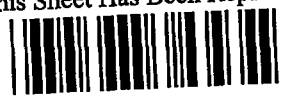
This Sheet Has Been Replaced



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

(2) INFORMATION FOR SEQ ID NO:1894:

This Sheet Has Been Replaced



(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...310

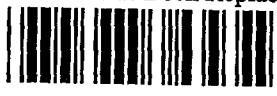
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1894

```
Val Val Val Ile Arg Leu Val Leu Asn Met Leu Thr Cys Gln Ile Ser
1               5                   10                  15
Tyr Ile Arg Ile Ser Tyr Leu Val Ser Val Ser Asp Phe Val Ile Cys
            20                  25                  30
Lys Glu Arg Phe Met Asp Glu Ile Lys Thr Leu Leu Val Asp Phe Phe
        35                  40                  45
Pro Gln Ala Lys His Phe Gly Ile Ile Leu Ile Lys Ala Ile Val Val
    50                  55                  60
Phe Cys Ile Gly Phe Tyr Phe Ser Phe Phe Leu Arg Asn Lys Thr Met
```

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

(2) INFORMATION FOR SEQ ID NO:1895:

This Sheet Has Been Replaced



(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:1895

```
Ser Lys Arg Thr Gln Gln Thr Phe Phe Leu Phe Ile Asp Glu Thr Lys
1               5                   10                  15
Asp Tyr Ile Met His Pro Ile Met Phe Ala Tyr Ile Ala Asn Ala Leu
            20                  25                  30
Ala Gln Ala Arg Lys Ile Asn Gly Thr Leu Cys Met Ala Phe Gln Lys
        35                  40                  45
Ile Ser Gln Val Lys Glu Leu Gly Ile Asp Lys Ala Lys Ser Leu Ile
    50                  55                  60
Gly Asn Leu Ser Gln Val Ile Ile Tyr Pro Thr Lys Asp Thr Asp Glu
65                  70                  75                  80
Leu Ile Glu Cys Gly Val Pro Leu Ser Asp Ser Glu Ile Asn Phe Leu
                85                  90                  95
```

```
His Asn Thr Asp Met Arg Ala Arg Gln Val Leu Val Lys Asn Ile Val
            100                 105                 110
Thr Asn Ala Ser Ala Phe Ile Glu Ile Asp Leu Lys Lys Ile Cys Lys
        115                 120                 125
Asn Tyr Phe Ile Phe Leu Ile Ala Met Leu Val Ile Glu Lys Ser Ser
    130                 135                 140
Met Ile Leu Lys Lys Gln Thr Lys Lys Leu Ile Arg Lys Ser Ile
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:1896:

(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

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1896

```
Leu Leu Lys Asn Ile Asp Glu Lys Lys Leu Ser Val Ser Lys Val Asn
1               5                   10                  15
Glu Lys Arg His Met Asp Phe Lys Lys Cys Pro Asn Phe Glu Lys Lys
            20                  25                  30
Cys Ala Phe Leu Cys Phe Ser Asn Leu Val Leu Leu Ile Glu Ile His
        35                  40                  45
Ser Lys Gly Leu His Met Gln Lys Lys Lys Pro Lys Asn Pro Gln Pro
    50                  55                  60
Asn Leu Phe Ser Ile Leu Asp Lys Gly Asp Val Ala Thr Asn Asn Pro
65                  70                  75                  80
Val Glu Glu Ser Asp Lys Ala Asn Lys Ile Gln Glu Pro Leu Pro Tyr
                85                  90                  95
Val Val Lys Thr Gln Ile Asn Lys Ala Ser Met Ile Ser Arg Asp Pro
            100                 105                 110
Ile Glu Trp Ala Lys Tyr Leu Ser Phe Glu Lys Arg Val Tyr Lys Asp
        115                 120                 125
Asn Ser Lys Glu Asp Val Asn Phe Phe Ala Asn Gly Glu Ile Lys Glu
    130                 135                 140
Ser Ser Arg Val Tyr Glu Ala Asn Lys Glu Gly Phe Glu Arg Arg Ile
145                 150                 155                 160
Thr Lys Arg Tyr Asp Leu Ile Asp Arg Asn Ile Asp Arg Asn Arg Glu
                165                 170                 175
Phe Phe Ile Lys Glu Ile Glu Ile Leu Thr His Thr Asn Ser Leu Lys
            180                 185                 190
Glu Leu Lys Glu Gln Gly Leu Glu Ile Gln Leu Thr His His Asn Glu
        195                 200                 205
Thr His Lys Lys Ala Leu Glu Asn Gly Asn Glu Ile Val Lys Glu Tyr
    210                 215                 220
Asp His Leu Lys Asp Ile Tyr Gln Glu Val Glu Arg Thr Lys Asp Gly
225                 230                 235                 240
Gly Leu Val Arg Glu Ile Ile Pro Ser Ile Ser Ser Ala Glu Tyr Phe
                245                 250                 255
Thr Leu
```

(2) INFORMATION FOR SEQ ID NO:1897:

(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:1897

TATACCATGG TGGGCGCTAA 20

(2) INFORMATION FOR SEQ ID NO:1898:

(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:1898

ATGAATTCGA GTAAGGATTT TTG 23

(2) INFORMATION FOR SEQ ID NO:1899:

(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

This Sheet Has Been Replaced



SUBSTITUTE SHEET (RULE 26)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1899

TTAACCATGG TGAAAAGCGA TA 22

(2) INFORMATION FOR SEQ ID NO:1900:

(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:1900

TAGAATTCGC ATAACGATCA ATC 23

(2) INFORMATION FOR SEQ ID NO:1901:

(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:1901

ATATCCATGG TGAGTTTGAT GA 22

(2) INFORMATION FOR SEQ ID NO:1902:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs

This Sheet Has Been Replaced



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

(ii) MOLECULE TYPE: DNA (genomic)

(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:1902

ATGAATTCAA TTTTTTATTT TGCCA 25

(2) INFORMATION FOR SEQ ID NO:1903:

(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:1903

AATTCCATGG TGGGGGCTAT G 21

(2) INFORMATION FOR SEQ ID NO:1904:

(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

This Sheet Has Been Replaced



(B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1904

ATGAATTCTC GATAGCCAAA ATC 23

(2) INFORMATION FOR SEQ ID NO:1905:

(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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1905

AATTCCATGG TGCATAACTT CCATT 25

(2) INFORMATION FOR SEQ ID NO:1906:

(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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1906

AAGAATTCTC TAGCATCCAA ATGGA 25

(2) INFORMATION FOR SEQ ID NO:1907:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

This Sheet Has Been Replaced



(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:1907

ATTTCCATGG TCATGTCTCA TATT 24

(2) INFORMATION FOR SEQ ID NO:1908:

(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:1908

ATGAATTCCA TCTTTTATTC CAC 23

(2) INFORMATION FOR SEQ ID NO:1909:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1909

AACCATGGTG ATTTTAAGCA TTGAAAG 27

This Sheet Has Been Replaced



This Sheet Has Been Replaced

(2) INFORMATION FOR SEQ ID NO:1910:

(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:1910

AAGAATTCCA CTCAAAATTT TTTAACAG 28

(2) INFORMATION FOR SEQ ID NO:1911:

(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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1911

GATCATCCAT ATGTTATCTT CTAAT 25

(2) INFORMATION FOR SEQ ID NO:1912:

(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

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1912

TGAATTCAAC CATTTTAACC CTG 23

(2) INFORMATION FOR SEQ ID NO::1913

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1913

TATACCATGG TGAAATTTTT TCTTTTA 27

(2) INFORMATION FOR SEQ ID NO:1914:

(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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1914

AGAATTCAAT TGCGTCTTGT AAAAG 25

(2) INFORMATION FOR SEQ ID NO:1915:

(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:1915

TATACCATGG TGATGGACAA ACTC 24

(2) INFORMATION FOR SEQ ID NO:1916:

(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:1916

ATGAATTCCC ACTTGGGGCG ATA 23

(2) INFORMATION FOR SEQ ID NO:1917:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

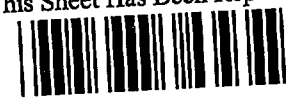
(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature

This Sheet Has Been Replaced



(B) LOCATION 1...25

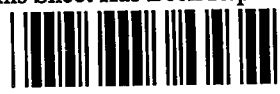
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1917

TTATGGATCC AAACCAATTA AAACT 25

(2) INFORMATION FOR SEQ ID NO:1918:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1918

TATCTCGAGT TATAGAGAAG GGC 23

(2) INFORMATION FOR SEQ ID NO:1919:

(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:1919

TTAACCATGG TGAAAAGCGA TA 22

(2) INFORMATION FOR SEQ ID NO:1920:

(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:1920

TAGAATTCGC CTCTAAAACT TTAG 24

(2) INFORMATION FOR SEQ ID NO:1921:

(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:1921

TTAACCATGG TGAAAAGCGA TA 22

(2) INFORMATION FOR SEQ ID NO:1922:

(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:1922

TAGAATTCGC ATAACGATCA ATC 23

This Sheet Has Been Replaced



(2) INFORMATION FOR SEQ ID NO:1923:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

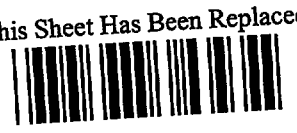
(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...22

This Sheet Has Been Replaced



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1923

ATATCCATGG TGAGTTTGAT GA 22

(2) INFORMATION FOR SEQ ID NO:1924:

(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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1924

ATGAATTCAA TTTTTTATTT TGCCA 25

(2) INFORMATION FOR SEQ ID NO:1925:

(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:1925

AATTCCATGG CTATCCAAAT CCG 23

(2) INFORMATION FOR SEQ ID NO:1926:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1926

ATGAATTCGC CAAAATCGTA GTATT 25

(2) INFORMATION FOR SEQ ID NO:1927:

(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:1927

GATACCATGG AATTTATGAA AAAG 24

(2) INFORMATION FOR SEQ ID NO:1928:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs

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

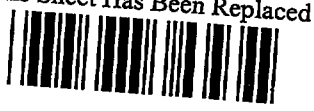
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1928

TGAATTCGAA AAAGTGTAGT TATAC 25

(2) INFORMATION FOR SEQ ID NO::1929

(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:1929

CCCTTCATTT TAGAAATCG 19

(2) INFORMATION FOR SEQ ID NO:1930:

(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:1930

ATTTCAACCA ATTCAATGCG 20

(2) INFORMATION FOR SEQ ID NO:1931:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

This Sheet Has Been Replaced



(ii) MOLECULE TYPE: DNA (genomic)

(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:1931

GCCCCTTTTG ATTTGAAGCT 20

