

SEQUENCE LISTING

<110> Technische Universität München
 <120> Method for the detection of H. pylori infection
 <130> G 10023 PCT
 <150> EP 13 004 038.9
 <151> 2013-08-13
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 <170> PatentIn version 3.3
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 <213> H. pylori

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Asn Ile Lys Val Asp Val Glu Ser Leu Ala Gln Gly Asp Ile Asn Glu
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Asp Asn Ala Val Ala Ser Tyr Asp Pro Asp Gln Lys Pro Ile Val Asp
35 40 45

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

Arg Glu Glu Tyr Ser Asn Lys Ala Ile Lys Asn Pro Ala Lys Lys Asn

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

Gly Ser His Asn Gly Ile Glu Pro Glu Lys Val Ser Leu Leu Tyr Gly
 305 310 315 320

Gly Asn Gly Gly Pro Lys Ala Lys His Asp Trp Asn Ala Thr Val Gly
 325 330 335

Tyr Lys Asp Gln Gln Gly Asn Asn Val Ala Thr Ile Ile Asn Val His
 340 345 350

Met Lys Asn Gly Ser Gly Leu Val Ile Ala Gly Gly Glu Lys Gly Ile
 355 360 365

Asn Asn Pro Ser Phe Tyr Leu Tyr Lys Glu Asp Gln Leu Thr Gly Ser
 370 375 380

Gln Arg Ala Leu Ser Gln Glu Glu Ile Arg Asn Lys Val Asp Phe Met
 385 390 395 400

Glu Phe Leu Ala Gln Asn Asn Ala Lys Leu Asp Asn Leu Ser Glu Lys
 405 410 415

Glu Glu Glu Lys Phe Arg Asn Glu Ile Lys Asp Phe Gln Lys Asp Ser
 420 425 430

Lys Ala Tyr Leu Asp Ala Leu Gly Asn Asp Arg Ile Ala Phe Val Ser
 435 440 445

Lys Lys Asp Thr Lys His Ser Ala Leu Ile Thr Glu Phe Gly Asn Gly
 450 455 460

Asp Leu Ser Tyr Thr Leu Lys Asp Tyr Gly Lys Lys Ala Asp Lys Ala
 465 470 475 480

Leu Asp Arg Glu Lys Asn Val Thr Leu Gln Gly Asn Leu Lys His Asp
 485 490 495

Gly Val Met Phe Val Asp Tyr Ser Asn Phe Lys Tyr Thr Asn Ala Ser
 500 505 510

Lys Asn Pro Asn Lys Gly Val Gly Val Thr Asn Gly Val Ser His Leu
 515 520 525

Glu Ala Gly Phe Ser Lys Val Ala Val Phe Asn Leu Pro Asp Leu Asn
 530 535 540

Asn Leu Ala Ile Thr Ser Leu Val Arg Arg Asp Leu Glu Asp Lys Leu
545 550 555 560

Ile Ala Lys Gly Leu Ser Pro Gln Glu Thr Asn Lys Leu Val Lys Asp
565 570 575

Phe Leu Ser Ser Asn Lys Glu Leu Val Gly Lys Ala Leu Asn Phe Asn
580 585 590

Lys Ala Val Ala Glu Ala Lys Asn Thr Gly Asn Tyr Asp Glu Val Lys
595 600 605

Gln Ala Gln Lys Asp Leu Glu Lys Ser Leu Lys Lys Arg Glu Arg Leu
610 615 620

Glu Lys Glu Val Ala Lys Lys Leu Glu Ser Lys Ser Gly Asn Lys Asn
625 630 635 640

Lys Met Glu Ala Lys Ser Gln Ala Asn Ser Gln Lys Asp Glu Ile Phe
645 650 655

Ala Leu Ile Asn Lys Glu Ala Asn Arg Glu Ala Arg Ala Ile Thr Tyr
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Ala Gln Asn Leu Lys Gly Ile Lys Arg Glu Leu Ser Asp Lys Leu Glu
675 680 685

Asn Val Asn Lys Asn Leu Lys Asp Phe Ser Lys Ser Phe Asp Glu Phe
690 695 700

Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys Ser Glu Glu Thr Leu Lys
705 710 715 720

