

ST25.txt

SEQUENCE LISTING

<110> UNIVERSITE D'Auvergne Clermont I

<120> Antagonist for the prevention or treatment of inflammatory bowel disease, and more particularly of Crohn's disease

<130> BET10A0547

<160> 15

<170> PatentIn version 3.4

<210> 1

<211> 803

<212> PRT

<213> homo sapiens

<400> 1

Met Arg Ala Leu Trp Val Leu Gly Leu Cys Cys Val Leu Leu Thr Phe  
1 5 10 15

Gly Ser Val Arg Ala Asp Asp Glu Val Asp Val Asp Gly Thr Val Glu  
20 25 30

Glu Asp Leu Gly Lys Ser Arg Glu Gly Ser Arg Thr Asp Asp Glu Val  
35 40 45

Val Gln Arg Glu Glu Glu Ala Ile Gln Leu Asp Gly Leu Asn Ala Ser  
50 55 60

Gln Ile Arg Glu Leu Arg Glu Lys Ser Glu Lys Phe Ala Phe Gln Ala  
65 70 75 80

Glu Val Asn Arg Met Met Lys Leu Ile Ile Asn Ser Leu Tyr Lys Asn  
85 90 95

Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ala Ser Asp Ala Leu  
100 105 110

Asp Lys Ile Arg Leu Ile Ser Leu Thr Asp Glu Asn Ala Leu Ser Gly  
115 120 125

Asn Glu Glu Leu Thr Val Lys Ile Lys Cys Asp Lys Glu Lys Asn Leu  
130 135 140

Leu His Val Thr Asp Thr Gly Val Gly Met Thr Arg Glu Glu Leu Val  
145 150 155 160

Lys Asn Leu Gly Thr Ile Ala Lys Ser Gly Thr Ser Glu Phe Leu Asn  
165 170 175

Lys Met Thr Glu Ala Gln Glu Asp Gly Gln Ser Thr Ser Glu Leu Ile  
180 185 190

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Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Leu Val Ala Asp Lys  
 195 200 205  
 Val Ile Val Thr Ser Lys His Asn Asn Asp Thr Gln His Ile Trp Glu  
 210 215 220  
 Ser Asp Ser Asn Glu Phe Ser Val Ile Ala Asp Pro Arg Gly Asn Thr  
 225 230 235 240  
 Leu Gly Arg Gly Thr Thr Ile Thr Leu Val Leu Lys Glu Glu Ala Ser  
 245 250 255  
 Asp Tyr Leu Glu Leu Asp Thr Ile Lys Asn Leu Val Lys Lys Tyr Ser  
 260 265 270  
 Gln Phe Ile Asn Phe Pro Ile Tyr Val Trp Ser Ser Lys Thr Glu Thr  
 275 280 285  
 Val Glu Glu Pro Met Glu Glu Glu Glu Ala Ala Lys Glu Glu Lys Glu  
 290 295 300  
 Glu Ser Asp Asp Glu Ala Ala Val Glu Glu Glu Glu Glu Lys Lys  
 305 310 315 320  
 Pro Lys Thr Lys Lys Val Glu Lys Thr Val Trp Asp Trp Glu Leu Met  
 325 330 335  
 Asn Asp Ile Lys Pro Ile Trp Gln Arg Pro Ser Lys Glu Val Glu Glu  
 340 345 350  
 Asp Glu Tyr Lys Ala Phe Tyr Lys Ser Phe Ser Lys Glu Ser Asp Asp  
 355 360 365  
 Pro Met Ala Tyr Ile His Phe Thr Ala Glu Gly Glu Val Thr Phe Lys  
 370 375 380  
 Ser Ile Leu Phe Val Pro Thr Ser Ala Pro Arg Gly Leu Phe Asp Glu  
 385 390 395 400  
 Tyr Gly Ser Lys Lys Ser Asp Tyr Ile Lys Leu Tyr Val Arg Arg Val  
 405 410 415  
 Phe Ile Thr Asp Asp Phe His Asp Met Met Pro Lys Tyr Leu Asn Phe  
 420 425 430  
 Val Lys Gly Val Val Asp Ser Asp Asp Leu Pro Leu Asn Val Ser Arg  
 435 440 445  
 Glu Thr Leu Gln Gln His Lys Leu Leu Lys Val Ile Arg Lys Lys Leu  
 450 455 460