(2) INFORMATION FOR SEQ ID NO:1932:

(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:1932

TCGCTCCAAG ATACCAAGAA GT 22

(2) INFORMATION FOR SEQ ID NO::1933

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1933

CTTGAATTAG GGGCAAAGAT CG 22

(2) INFORMATION FOR SEQ ID NO:1934:

(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:1934

ATGCGTTTTT ACCCAAAGAA GT 22

(2) INFORMATION FOR SEQ ID NO:1935:

(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:1935

ATAACGCCAC TTCCTTATTG GT 22

(2) INFORMATION FOR SEQ ID NO:1936:

(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:1936

CTTTGGGTAA AAACGCATC 19

(2) INFORMATION FOR SEQ ID NO:1937:

(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:1937

CGATCTTTGA TCCTAATTCA 20

(2) INFORMATION FOR SEQ ID NO:1938:

(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

This Sheet Has Been Replaced



This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1938

ATCAAGTTGC CTATGCTGA 19

(2) INFORMATION FOR SEQ ID NO:1939:

(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:1939

TTGAACACTT TTGATTATGC GG 22

(2) INFORMATION FOR SEQ ID NO:1940:

(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:1940

GGATTATGCG ATTGTTTTAC AAG 23

(2) INFORMATION FOR SEQ ID NO:1941:

(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:1941

GTCTTTAGCA AAAATGGCGT C 21

(2) INFORMATION FOR SEQ ID NO:1942:

(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:1942

AATGAGCGTA AGAGAGCCTT C 21

(2) INFORMATION FOR SEQ ID NO:1943:

(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

This Sheet Has Been Replaced



(B) LOCATION 1...18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1943

CTTATGGGGG TATTGTCA 18

(2) INFORMATION FOR SEQ ID NO:1944:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1944

AGCATGTGGG TATCCAGC 18

(2) INFORMATION FOR SEQ ID NO:1945:

(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:1945

AGGTTGTTGC CTAAAGACT 19

(2) INFORMATION FOR SEQ ID NO:1946:

(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:1946

CTGCCTCCAC CTTTGATC 18

(2) INFORMATION FOR SEQ ID NO:1947:

(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

This Sheet Has Been Replaced



(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1947

ACCAATATCA ATTGGCACT 19

(2) INFORMATION FOR SEQ ID NO:1948:

(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:1948

ACTTGGAAAA GCTCTGCA 18

(2) INFORMATION FOR SEQ ID NO:1949:

(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:1949

CTTGCTTGTC ATATCTAGC 19

(2) INFORMATION FOR SEQ ID NO:1950:

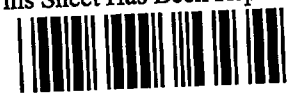
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

This Sheet Has Been Replaced



(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1950

GTTGAAGTGT TGGTGCTA 18

(2) INFORMATION FOR SEQ ID NO:1951:

(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:1951

CAAGCAAGTG GTTTGGTTTT AG 22

(2) INFORMATION FOR SEQ ID NO:1952:

(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:1952

TGGAAAGAGC AAATCATTGA AG 22

(2) INFORMATION FOR SEQ ID NO:1953:

(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

This Sheet Has Been Replaced



(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:1953

GCCCATAATC AAAAAGCCCA T 21

(2) INFORMATION FOR SEQ ID NO:1954:

(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

This Sheet Has Been Replaced


(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1954

CTAAAACCAA ACCACTTGCT TGTC 24

(2) INFORMATION FOR SEQ ID NO:1955:

(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:1955

GTAAAACGAC GGCCAG 16

(2) INFORMATION FOR SEQ ID NO:1956:

(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

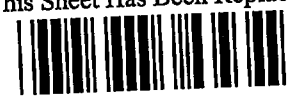
(ix) FEATURE:
(A) NAME/KEY: misc_feature

(B) LOCATION 1...17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1956

CAGGAAACAG CTATGAC 17

This Sheet Has Been Replaced



CLAIMS

1. 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: 1020, SEQ ID NO: 1021, SEQ ID NO: 1036, SEQ ID NO: 1050, SEQ ID NO: 1071, SEQ ID NO: 1101, SEQ ID NO: 1135, SEQ ID NO: 1276, SEQ ID NO: 1150, SEQ ID NO: 1187, SEQ ID NO: 1192, SEQ ID NO: 1361, SEQ ID NO: 1379, SEQ ID NO: 1399, SEQ ID NO: 1403, SEQ ID NO: 1400, SEQ ID NO: 1189, SEQ ID NO: 1002, SEQ ID NO: 1213, SEQ ID NO: 1214, SEQ ID NO: 1215, SEQ ID NO: 1234, SEQ ID NO: 1236, SEQ ID NO: 1237, SEQ ID NO: 1224, SEQ ID NO: 1251, SEQ ID NO: 1262, SEQ ID NO: 1149, SEQ ID NO: 1220, SEQ ID NO: 1240, SEQ ID NO: 1164, SEQ ID NO: 1165, SEQ ID NO: 1404, SEQ ID NO: 1144, SEQ ID NO: 1182, SEQ ID NO: 1157, SEQ ID NO: 1160, SEQ ID NO: 1300, SEQ ID NO: 1321, SEQ ID NO: 1323, SEQ ID NO: 1329, SEQ ID NO: 1332, SEQ ID NO: 1345, SEQ ID NO: 1358, SEQ ID NO: 1375, SEQ ID NO: 1417, SEQ ID NO: 1283, SEQ ID NO: 1335, SEQ ID NO: 1368, SEQ ID NO: 1179, SEQ ID NO: 1255, SEQ ID NO: 1258, SEQ ID NO: 1044, SEQ ID NO: 1273, SEQ ID NO: 1219, SEQ ID NO: 1274, SEQ ID NO: 1210, SEQ ID NO: 1422, SEQ ID NO: 1302, SEQ ID NO: 1308, SEQ ID NO: 1310, SEQ ID NO: 1331, SEQ ID NO: 1432, SEQ ID NO: 1052, SEQ ID NO: 1091, SEQ ID NO: 1421, SEQ ID NO: 1069, SEQ ID NO: 1005, SEQ ID NO: 1007, SEQ ID NO: 1166, SEQ ID NO: 1177, SEQ ID NO: 1193, SEQ ID NO: 1206, SEQ ID NO: 1207, SEQ ID NO: 1304, SEQ ID NO: 1305, SEQ ID NO: 1346, SEQ ID NO: 1348, SEQ ID NO: 1350, SEQ ID NO: 1032, SEQ ID NO: 1053, SEQ ID NO: 1081, SEQ ID NO: 1124, SEQ ID NO: 1382, SEQ ID NO: 1437, SEQ ID NO: 1263, SEQ ID NO: 1173, SEQ ID NO: 1405, SEQ ID NO: 1406, SEQ ID NO: 1410, SEQ ID NO: 1086, SEQ ID NO: 1322, SEQ ID NO: 1266, SEQ ID NO: 1282, SEQ ID NO: 1271, SEQ ID NO: 1208, SEQ ID NO: 1126, SEQ ID NO: 1270, SEQ ID NO: 1278, SEQ ID NO: 1419, SEQ ID NO: 1125, SEQ ID NO: 1181, SEQ ID NO: 1416, SEQ ID NO: 1096, SEQ ID NO: 1082, SEQ ID NO: 1146, SEQ ID NO: 1145, SEQ ID NO: 1108, SEQ ID NO: 1148, SEQ ID NO: 1337, SEQ ID NO: 1338, SEQ ID NO: 1424, SEQ ID NO: 1000, SEQ ID NO: 1027, SEQ ID NO: 1175, SEQ ID NO: 1330, SEQ ID NO: 217, SEQ ID NO: 217, SEQ ID NO: 367, SEQ ID NO: 911,SEQ ID NO: 944, SEQ ID NO: 18, SEQ ID NO: 107, SEQ ID NO: 894, SEQ ID NO: 943, SEQ ID NO: 203, SEQ ID NO: 85, SEQ ID NO: 290, SEQ ID NO: 5, SEQ ID NO: 199, SEQ ID NO: 992, SEQ ID NO: 934, SEQ ID NO: 899, SEQ ID NO: 302, SEQ ID NO: 215, SEQ ID NO: 893, SEQ ID NO: 984, SEQ ID NO: 97,SEQ ID NO: 22, SEQ ID NO: 49, SEQ ID NO: 309, SEQ ID NO: 150, SEQ ID NO: 240, SEQ ID NO: 957, SEQ ID NO: 57, SEQ ID NO: 2, SEQ ID NO: 92, SEQ ID NO: 255, SEQ ID NO: 164, SEQ ID NO: 201, SEQ ID NO: 278, SEQ ID NO: 245, SEQ ID NO: 921, SEQ ID NO: 896, SEQ ID NO: 248, SEQ ID NO: 159, SEQ ID NO: 979, SEQ ID NO: 194, SEQ ID NO: 194, SEQ ID NO: 946, SEQ

ID NO: 916, SEQ ID NO: 76, SEQ ID NO: 905, SEQ ID NO: 914, SEQ ID NO: 931, SE ID NO: 50, SEQ ID NO: 250, SEQ ID NO: 969, SEQ ID NO: 66,SEQ ID NO: 275, SEQ ID NO: 330, SEQ ID NO: 204, SEQ ID NO: 383, SEQ ID NO: 303, SEQ ID NO: 70, SEQ ID NO: 983, SEQ ID NO: 972, SEQ ID NO: 929, SEQ ID NO: 972, SEQ ID NO: 936, SEQ ID NO: 267, SEQ ID NO: 197, SEQ ID NO: 55, SEQ ID NO: 54, SEQ ID NO: 210, SEQ ID NO: 90, SEQ ID NO: 15, SEQ ID NO: 913, SEQ ID NO: 227, SEQ ID NO: 79, SEQ ID NO: 191, SEQ ID NO: 238, SEQ ID NO: 274, SEQ ID NO: 27, SEQ ID NO: 258, SEQ ID NO: 295, SEQ ID NO: 10, SEQ ID NO: 160, SEQ ID NO: 225, SEQ ID NO: 964, SEQ ID NO: 166, SEQ ID NO: 56, SEQ ID NO: 980,SEQ ID NO: 903, SEQ ID NO: 261, SEQ ID NO: 71, SEQ ID NO: 955, SEQ ID NO: 361, SEQ ID NO: 58, SEQ ID NO: 114, SEQ ID NO: 940, SEQ ID NO: 960, SEQ ID NO: 144, SEQ ID NO: 362, SEQ ID NO: 40, SEQ ID NO: 285, SEQ ID NO: 11, SEQ ID NO: 161, SEQ ID NO: 974, SEQ ID NO: 111, SEQ ID NO: 316, SEQ ID NO: 257, SEQ ID NO: 78, SEQ ID NO: 966, SEQ ID NO: 352, SEQ ID NO: 981, SEQ ID NO: 158, SEQ ID NO: 989, SEQ ID NO: 963, SEQ ID NO: 48, SEQ ID NO: 68, SEQ ID NO: 135, SEQ ID NO: 910, SEQ ID NO: 236, SEQ ID NO: 241, SEQ ID NO: 949, SEQ ID NO: 945, SEQ ID NO: 207, SEQ ID NO: 977, SEQ ID NO: 978, SEQ ID NO: 994, SEQ ID NO: 163, SEQ ID NO: 256, SEQ ID NO: 287, SEQ ID NO: 184, SEQ ID NO: 45, SEQ ID NO: 136, SEQ ID NO: 214, SEQ ID NO: 16, SEQ ID NO: 192, SEQ ID NO: 373, SEQ ID NO: 892, SEQ ID NO: 239, SEQ ID NO: 34, SEQ ID NO: 340, SEQ ID NO: 41, SEQ ID NO: 332, SEQ ID NO: 134, and SEQ ID NO: 330.

2. The purified nucleic acid of claim 1, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* flagella-associated polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1020, SEQ ID NO: 1021, SEQ ID NO: 1036, SEQ ID NO: 1050, SEQ ID NO: 1071, SEQ ID NO: 1101, SEQ ID NO: 1135, SEQ ID NO: 1276, SEQ ID NO: 1150, SEQ ID NO: 1187, SEQ ID NO: 1192, SEQ ID NO: 1361, SEQ ID NO: 1379, SEQ ID NO: 1399, SEQ ID NO: 1403, SEQ ID NO: 1400, SEQ ID NO: 1189, SEQ ID NO: 217, SEQ ID NO: 367, SEQ ID NO: 911,SEQ ID NO: 944, SEQ ID NO: 18, SEQ ID NO: 107, SEQ ID NO: 894, SEQ ID NO: 943, SEQ ID NO: 203, SEQ ID NO: 85, SEQ ID NO: 290, SEQ ID NO: 5, SEQ ID NO: 199, SEQ ID NO: 992, SEQ ID NO: 934, SEQ ID NO: 899, SEQ ID NO: 302, and SEQ ID NO: 215.

3. The purified nucleic acid of claim 1, 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: 1002, SEQ ID NO: 1213, SEQ ID NO: 1214, SEQ ID NO: 1215, SEQ ID NO: 1234, SEQ ID NO: 1236, SEQ ID NO: 1237, SEQ ID NO: 1224, SEQ ID NO: 1251, SEQ ID NO: 1262, SEQ ID NO: 1149, SEQ ID NO: 1220, SEQ ID NO: 1240, SEQ ID NO: 1164, SEQ ID NO: 1165, SEQ ID NO: 1404, SEQ ID NO: 1144, SEQ ID NO: 1182, SEQ ID NO:

1157, SEQ ID NO: 1160, SEQ ID NO: 1300, SEQ ID NO: 1321, SEQ ID NO: 1323, SEQ ID NO: 1329, SEQ ID NO: 1332, SEQ ID NO: 1345, SEQ ID NO: 1358, SEQ ID NO: 1375, SEQ ID NO: 1417, SEQ ID NO: 1283, SEQ ID NO: 1335, SEQ ID NO: 1368, SEQ ID NO: 1179, SEQ ID NO: 1255, SEQ ID NO: 1258, SEQ ID NO: 1044, SEQ ID NO: 1273, SEQ ID NO: 893, SEQ ID NO: 984, SEQ ID NO: 97,SEQ ID NO: 22, SEQ ID NO: 49, SEQ ID NO: 309, SEQ ID NO: 150, SEQ ID NO: 240, SEQ ID NO: 957, SEQ ID NO: 57, SEQ ID NO: 2, SEQ ID NO: 92, SEQ ID NO: 255, SEQ ID NO: 164, SEQ ID NO: 201, SEQ ID NO: 278, SEQ ID NO: 245, SEQ ID NO: 921, SEQ ID NO: 896, SEQ ID NO: 248, SEQ ID NO: 159, SEQ ID NO: 979, SEQ ID NO: 194, SEQ ID NO: 194, SEQ ID NO: 946, SEQ ID NO: 916, SEQ ID NO: 76, SEQ ID NO: 905, SEQ ID NO: 914, SEQ ID NO: 931, SEQ ID NO: 50, SEQ ID NO: 250, SEQ ID NO: 969, SEQ ID NO: 66,SEQ ID NO: 275, SEQ ID NO: 330, SEQ ID NO: 204, SEQ ID NO: 383, SEQ ID NO: 303, SEQ ID NO: 70, SEQ ID NO: 983, SEQ ID NO: 972, SEQ ID NO: 929, SEQ ID NO: 972, SEQ ID NO: 936, SEQ ID NO: 267, SEQ ID NO: 197, SEQ ID NO: 55, SEQ ID NO: 54, and SEQ ID NO: 210.