Ala Leu Lys Gly Ser Val Lys Asp Leu Gly Ile Asn Pro Glu Trp Ile
725 730 735

Ser Lys Val Glu Asn Leu Asn Ala Ala Leu Asn Glu Phe Lys Asn Gly
740 745 750

Lys Asn Lys Asp Phe Ser Lys Val Thr Gln Ala Lys Ser Asp Leu Glu
755 760 765

Asn Ser Val Lys Asp Val Ile Ile Asn Gln Lys Val Thr Asp Lys Val
770 775 780

Asp Asn Leu Asn Gln Ala Val Ser Val Ala Lys Ala Thr Gly Asp Phe
785 790 795 800

Ser Arg Val Glu Gln Ala Leu Ala Asp Leu Lys Asn Phe Ser Lys Glu
805 810 815

Gln Leu Ala Gln Gln Ala Gln Lys Asn Glu Asp Phe Asn Thr Gly Lys
820 825 830

Asn Ser Ala Leu Tyr Gln Ser Val Lys Asn Gly Val Asn Gly Thr Leu
835 840 845

Val Gly Asn Gly Leu Ser Lys Ala Glu Ala Thr Thr Leu Ser Lys Asn
850 855 860

Phe Ser Asp Ile Lys Lys Glu Leu Asn Ala Lys Leu Gly Asn Phe Asn
865 870 875 880

Asn Asn Asn Asn Asn Gly Leu Lys Asn Ser Thr Glu Pro Ile Tyr Ala
885 890 895

Lys Val Asn Lys Lys Lys Ala Gly Gln Ala Ala Ser Pro Glu Glu Pro
900 905 910

Ile Tyr Ala Gln Val Ala Lys Lys Val Asn Ala Lys Ile Asp Arg Leu
915 920 925

Asn Gln Ile Ala Ser Gly Leu Gly Val Val Gly Gln Ala Val Gly Phe
930 935 940

Pro Leu Lys Arg His Asp Lys Val Gly Asp Leu Ser Lys Val Gly Gln
945 950 955 960

Ser Val Ser Pro Glu Pro Ile Tyr Ala Thr Ile Asp Asp Leu Gly Gly
965 970 975

Pro Phe Pro Leu Lys Arg His Asp Lys Val Gly Asp Leu Ser Lys Val
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Gly Leu Ser Val Ser Pro Glu Pro Ile Tyr Ala Thr Ile Asp Asp Leu
995 1000 1005

Gly Gly Pro Phe Pro Leu Lys Arg His Asp Lys Val Gly Asp Leu

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Ser Lys Val Gly Leu Ser Arg Glu Gln Gln Leu Lys Gln Lys Ile				
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Asp Asn Leu Ser Gln Ala Val Ser Glu Ala Lys Ala Gly Phe Phe				
1040		1045		1050
Gly Asn Leu Glu Gln Thr Ile Asp Asn Leu Lys Asp Ser Ala Lys				
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Asn Asn Pro Val Ser Leu Trp Ala Glu Gly Ala Lys Lys Val Pro				
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Ala Ser Leu Ser Ala Lys Leu Asp Asn Tyr Ala Thr Asn Ser His				
1085		1090		1095
Thr Arg Ile Asn Ser Asn Ile Gln Ser Gly Ala Ile Asn Glu Lys				
1100		1105		1110
Ala Thr Gly Met Leu Thr Gln Lys Asn Pro Glu Trp Leu Lys Leu				
1115		1120		1125
Val Asn Asp Lys Ile Val Ala His Asn Val Gly Ser Val Pro Leu				
1130		1135		1140
Leu Glu Tyr Asp Lys Ile Gly Phe Asn Gln Lys Ser Met Lys Asp				
1145		1150		1155
Tyr Ser Asp Ser Phe Lys Phe Ser Thr Glu Leu Asn Asn Ala Val				
1160		1165		1170
Lys Asp Val Lys Ser Gly Phe Thr Gln Phe Leu Ala Asn Ala Phe				
1175		1180		1185
Ser Thr Gly Tyr Tyr Arg Leu Ala Gly Glu Asn Ala Glu His Gly				
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Ile Lys Asn Val Asn Thr Lys Gly Gly Ser Lys Asn Leu Lys Gly				
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Leu Val Leu Ala Gly Ala Leu Ile Ser Ala Ile Pro Gln Glu Ser His
          20           25           30