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Val Arg Lys Thr Leu Asp Met Ile Lys Lys Ile Ala Asp Asp Lys Tyr  
465 470 475 480

Asn Asp Thr Phe Trp Lys Glu Phe Gly Thr Asn Ile Lys Leu Gly Val  
485 490 495

Ile Glu Asp His Ser Asn Arg Thr Arg Leu Ala Lys Leu Leu Arg Phe  
500 505 510

Gln Ser Ser His His Pro Thr Asp Ile Thr Ser Leu Asp Gln Tyr Val  
515 520 525

Glu Arg Met Lys Glu Lys Gln Asp Lys Ile Tyr Phe Met Ala Gly Ser  
530 535 540

Ser Arg Lys Glu Ala Glu Ser Ser Pro Phe Val Glu Arg Leu Leu Lys  
545 550 555 560

Lys Gly Tyr Glu Val Ile Tyr Leu Thr Glu Pro Val Asp Glu Tyr Cys  
565 570 575

Ile Gln Ala Leu Pro Glu Phe Asp Gly Lys Arg Phe Gln Asn Val Ala  
580 585 590

Lys Glu Gly Val Lys Phe Asp Glu Ser Glu Lys Thr Lys Glu Ser Arg  
595 600 605

Glu Ala Val Glu Lys Glu Phe Glu Pro Leu Leu Asn Trp Met Lys Asp  
610 615 620

Lys Ala Leu Lys Asp Lys Ile Glu Lys Ala Val Val Ser Gln Arg Leu  
625 630 635 640

Thr Glu Ser Pro Cys Ala Leu Val Ala Ser Gln Tyr Gly Trp Ser Gly  
645 650 655

Asn Met Glu Arg Ile Met Lys Ala Gln Ala Tyr Gln Thr Gly Lys Asp  
660 665 670

Ile Ser Thr Asn Tyr Tyr Ala Ser Gln Lys Lys Thr Phe Glu Ile Asn  
675 680 685

Pro Arg His Pro Leu Ile Arg Asp Met Leu Arg Arg Ile Lys Glu Asp  
690 695 700

Glu Asp Asp Lys Thr Val Leu Asp Leu Ala Val Val Leu Phe Glu Thr  
705 710 715 720

Ala Thr Leu Arg Ser Gly Tyr Leu Leu Pro Asp Thr Lys Ala Tyr Gly  
725 730 735

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Asp Arg Ile Glu Arg Met Leu Arg Leu Ser Leu Asn Ile Asp Pro Asp  
740 745 750

Ala Lys Val Glu Glu Glu Pro Glu Glu Glu Pro Glu Glu Thr Ala Glu  
755 760 765

Asp Thr Thr Glu Asp Thr Glu Gln Asp Glu Asp Glu Glu Met Asp Val  
770 775 780

Gly Thr Asp Glu Glu Glu Glu Thr Ala Lys Glu Ser Thr Ala Glu Lys  
785 790 795 800

Asp Glu Leu

<210> 2  
<211> 358  
<212> PRT  
<213> AIEC strain LF82

<400> 2

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala  
1 5 10 15

Thr Val Ala Gln Ala Ala Pro Lys Asp Asn Thr Trp Tyr Thr Gly Ala  
20 25 30

Lys Leu Gly Trp Ser Gln Tyr His Asp Thr Gly Phe Phe Thr Ile Asn  
35 40 45

Asn Asn Gly Pro Thr His Glu Asn Gln Leu Gly Ala Gly Ala Phe Gly  
50 55 60

Gly Tyr Gln Val Asn Pro Tyr Val Gly Phe Glu Met Gly Tyr Asp Trp  
65 70 75 80

Leu Gly Arg Met Pro Tyr Lys Gly Ser Val Glu Asn Gly Ala Tyr Lys  
85 90 95

Ala Gln Gly Val Gln Leu Thr Ala Phe Thr Lys Leu Gly Tyr Pro Ile  
100 105 110

Thr Asp Asp Leu Asp Val Tyr Thr Arg Leu Gly Gly Met Val Trp Arg  
115 120 125

Ala Asp Thr Lys Ser Asn Phe Asp Gly Lys Asn His Asp Thr Gly Val  
130 135 140

Ser Pro Val Phe Ala Gly Gly Val Glu Tyr Ala Ile Thr Pro Glu Ile  
145 150 155 160