4. The purified nucleic acid of claim 1, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* transporter polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1219, SEQ ID NO: 1274, SEQ ID NO: 1210, SEQ ID NO: 1422, SEQ ID NO: 1302, SEQ ID NO: 1308, SEQ ID NO: 1310, SEQ ID NO: 1331, SEQ ID NO: 1432, SEQ ID NO: 1052, SEQ ID NO: 1091, SEQ ID NO: 1421, SEQ ID NO: 1069, SEQ ID NO: 1005, SEQ ID NO: 1007, SEQ ID NO: 1166, SEQ ID NO: 1177, SEQ ID NO: 1193, SEQ ID NO: 1206, SEQ ID NO: 1207, SEQ ID NO: 1304, SEQ ID NO: 1305, SEQ ID NO: 1346, SEQ ID NO: 1348, SEQ ID NO: 1350, SEQ ID NO: 1032, SEQ ID NO: 1053, SEQ ID NO: 1081, SEQ ID NO: 1124, SEQ ID NO: 1382, SEQ ID NO: 1437, SEQ ID NO: 1263, SEQ ID NO: 90, SEQ ID NO: 15, SEQ ID NO: 913, SEQ ID NO: 227, SEQ ID NO: 79, SEQ ID NO: 191, SEQ ID NO: 238, SEQ ID NO: 274, SEQ ID NO: 27, SEQ ID NO: 258, SEQ ID NO: 295, SEQ ID NO: 10, SEQ ID NO: 160, SEQ ID NO: 225, SEQ ID NO: 964, SEQ ID NO: 166, SEQ ID NO: 56, SEQ ID NO: 980,SEQ ID NO: 903, SEQ ID NO: 261, SEQ ID NO: 71, SEQ ID NO: 955, SEQ ID NO: 361, SEQ ID NO: 58, SEQ ID NO: 114, SEQ ID NO: 940, SEQ ID NO: 960, SEQ ID NO: 144, SEQ ID NO: 362, SEQ ID NO: 40, SEQ ID NO: 285, SEQ ID NO: 11, SEQ ID NO: 161, SEQ ID NO: 974, SEQ ID NO: 111, SEQ ID NO: 316, SEQ ID NO: 257, SEQ ID NO: 78, and SEQ ID NO: 966.

5. The purified nucleic acid of claim 1, wherein said *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: 1173, SEQ ID NO: 1405, SEQ ID NO: 1406, SEQ ID NO: 1410, SEQ ID NO: 1086, SEQ ID NO: 1322, SEQ ID NO: 1266, SEQ ID NO: 1282, SEQ ID NO: 1271, SEQ ID NO:

1208, SEQ ID NO: 1126, SEQ ID NO: 1270, SEQ ID NO: 1278, SEQ ID NO: 1419, SEQ ID NO: 1125, SEQ ID NO: 1181, SEQ ID NO: 1416, SEQ ID NO: 1096, SEQ ID NO: 1082, SEQ ID NO: 1146, SEQ ID NO: 1145, SEQ ID NO: 1108, SEQ ID NO: 1148, SEQ ID NO: 1337, SEQ ID NO: 1338, SEQ ID NO: 1424, SEQ ID NO: 1000, SEQ ID NO: 1027, SEQ ID NO: 1175, SEQ ID NO: 1330, SEQ ID NO: 352, SEQ ID NO: 981, SEQ ID NO: 158, SEQ ID NO: 989, SEQ ID NO: 963, SEQ ID NO: 48, SEQ ID NO: 68, SEQ ID NO: 135, SEQ ID NO: 910, SEQ ID NO: 236, SEQ ID NO: 241, SEQ ID NO: 949, SEQ ID NO: 945, SEQ ID NO: 207, and SEQ ID NO: 977.

6. A recombinant expression vector comprising the nucleic acid of claim 1 operably linked to a transcription regulatory element.

7. A cell comprising a recombinant expression vector of claim 6.

8. A method for producing an *H. pylori* polypeptide comprising culturing a cell of claim 7 under conditions that permit expression of the polypeptide.

9. 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: 1147, SEQ ID NO: 1288, SEQ ID NO: 1324, SEQ ID NO: 1363, SEQ ID NO: 997, SEQ ID NO: 1015, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1099, SEQ ID NO: 1229, SEQ ID NO: 1250, SEQ ID NO: 1268, SEQ ID NO: 1293, SEQ ID NO: 1339, SEQ ID NO: 1408, SEQ ID NO: 1429, SEQ ID NO: 1434, SEQ ID NO: 1228, SEQ ID NO: 1031, SEQ ID NO: 1034, SEQ ID NO: 1008, SEQ ID NO: 1061, SEQ ID NO: 1064, SEQ ID NO: 1191, SEQ ID NO: 1217, SEQ ID NO: 1365, SEQ ID NO: 1394, SEQ ID NO: 1414, SEQ ID NO: 1415, SEQ ID NO: 1435, SEQ ID NO: 1058, SEQ ID NO: 1059, SEQ ID NO: 1080, SEQ ID NO: 1128, SEQ ID NO: 1133, SEQ ID NO: 1211, SEQ ID NO: 1252, SEQ ID NO: 1253, SEQ ID NO: 1286, SEQ ID NO: 1289, SEQ ID NO: 1291, SEQ ID NO: 1303, SEQ ID NO: 1396, SEQ ID NO: 996, SEQ ID NO: 1095, SEQ ID NO: 1156, SEQ ID NO: 1158, SEQ ID NO: 1159, SEQ ID NO: 1277, SEQ ID NO: 1038, SEQ ID NO: 1257, SEQ ID NO: 1357, SEQ ID NO: 1436, SEQ ID NO: 1047, SEQ ID NO: 1055, SEQ ID NO: SEQ ID NO: 1141, SEQ ID NO: 1227, SEQ ID NO: 1327, SEQ ID NO: 1412, SEQ ID NO: 1003, SEQ ID NO: 1087, SEQ ID NO: 1116, SEQ ID NO: 1130, SEQ ID NO: 1132, SEQ ID NO: 1185, SEQ ID NO: 1188, SEQ ID NO: 1198, SEQ ID NO: 1218, SEQ ID NO: 1244, SEQ ID NO: 1306, SEQ ID NO: 1325, SEQ ID NO: 1397, SEQ ID NO: 1398, SEQ ID NO: 1407, SEQ ID NO: 1433, SEQ ID NO: 1216, SEQ ID NO: 1239, SEQ ID NO: 1362, SEQ ID NO: 1017, SEQ ID NO: 1019, SEQ ID NO: 1360, SEQ ID NO: 1423, SEQ ID NO: 1425, SEQ ID NO: 1374, SEQ ID NO: 1028, SEQ ID NO: 1037, SEQ ID NO: 1077, SEQ ID NO: 1115, SEQ ID NO: 1232, SEQ ID NO: 1241, SEQ ID NO: 1267, SEQ ID NO: 1163, SEQ ID NO:

1068, SEQ ID NO: 1025, SEQ ID NO: 1042, SEQ ID NO: 1046, SEQ ID NO: 1056, SEQ ID NO: 1039, SEQ ID NO: 1072, SEQ ID NO: 1073, SEQ ID NO: 1092, SEQ ID NO: 1100, SEQ ID NO: 1102, SEQ ID NO: 1103, SEQ ID NO: 1104, SEQ ID NO: 1111, SEQ ID NO: 1119, SEQ ID NO: 1136, SEQ ID NO: 1137, SEQ ID NO: 1140, SEQ ID NO: 1142, SEQ ID NO: 1233, SEQ ID NO: 1238, SEQ ID NO: 1243, SEQ ID NO: 1245, SEQ ID NO: 1247, SEQ ID NO: 1249, SEQ ID NO: 1261, SEQ ID NO: 1269, SEQ ID NO: 1279, SEQ ID NO: 1284, SEQ ID NO: 1290, SEQ ID NO: 1297, SEQ ID NO: 1328, SEQ ID NO: 1370, SEQ ID NO: 1372, SEQ ID NO: 1377, SEQ ID NO: 1383, SEQ ID NO: 1384, SEQ ID NO: 1385, SEQ ID NO: 1388, SEQ ID NO: 1401, SEQ ID NO: 1402, SEQ ID NO: 1418, SEQ ID NO: 1420, SEQ ID NO: 1427, SEQ ID NO: 1070, SEQ ID NO: 1151, SEQ ID NO: 1176, SEQ ID NO: 999, SEQ ID NO: 1006, SEQ ID NO: 1012, SEQ ID NO: 1018, SEQ ID NO: 1030, SEQ ID NO: 1033, SEQ ID NO: 1041, SEQ ID NO: 1049, SEQ ID NO: 1054, SEQ ID NO: 1057, SEQ ID NO: 1090, SEQ ID NO: 1097, SEQ ID NO: 1129, SEQ ID NO: 1139, SEQ ID NO: 1143, SEQ ID NO: 1152, SEQ ID NO: 1153, SEQ ID NO: 1155, SEQ ID NO: 1161, SEQ ID NO: 1162, SEQ ID NO: 1169, SEQ ID NO: 1170, SEQ ID NO: 1171, SEQ ID NO: 1180, SEQ ID NO: 1194, SEQ ID NO: 1195, SEQ ID NO: 1199, SEQ ID NO: 1200, SEQ ID NO: 1201, SEQ ID NO: 1202, SEQ ID NO: 1205, SEQ ID NO: 1312, SEQ ID NO: 1336, SEQ ID NO: 1349, SEQ ID NO: 1355, SEQ ID NO: 1359, SEQ ID NO: 1413, SEQ ID NO: 1426, SEQ ID NO: 1430, SEQ ID NO: 882, SEQ ID NO: 382, SEQ ID NO: 130, SEQ ID NO: 230, SEQ ID NO: 269, SEQ ID NO: 312, SEQ ID NO: 211, SEQ ID NO: 959, SEQ ID NO: 938, SEQ ID NO: 110, SEQ ID NO: 244, SEQ ID NO: 328, SEQ ID NO: 235, SEQ ID NO: 315, SEQ ID NO: 296, SEQ ID NO: 976, SEQ ID NO: 321, SEQ ID NO: 43, SEQ ID NO: 281, SEQ ID NO: 326, SEQ ID NO: 272, SEQ ID NO: 344, SEQ ID NO: 139, SEQ ID NO: 30, SEQ ID NO: 220, SEQ ID NO: 364, SEQ ID NO: 369, SEQ ID NO: 372, SEQ ID NO: 991, SEQ ID NO: 128, SEQ ID NO: 347, SEQ ID NO: 52, SEQ ID NO: 12, SEQ ID NO: 247, SEQ ID NO: 64, SEQ ID NO: 101, SEQ ID NO: 338, SEQ ID NO: 83, SEQ ID NO: 46, SEQ ID NO: 348, SEQ ID NO: 223, SEQ ID NO: 39, SEQ ID NO: 232, SEQ ID NO: 168, SEQ ID NO: 65, SEQ ID NO: 952, SEQ ID NO: 341, SEQ ID NO: 69, SEQ ID NO: 924, SEQ ID NO: 4, SEQ ID NO: 197, SEQ ID NO: 313, SEQ ID NO: 119, SEQ ID NO: 188, SEQ ID NO: 956, SEQ ID NO: 935, SEQ ID NO: 246, SEQ ID NO: 196, SEQ ID NO: 376, SEQ ID NO: 172, SEQ ID NO: 25, SEQ ID NO: 126, SEQ ID NO: 951, SEQ ID NO: 147, SEQ ID NO: 895, SEQ ID NO: 14, SEQ ID NO: 154, SEQ ID NO: 277, SEQ ID NO: 363, SEQ ID NO: 342, SEQ ID NO: 378, SEQ ID NO: 130, SEQ ID NO: 198, SEQ ID NO: 243, SEQ ID NO: 19, SEQ ID NO: 9, SEQ ID NO: 149, SEQ ID NO: 167, SEQ ID NO: 349, SEQ ID NO: 209, SEQ ID NO: 990, SEQ ID NO: 185, SEQ ID NO: 883, SEQ ID NO: 8, SEQ ID NO: 887, SEQ ID NO: 350, SEQ ID NO: 987, SEQ ID NO: 63, SEQ ID NO: 249, SEQ ID NO: 118, SEQ ID NO: 132, SEQ ID NO: 47, SEQ ID NO: 106, SEQ ID NO: 324, SEQ ID NO: 155, SEQ ID NO: 121, SEQ ID NO: 153, SEQ ID NO: 87, SEQ ID NO: 986,

SEQ ID NO: 262, SEQ ID NO: 333, SEQ ID NO: 36, SEQ ID NO: 982, SEQ ID NO: 180, SEQ ID NO: 84, SEQ ID NO: 900, SEQ ID NO: 20, SEQ ID NO: 7, SEQ ID NO: 61, SEQ ID NO: 253, SEQ ID NO: 120, SEQ ID NO: 268, SEQ ID NO: 299, SEQ ID NO: 942, SEQ ID NO: 173, SEQ ID NO: 187, SEQ ID NO: 187, SEQ ID NO: 234, SEQ ID NO: 112, SEQ ID NO: 324, SEQ ID NO: 971, SEQ ID NO: 62, SEQ ID NO: 308, SEQ ID NO: 74, SEQ ID NO: 1, SEQ ID NO: 266, SEQ ID NO: 337, SEQ ID NO: 93, SEQ ID NO: 44, SEQ ID NO: 335, SEQ ID NO: 368, SEQ ID NO: 208, SEQ ID NO: 358, SEQ ID NO: 923, SEQ ID NO: 310, SEQ ID NO: 26, SEQ ID NO: 279, SEQ ID NO: 890, SEQ ID NO: 325, SEQ ID NO: 109, SEQ ID NO: 143, SEQ ID NO: 918, SEQ ID NO: 252, SEQ ID NO: 953, SEQ ID NO: 902, SEQ ID NO: 174, SEQ ID NO: 73, SEQ ID NO: 898, SEQ ID NO: 300, SEQ ID NO: 356, SEQ ID NO: 298, SEQ ID NO: 354, SEQ ID NO: 138, SEQ ID NO: 319, SEQ ID NO: 80, SEQ ID NO: 933, SEQ ID NO: 891, SEQ ID NO: 366, SEQ ID NO: 113, SEQ ID NO: 320, SEQ ID NO: 915, SEQ ID NO: 351, SEQ ID NO: 162, SEQ ID NO: 965, SEQ ID NO: 67, SEQ ID NO: 314, SEQ ID NO: 904, SEQ ID NO: 345, SEQ ID NO: 374, SEQ ID NO: 962, SEQ ID NO: 270, SEQ ID NO: 186, SEQ ID NO: 60, SEQ ID NO: 379, SEQ ID NO: 889, SEQ ID NO: 967, SEQ ID NO: 973, SEQ ID NO: 280, SEQ ID NO: 170, SEQ ID NO: 985, and SEQ ID NO: 932.

10. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in energy conversion encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1147, SEQ ID NO: 1288, SEQ ID NO: 1324, SEQ ID NO: 1363, SEQ ID NO: 882, SEQ ID NO: 382, SEQ ID NO: 130, and SEQ ID NO: 230.

11. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in amino acid metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 997, SEQ ID NO: 1015, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1099, SEQ ID NO: 1229, SEQ ID NO: 1250, SEQ ID NO: 1268, SEQ ID NO: 1293, SEQ ID NO: 1339, SEQ ID NO: 1408, SEQ ID NO: 1429, SEQ ID NO: 1434, SEQ ID NO: 1228, SEQ ID NO: 1031, SEQ ID NO: 1034, SEQ ID NO: 1008, SEQ ID NO: 269, SEQ ID NO: 312, SEQ ID NO: 211, SEQ ID NO: 959, SEQ ID NO: 938, SEQ ID NO: 110, SEQ ID NO: 244, SEQ ID NO: 328, SEQ ID NO: 235, SEQ ID NO: 315, SEQ ID NO: 296, SEQ ID NO: 976, SEQ ID NO: 321, SEQ ID NO: 43, SEQ ID NO: 281, SEQ ID NO: 326, and SEQ ID NO: 272.

12. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in nucleotide metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1061, SEQ ID NO: 1064, SEQ ID NO: 1191, SEQ ID NO: 1217,

SEQ ID NO: 1365, SEQ ID NO: 1394, SEQ ID NO: 1414, SEQ ID NO: 1415, SEQ ID NO: 1435, SEQ ID NO: 1058, SEQ ID NO: 1059, SEQ ID NO: 344, SEQ ID NO: 139, SEQ ID NO: 30, SEQ ID NO: 220, SEQ ID NO: 364, SEQ ID NO: 369, SEQ ID NO: 372, SEQ ID NO: 991, SEQ ID NO: 128, SEQ ID NO: 347, and SEQ ID NO: 52.

13. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in carbohydrate metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1080, SEQ ID NO: 1128, SEQ ID NO: 1133, SEQ ID NO: 1211, SEQ ID NO: 1252, SEQ ID NO: 1253, SEQ ID NO: 1286, SEQ ID NO: 1289, SEQ ID NO: 1291, SEQ ID NO: 1303, SEQ ID NO: 1396, SEQ ID NO: 996, SEQ ID NO: 12, SEQ ID NO: 247, SEQ ID NO: 64, SEQ ID NO: 101, SEQ ID NO: 338, SEQ ID NO: 83, SEQ ID NO: 46, SEQ ID NO: 348, SEQ ID NO: 223, SEQ ID NO: 39, SEQ ID NO: 232, and SEQ ID NO: 168.

14. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in cofactor metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1095, SEQ ID NO: 1156, SEQ ID NO: 1158, SEQ ID NO: 1159, SEQ ID NO: 1277, SEQ ID NO: 1038, SEQ ID NO: 65, SEQ ID NO: 952, SEQ ID NO: 341, SEQ ID NO: 69, SEQ ID NO: 924, and SEQ ID NO: 4.

15. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in lipid metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1257, SEQ ID NO: 1357, SEQ ID NO: 1436, SEQ ID NO: 197, SEQ ID NO: 313, and SEQ ID NO: 119.

16. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in mRNA translation and ribosome biogenesis encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1047, SEQ ID NO: 1055, SEQ ID NO: SEQ ID NO: 1141, SEQ ID NO: 1227, SEQ ID NO: 1327, SEQ ID NO: 1412, SEQ ID NO: 188, SEQ ID NO: 956, SEQ ID NO: 935, SEQ ID NO: 246, SEQ ID NO: 196, and SEQ ID NO: 376.

17. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in genome replication, transcription, recombination and repair encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1003, SEQ ID NO: 1087,

SEQ ID NO: 1116, SEQ ID NO: 1130, SEQ ID NO: 1132, SEQ ID NO: 1185, SEQ ID NO: 1188, SEQ ID NO: 1198, SEQ ID NO: 1218, SEQ ID NO: 1244, SEQ ID NO: 1306, SEQ ID NO: 1325, SEQ ID NO: 1397, SEQ ID NO: 1398, SEQ ID NO: 1407, SEQ ID NO: 1433, SEQ ID NO: 172, SEQ ID NO: 25, SEQ ID NO: 126, SEQ ID NO: 951, SEQ ID NO: 147, SEQ ID NO: 895, SEQ ID NO: 14, SEQ ID NO: 154, SEQ ID NO: 277, SEQ ID NO: 363, SEQ ID NO: 342, SEQ ID NO: 378, SEQ ID NO: 130, SEQ ID NO: 198, SEQ ID NO: 243, SEQ ID NO: 19, and SEQ ID NO: 9.

18. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in outer membrane or cell wall biosynthesis encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1216, SEQ ID NO: 1239, SEQ ID NO: 1362, SEQ ID NO: 1017, SEQ ID NO: 1019, SEQ ID NO: 1360, SEQ ID NO: 149, SEQ ID NO: 167, SEQ ID NO: 349, SEQ ID NO: 209, SEQ ID NO: 990, SEQ ID NO: 185, SEQ ID NO: 883, and SEQ ID NO: 8.

19. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide is an *H. pylori* chaperone polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1423, SEQ ID NO: 1425, SEQ ID NO: 1374, SEQ ID NO: 887, SEQ ID NO: 350, and SEQ ID NO: 987.

20. A recombinant expression vector comprising the nucleic acid of claim 9 operably linked to a transcription regulatory element.

21. A cell comprising a recombinant expression vector of claim 20.

22. A method for producing an *H. pylori* polypeptide comprising culturing a cell of claim 21 under conditions that permit expression of the polypeptide.

23. An isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* secreted or periplasmic polypeptide or a fragment thereof, said nucleic acid selected from the group consisting of SEQ ID NO: 1004, SEQ ID NO: 1138, SEQ ID NO: 1067, SEQ ID NO: 1078, SEQ ID NO: 1314, SEQ ID NO: 1319, SEQ ID NO: 1378, SEQ ID NO: 1105, SEQ ID NO: 1114, SEQ ID NO: 1118, SEQ ID NO: 1120, SEQ ID NO: 1123, SEQ ID NO: 1127, SEQ ID NO: 1212, SEQ ID NO: 1223, SEQ ID NO: 1225, SEQ ID NO: 1246, SEQ ID NO: 1248, SEQ ID NO: 1259, SEQ ID NO: 1264, SEQ ID NO: 1265, SEQ ID NO: 1281, SEQ ID NO: 1285, SEQ ID NO: 1294, SEQ ID NO: 1298, SEQ ID NO: 1299, SEQ ID NO: 1315, SEQ ID NO: 1316, SEQ ID NO: 1317, SEQ ID NO: 1318, SEQ ID NO: 1344, SEQ ID NO: 1351, SEQ ID NO: 1353, SEQ ID NO: 1373, SEQ ID

NO: 1380, SEQ ID NO: 1387, SEQ ID NO: 1389, SEQ ID NO: 1393, SEQ ID NO: 1411, SEQ ID NO: 1428, SEQ ID NO: 1431, SEQ ID NO: 1439, SEQ ID NO: 1043, SEQ ID NO: 1183, SEQ ID NO: 1184, SEQ ID NO: 1196, SEQ ID NO: 1197, SEQ ID NO: 1203, SEQ ID NO: 995, SEQ ID NO: 998, SEQ ID NO: 1001, SEQ ID NO: 1022, SEQ ID NO: 1023, SEQ ID NO: 1029, SEQ ID NO: 1040, SEQ ID NO: 1051, SEQ ID NO: 1062, SEQ ID NO: 1154, SEQ ID NO: 1320, SEQ ID NO: 1075, SEQ ID NO: 1106, SEQ ID NO: 1109, SEQ ID NO: 1134, SEQ ID NO: 1221, SEQ ID NO: 1226, SEQ ID NO: 1235, SEQ ID NO: 1301, SEQ ID NO: 1311, SEQ ID NO: 1326, SEQ ID NO: 1341, SEQ ID NO: 1354, SEQ ID NO: 1364, SEQ ID NO: 1366, SEQ ID NO: 1376, SEQ ID NO: 1391, SEQ ID NO: 1395, SEQ ID NO: 1445, SEQ ID NO: 1079, SEQ ID NO: 1186, SEQ ID NO: 1010, SEQ ID NO: 1016, SEQ ID NO: 1172, SEQ ID NO: 1174, SEQ ID NO: 117, SEQ ID NO: 254, SEQ ID NO: 24, SEQ ID NO: 242, SEQ ID NO: 950, SEQ ID NO: 263, SEQ ID NO: 286, SEQ ID NO: 947, SEQ ID NO: 51, SEQ ID NO: 177, SEQ ID NO: 156, SEQ ID NO: 190, SEQ ID NO: 375, SEQ ID NO: 222, SEQ ID NO: 21, SEQ ID NO: 912, SEQ ID NO: 148, SEQ ID NO: 202, SEQ ID NO: 224, SEQ ID NO: 112, SEQ ID NO: 32, SEQ ID NO: 339, SEQ ID NO: 182, SEQ ID NO: 228, SEQ ID NO: 152, SEQ ID NO: 219, SEQ ID NO: 137, SEQ ID NO: 318, SEQ ID NO: 141, SEQ ID NO: 165, SEQ ID NO: 334, SEQ ID NO: 13, SEQ ID NO: 297, SEQ ID NO: 35, SEQ ID NO: 216, SEQ ID NO: 908, SEQ ID NO: 124, SEQ ID NO: 75, SEQ ID NO: 927, SEQ ID NO: 221, SEQ ID NO: 178, SEQ ID NO: 169, SEQ ID NO: 293, SEQ ID NO: 289, SEQ ID NO: 926, SEQ ID NO: 948, SEQ ID NO: 115, SEQ ID NO: 251, SEQ ID NO: 345, SEQ ID NO: 17, SEQ ID NO: 920, SEQ ID NO: 95, SEQ ID NO: 86, SEQ ID NO: 360, SEQ ID NO: 271, SEQ ID NO: 970, SEQ ID NO: 288, SEQ ID NO: 282, SEQ ID NO: 98, SEQ ID NO: 29, SEQ ID NO: 317, SEQ ID NO: 343, SEQ ID NO: 291, SEQ ID NO: 108, SEQ ID NO: 377, SEQ ID NO: 305, SEQ ID NO: 305, SEQ ID NO: 100, SEQ ID NO: 988, SEQ ID NO: 212, SEQ ID NO: 884, SEQ ID NO: 37, SEQ ID NO: 968, SEQ ID NO: 975, SEQ ID NO: 237, SEQ ID NO: 335, SEQ ID NO: 260, SEQ ID NO: 370, SEQ ID NO: 91, SEQ ID NO: 276, SEQ ID NO: 311, SEQ ID NO: 173, SEQ ID NO: 102, SEQ ID NO: 304, SEQ ID NO: 380, SEQ ID NO: 127, SEQ ID NO: 993, SEQ ID NO: 925, SEQ ID NO: 181, and SEQ ID NO: 171.

24. A recombinant expression vector comprising the nucleic acid of claim 23 operably linked to a transcription regulatory element.

25. A cell comprising a recombinant expression vector of claim 24.

26. A method for producing an *H. pylori* polypeptide comprising culturing a cell of claim 25 under conditions that permit expression of the polypeptide.

27. An isolated nucleic acid comprising a nucleotide sequence encoding an *h. pylori* surface or membrane polypeptide or a fragment thereof, said nucleic acid selected from the group consisting of SEQ ID NO: 1060, SEQ ID NO: 1110, SEQ ID NO: 1112, SEQ ID NO: 1230, SEQ ID NO: 1260, SEQ ID NO: 1280, SEQ ID NO: 1292, SEQ ID NO: 1296, SEQ ID NO: 1307, SEQ ID NO: 1442, SEQ ID NO: 1444, SEQ ID NO: 1122, SEQ ID NO: 1254, SEQ ID NO: 1256, SEQ ID NO: 1272, SEQ ID NO: 1275, SEQ ID NO: 1309, SEQ ID NO: 1313, SEQ ID NO: 1347, SEQ ID NO: 1352, SEQ ID NO: 1356, SEQ ID NO: 1438, SEQ ID NO: 1441, SEQ ID NO: 1009, SEQ ID NO: 1026, SEQ ID NO: 1048, SEQ ID NO: 1063, SEQ ID NO: 1190, SEQ ID NO: 1083, SEQ ID NO: 1113, SEQ ID NO: 1222, SEQ ID NO: 1295, SEQ ID NO: 1343, SEQ ID NO: 1392, SEQ ID NO: 1443, SEQ ID NO: 1085, SEQ ID NO: 1093, SEQ ID NO: 1117, SEQ ID NO: 1121, SEQ ID NO: 1131, SEQ ID NO: 1287, SEQ ID NO: 1440, SEQ ID NO: 1209, SEQ ID NO: 1342, SEQ ID NO: 1381, SEQ ID NO: 1390, SEQ ID NO: 1409, SEQ ID NO: 1035, SEQ ID NO: 1014, SEQ ID NO: 1088, SEQ ID NO: 1242, SEQ ID NO: 1178, SEQ ID NO: 1089, SEQ ID NO: 1340, SEQ ID NO: 1074, SEQ ID NO: 1107, SEQ ID NO: 1204, SEQ ID NO: 1066, SEQ ID NO: 381, SEQ ID NO: 229, SEQ ID NO: 323, SEQ ID NO: 371, SEQ ID NO: 284, SEQ ID NO: 116, SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 907, SEQ ID NO: 193, SEQ ID NO: 145, SEQ ID NO: 59, SEQ ID NO: 322, SEQ ID NO: 94, SEQ ID NO: 306, SEQ ID NO: 939, SEQ ID NO: 205, SEQ ID NO: 123, SEQ ID NO: 906, SEQ ID NO: 928, SEQ ID NO: 346, SEQ ID NO: 129, SEQ ID NO: 307, SEQ ID NO: 133, SEQ ID NO: 131, SEQ ID NO: 886, SEQ ID NO: 179, SEQ ID NO: 104, SEQ ID NO: 213, SEQ ID NO: 359, SEQ ID NO: 140, SEQ ID NO: 146, SEQ ID NO: 327, SEQ ID NO: 365, SEQ ID NO: 33, SEQ ID NO: 331, SEQ ID NO: 175, SEQ ID NO: 200, SEQ ID NO: 292, SEQ ID NO: 23, SEQ ID NO: 336, SEQ ID NO: 301, SEQ ID NO: 28, SEQ ID NO: 941, SEQ ID NO: 103, SEQ ID NO: 231, SEQ ID NO: 176, SEQ ID NO: 31, SEQ ID NO: 917, SEQ ID NO: 151, SEQ ID NO: 922, SEQ ID NO: 265, SEQ ID NO: 142, SEQ ID NO: 259, SEQ ID NO: 122, SEQ ID NO: 206, SEQ ID NO: 96, SEQ ID NO: 353, SEQ ID NO: 38, SEQ ID NO: 89, SEQ ID NO: 77, SEQ ID NO: 954, SEQ ID NO: 264, SEQ ID NO: 937, SEQ ID NO: 226, SEQ ID NO: 283, SEQ ID NO: 88, SEQ ID NO: 125, SEQ ID NO: 183, SEQ ID NO: 195, SEQ ID NO: 81, SEQ ID NO: 901, SEQ ID NO: 82, SEQ ID NO: 42, SEQ ID NO: 881, and SEQ ID NO: 885.

28. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least one membrane spanning region encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1060, SEQ ID NO: 1110, SEQ ID NO: 1112, SEQ ID NO: 1230, SEQ ID NO: 1260, SEQ ID NO: 1280, SEQ ID NO: 1292, SEQ ID NO: 1296, SEQ ID NO: 1307, SEQ ID NO: 1442, SEQ ID NO: 1444, SEQ ID NO: 381, SEQ ID NO: 229, SEQ ID NO: 323, SEQ ID NO: 371, SEQ ID NO: 284, SEQ ID NO:

This Sheet Has Been Replaced

116, SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 907, SEQ ID NO: 193, SEQ ID NO: 145, SEQ ID NO: 59, SEQ ID NO: 322, SEQ ID NO: 94, SEQ ID NO: 306, and SEQ ID NO: 881.

29. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least two membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1122, SEQ ID NO: 1254, SEQ ID NO: 1256, SEQ ID NO: 1272, SEQ ID NO: 1275, SEQ ID NO: 1309, SEQ ID NO: 1313, SEQ ID NO: 1347, SEQ ID NO: 1352, SEQ ID NO: 1356, SEQ ID NO: 1438, SEQ ID NO: 1441, SEQ ID NO: 1009, SEQ ID NO: 1026, SEQ ID NO: 1048, SEQ ID NO: 1063, SEQ ID NO: 1190, SEQ ID NO: 939, SEQ ID NO: 205, SEQ ID NO: 123, SEQ ID NO: 906, SEQ ID NO: 928, SEQ ID NO: 346, SEQ ID NO: 129, SEQ ID NO: 307, SEQ ID NO: 133, SEQ ID NO: 131, SEQ ID NO: 886, SEQ ID NO: 179, SEQ ID NO: 104, SEQ ID NO: 213, SEQ ID NO: 359, SEQ ID NO: 140, SEQ ID NO: 146, SEQ ID NO: 327, and SEQ ID NO: 365.

30. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least three membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1083, SEQ ID NO: 1113, SEQ ID NO: 1222, SEQ ID NO: 1295, SEQ ID NO: 1343, SEQ ID NO: 1392, SEQ ID NO: 1443, SEQ ID NO: 33, SEQ ID NO: 331, SEQ ID NO: 175, SEQ ID NO: 200, SEQ ID NO: 292, SEQ ID NO: 23, and SEQ ID NO: 336.

31. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least four membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1085, SEQ ID NO: 1093, SEQ ID NO: 1117, SEQ ID NO: 1121, SEQ ID NO: 1131, SEQ ID NO: 1287, SEQ ID NO: 1440, SEQ ID NO: 1209, SEQ ID NO: 301, SEQ ID NO: 28, SEQ ID NO: 941, SEQ ID NO: 103, SEQ ID NO: 231, SEQ ID NO: 176, SEQ ID NO: 31, SEQ ID NO: 917, SEQ ID NO: 151, and SEQ ID NO: 922.

32. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least five membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1342, SEQ ID NO: 1381, SEQ ID NO: 1390, SEQ ID NO: 1409, SEQ ID NO: 1035, SEQ ID NO: 265, SEQ ID NO: 142, SEQ ID NO: 259, SEQ ID NO: 122, SEQ ID NO: 206, and SEQ ID NO: 885.

This Sheet Has Been Replaced

33. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least six membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1014, SEQ ID NO: 1088, SEQ ID NO: 1242, SEQ ID NO: 1178, SEQ ID NO: 96, SEQ ID NO: 353, SEQ ID NO: 38, SEQ ID NO: 89, SEQ ID NO: 77, SEQ ID NO: 954, and SEQ ID NO: 264.

34. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least seven membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1089, SEQ ID NO: 1340, SEQ ID NO: 1074, SEQ ID NO: 1107, SEQ ID NO: 1204, SEQ ID NO: 1066, SEQ ID NO: 937, SEQ ID NO: 226, SEQ ID NO: 283, SEQ ID NO: 88, SEQ ID NO: 125, SEQ ID NO: 183, SEQ ID NO: 195, SEQ ID NO: 81, SEQ ID NO: 901, SEQ ID NO: 82, and SEQ ID NO: 42.

35. A recombinant expression vector comprising the nucleic acid of claim 27 operably linked to a transcription regulatory element.

36. A cell comprising a recombinant expression vector of claim 35.

37. A method for producing an *H. pylori* polypeptide comprising culturing a cell of claim 36 under conditions that permit expression of the polypeptide.

38. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a nucleic acid of claim 1.

39. A vaccine composition of claim 38, further comprising a pharmaceutically acceptable carrier.

40. A vaccine composition of claim 39, wherein the pharmaceutically acceptable carrier is an adjuvant.

41. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 38, such that treatment of *H. pylori* infection occurs.

42. A method of claim 41, wherein the treatment is a prophylactic treatment.

43. A method of claim 41, wherein the treatment is a therapeutic treatment.

44. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a nucleic acid of claim 9.

45. A vaccine composition of claim 44, further comprising a pharmaceutically acceptable carrier.

46. A vaccine composition of claim 45, wherein the pharmaceutically acceptable carrier is an adjuvant.

47. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 44, such that treatment of *H. pylori* infection occurs.

48. A method of claim 47, wherein the treatment is a prophylactic treatment.

49. A method of claim 47, wherein the treatment is a therapeutic treatment.

50. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a nucleic acid of claim 23.

51. A vaccine composition of claim 50, further comprising a pharmaceutically acceptable carrier.

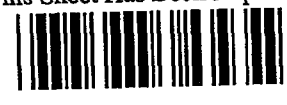
52. A vaccine composition of claim 51, wherein the pharmaceutically acceptable carrier is an adjuvant.

53. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 50, such that treatment of *H. pylori* infection occurs.

54. A method of claim 53, wherein the treatment is a prophylactic treatment.

55. A method of claim 53, wherein the treatment is a therapeutic treatment.

This Sheet Has Been Replaced



56. A purified *H. pylori* cell envelope polypeptide or a fragment thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 1471, SE ID NO: 1472, SEQ ID NO: 1487, SEQ ID NO: 1501, SEQ ID NO: 1522, SEQ ID NO: 1552, SEQ ID NO: 1586, SEQ ID NO: 1727, SEQ ID NO: 1601, SEQ ID NO: 1638, SEQ ID NO: 1643, SEQ ID NO: 1812, SEQ ID NO: 1830, SEQ ID NO: 1850, SEQ ID NO: 1854, SEQ ID NO: 1851, SEQ ID NO: 1640, SEQ ID NO: 1453, SEQ ID NO: 1664, SEQ ID NO: 1665, SEQ ID NO: 1666, SEQ ID NO: 1685, SEQ ID NO: 1687, SEQ ID NO: 1688, SEQ ID NO: 1675, SEQ ID NO: 1702, SEQ ID NO: 1713, SEQ ID NO: 1600, SEQ ID NO: 1671, SEQ ID NO: 1691, SEQ ID NO: 1615, SEQ ID NO: 1616, SEQ ID NO: 1855, SEQ ID NO: 1595, SEQ ID NO: 1633, SEQ ID NO: 1608, SEQ ID NO: 1611, SEQ ID NO: 1751, SEQ ID NO: 1772, SEQ ID NO: 1774, SEQ ID NO: 1780, SEQ ID NO: 1783, SEQ ID NO: 1796, SEQ ID NO: 1809, SEQ ID NO: 1826, SEQ ID NO: 1868, SEQ ID NO: 1734, SEQ ID NO: 1786, SEQ ID NO: 1819, SEQ ID NO: 1630, SEQ ID NO: 1706, SEQ ID NO: 1709, SEQ ID NO: 1495, SEQ ID NO: 1724, SEQ ID NO: 1670, SEQ ID NO: 1725, SEQ ID NO: 1661, SEQ ID NO: 1873, SEQ ID NO: 1753, SEQ ID NO: 1759, SEQ ID NO: 1761, SEQ ID NO: 1782, SEQ ID NO: 1883, SEQ ID NO: 1503, SEQ ID NO: 1542, SEQ ID NO: 1872, SEQ ID NO: 1520, SEQ ID NO: 1456, SEQ ID NO: 1458, SEQ ID NO: 1617, SEQ ID NO: 1628, SEQ ID NO: 1644, SEQ ID NO: 1657, SEQ ID NO: 1658, SEQ ID NO: 1755, SEQ ID NO: 1756, SEQ ID NO: 1797, SEQ ID NO: 1799, SEQ ID NO: 1801, SEQ ID NO: 1483, SEQ ID NO: 1504, SEQ ID NO: 1532, SEQ ID NO: 1575, SEQ ID NO: 1833, SEQ ID NO: 1888, SEQ ID NO: 1714, SEQ ID NO: 1624, SEQ ID NO: 1856, SEQ ID NO: 1857, SEQ ID NO: 1861, SEQ ID NO: 1537, SEQ ID NO: 1773, SEQ ID NO: 1717, SEQ ID NO: 1733, SEQ ID NO: 1722, SEQ ID NO: 1659, SEQ ID NO: 1577, SEQ ID NO: 1721, SEQ ID NO: 1729, SEQ ID NO: 1870, SEQ ID NO: 1576, SEQ ID NO: 1632, SEQ ID NO: 1867, SEQ ID NO: 1547, SEQ ID NO: 1533, SEQ ID NO: 1597, SEQ ID NO: 1596, SEQ ID NO: 1559, SEQ ID NO: 1599, SEQ ID NO: 1788, SEQ ID NO: 1789, SEQ ID NO: 1875, SEQ ID NO: 1451, SEQ ID NO: 1478, SEQ ID NO: 1626, SEQ ID NO: 1781, SEQ ID NO: 660, SEQ ID NO: 660, SEQ ID NO: 855, SEQ ID NO: 534, SEQ ID NO: 675, SEQ ID NO: 404, SEQ ID NO: 518, SEQ ID NO: 464, SEQ ID NO: 672, SEQ ID NO: 640, SEQ ID NO: 490, SEQ ID NO: 755, SEQ ID NO: 389, SEQ ID NO: 635, SEQ ID NO: 877, SEQ ID NO: 637, SEQ ID NO: 477, SEQ ID NO: 772, SEQ ID NO: 658, SEQ ID NO: 463, SEQ ID NO: 852, SEQ ID NO: 503, SEQ ID NO: 411, SEQ ID NO: 441, SEQ ID NO: 782, SEQ ID NO: 575, SEQ ID NO: 691, SEQ ID NO: 724, SEQ ID NO: 452, SEQ ID NO: 386, SEQ ID NO: 497, SEQ ID NO: 712, SEQ ID NO: 591, SEQ ID NO: 638, SEQ ID NO: 740, SEQ ID NO: 697, SEQ ID NO: 569, SEQ ID NO: 470, SEQ ID NO: 700, SEQ ID NO: 586, SEQ ID NO: 823, SEQ ID NO: 627, SEQ ID NO: 627, SEQ ID NO: 684, SEQ ID NO: 551, SEQ ID NO: 478, SEQ ID NO: 508, SEQ ID NO: 545, SEQ ID NO: 628, SEQ ID NO: 443, SEQ ID NO: 702, SEQ ID NO: 776, SEQ ID NO: 461, SEQ ID NO: 737, SEQ ID NO:

809, SEQ ID NO: 642, SEQ ID NO: 879, SEQ ID NO: 773, SEQ ID NO: 468, SEQ ID NO: 842, SEQ ID NO: 788, SEQ ID NO: 624, SEQ ID NO: 788, SEQ ID NO: 644, SEQ ID NO: 727, SEQ ID NO: 631, SEQ ID NO: 450, SEQ ID NO: 448, SEQ ID NO: 653, SEQ ID NO: 495, SEQ ID NO: 400, SEQ ID NO: 541, SEQ ID NO: 673, SEQ ID NO: 482, SEQ ID NO: 622, SEQ ID NO: 689, SEQ ID NO: 736, SEQ ID NO: 417, SEQ ID NO: 716, SEQ ID NO: 762, SEQ ID NO: 395, SEQ ID NO: 587, SEQ ID NO: 669, SEQ ID NO: 758, SEQ ID NO: 593, SEQ ID NO: 451, SEQ ID NO: 827, SEQ ID NO: 502, SEQ ID NO: 719, SEQ ID NO: 469, SEQ ID NO: 715, SEQ ID NO: 847, SEQ ID NO: 453, SEQ ID NO: 527, SEQ ID NO: 652, SEQ ID NO: 745, SEQ ID NO: 567, SEQ ID NO: 848, SEQ ID NO: 430, SEQ ID NO: 748, SEQ ID NO: 396, SEQ ID NO: 588, SEQ ID NO: 795, SEQ ID NO: 523, SEQ ID NO: 791, SEQ ID NO: 714, SEQ ID NO: 481, SEQ ID NO: 765, SEQ ID NO: 837, SEQ ID NO: 833, SEQ ID NO: 585, SEQ ID NO: 865, SEQ ID NO: 764, SEQ ID NO: 440, SEQ ID NO: 465, SEQ ID NO: 555, SEQ ID NO: 526, SEQ ID NO: 687, SEQ ID NO: 692, SEQ ID NO: 693, SEQ ID NO: 677, SEQ ID NO: 649, SEQ ID NO: 812, SEQ ID NO: 820, SEQ ID NO: 880, SEQ ID NO: 590, SEQ ID NO: 713, SEQ ID NO: 750, SEQ ID NO: 613, SEQ ID NO: 437, SEQ ID NO: 556, SEQ ID NO: 657, SEQ ID NO: 402, SEQ ID NO: 623, SEQ ID NO: 862, SEQ ID NO: 449, SEQ ID NO: 690, SEQ ID NO: 424, SEQ ID NO: 821, SEQ ID NO: 432, SEQ ID NO: 811, SEQ ID NO: 554, and SEQ ID NO: 809.