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Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile
          35           40           45

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Ala Thr Gly Thr Ala Val Gly Thr Val Ser Gly Leu Leu Ser Trp Gly
          50           55           60

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Leu Lys Gln Ala Glu Glu Ala Asn Lys Asn Pro Asp Lys Pro Asp Lys
65           70           75           80

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Val Trp Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys
          85           90           95

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Glu Tyr Asp Leu Tyr Lys Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly
          100          105          110

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Trp Asp Trp Gly Asn Ala Ala Arg His Tyr Trp Val Lys Gly Gly Gln
115 120 125

Trp Asn Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Lys
130 135 140

Leu Ser Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met
145 150 155 160

Gln Lys Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr
165 170 175

Ser Tyr Lys Asp Ala Ala Asp Arg Thr Thr Arg Val Asn Phe Asn Ala
180 185 190

Lys Asn Ile Ser Ile Asp Asn Phe Val Glu Ile Asn Asn Arg Val Gly
195 200 205

Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala
210 215 220

Ser Glu Gly Ile Thr Ser Asp Lys Asn Ala Glu Ile Ser Leu Tyr Asp
225 230 235 240

Gly Ala Thr Leu Asn Leu Ala Ser Ser Ser Val Lys Leu Met Gly Asn
245 250 255

Val Trp Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser
260 265 270

Tyr Ser Thr Ile Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn
275 280 285

His Leu Thr Val Gly Asp Lys Asn Ala Ala Gln Ala Gly Ile Ile Ala
290 295 300

Ser Asn Lys Thr His Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly
305 310 315 320

Leu Asn Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Asn
325 330 335

Asn Thr Pro Ser Gln Ser Gly Thr Lys Asn Asp Lys Asn Glu Ser Ala
340 345 350

Lys Asn Asp Lys Gln Glu Ser Ser Gln Asn Asn Ser Asn Thr Gln Val
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Ile Asn Pro Pro Asn Ser Thr Gln Lys Thr Glu Ile Gln Pro Thr Gln
 370 375 380

Val Ile Asp Gly Pro Phe Ala Gly Gly Lys Asp Thr Val Val Asn Ile
 385 390 395 400

Asn Arg Ile Asn Thr Asn Ala Asp Gly Thr Ile Arg Val Gly Gly Phe
 405 410 415

Lys Ala Ser Leu Thr Thr Asn Ala Ala His Leu His Ile Gly Lys Gly
 420 425 430

Gly Val Asn Leu Ser Asn Gln Ala Ser Gly Arg Thr Leu Leu Val Glu
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Asn Leu Thr Gly Asn Ile Thr Val Asp Gly Pro Leu Arg Val Asn Asn
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Gln Val Gly Gly Tyr Ala Leu Ala Gly Ser Ser Ala Asn Phe Glu Phe
 465 470 475 480

Lys Ala Gly Val Asp Thr Lys Asn Gly Thr Ala Thr Phe Asn Asn Asp
 485 490 495

Ile Ser Leu Gly Arg Phe Val Asn Leu Lys Val Asp Ala His Thr Ala
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Asn Phe Lys Gly Ile Asp Thr Gly Asn Gly Gly Phe Asn Thr Leu Asp
 515 520 525

