

SequenceListing454w000_ST25
SEQUENCE LISTING

<110> CEDARS-SINAI MEDICAL CENTER
PIMENTEL, Mark
CHANG, Christopher

<120> DIAGNOSIS AND TREATMENT OF IRRITABLE BOWEL SYNDROME AND
INFLAMMATORY BOWEL DISEASE

<130> 065472-000454w000

<150> 61/888,658
<151> 2013-10-09

<160> 8

<170> PatentIn version 3.5

<210> 1
<211> 267
<212> PRT
<213> Campylobacter coli

<400> 1

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

Ala Leu Glu Asn Tyr Asn Thr Gly Thr Trp Asn Leu Gln Gly Ser Ser
20 25 30

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

Gly Ala Asn Pro Met Asp Val Leu Ala Val Gln Glu Ala Gly Val Leu
50 55 60

Pro Ser Thr Ala Met Met Thr Pro Arg Gln Val Gln Pro Val Gly Val
65 70 75 80

Gly Ile Pro Ile His Glu Tyr Ile Trp Asn Leu Gly Ser Val Ser Arg
85 90 95

Pro Ser Ser Val Tyr Ile Tyr Tyr Ser Arg Val Asp Val Gly Ala Asn
100 105 110

Arg Val Asn Leu Ala Ile Val Ser Arg Val Gln Ala Asp Glu Val Phe
115 120 125

Val Leu Pro Pro Pro Thr Val Ala Ser Arg Pro Ile Ile Gly Ile Arg
130 135 140

Ile Gly Asn Asp Ala Phe Phe Asn Ile His Ala Leu Ala Ser Gly Gly
145 150 155 160

Asn Asp Ala Gly Ala Ile Val Ala Ala Val Asp Met Phe Phe Arg Asn
165 170 175

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Arg Pro Asp Ile Asn Trp Met Ile Leu Gly Asp Phe Asn Arg Glu Ser
180 185 190

Gly Ala Leu Val Thr Leu Leu Asp Pro Asp Leu Arg Ala Arg Thr Arg
195 200 205

Val Val Val Pro Pro Ser Ser Thr Gln Thr Ser Gly Arg Thr Ile Asp
210 215 220

Tyr Ala Ile Thr Gly Asn Ser Asn Thr Ala Ala Leu Tyr Asn Pro Pro
225 230 235 240

Pro Ile Val Ala Ile Leu Ala Leu Glu Gly Leu Arg Thr Phe Leu Ala
245 250 255

Ser Asp His Phe Pro Val Asn Phe Arg Arg Pro
260 265

<210> 2
<211> 804
<212> DNA
<213> Campylobacter coli

<400> 2
atgaaaaaaa tagtattttt gattttaagt tttaatgtat tatttgccgc tttagaaaat 60
tacaacaccg gaacttgaa tttgcaaggc tcatcagctg caactgaaag caaatggaat 120
gttagtataa gacaactcat aaccggtgca aatcctatgg atgttttagc tgttcaagaa 180
gcggggggtt tacctagtac agctatgatg actcctagac aggtacaacc cgtgggcgtg 240
ggatttccta tacatgaata catatggaat ttaggctctg tatcaagacc tagctctgtt 300
tatatatatt attctagagt ggatgtagga gcaaatcgtg tgaatttagc tatcgtttagc 360
agagtgcaag cggatgaagt ttttgtttta cccctccaa cagttgcttc aagacctatt 420
ataggcatac gcataggcaa tgatgctttt ttcaatatac acgctctagc aagtggggga 480
aatgacgcag gagccattgt cgctgctgtg gatatgtttt ttagaaatag acctgatatt 540
aattggatga ttttaggcga ttttaataga gaatcaggcg ccttagtaac cttgctagat 600
cctgacttaa gagcacgcac tcgcgtagtt gttccgcctt cttctacgca aacaagtgga 660
agaacgattg attatgctat cactggaaat tccaacactg cagctttata caaccacca 720
ccgatatgtt cgatttttagc tttagaagga ttaagaacct ttttggcttc agatcatttt 780
cctgtaaatt ttagaagacc ttag 804