57. The purified polypeptide of claim 56, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* flagella-associated polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1471, SEQ ID NO: 1472, SEQ ID NO: 1487, SEQ ID NO: 1501, SEQ ID NO: 1522, SEQ ID NO: 1552, SEQ ID NO: 1586, SEQ ID NO: 1727, SEQ ID NO: 1601, SEQ ID NO: 1638, SEQ ID NO: 1643, SEQ ID NO: 1812, SEQ ID NO: 1830, SEQ ID NO: 1850, SEQ ID NO: 1854, SEQ ID NO: 1851, SEQ ID NO: 1640, SEQ ID NO: 660, SEQ ID NO: 660, SEQ ID NO: 855, SEQ ID NO: 534, SEQ ID NO: 675, SEQ ID NO: 404, SEQ ID NO: 518, SEQ ID NO: 464, SEQ ID NO: 672, SEQ ID NO: 640, SEQ ID NO: 490, SEQ ID NO: 755, SEQ ID NO: 389, SEQ ID NO: 635, SEQ ID NO: 877, SEQ ID NO: 637, SEQ ID NO: 477, SEQ ID NO: 772, and SEQ ID NO: 658.

58. The purified polypeptide of claim 56, 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: 1453, SEQ ID NO: 1664, SEQ ID NO: 1665, SEQ ID NO: 1666, SEQ ID NO: 1685, SEQ ID NO: 1687, SEQ ID NO: 1688, SEQ ID NO: 1675, SEQ ID NO: 1702, SEQ ID NO: 1713, SEQ ID NO: 1600, SEQ ID NO: 1671, SEQ ID NO: 1691, SEQ ID NO: 1615, SEQ ID NO: 1616, SEQ ID NO: 1855, SEQ ID NO: 1595, SEQ ID NO: 1633, SEQ ID NO: 1608, SEQ ID NO: 1611, SEQ

ID NO: 1751, SEQ ID NO: 1772, SEQ ID NO: 1774, SEQ ID NO: 1780, SEQ ID NO: 1783, SEQ ID NO: 1796, SEQ ID NO: 1809, SEQ ID NO: 1826, SEQ ID NO: 1868, SEQ ID NO: 1734, SEQ ID NO: 1786, SEQ ID NO: 1819, SEQ ID NO: 1630, SEQ ID NO: 1706, SEQ ID NO: 1709, SEQ ID NO: 1495, SEQ ID NO: 1724, SEQ ID NO: 463, SEQ ID NO: 852, SEQ ID NO: 503, SEQ ID NO: 411, SEQ ID NO: 441, SEQ ID NO: 782, SEQ ID NO: 575, SEQ ID NO: 691, SEQ ID NO: 724, SEQ ID NO: 452, SEQ ID NO: 386, SEQ ID NO: 497, SEQ ID NO: 712, SEQ ID NO: 591, SEQ ID NO: 638, SEQ ID NO: 740, SEQ ID NO: 697, SEQ ID NO: 569, SEQ ID NO: 470, SEQ ID NO: 700, SEQ ID NO: 586, SEQ ID NO: 823, SEQ ID NO: 627, SEQ ID NO: 627, SEQ ID NO: 684, SEQ ID NO: 551, SEQ ID NO: 478, SEQ ID NO: 508, SEQ ID NO: 545, SEQ ID NO: 628, SEQ ID NO: 443, SEQ ID NO: 702, SEQ ID NO: 776, SEQ ID NO: 461, SEQ ID NO: 737, SEQ ID NO: 809, SEQ ID NO: 642, SEQ ID NO: 879, SEQ ID NO: 773, SEQ ID NO: 468, SEQ ID NO: 842, SEQ ID NO: 788, SEQ ID NO: 624, SEQ ID NO: 788, SEQ ID NO: 644, SEQ ID NO: 727, SEQ ID NO: 631, SEQ ID NO: 450, SEQ ID NO: 448, and SEQ ID NO: 653.

59. The purified polypeptide of claim 56, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* transporter polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1670, SEQ ID NO: 1725, SEQ ID NO: 1661, SEQ ID NO: 1873, SEQ ID NO: 1753, SEQ ID NO: 1759, SEQ ID NO: 1761, SEQ ID NO: 1782, SEQ ID NO: 1883, SEQ ID NO: 1503, SEQ ID NO: 1542, SEQ ID NO: 1872, SEQ ID NO: 1520, SEQ ID NO: 1456, SEQ ID NO: 1458, SEQ ID NO: 1617, SEQ ID NO: 1628, SEQ ID NO: 1644, SEQ ID NO: 1657, SEQ ID NO: 1658, SEQ ID NO: 1755, SEQ ID NO: 1756, SEQ ID NO: 1797, SEQ ID NO: 1799, SEQ ID NO: 1801, SEQ ID NO: 1483, SEQ ID NO: 1504, SEQ ID NO: 1532, SEQ ID NO: 1575, SEQ ID NO: 1833, SEQ ID NO: 1888, SEQ ID NO: 1714, SEQ ID NO: 495, SEQ ID NO: 400, SEQ ID NO: 541, SEQ ID NO: 673, SEQ ID NO: 482, SEQ ID NO: 622, SEQ ID NO: 689, SEQ ID NO: 736, SEQ ID NO: 417, SEQ ID NO: 716, SEQ ID NO: 762, SEQ ID NO: 395, SEQ ID NO: 587, SEQ ID NO: 669, SEQ ID NO: 758, SEQ ID NO: 593, SEQ ID NO: 451, SEQ ID NO: 827, SEQ ID NO: 502, SEQ ID NO: 719, SEQ ID NO: 469, SEQ ID NO: 715, SEQ ID NO: 847, SEQ ID NO: 453, SEQ ID NO: 527, SEQ ID NO: 652, SEQ ID NO: 745, SEQ ID NO: 567, SEQ ID NO: 848, SEQ ID NO: 430, SEQ ID NO: 748, SEQ ID NO: 396, SEQ ID NO: 588, SEQ ID NO: 795, SEQ ID NO: 523, SEQ ID NO: 791, SEQ ID NO: 714, SEQ ID NO: 481, and SEQ ID NO: 765.

60. The purified polypeptide of claim 56, 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: 1624, SEQ ID NO: 1856, SEQ ID NO: 1857, SEQ ID NO: 1861, SEQ ID NO: 1537, SEQ ID NO: 1773, SEQ ID NO:

1717, SEQ ID NO: 1733. SEQ ID NO: 1722, SEQ ID NO: 1659, SEQ ID NO: 1577, SEQ ID NO: 1721, SEQ ID NO: 1729, SEQ ID NO: 1870, SEQ ID NO: 1576, SEQ ID NO: 1632, SEQ ID NO: 1867, SEQ ID NO: 1547, SEQ ID NO: 1533, SEQ ID NO: 1597, SEQ ID NO: 1596, SEQ ID NO: 1559, SEQ ID NO: 1599, SEQ ID NO: 1788, SEQ ID NO: 1789, SEQ ID NO: 1875, SEQ ID NO: 1451, SEQ ID NO: 1478, SEQ ID NO: 1626, SEQ ID NO: 1781, SEQ ID NO: 837, SEQ ID NO: 833, SEQ ID NO: 585, SEQ ID NO: 865, SEQ ID NO: 764, SEQ ID NO: 440, SEQ ID NO: 465, SEQ ID NO: 555, SEQ ID NO: 526, SEQ ID NO: 687, SEQ ID NO: 692, SEQ ID NO: 693, SEQ ID NO: 677, SEQ ID NO: 649, and SEQ ID NO: 812.

61. A purified *H. pylori* cytoplasmic polypeptide or a fragment thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 1598, SEQ ID NO: 1739, SEQ ID NO: 1775, SEQ ID NO: 1814, SEQ ID NO: 1448, SEQ ID NO: 1466, SEQ ID NO: 1535, SEQ ID NO: 1545, SEQ ID NO: 1550, SEQ ID NO: 1680, SEQ ID NO: 1701, SEQ ID NO: 1719, SEQ ID NO: 1744, SEQ ID NO: 1790, SEQ ID NO: 1859, SEQ ID NO: 1880, SEQ ID NO: 1885, SEQ ID NO: 1679, SEQ ID NO: 1482, SEQ ID NO: 1485, SEQ ID NO: 1459, SEQ ID NO: 1512, SEQ ID NO: 1515, SEQ ID NO: 1642, SEQ ID NO: 1668, SEQ ID NO: 1816, SEQ ID NO: 1845, SEQ ID NO: 1865, SEQ ID NO: 1866, SEQ ID NO: 1886, SEQ ID NO: 1509, SEQ ID NO: 1510, SEQ ID NO: 1531, SEQ ID NO: 1579, SEQ ID NO: 1584, SEQ ID NO: 1662, SEQ ID NO: 1703, SEQ ID NO: 1704, SEQ ID NO: 1737, SEQ ID NO: 1740, SEQ ID NO: 1742, SEQ ID NO: 1754, SEQ ID NO: 1847, SEQ ID NO: 1447, SEQ ID NO: 1546, SEQ ID NO: 1607, SEQ ID NO: 1609, SEQ ID NO: 1610, SEQ ID NO: 1728, SEQ ID NO: 1489, SEQ ID NO: 1708, SEQ ID NO: 1808, SEQ ID NO: 1887, SEQ ID NO: 1498, SEQ ID NO: 1506, SEQ ID NO: 1592, SEQ ID NO: 1678, SEQ ID NO: 1778, SEQ ID NO: 1863, SEQ ID NO: 1454, SEQ ID NO: 1538, SEQ ID NO: 1567, SEQ ID NO: 1581, SEQ ID NO: 1583, SEQ ID NO: 1636, SEQ ID NO: 1639, SEQ ID NO: 1649, SEQ ID NO: 1669, SEQ ID NO: 1695, SEQ ID NO: 1757, SEQ ID NO: 1776, SEQ ID NO: 1848, SEQ ID NO: 1849, SEQ ID NO: 1858, SEQ ID NO: 1884, SEQ ID NO: 1667, SEQ ID NO: 1690, SEQ ID NO: 1813, SEQ ID NO: 1468, SEQ ID NO: 1470, SEQ ID NO: 1811, SEQ ID NO: 1874, SEQ ID NO: 1876, SEQ ID NO: 1825, SEQ ID NO: 1479, SEQ ID NO: 1488, SEQ ID NO: 1528, SEQ ID NO: 1566, SEQ ID NO: 1683, SEQ ID NO: 1692, SEQ ID NO: 1718, SEQ ID NO: 1614, SEQ ID NO: 1519, SEQ ID NO: 1476, SEQ ID NO: 1493, SEQ ID NO: 1497, SEQ ID NO: 1507, SEQ ID NO: 1490, SEQ ID NO: 1523, SEQ ID NO: 1524, SEQ ID NO: 1543, SEQ ID NO: 1551, SEQ ID NO: 1553, SEQ ID NO: 1554, SEQ ID NO: 1555, SEQ ID NO: 1562, SEQ ID NO: 1570, SEQ ID NO: 1587, SEQ ID NO: 1588, SEQ ID NO: 1591, SEQ ID NO: 1593, SEQ ID NO: 1684, SEQ ID NO: 1689, SEQ ID NO: 1694, SEQ ID NO: 1696, SEQ ID NO: 1698, SEQ ID NO: 1700, SEQ ID NO: 1712, SEQ ID NO: 1720, SEQ ID NO: 1730, SEQ ID NO: 1735, SEQ ID NO: 1741, SEQ ID NO: 1748, SEQ