Phe Ser Gly Val Thr Asp Lys Val Asn Ile Asn Lys Leu Ile Thr Ala
 530 535 540

Ser Thr Asn Val Ala Val Lys Asn Phe Asn Ile Asn Glu Leu Ile Val
 545 550 555 560

Lys Thr Asn Gly Ile Ser Val Gly Glu Tyr Thr His Phe Ser Glu Asp
 565 570 575

Ile Gly Ser Gln Ser Arg Ile Asn Thr Val Arg Leu Glu Thr Gly Thr

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Val Ile Asp Glu Phe Tyr Tyr Ser Pro Trp Asn Tyr Phe Asp Ala Arg		
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Asn Val Lys Asn Val Glu Ile Thr Arg Lys Phe Ala Ser Ser Thr Pro		
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Glu Asn Pro Trp Gly Thr Ser Lys Leu Met Phe Asn Asn Leu Thr Leu		
	645	650
Gly Gln Asn Ala Val Met Asp Tyr Ser Gln Phe Ser Asn Leu Thr Ile		
	660	665
Gln Gly Asp Phe Ile Asn Asn Gln Gly Thr Ile Asn Tyr Leu Val Arg		
	675	680
Gly Gly Lys Val Ala Thr Leu Ser Val Gly Asn Ala Ala Ala Met Met		
	690	695
Phe Asn Asn Asp Ile Asp Ser Ala Thr Gly Phe Tyr Lys Pro Leu Ile		
705	710	715
Lys Ile Asn Ser Ala Gln Asp Leu Ile Lys Asn Thr Glu His Val Leu		
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Leu Lys Ala Lys Ile Ile Gly Tyr Gly Asn Val Ser Thr Gly Thr Asn		
	740	745
Ser Ile Ser Asn Val Asn Leu Glu Glu Gln Phe Lys Glu Arg Leu Ala		
	755	760
Leu Tyr Asn Asn Asn Asn Arg Met Asp Thr Cys Val Val Arg Asn Thr		
	770	775
Asp Asp Ile Lys Ala Cys Gly Met Ala Ile Gly Asn Gln Ser Met Val		
785	790	795
Asn Asn Pro Asp Asn Tyr Lys Tyr Leu Ile Gly Lys Ala Trp Lys Asn		
	805	810
		815

Ile Gly Ile Ser Lys Thr Ala Asn Gly Ser Lys Ile Ser Val Tyr Tyr
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Leu Gly Asn Ser Thr Pro Thr Glu Asn Gly Gly Asn Thr Thr Asn Leu
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Pro Thr Asn Thr Thr Asn Asn Ala Arg Ser Ala Asn Tyr Ala Leu Val
 850 855 860

Lys Asn Ala Pro Phe Ala His Ser Ala Thr Pro Asn Leu Val Ala Ile
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Asn Gln His Asp Phe Gly Thr Ile Glu Ser Val Phe Glu Leu Ala Asn
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Arg Ser Lys Asp Ile Asp Thr Leu Tyr Thr His Ser Gly Val Gln Gly
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Arg Asp Leu Leu Gln Thr Leu Leu Ile Asp Ser His Asp Ala Gly Tyr
 915 920 925

Ala Arg Gln Met Ile Asp Asn Thr Ser Thr Gly Glu Ile Thr Lys Gln
 930 935 940

Leu Asn Ala Ala Thr Asp Ala Leu Asn Asn Ile Ala Ser Leu Glu His
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Lys Thr Ser Gly Leu Gln Thr Leu Ser Leu Ser Asn Ala Met Ile Leu
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Asn Ser Arg Leu Val Asn Leu Ser Arg Lys His Thr Asn His Ile Asp
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Ser Phe Ala Gln Arg Leu Gln Ala Leu Lys Gly Gln Arg Phe Ala Ser
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Leu Glu Ser Ala Ala Glu Val Leu Tyr Gln Phe Ala Pro Lys Tyr
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Glu Lys Pro Thr Asn Val Trp Ala Asn Ala Ile Gly Gly Ala Ser
 1025 1030 1035