<210> 3
<211> 17
<212> PRT
<213> Campylobacter jejuni

<400> 3
Leu Asp Tyr Ala Ile Thr Gly Asn Ser Asn Arg Gln Gln Thr Tyr Thr

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1 5 10 15

Pro

<210> 4
 <211> 18
 <212> PRT
 <213> Campylobacter jejuni

<400> 4

Cys Leu Asp Tyr Ala Ile Thr Gly Asn Ser Asn Arg Gln Gln Thr Tyr
 1 5 10 15

Thr Pro

<210> 5
 <211> 265
 <212> PRT
 <213> Campylobacter jejuni

<400> 5

Met Lys Lys Ile Ile Cys Leu Phe Leu Ser Phe Asn Leu Ala Phe Ala
 1 5 10 15

Asn Leu Glu Asn Phe Asn Val Gly Thr Trp Asn Leu Gln Gly Ser Ser
 20 25 30

Ala Ala Thr Glu Ser Lys Trp Ser Val Ser Val Arg Gln Leu Val Ser
 35 40 45

Gly Ala Asn Pro Leu Asp Ile Leu Met Ile Gln Glu Ala Gly Thr Leu
 50 55 60

Pro Arg Thr Ala Thr Pro Thr Gly Arg His Val Gln Gln Gly Gly Thr
 65 70 75 80

Pro Ile Asp Glu Tyr Glu Trp Asn Leu Gly Thr Leu Ser Arg Pro Asp
 85 90 95

Arg Val Phe Ile Tyr Tyr Ser Arg Val Asp Val Gly Ala Asn Arg Val
 100 105 110

Asn Leu Ala Ile Val Ser Arg Met Gln Ala Glu Glu Val Ile Val Leu
 115 120 125

Pro Pro Pro Thr Thr Val Ser Arg Pro Ile Ile Gly Ile Arg Asn Gly
 130 135 140

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

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Val Gly Ala Ile Ile Thr Ala Val Asp Ala His Phe Ala Asn Met Pro
165 170 175