ID NO: 1779, SEQ ID NO: 1821, SEQ ID NO: 1823, SEQ ID NO: 1828, SEQ ID NO: 1834, SEQ ID NO: 1835, SEQ ID NO: 1836, SEQ ID NO: 1839, SEQ ID NO: 1852, SEQ ID NO: 1853, SEQ ID NO: 1869, SEQ ID NO: 1871, SEQ ID NO: 1878, SEQ ID NO: 1521, SEQ ID NO: 1602, SEQ ID NO: 1627, SEQ ID NO: 1450, SEQ ID NO: 1457, SEQ ID NO: 1463, SEQ ID NO: 1469, SEQ ID NO: 1481, SEQ ID NO: 1484, SEQ ID NO: 1492, SEQ ID NO: 1500, SEQ ID NO: 1505, SEQ ID NO: 1508, SEQ ID NO: 1541, SEQ ID NO: 1548, SEQ ID NO: 1580, SEQ ID NO: 1590, SEQ ID NO: 1594, SEQ ID NO: 1603, SEQ ID NO: 1604, SEQ ID NO: 1606, SEQ ID NO: 1612, SEQ ID NO: 1613, SEQ ID NO: 1620, SEQ ID NO: 1621, SEQ ID NO: 1622, SEQ ID NO: 1631, SEQ ID NO: 1645, SEQ ID NO: 1646, SEQ ID NO: 1650, SEQ ID NO: 1651, SEQ ID NO: 1652, SEQ ID NO: 1653, SEQ ID NO: 1656, SEQ ID NO: 1763, SEQ ID NO: 1787, SEQ ID NO: 1800, SEQ ID NO: 1806, SEQ ID NO: 1810, SEQ ID NO: 1864, SEQ ID NO: 1877, SEQ ID NO: 1881, SEQ ID NO: 390, SEQ ID NO: 876, SEQ ID NO: 547, SEQ ID NO: 678, SEQ ID NO: 729, SEQ ID NO: 786, SEQ ID NO: 654, SEQ ID NO: 734, SEQ ID NO: 646, SEQ ID NO: 522, SEQ ID NO: 696, SEQ ID NO: 807, SEQ ID NO: 683, SEQ ID NO: 790, SEQ ID NO: 763, SEQ ID NO: 806, SEQ ID NO: 799, SEQ ID NO: 434, SEQ ID NO: 743, SEQ ID NO: 804, SEQ ID NO: 733, SEQ ID NO: 826, SEQ ID NO: 562, SEQ ID NO: 420, SEQ ID NO: 664, SEQ ID NO: 850, SEQ ID NO: 857, SEQ ID NO: 861, SEQ ID NO: 872, SEQ ID NO: 544, SEQ ID NO: 830, SEQ ID NO: 446, SEQ ID NO: 397, SEQ ID NO: 699, SEQ ID NO: 459, SEQ ID NO: 509, SEQ ID NO: 818, SEQ ID NO: 488, SEQ ID NO: 438, SEQ ID NO: 831, SEQ ID NO: 667, SEQ ID NO: 429, SEQ ID NO: 680, SEQ ID NO: 597, SEQ ID NO: 460, SEQ ID NO: 709, SEQ ID NO: 822, SEQ ID NO: 466, SEQ ID NO: 584, SEQ ID NO: 388, SEQ ID NO: 631, SEQ ID NO: 787, SEQ ID NO: 532, SEQ ID NO: 619, SEQ ID NO: 723, SEQ ID NO: 641, SEQ ID NO: 698, SEQ ID NO: 630, SEQ ID NO: 869, SEQ ID NO: 601, SEQ ID NO: 415, SEQ ID NO: 542, SEQ ID NO: 704, SEQ ID NO: 572, SEQ ID NO: 467, SEQ ID NO: 399, SEQ ID NO: 579, SEQ ID NO: 739, SEQ ID NO: 849, SEQ ID NO: 824, SEQ ID NO: 871, SEQ ID NO: 547, SEQ ID NO: 633, SEQ ID NO: 695, SEQ ID NO: 405, SEQ ID NO: 394, SEQ ID NO: 761, SEQ ID NO: 574, SEQ ID NO: 596, SEQ ID NO: 832, SEQ ID NO: 651, SEQ ID NO: 867, SEQ ID NO: 614, SEQ ID NO: 401, SEQ ID NO: 393, SEQ ID NO: 413, SEQ ID NO: 835, SEQ ID NO: 863, SEQ ID NO: 458, SEQ ID NO: 701, SEQ ID NO: 531, SEQ ID NO: 550, SEQ ID NO: 439, SEQ ID NO: 516, SEQ ID NO: 802, SEQ ID NO: 581, SEQ ID NO: 535, SEQ ID NO: 578, SEQ ID NO: 492, SEQ ID NO: 858, SEQ ID NO: 720, SEQ ID NO: 813, SEQ ID NO: 426, SEQ ID NO: 834, SEQ ID NO: 609, SEQ ID NO: 489, SEQ ID NO: 480, SEQ ID NO: 406, SEQ ID NO: 392, SEQ ID NO: 456, SEQ ID NO: 707, SEQ ID NO: 533, SEQ ID NO: 728, SEQ ID NO: 769, SEQ ID NO: 671, SEQ ID NO: 602, SEQ ID NO: 618, SEQ ID NO: 618, SEQ ID NO: 682, SEQ ID NO: 524, SEQ ID NO: 802, SEQ ID NO: 785, SEQ ID NO: 457, SEQ ID NO: 781, SEQ ID NO: 473, SEQ ID NO: 384, SEQ ID NO: 726, SEQ ID

NO: 817, SEQ ID NO: 498, SEQ ID NO: 436, SEQ ID NO: 815, SEQ ID NO: 856, SEQ ID NO: 650, SEQ ID NO: 844, SEQ ID NO: 580, SEQ ID NO: 783, SEQ ID NO: 416, SEQ ID NO: 741, SEQ ID NO: 442, SEQ ID NO: 803, SEQ ID NO: 520, SEQ ID NO: 566, SEQ ID NO: 557, SEQ ID NO: 706, SEQ ID NO: 710, SEQ ID NO: 487, SEQ ID NO: 603, SEQ ID NO: 472, SEQ ID NO: 476, SEQ ID NO: 770, SEQ ID NO: 841, SEQ ID NO: 768, SEQ ID NO: 839, SEQ ID NO: 560, SEQ ID NO: 796, SEQ ID NO: 483, SEQ ID NO: 634, SEQ ID NO: 445, SEQ ID NO: 853, SEQ ID NO: 525, SEQ ID NO: 798, SEQ ID NO: 549, SEQ ID NO: 836, SEQ ID NO: 589, SEQ ID NO: 760, SEQ ID NO: 462, SEQ ID NO: 789, SEQ ID NO: 507, SEQ ID NO: 828, SEQ ID NO: 866, SEQ ID NO: 754, SEQ ID NO: 730, SEQ ID NO: 617, SEQ ID NO: 455, SEQ ID NO: 873, SEQ ID NO: 435, SEQ ID NO: 766, SEQ ID NO: 793, SEQ ID NO: 742, SEQ ID NO: 599, SEQ ID NO: 854, and SEQ ID NO: 632.

62. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in energy conversion selected from the group consisting of SEQ ID NO: 1598, SEQ ID NO: 1739, SEQ ID NO: 1775, SEQ ID NO: 1814, SEQ ID NO: 390, SEQ ID NO: 876, SEQ ID NO: 547, SEQ ID NO: 678.

63. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in amino acid metabolism selected from the group consisting of SEQ ID NO: 1448, SEQ ID NO: 1466, SEQ ID NO: 1535, SEQ ID NO: 1545, SEQ ID NO: 1550, SEQ ID NO: 1680, SEQ ID NO: 1701, SEQ ID NO: 1719, SEQ ID NO: 1744, SEQ ID NO: 1790, SEQ ID NO: 1859, SEQ ID NO: 1880, SEQ ID NO: 1885, SEQ ID NO: 1679, SEQ ID NO: 1482, SEQ ID NO: 1485, SEQ ID NO: 1459, SEQ ID NO: 729, SEQ ID NO: 786, SEQ ID NO: 654, SEQ ID NO: 734, SEQ ID NO: 646, SEQ ID NO: 522, SEQ ID NO: 696, SEQ ID NO: 807, SEQ ID NO: 683, SEQ ID NO: 790, SEQ ID NO: 763, SEQ ID NO: 806, SEQ ID NO: 799, SEQ ID NO: 434, SEQ ID NO: 743, SEQ ID NO: 804, SEQ ID NO: 733.

64. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in nucleotide metabolism selected from the group consisting of SEQ ID NO: 1512, SEQ ID NO: 1515, SEQ ID NO: 1642, SEQ ID NO: 1668, SEQ ID NO: 1816, SEQ ID NO: 1845, SEQ ID NO: 1865, SEQ ID NO: 1866, SEQ ID NO: 1886, SEQ ID NO: 1509, SEQ ID NO: 1510, SEQ ID NO: 826, SEQ ID NO: 562, SEQ ID NO: 420, SEQ ID NO: 664, SEQ ID NO: 850, SEQ ID NO: 857, SEQ ID NO: 861, SEQ ID NO: 872, SEQ ID NO: 544, SEQ ID NO: 830, and SEQ ID NO: 446.

This Sheet Has Been Replaced

65. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in carbohydrate metabolism selected from the group consisting of SEQ ID NO: 1531, SEQ ID NO: 1579, SEQ ID NO: 1584, SEQ ID NO: 1662, SEQ ID NO: 1703, SEQ ID NO: 1704, SEQ ID NO: 1737, SEQ ID NO: 1740, SEQ ID NO: 1742, SEQ ID NO: 1754, SEQ ID NO: 1847, SEQ ID NO: 1447, SEQ ID NO: 397, SEQ ID NO: 699, SEQ ID NO: 459, SEQ ID NO: 509, SEQ ID NO: 818, SEQ ID NO: 488, SEQ ID NO: 438, SEQ ID NO: 831, SEQ ID NO: 667, SEQ ID NO: 429, SEQ ID NO: 680, and SEQ ID NO: 597.

66. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in cofactor metabolism selected from the group consisting of SEQ ID NO: 1546, SEQ ID NO: 1607, SEQ ID NO: 1609, SEQ ID NO: 1610, SEQ ID NO: 1728, SEQ ID NO: 1489, SEQ ID NO: 460, SEQ ID NO: 709, SEQ ID NO: 822, SEQ ID NO: 466, SEQ ID NO: 584, and SEQ ID NO: 388.

67. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in lipid metabolism selected from the group consisting of SEQ ID NO: 1708, SEQ ID NO: 1808, SEQ ID NO: 1887, SEQ ID NO: 631, SEQ ID NO: 787, and SEQ ID NO: 532.

68. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in mRNA translation and ribosome biogenesis selected from the group consisting of SEQ ID NO: 1498, SEQ ID NO: 1506, SEQ ID NO: 1592, SEQ ID NO: 1678, SEQ ID NO: 1778, SEQ ID NO: 1863, SEQ ID NO: 619, SEQ ID NO: 723, SEQ ID NO: 641, SEQ ID NO: 698, SEQ ID NO: 630, and SEQ ID NO: 869.

69. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in genome replication, transcription, recombination and repair selected from the group consisting of SEQ ID NO: 1454, SEQ ID NO: 1538, SEQ ID NO: 1567, SEQ ID NO: 1581, SEQ ID NO: 1583, SEQ ID NO: 1636, SEQ ID NO: 1639, SEQ ID NO: 1649, SEQ ID NO: 1669, SEQ ID NO: 1695, SEQ ID NO: 1757, SEQ ID NO: 1776, SEQ ID NO: 1848, SEQ ID NO: 1849, SEQ ID NO: 1858, SEQ ID NO: 1884, SEQ ID NO: 601, SEQ ID NO: 415, SEQ ID NO: 542, SEQ ID NO: 704, SEQ ID NO: 572, SEQ ID NO: 467, SEQ ID NO: 399, SEQ ID NO: 579, SEQ ID NO: 739, SEQ ID NO: 849, SEQ ID NO: 824, SEQ ID NO: 871, SEQ ID NO: 547, SEQ ID NO: 633, SEQ ID NO: 695, SEQ ID NO: 405, SEQ ID NO: 394, and SEQ ID NO: 761.

70. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in outer membrane or cell wall biosynthesis selected from the group consisting of SEQ ID NO: 1667, SEQ ID NO: 1690, SEQ ID NO: 1813, SEQ ID NO: 1468, SEQ ID NO: 1470, SEQ ID NO: 1811, SEQ ID NO: 574, SEQ ID NO: 596, SEQ ID NO: 832, SEQ ID NO: 651, SEQ ID NO: 867, SEQ ID NO: 614, SEQ ID NO: 401, and SEQ ID NO: 393.

71. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* chaperone polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1874, SEQ ID NO: 1876, SEQ ID NO: 1825, SEQ ID NO: 413, SEQ ID NO: 835, and SEQ ID NO: 863.