Leu Asn Asn Gly Gly Asn Ala Ser Leu Tyr Gly Thr Ser Ala Gly
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Phe	Gly	Ser	Tyr	Gly	Tyr	Ser	Ser	Phe	Ser	Asn	Arg	Ala	Asn	Ser
1070						1075					1080			
Leu	Asn	Ser	Gly	Ala	Asn	Asn	Ala	Asn	Phe	Gly	Val	Tyr	Ser	Arg
1085						1090					1095			
Ile	Phe	Ala	Asn	Gln	His	Glu	Phe	Asp	Phe	Glu	Ala	Gln	Gly	Ala
1100						1105					1110			
Leu	Gly	Ser	Asp	Gln	Ser	Ser	Leu	Asn	Phe	Lys	Ser	Ala	Leu	Leu
1115						1120					1125			
Gln	Asp	Leu	Asn	Gln	Ser	Tyr	His	Tyr	Leu	Ala	Tyr	Ser	Ala	Ala
1130						1135					1140			
Thr	Arg	Ala	Ser	Tyr	Gly	Tyr	Asp	Phe	Ala	Phe	Phe	Arg	Asn	Ala
1145						1150					1155			
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1175						1180					1185			
Gly	Ser	Ser	Ser	Gln	His	Leu	Phe	Asn	Ala	Asn	Ala	Asn	Val	Glu
1190						1195					1200			
Ala	Arg	Tyr	Tyr	Tyr	Gly	Asp	Thr	Ser	Tyr	Phe	Tyr	Met	Asn	Ala
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Gly	Val	Leu	Gln	Glu	Phe	Ala	Arg	Phe	Gly	Ser	Asn	Asn	Ala	Ala
1220						1225					1230			
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Thr	His	Ala	Arg	Val	Met	Met	Gly	Gly	Glu	Leu	Gln	Leu	Ala	Lys
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Glu	Val	Phe	Leu	Asn	Leu	Gly	Val	Val	Tyr	Leu	His	Asn	Leu	Ile
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caaagtggca ctaaaaacga caaaaatgaa agcgctaaaa acgacaaaca agagagcagt 1080
caaaataata gtaacactca ggtcattaac ccaccaata gcacgcaaaa aacagaaatt 1140

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gtcaatctct ccaggaagca caccaaccat attgactcgt tcgctcaacg cttacaagct 3000
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<210> 11
 <211> 546
 <212> PRT
 <213> H. pylori

<220>
 <221> MISC_FEATURE
 <223> H. pylori strain G27

<400> 11

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Glu Gly Val Arg Gln Leu His Asp Ala Val Lys Val Thr Met Gly Pro
 20 25 30

Arg Gly Arg Asn Val Leu Ile Gln Lys Ser Tyr Gly Ala Pro Ser Ile
 35 40 45

Thr Lys Asp Gly Val Ser Val Ala Lys Glu Ile Glu Leu Ser Cys Pro

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

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

Gly Leu Ser Leu Glu Asn Ala Glu Val Glu Phe Leu Gly Lys Ala Gly
 305 310 315 320

Arg Ile Val Ile Asp Lys Asp Asn Thr Thr Ile Val Asp Gly Lys Gly
 325 330 335

His Ser Asp Asp Val Lys Asp Arg Val Ala Gln Ile Lys Thr Gln Ile
 340 345 350

Ala Ser Thr Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu
 355 360 365

Ala Lys Leu Ser Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Ser
 370 375 380

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

Ala Thr Lys Ala Ala Val Glu Glu Gly Ile Val Ile Gly Gly Gly Ala
 405 410 415

Ala Leu Ile Arg Ala Ala Gln Lys Val His Leu Asn Leu His Asp Asp
 420 425 430

Glu Lys Val Gly Tyr Glu Ile Ile Met Arg Ala Ile Lys Ala Pro Leu
 435 440 445

Ala Gln Ile Ala Ile Asn Ala Gly Tyr Asp Gly Gly Val Val Val Asn
 450 455 460

Glu Val Glu Lys His Glu Gly His Phe Gly Phe Asn Ala Ser Asn Gly
 465 470 475 480

Lys Tyr Val Asp Met Phe Lys Glu Gly Ile Ile Asp Pro Leu Lys Val
 485 490 495

Glu Arg Ile Ala Leu Gln Asn Ala Val Ser Val Ser Ser Leu Leu Leu
 500 505 510

Thr Thr Glu Ala Thr Val His Glu Ile Lys Glu Glu Lys Ala Ala Pro
 515 520 525

Ala Met Pro Asp Met Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly
 530 535 540