Gln Val Asn Trp Met Ile Ala Gly Asp Phe Asn Arg Asp Pro Ser Thr
180 185 190

Ile Thr Ser Thr Val Asp Arg Glu Leu Ala Asn Arg Ile Arg Val Val
195 200 205

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

Ile Thr Gly Asn Ser Asn Arg Gln Gln Thr Tyr Thr Pro Pro Leu Leu
225 230 235 240

Ala Ala Ile Leu Met Leu Ala Ser Leu Arg Ser His Ile Val Ser Asp
245 250 255

His Phe Pro Val Asn Phe Arg Lys Phe
260 265

<210> 6
<211> 51
<212> DNA
<213> Campylobacter jejuni

<400> 6
cttgattatg caattacagg aaattcaaat agacaacaaa cctatactcc a

51

<210> 7
<211> 1066
<212> PRT
<213> Homo sapiens

<400> 7

Met Pro Val Phe His Thr Arg Thr Ile Glu Ser Ile Leu Glu Pro Val
1 5 10 15

Ala Gln Gln Ile Ser His Leu Val Ile Met His Glu Glu Gly Glu Val
20 25 30

Asp Gly Lys Ala Ile Pro Asp Leu Thr Ala Pro Val Ala Ala Val Gln
35 40 45

Ala Ala Val Ser Asn Leu Val Arg Val Gly Lys Glu Thr Val Gln Thr
50 55 60

Thr Glu Asp Gln Ile Leu Lys Arg Asp Met Pro Pro Ala Phe Ile Lys
65 70 75 80

Val Glu Asn Ala Cys Thr Lys Leu Val Gln Ala Ala Gln Met Leu Gln
85 90 95

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

Arg Gly Ile Leu Ser Gly Thr Ser Asp Leu Leu Leu Thr Phe Asp Glu
115 120 125

Ala Glu Val Arg Lys Ile Ile Arg Val Cys Lys Gly Ile Leu Glu Tyr
130 135 140

Leu Thr Val Ala Glu Val Val Glu Thr Met Glu Asp Leu Val Thr Tyr
145 150 155 160

Thr Lys Asn Leu Gly Pro Gly Met Thr Lys Met Ala Lys Met Ile Asp
165 170 175

Glu Arg Gln Gln Glu Leu Thr His Gln Glu His Arg Val Met Leu Val
180 185 190

Asn Ser Met Asn Thr Val Lys Glu Leu Leu Pro Val Leu Ile Ser Ala
195 200 205

Met Lys Ile Phe Val Thr Thr Lys Asn Ser Lys Asn Gln Gly Ile Glu
210 215 220

Glu Ala Leu Lys Asn Arg Asn Phe Thr Val Glu Lys Met Ser Ala Glu
225 230 235 240

Ile Asn Glu Ile Ile Arg Val Leu Gln Leu Thr Ser Trp Asp Glu Asp
245 250 255

Ala Trp Ala Ser Lys Asp Thr Glu Ala Met Lys Arg Ala Leu Ala Ser
260 265 270

Ile Asp Ser Lys Leu Asn Gln Ala Lys Gly Trp Leu Arg Asp Pro Ser
275 280 285

Ala Ser Pro Gly Asp Ala Gly Glu Gln Ala Ile Arg Gln Ile Leu Asp
290 295 300

Glu Ala Gly Lys Val Gly Glu Leu Cys Ala Gly Lys Glu Arg Arg Glu
305 310 315 320

Ile Leu Gly Thr Cys Lys Met Leu Gly Gln Met Thr Asp Gln Val Ala
325 330 335

Asp Leu Arg Ala Arg Gly Gln Gly Ser Ser Pro Val Ala Met Gln Lys
340 345 350

Ala Gln Gln Val Ser Gln Gly Leu Asp Val Leu Thr Ala Lys Val Glu
355 360 365

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Asn Ala Ala Arg Lys Leu Glu Ala Met Thr Asn Ser Lys Gln Ser Ile
 370 375 380
 Ala Lys Lys Ile Asp Ala Ala Gln Asn Trp Leu Ala Asp Pro Asn Gly
 385 390 395 400
 Gly Pro Glu Gly Glu Glu Gln Ile Arg Gly Ala Leu Ala Glu Ala Arg
 405 410 415
 Lys Ile Ala Glu Leu Cys Asp Asp Pro Lys Glu Arg Asp Asp Ile Leu
 420 425 430
 Arg Ser Leu Gly Glu Ile Ser Ala Leu Thr Ser Lys Leu Ala Asp Leu
 435 440 445
 Arg Arg Gln Gly Lys Gly Asp Ser Pro Glu Ala Arg Ala Leu Ala Lys
 450 455 460
 Gln Val Ala Thr Ala Leu Gln Asn Leu Gln Thr Lys Thr Asn Arg Ala
 465 470 475 480
 Val Ala Asn Ser Arg Pro Ala Lys Ala Val His Leu Glu Gly Lys
 485 490 495
 Ile Glu Gln Ala Gln Arg Trp Ile Asp Asn Pro Thr Val Asp Asp Arg
 500 505 510
 Gly Val Gly Gln Ala Ala Ile Arg Gly Leu Val Ala Glu Gly His Arg
 515 520 525
 Leu Ala Asn Val Met Met Gly Pro Tyr Arg Gln Asp Leu Leu Ala Lys
 530 535 540
 Cys Asp Arg Val Asp Gln Leu Thr Ala Gln Leu Ala Asp Leu Ala Ala
 545 550 555 560
 Arg Gly Glu Gly Glu Ser Pro Gln Ala Arg Ala Leu Ala Ser Gln Leu
 565 570 575
 Gln Asp Ser Leu Lys Asp Leu Lys Ala Arg Met Gln Glu Ala Met Thr
 580 585 590
 Gln Glu Val Ser Asp Val Phe Ser Asp Thr Thr Thr Pro Ile Lys Leu
 595 600 605
 Leu Ala Val Ala Ala Thr Ala Pro Pro Asp Ala Pro Asn Arg Glu Glu
 610 615 620
 Val Phe Asp Glu Arg Ala Ala Asn Phe Glu Asn His Ser Gly Lys Leu
 625 630 635 640

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Gly Ala Thr Ala Glu Lys Ala Ala Ala Val Gly Thr Ala Asn Lys Ser
645 650 655

Thr Val Glu Gly Ile Gln Ala Ser Val Lys Thr Ala Arg Glu Leu Thr
660 665 670

Pro Gln Val Val Ser Ala Ala Arg Ile Leu Leu Arg Asn Pro Gly Asn
675 680 685

Gln Ala Ala Tyr Glu His Phe Glu Thr Met Lys Asn Gln Trp Ile Asp
690 695 700

Asn Val Glu Lys Met Thr Gly Leu Val Asp Glu Ala Ile Asp Thr Lys
705 710 715 720

Ser Leu Leu Asp Ala Ser Glu Glu Ala Ile Lys Lys Asp Leu Asp Lys
725 730 735

Cys Lys Val Ala Met Ala Asn Ile Gln Pro Gln Met Leu Val Ala Gly
740 745 750

Ala Thr Ser Ile Ala Arg Arg Ala Asn Arg Ile Leu Leu Val Ala Lys
755 760 765

Arg Glu Val Glu Asn Ser Glu Asp Pro Lys Phe Arg Glu Ala Val Lys
770 775 780

Ala Ala Ser Asp Glu Leu Ser Lys Thr Ile Ser Pro Met Val Met Asp
785 790 795 800

Ala Lys Ala Val Ala Gly Asn Ile Ser Asp Pro Gly Leu Gln Lys Ser
805 810 815

Phe Leu Asp Ser Gly Tyr Arg Ile Leu Gly Ala Val Ala Lys Val Arg
820 825 830

Glu Ala Phe Gln Pro Gln Glu Pro Asp Phe Pro Pro Pro Pro Asp
835 840 845

Leu Glu Gln Leu Arg Leu Thr Asp Glu Leu Ala Pro Pro Lys Pro Pro
850 855 860

Leu Pro Glu Gly Glu Val Pro Pro Pro Arg Pro Pro Pro Pro Glu Glu
865 870 875 880

Lys Asp Glu Glu Phe Pro Glu Gln Lys Ala Gly Glu Val Ile Asn Gln
885 890 895

Pro Met Met Met Ala Ala Arg Gln Leu His Asp Glu Ala Arg Lys Trp
900 905 910

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Ser Ser Lys Gly Asn Asp Ile Ile Ala Ala Ala Lys Arg Met Ala Leu
915 920 925