72. A purified *H. pylori* secreted or periplasmic polypeptide or a fragment thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 1455, SEQ ID NO: 1589, SEQ ID NO: 1518, SEQ ID NO: 1529, SEQ ID NO: 1765, SEQ ID NO: 1770, SEQ ID NO: 1829, SEQ ID NO: 1556, SEQ ID NO: 1565, SEQ ID NO: 1569, SEQ ID NO: 1571, SEQ ID NO: 1574, SEQ ID NO: 1578, SEQ ID NO: 1663, SEQ ID NO: 1674, SEQ ID NO: 1676, SEQ ID NO: 1697, SEQ ID NO: 1699, SEQ ID NO: 1710, SEQ ID NO: 1715, SEQ ID NO: 1716, SEQ ID NO: 1732, SEQ ID NO: 1736, SEQ ID NO: 1745, SEQ ID NO: 1749, SEQ ID NO: 1750, SEQ ID NO: 1766, SEQ ID NO: 1767, SEQ ID NO: 1768, SEQ ID NO: 1769, SEQ ID NO: 1795, SEQ ID NO: 1802, SEQ ID NO: 1804, SEQ ID NO: 1824, SEQ ID NO: 1831, SEQ ID NO: 1838, SEQ ID NO: 1840, SEQ ID NO: 1844, SEQ ID NO: 1862, SEQ ID NO: 1879, SEQ ID NO: 1882, SEQ ID NO: 1890, SEQ ID NO: 1494, SEQ ID NO: 1634, SEQ ID NO: 1635, SEQ ID NO: 1647, SEQ ID NO: 1648, SEQ ID NO: 1654, SEQ ID NO: 1446, SEQ ID NO: 1449, SEQ ID NO: 1452, SEQ ID NO: 1473, SEQ ID NO: 1474, SEQ ID NO: 1480, SEQ ID NO: 1491, SEQ ID NO: 1502, SEQ ID NO: 1513, SEQ ID NO: 1605, SEQ ID NO: 1771, SEQ ID NO: 1526, SEQ ID NO: 1557, SEQ ID NO: 1560, SEQ ID NO: 1585, SEQ ID NO: 1672, SEQ ID NO: 1677, SEQ ID NO: 1686, SEQ ID NO: 1752, SEQ ID NO: 1762, SEQ ID NO: 1777, SEQ ID NO: 1792, SEQ ID NO: 1805, SEQ ID NO: 1815, SEQ ID NO: 1817, SEQ ID NO: 1827, SEQ ID NO: 1842, SEQ ID NO: 1846, SEQ ID NO: 1896, SEQ ID NO: 1530, SEQ ID NO: 1637, SEQ ID NO: 1461, SEQ ID NO: 1467, SEQ ID NO: 1623, SEQ ID NO: 1625, SEQ ID NO: 530, SEQ ID NO: 708, SEQ ID NO: 414, SEQ ID NO: 694, SEQ ID NO: 703, SEQ ID NO: 721, SEQ ID NO: 749, SEQ ID NO: 685, SEQ ID NO: 444, SEQ ID NO: 606, SEQ ID NO: 582, SEQ ID NO: 621, SEQ ID NO: 868, SEQ ID NO: 666, SEQ ID NO: 408, SEQ ID NO: 538, SEQ ID NO: 573, SEQ ID NO: 639, SEQ ID NO: 668, SEQ ID NO: 524, SEQ ID NO: 422, SEQ ID NO: 819, SEQ ID NO: 611, SEQ ID NO: 674, SEQ ID NO: 577, SEQ ID NO: 663, SEQ ID NO: 558, SEQ

This Sheet Has Been Replaced

ID NO: 794, SEQ ID NO: 564, SEQ ID NO: 592, SEQ ID NO: 814, SEQ ID NO: 398, SEQ ID NO: 767, SEQ ID NO: 425, SEQ ID NO: 659, SEQ ID NO: 517, SEQ ID NO: 539, SEQ ID NO: 475, SEQ ID NO: 615, SEQ ID NO: 665, SEQ ID NO: 607, SEQ ID NO: 598, SEQ ID NO: 759, SEQ ID NO: 752, SEQ ID NO: 595, SEQ ID NO: 686, SEQ ID NO: 528, SEQ ID NO: 705, SEQ ID NO: 828, SEQ ID NO: 403, SEQ ID NO: 561, SEQ ID NO: 500, SEQ ID NO: 491, SEQ ID NO: 846, SEQ ID NO: 732, SEQ ID NO: 778, SEQ ID NO: 751, SEQ ID NO: 744, SEQ ID NO: 504, SEQ ID NO: 419, SEQ ID NO: 792, SEQ ID NO: 825, SEQ ID NO: 756, SEQ ID NO: 519, SEQ ID NO: 870, SEQ ID NO: 777, SEQ ID NO: 808, SEQ ID NO: 506, SEQ ID NO: 864, SEQ ID NO: 655, SEQ ID NO: 407, SEQ ID NO: 427, SEQ ID NO: 774, SEQ ID NO: 797, SEQ ID NO: 688, SEQ ID NO: 815, SEQ ID NO: 718, SEQ ID NO: 859, SEQ ID NO: 775, SEQ ID NO: 874, SEQ ID NO: 543, SEQ ID NO: 878, SEQ ID NO: 594, SEQ ID NO: 610, and SEQ ID NO: 600.

73. A purified *H. pylori* surface or membrane polypeptide or a fragment thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 1511, SEQ ID NO: 1561, SEQ ID NO: 1563, SEQ ID NO: 1681, SEQ ID NO: 1711, SEQ ID NO: 1731, SEQ ID NO: 1743, SEQ ID NO: 1747, SEQ ID NO: 1758, SEQ ID NO: 1893, SEQ ID NO: 1895, SEQ ID NO: 1573, SEQ ID NO: 1705, SEQ ID NO: 1707, SEQ ID NO: 1723, SEQ ID NO: 1726, SEQ ID NO: 1760, SEQ ID NO: 1764, SEQ ID NO: 1798, SEQ ID NO: 1803, SEQ ID NO: 1807, SEQ ID NO: 1889, SEQ ID NO: 1892, SEQ ID NO: 1460, SEQ ID NO: 1477, SEQ ID NO: 1499, SEQ ID NO: 1514, SEQ ID NO: 1641, SEQ ID NO: 1534, SEQ ID NO: 1564, SEQ ID NO: 1673, SEQ ID NO: 1746, SEQ ID NO: 1794, SEQ ID NO: 1843, SEQ ID NO: 1894, SEQ ID NO: 1536, SEQ ID NO: 1544, SEQ ID NO: 1568, SEQ ID NO: 1572, SEQ ID NO: 1582, SEQ ID NO: 1738, SEQ ID NO: 1891, SEQ ID NO: 1660, SEQ ID NO: 1793, SEQ ID NO: 1832, SEQ ID NO: 1841, SEQ ID NO: 1860, SEQ ID NO: 1486, SEQ ID NO: 1465, SEQ ID NO: 1539, SEQ ID NO: 1693, SEQ ID NO: 1629, SEQ ID NO: 1540, SEQ ID NO: 1791, SEQ ID NO: 1525, SEQ ID NO: 1558, SEQ ID NO: 1655, SEQ ID NO: 1517, SEQ ID NO: 875, SEQ ID NO: 676, SEQ ID NO: 801, SEQ ID NO: 860, SEQ ID NO: 747, SEQ ID NO: 529, SEQ ID NO: 387, SEQ ID NO: 391, SEQ ID NO: 515, SEQ ID NO: 625, SEQ ID NO: 568, SEQ ID NO: 454, SEQ ID NO: 800, SEQ ID NO: 499, SEQ ID NO: 779, SEQ ID NO: 648, SEQ ID NO: 643, SEQ ID NO: 537, SEQ ID NO: 511, SEQ ID NO: 616, SEQ ID NO: 829, SEQ ID NO: 546, SEQ ID NO: 780, SEQ ID NO: 553, SEQ ID NO: 549, SEQ ID NO: 410, SEQ ID NO: 608, SEQ ID NO: 513, SEQ ID NO: 656, SEQ ID NO: 845, SEQ ID NO: 563, SEQ ID NO: 570, SEQ ID NO: 805, SEQ ID NO: 851, SEQ ID NO: 423, SEQ ID NO: 810, SEQ ID NO: 604, SEQ ID NO: 636, SEQ ID NO: 757, SEQ ID NO: 412, SEQ ID NO: 816, SEQ ID NO: 771, SEQ ID NO: 418, SEQ ID NO: 662, SEQ ID NO: 512, SEQ ID NO: 679, SEQ ID NO: 605, SEQ ID NO: 421, SEQ ID NO: 552, SEQ ID

NO: 576, SEQ ID NO: 571, SEQ ID NO: 725, SEQ ID NO: 565, SEQ ID NO: 717, SEQ ID NO: 536, SEQ ID NO: 647, SEQ ID NO: 501, SEQ ID NO: 838, SEQ ID NO: 428, SEQ ID NO: 494, SEQ ID NO: 479, SEQ ID NO: 711, SEQ ID NO: 722 ,SEQ ID NO: 645, SEQ ID NO: 670, SEQ ID NO: 746, SEQ ID NO: 493, SEQ ID NO: 540, SEQ ID NO: 612, SEQ ID NO: 629, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 433, SEQ ID NO: 385, and SEQ ID NO: 409.

74. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least one membrane spanning region selected from the group consisting of SEQ ID NO: 1511, SEQ ID NO: 1561, SEQ ID NO: 1563, SEQ ID NO: 1681, SEQ ID NO: 1711, SEQ ID NO: 1731, SEQ ID NO: 1743, SEQ ID NO: 1747, SEQ ID NO: 1753, SEQ ID NO: 1893, SEQ ID NO: 1895, SEQ ID NO: 875, SEQ ID NO: 676, SEQ ID NO: 801, SEQ ID NO: 860, SEQ ID NO: 747, SEQ ID NO: 529, SEQ ID NO: 387, SEQ ID NO: 391, SEQ ID NO: 515, SEQ ID NO: 625, SEQ ID NO: 568, SEQ ID NO: 454, SEQ ID NO: 800, SEQ ID NO: 499, SEQ ID NO: 779, and SEQ ID NO: 385.

75. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least two membrane spanning regions selected from the group consisting of SEQ ID NO: 1573, SEQ ID NO: 1705, SEQ ID NO: 1707, SEQ ID NO: 1723, SEQ ID NO: 1726, SEQ ID NO: 1760, SEQ ID NO: 1764, SEQ ID NO: 1798, SEQ ID NO: 1803, SEQ ID NO: 1807, SEQ ID NO: 1889, SEQ ID NO: 1892, SEQ ID NO: 1460, SEQ ID NO: 1477, SEQ ID NO: 1499, SEQ ID NO: 1514, SEQ ID NO: 1641, SEQ ID NO: 648, SEQ ID NO: 643, SEQ ID NO: 537, SEQ ID NO: 511, SEQ ID NO: 616, SEQ ID NO: 829, SEQ ID NO: 546, SEQ ID NO: 780, SEQ ID NO: 553, SEQ ID NO: 549, SEQ ID NO: 410, SEQ ID NO: 608, SEQ ID NO: 513, SEQ ID NO: 656, SEQ ID NO: 845, SEQ ID NO: 563, SEQ ID NO: 570, SEQ ID NO: 805, and SEQ ID NO: 851.

76. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least three membrane spanning regions selected from the group consisting of SEQ ID NO: 1534, SEQ ID NO: 1564, SEQ ID NO: 1673, SEQ ID NO: 1746, SEQ ID NO: 1794, SEQ ID NO: 1843, SEQ ID NO: 1894, SEQ ID NO: 423, SEQ ID NO: 810, SEQ ID NO: 604, SEQ ID NO: 636, SEQ ID NO: 757, SEQ ID NO: 412, and SEQ ID NO: 816.

77. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least four membrane spanning regions selected from the group consisting

of SEQ ID NO: 1536, SEQ ID NO: 1544, SEQ ID NO: 1568, SEQ ID NO: 1572, SEQ ID NO: 1582, SEQ ID NO: 1738, SEQ ID NO: 1891, SEQ ID NO: 1660, SEQ ID NO: 771, SEQ ID NO: 418, SEQ ID NO: 662, SEQ ID NO: 512, SEQ ID NO: 679, SEQ ID NO: 605, SEQ ID NO: 421, SEQ ID NO: 552, SEQ ID NO: 576, and SEQ ID NO: 571.

78. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least five membrane spanning regions selected from the group consisting of SEQ ID NO: 1793, SEQ ID NO: 1832, SEQ ID NO: 1841, SEQ ID NO: 1860, SEQ ID NO: 1486, SEQ ID NO: 725, SEQ ID NO: 565, SEQ ID NO: 717, SEQ ID NO: 536, SEQ ID NO: 647, SEQ ID NO: 409.

79. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least six membrane spanning regions selected from the group consisting of SEQ ID NO: 1465, SEQ ID NO: 1539, SEQ ID NO: 1693, SEQ ID NO: 1629, SEQ ID NO: 501, SEQ ID NO: 838, SEQ ID NO: 428, SEQ ID NO: 494, SEQ ID NO: 479, SEQ ID NO: 711, and SEQ ID NO: 722.

80. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least seven membrane spanning regions selected from the group consisting of SEQ ID NO: 1540, SEQ ID NO: 1791, SEQ ID NO: 1525, SEQ ID NO: 1558, SEQ ID NO: 1655, SEQ ID NO: 1517, SEQ ID NO: 645, SEQ ID NO: 670, SEQ ID NO: 746, SEQ ID NO: 493, SEQ ID NO: 540, SEQ ID NO: 612, SEQ ID NO: 629, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, and SEQ ID NO: 433.

81. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 56.

82. A vaccine composition of claim 81, further comprising a pharmaceutically acceptable carrier.

83. A vaccine composition of claim 82, wherein the pharmaceutically acceptable carrier is an adjuvant.

84. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 81, such that treatment of *H. pylori* infection occurs.

This Sheet Has Been Replaced

85. A method of claim 84, wherein the treatment is a prophylactic treatment.

86. A method of claim 84, wherein the treatment is a therapeutic treatment.

87. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 61.

88. A vaccine composition of claim 87, further comprising a pharmaceutically acceptable carrier.

89. A vaccine composition of claim 88, wherein the pharmaceutically acceptable carrier is an adjuvant.

90. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 87, such that treatment of *H. pylori* infection occurs.

91. A method of claim 90, wherein the treatment is a prophylactic treatment.

92. A method of claim 90, wherein the treatment is a therapeutic treatment.

93. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 72.

94. A vaccine composition of claim 93, further comprising a pharmaceutically acceptable carrier.

95. A vaccine composition of claim 94, wherein the pharmaceutically acceptable carrier is an adjuvant.

96. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 93, such that treatment of *H. pylori* infection occurs.

97. A method of claim 96, wherein the treatment is a prophylactic treatment.

This Sheet Has Been Replaced

SUBSTITUTE SHEET (RULE 26)

98. A method of claim 96, wherein the treatment is a therapeutic treatment.

99. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 73.

100. A vaccine composition of claim 99, further comprising a pharmaceutically acceptable carrier.

101. A vaccine composition of claim 100, wherein the pharmaceutically acceptable carrier is an adjuvant.

102. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 99, such that treatment of *H. pylori* infection occurs.

103. A method of claim 102, wherein the treatment is a prophylactic treatment.

104. A method of claim 102, wherein the treatment is a therapeutic treatment.

105. 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 1 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.

106. 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 9 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.

107. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising:

This Sheet Has Been Replaced

(a) contacting a sample with a nucleic acid of claim 23 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.

108. 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 27 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.

This Sheet Has Been Replaced