Met Met
 545

<210> 12
 <211> 1641
 <212> DNA
 <213> H. pylori

<220>
 <221> misc_feature
 <223> H. pylori strain G27

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 aaaagctatg gcgctccaag catcaccaaa gatggcgtga gcgtggctaa agagattgaa 180
 ttaagttgcc cgggtggctaa catgggcgtc caactcgtta aagaggtagc gagcaaaacc 240
 gctgatgctg ccggcgatgg cacgaccaca gcgaccgtgc tggcttatag cattttttaa 300
 gaaggtttga ggaatatcac ggctggggct aaccctattg aagtgaacg aggcattgat 360
 aaagccgctg aagcgatcat caatgagctt aaaaaagcga gcaaaaaagt aggcggtaaa 420
 gaagaaatca cccaagtagc gaccatttct gccaaactccg atcacaatat cgggaaaactc 480
 atcgctgacg ctatggaaaa agtgggtaaa gatggcgtga tcaactgttg agaggctaag 540
 ggcattgaag acgaattaga tgtcgtagaa ggcatgcaat ttgatagagg ctatctctcc 600
 ccttattttg taacgaacgc tgagaaaatg accgctcaat tggataacgc ttacatcctt 660
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 ctagtgggtga ataaattaag aggcgtgttg aatatcgtag cggttaaagc tccaggcttt 840
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 aaagaaaaat tgcaagaaag gttggccaaa ctctctggcg gtgtggctgt gattaaagtg 1140
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<210> 13
<211> 265
<212> PRT
<213> H. pylori

<220>
<221> MISC_FEATURE
<223> H. pylori 26695

<400> 13

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Gly Ala Ala Pro Lys His Ser Val Ser Ala Asn Asp Lys Arg Met Gln
20 25 30

Asp Asn Leu Val Ser Val Ile Glu Lys Gln Thr Asn Lys Lys Val Arg
35 40 45

Ile Leu Glu Ile Lys Pro Leu Lys Ser Ser Gln Asp Leu Lys Met Val
50 55 60

Val Ile Glu Asp Pro Asp Thr Lys Tyr Asn Ile Pro Leu Val Val Ser
65 70 75 80

Lys Asp Gly Asn Leu Ile Ile Gly Leu Ser Asn Ile Phe Phe Ser Asn
85 90 95

Lys Ser Asp Asp Val Gln Leu Val Ala Glu Thr Asn Gln Lys Val Gln
100 105 110

Ala Leu Asn Ala Thr Gln Gln Asn Ser Ala Lys Leu Asn Ala Ile Phe

115	120	125
Asn Glu Ile Pro Ala Asp Tyr Ala Ile Glu Leu Pro Ser Thr Asn Ala		
130	135	140
Ala Asn Lys Asp Lys Ile Leu Tyr Ile Val Ser Asp Pro Met Cys Pro		
145	150	155 160
His Cys Gln Lys Glu Leu Thr Lys Leu Arg Asp His Leu Lys Glu Asn		
165	170	175
Thr Val Arg Met Val Val Val Gly Trp Leu Gly Val Asn Ser Ala Lys		
180	185	190
Lys Ala Ala Leu Ile Gln Glu Glu Met Ala Lys Ala Arg Ala Arg Gly		
195	200	205
Ala Ser Val Glu Asp Lys Ile Ser Ile Leu Glu Lys Ile Tyr Ser Thr		
210	215	220
Gln Tyr Asp Ile Asn Ala Gln Lys Glu Pro Glu Asp Leu Arg Thr Lys		
225	230	235 240
Val Glu Asn Thr Thr Lys Lys Ile Phe Glu Ser Gly Val Ile Lys Gly		
245	250	255
Val Pro Phe Leu Tyr His Tyr Lys Ala		
260	265	

<210> 14
 <211> 798
 <212> DNA
 <213> H. pylori

<220>
 <221> misc_feature
 <223> H. pylori 26695

<400> 14	
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aaacagacca ataaaaaggt gcgtatttta gaaatcaaac ctttaaaatc tagccaggat	180
ttaaaaatgg tcgttattga agatccggac actaaataca atatcccgt tgtggtgagt	240
aaggatggta atttaatcat agggcttagc aacatattct ttagcaataa aagcgatgat	300

gtgcaattag ttgcagaaac caatcaaaaa gttcaagctc ttaacgccac ccaacaaaaat 360
 agcgcgaaat tgaacgctat ttttaatgaa ataccggctg attatgcgat agagttgccc 420
 tctactaacg ctgcaaataa ggataaaatc ctttatattg tctctgatcc catgtgcccc 480
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 gtcgtggtgg ggtggcttgg ggtcaattca gctaaaaaag cggctttaat ccaagaagaa 600
 atggcgaaag ctagggctag gggagcgagc gtggaagata agatctctat tcttgaaaag 660
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<210> 15
 <211> 325
 <212> PRT
 <213> H. pylori