Leu Met Ala Glu Met Ser Arg Leu Val Arg Gly Gly Ser Gly Thr Lys
930 935 940

Arg Ala Leu Ile Gln Cys Ala Lys Asp Ile Ala Lys Ala Ser Asp Glu
945 950 955 960

Val Thr Arg Leu Ala Lys Glu Val Ala Lys Gln Cys Thr Asp Lys Arg
965 970 975

Ile Arg Thr Asn Leu Leu Gln Val Cys Glu Arg Ile Pro Thr Ile Ser
980 985 990

Thr Gln Leu Lys Ile Leu Ser Thr Val Lys Ala Thr Met Leu Gly Arg
995 1000 1005

Thr Asn Ile Ser Asp Glu Glu Ser Glu Gln Ala Thr Glu Met Leu
1010 1015 1020

Val His Asn Ala Gln Asn Leu Met Gln Ser Val Lys Glu Thr Val
1025 1030 1035

Arg Glu Ala Glu Ala Ala Ser Ile Lys Ile Arg Thr Asp Ala Gly
1040 1045 1050

Phe Thr Leu Arg Trp Val Arg Lys Thr Pro Trp Tyr Gln
1055 1060 1065

<210> 8
<211> 633
<212> PRT
<213> IpaA of Shigella

<400> 8

Met His Asn Val Asn Asn Thr Gln Ala Pro Thr Phe Leu Tyr Lys Ala
1 5 10 15

Thr Ser Pro Ser Ser Thr Glu Tyr Ser Glu Leu Lys Ser Lys Ile Ser
20 25 30

Asp Ile His Ser Ser Gln Thr Ser Leu Lys Thr Pro Ala Ser Val Ser
35 40 45

Glu Lys Glu Asn Phe Ala Thr Ser Phe Asn Gln Lys Cys Leu Asp Phe
50 55 60

Leu Phe Ser Ser Ser Gly Lys Glu Asp Val Leu Arg Ser Ile Tyr Ser
65 70 75 80

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

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Pro Gln Arg Ala Leu Val Gln Lys Val Thr Ser Val Leu Pro His Ser
355 360 365

Ile Ser Asp Thr Val Gln Thr Phe Ala Asn Asn Ser Ala Leu Glu Lys
370 375 380

Val Phe Asn His Thr Pro Asp Asn Ser Asp Gly Ile Gly Ser Asp Leu
385 390 395 400

Leu Thr Thr Ser Ser Gln Glu Arg Ser Ala Asn Asn Ser Leu Ser Arg
405 410 415

Gly His Arg Pro Leu Asn Ile Gln Asn Ser Ser Thr Thr Pro Pro Leu
420 425 430

His Pro Glu Gly Val Thr Ser Ser Asn Asp Asn Ser Ser Asp Thr Thr
435 440 445

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

Phe Asn Ser Asn Thr Asp Ser Lys Val Leu Gln Thr Asp Phe Leu Ser
465 470 475 480

Arg Asn Gly Asp Thr Tyr Leu Thr Arg Glu Thr Ile Phe Glu Ala Ser
485 490 495

Lys Lys Val Thr Asn Ser Leu Ser Asn Leu Ile Ser Leu Ile Gly Thr
500 505 510

Lys Ser Gly Thr Gln Glu Arg Glu Leu Gln Glu Lys Ser Lys Asp Ile
515 520 525

Thr Lys Ser Thr Thr Glu His Arg Ile Asn Asn Lys Leu Lys Val Thr
530 535 540

Asp Ala Asn Ile Arg Asn Tyr Val Thr Glu Thr Asn Ala Asp Thr Ile
545 550 555 560

Asp Lys Asn His Ala Ile Tyr Glu Lys Ala Lys Glu Val Ser Ser Ala
565 570 575

Leu Ser Lys Val Leu Ser Lys Ile Asp Asp Thr Ser Ala Glu Leu Leu
580 585 590

Thr Asp Asp Ile Ser Asp Leu Lys Asn Asn Asn Asp Ile Thr Ala Glu
595 600 605

Asn Asn Asn Ile Tyr Lys Ala Ala Lys Asp Val Thr Thr Ser Leu Ser
610 615 620

SequenceListing454w000_ST25
Lys Val Leu Lys Asn Ile Asn Lys Asp
625 630