

SequenceListing511W000_ST25
SEQUENCE LISTING

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

<120> METHODS AND SYSTEMS FOR DISTINGUISHING IRRITABLE BOWEL SYNDROME
FROM INFLAMMATORY BOWEL DISEASE AND CELIAC DISEASE

<130> 065472-000511W000

<150> 62/061,877
<151> 2014-10-09

<150> 62/085,825
<151> 2014-12-01

<160> 7

<170> PatentIn version 3.5

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

<400> 1

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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

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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

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

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<210> 2

<211> 804

<212> DNA

<213> Campylobacter coli

<400> 2

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gttagtataa gacaactcat aaccggtgca aatcctatgg atgttttagc tgttcaagaa      180
gcggggggttt tacctagtac agctatgatg actcctagac aggtacaacc cgtgggcgtg      240
ggatttccta tacatgaata catatggaat ttaggctctg tatcaagacc tagctctgtt      300
tatatatatt attctagagt ggatgtagga gcaaactcgtg tgaatttagc tatcgtagc      360
agagtgaag cggaatgaagt ttttgtttta cccctccaa cagttgcttc aagacctatt      420
ataggcatat 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
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<210> 3

<211> 17

<212> PRT

<213> Campylobacter jejuni

<400> 3

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Leu Asp Tyr Ala Ile Thr Gly Asn Ser Asn Arg Gln Gln Thr Tyr Thr
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Pro

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<210> 4
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 <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

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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

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

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<400> 6

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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

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

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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

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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

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 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

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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

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

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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 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