<220>
 <221> MISC_FEATURE
 <223> H. pylori J99

<400> 15

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Phe	Gly	Gly	Ala	Asn	Gly	Asn	Lys	Ile	Ser	Leu	Phe	Tyr	Asn	Asn	Glu
			20				25						30		

Leu	Tyr	Met	Val	Lys	Phe	Pro	Pro	Lys	Pro	Ser	Thr	His	Lys	Glu	Met
	35						40					45			

Ser	Tyr	Thr	Asn	Gly	Cys	Phe	Ser	Glu	Tyr	Val	Ala	Cys	His	Ile	Val
	50					55					60				

Asn	Ser	Leu	Gly	Leu	Lys	Val	Gln	Glu	Thr	Leu	Leu	Gly	Thr	Tyr	Lys
65					70					75					80

Asn	Lys	Ile	Val	Val	Ala	Cys	Lys	Asp	Phe	Thr	Thr	His	Gln	Tyr	Glu
			85						90					95	

Leu	Val	Asp	Phe	Leu	Ser	Leu	Lys	Asn	Thr	Met	Ile	Glu	Leu	Glu	Lys
			100					105					110		

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

Gln His Phe Ile Glu Pro Lys Val Leu Lys Cys Phe Phe Trp Asp Met
130 135 140

Phe Val Ala Asp Thr Leu Leu Gly Asn Phe Asp Arg His Asn Gly Asn
145 150 155 160

Trp Gly Phe Leu Arg Ala Ser Asn Ser Lys Glu Tyr Gln Ile Ala Pro
165 170 175

Ile Phe Asp Cys Gly Ser Cys Leu Tyr Pro Gln Ala Asp Asp Val Val
180 185 190

Cys Gln Lys Val Leu Ser Asn Ile Asp Glu Leu Asn Ala Arg Ile Tyr
195 200 205

Asn Phe Pro Gln Ser Ile Leu Lys Asp Asp Asn Asp Lys Lys Ile Asn
210 215 220

Tyr Tyr Asp Phe Leu Thr Gln Thr Asn Asn Lys Asp Cys Leu Asp Ala
225 230 235 240

Leu Leu Arg Ile Tyr Pro Arg Ile Asp Met Asn Lys Ile His Ser Ile
245 250 255

Ile Asp Asn Thr Pro Phe Met Ser Glu Ile His Lys Glu Phe Leu His
260 265 270

Thr Met Leu Asp Glu Arg Lys Ser Lys Ile Ile Asp Val Ala His Thr
275 280 285

Arg Ala Ile Glu Leu Ser Leu Gln His Lys Gln Ala His Ser Asn Pro
290 295 300

Tyr Asp Asn Ala Asp Asp Leu Asp Asn Ser Asn Glu Tyr Thr Pro Thr
305 310 315 320

Pro Lys Arg Arg Arg
325

<210> 16
<211> 978

<212> DNA
<213> H. pylori

<220>
<221> misc_feature
<223> H. pylori J99

<400> 16
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aatggaaata aaattagctt attttataat aatgaactct acatgggtcaa attccccct 120
aagccttcta cacataaaga aatgtcctat accaatgggtt gttttagtga atatgtagca 180
tgtcatatag tcaatagctt aggcttaaag gttcaagaaa cattgctagg cacttataaa 240
aataaaatcg tggttgcttg taaagatttt accacccatc aatacgagct tgtagatttt 300
ctaagtctaa aaaatactat gattgaatta gaaaaatcag gcaaagacac taatttgaat 360
gatgtgcttt atgccataga taaccagcat tttattgagc caaaagtttt aaaatgtttc 420
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tgggggttct taagagcctc aaattcaaaa gaatatcaaa tagctcccat ttttgattgt 540
ggctcttgtc tataccccca agctgatgat gtggtatgcc aaaaagtttt aagtaatatt 600
gatgaactca atgcaaggat ttataatttc cccaatcta tcttaaaaga tgacaacgat 660
aaaaaaatta actactatga tttcttaact caaaccaata ataaagattg ctttgatgca 720
ctaacttagga tatacccacg catagatatg aataaaatcc attcaattat tgataacaca 780
ccctttatga gcgaaataca caaagaatth ttacatacaa tgcttgatga aagaaaatca 840
aagattatag atgtagcaca cactagagct attgagttat ccttacaaca caaacaagct 900
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<210> 17
<211> 476
<212> PRT
<213> H. pylori

<220>
<221> MISC_FEATURE
<223> H. pylori strain G27

<400> 17

Met Met Lys Lys Thr Leu Phe Ile Ser Leu Ala Leu Ala Leu Ser Leu
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Asn Ala Gly Asn Ile Gln Ile Gln Asn Met Pro Lys Val Lys Glu Arg
20 25 30

Val Ser Val Pro Ser Lys Asp Asp Thr Ile Tyr Ser Tyr His Asp Ser
35 40 45

Ile Lys Asp Ser Ile Lys Ala Val Val Asn Ile Ser Thr Glu Lys Lys
50 55 60

Ile Lys Asn Asn Phe Ile Gly Gly Gly Val Phe Asn Asp Pro Phe Phe
65 70 75 80

Gln Gln Phe Phe Gly Asp Leu Gly Gly Met Ile Pro Lys Glu Arg Met
85 90 95

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

Val Thr Asn Asn His Val Ile Asp Gly Ala Asp Lys Ile Lys Val Thr
115 120 125

Ile Pro Gly Ser Asn Lys Glu Tyr Ser Ala Thr Leu Val Gly Thr Asp
130 135 140

Ser Glu Ser Asp Leu Ala Val Ile Arg Ile Thr Lys Asp Asn Leu Pro
145 150 155 160

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

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

Ile Val Ser Ala Leu Asn Lys Ser Gly Ile Gly Ile Asn Ser Tyr Glu
195 200 205

Asn Phe Ile Gln Thr Asp Ala Ser Ile Asn Pro Gly Asn Ser Gly Gly
210 215 220

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

Ile Ser Lys Thr Gly Gly Asn His Gly Ile Gly Phe Ala Ile Pro Ser
245 250 255

Asn Met Val Lys Asp Ile Val Thr Gln Leu Ile Lys Thr Gly Lys Ile
 260 265 270

Glu Arg Gly Tyr Leu Gly Val Gly Leu Gln Asp Leu Ser Gly Asp Leu
 275 280 285

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

Lys Asp Ser Pro Ala Lys Lys Val Gly Ile Leu Val Trp Asp Leu Ile
 305 310 315 320

Thr Glu Val Asn Gly Lys Lys Val Lys Asn Thr Asn Glu Leu Arg Asn
 325 330 335

Leu Ile Gly Ser Met Leu Pro Asn Gln Arg Val Thr Leu Lys Val Ile
 340 345 350

Arg Asp Lys Lys Glu Arg Thr Phe Thr Leu Thr Leu Ala Glu Arg Lys
 355 360 365

Asn Pro Asn Lys Lys Glu Thr Ile Ser Ala Gln Asn Gly Ala Gln Gly
 370 375 380

Gln Leu Asn Gly Leu Gln Val Glu Asp Leu Thr Gln Lys Thr Lys Arg
 385 390 395 400

Ser Met Arg Leu Ser Asp Asp Val Gln Gly Val Leu Val Ser Gln Val
 405 410 415

Asn Glu Asn Ser Pro Ala Glu Gln Ala Gly Phe Arg Gln Gly Asn Ile
 420 425 430

Ile Thr Lys Ile Glu Glu Ile Glu Val Lys Ser Val Ala Asp Phe Asn
 435 440 445

His Ala Leu Glu Lys Tyr Lys Gly Lys Pro Lys Arg Phe Leu Val Leu
 450 455 460

Asp Leu Asn Gln Gly Tyr Arg Ile Ile Leu Val Lys
 465 470 475

<210> 18

<211> 1431
 <212> DNA
 <213> H. pylori

<220>
 <221> misc_feature
 <223> H. pylori G27

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 acgatctatt cttaccacga ttctattaag gattcgatta aagcggtggt gaatatctct 180
 actgaaaaga agattaaaaa caattttata ggtggcgggtg tgtttaatga cccctttttc 240
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