Ala Thr Arg Leu Phe Thr Glu Tyr Gln Trp Thr Asn Asn Ile Gly Asp

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165

170

175

Ala His Thr Ile Gly Thr Arg Pro Asp Asn Gly Met Leu Ser Leu Gly  
 180 185 190

Val Ser Tyr Arg Phe Gly Gln Gly Glu Ala Ala Pro Val Val Ala Pro  
 195 200 205

Ala Pro Ala Pro Ala Pro Glu Val Gln Thr Lys His Phe Thr Leu Lys  
 210 215 220

Phe Thr Ser Asp Val Leu Phe Thr Phe Asn Lys Ala Thr Leu Lys Pro  
 225 230 235 240

Glu Gly Gln Ala Ala Leu Asp Gln Leu Tyr Ser Gln Leu Ser Asn Leu  
 245 250 255

Asp Pro Lys Asp Gly Ser Val Val Val Leu Gly Tyr Thr Asp Arg Ile  
 260 265 270

Gly Ser Asp Ala Tyr Asn Gln Ala Leu Ser Glu Arg Phe Thr Arg Ala  
 275 280 285

Gln Ser Val Val Asp Tyr Leu Ile Ser Lys Gly Ile Pro Ala Asp Lys  
 290 295 300

Ile Ser Ala Arg Gly Met Gly Glu Ser Asn Pro Val Thr Gly Asn Thr  
 305 310 315 320

Cys Asp Asn Val Lys Gln Arg Ala Ala Leu Ile Asp Cys Leu Ala Pro  
 325 330 335

Asp Arg Arg Val Glu Ile Glu Val Phe Thr Lys Gly Ile Lys Asp Val  
 340 345 350

Val Thr Gln Pro Gln Ala  
 355

<210> 3  
 <211> 358  
 <212> PRT  
 <213> E. Coli

<400> 3

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala  
 1 5 10 15

Thr Val Ala Gln Ala Ala Pro Lys Asp Asn Thr Trp Tyr Thr Gly Ala  
 20 25 30

Lys Leu Gly Trp Ser Gln Tyr His Asp Thr Gly Phe Phe Thr Ile Asn  
 35 40 45

## ST25.txt

Asn Asn Gly Pro Thr His Glu Asn Gln Leu Gly Ala Gly Ala Phe Gly  
 50 55 60  
 Gly Tyr Gln Val Asn Pro Tyr Val Gly Phe Glu Met Gly Tyr Asp Trp  
 65 70 75 80  
 Leu Gly Arg Met Pro Tyr Lys Gly Ser Val Glu Asn Gly Ala Tyr Lys  
 85 90 95  
 Ala Gln Gly Val Gln Leu Thr Ala Phe Thr Lys Leu Gly Tyr Pro Ile  
 100 105 110  
 Thr Asp Asp Leu Asp Ile Tyr Thr Arg Leu Gly Gly Met Val Trp Arg  
 115 120 125  
 Ala Asp Thr Lys Ser Asn Val Tyr Gly Lys Asn His Asp Thr Gly Val  
 130 135 140  
 Ser Pro Val Phe Ala Gly Gly Val Glu Tyr Ala Ile Thr Pro Glu Ile  
 145 150 155 160  
 Ala Thr Arg Leu Phe Thr Glu Tyr Gln Trp Thr Asn Asn Ile Gly Asp  
 165 170 175  
 Ala His Thr Ile Gly Thr Arg Pro Asp Asn Gly Met Leu Ser Leu Gly  
 180 185 190  
 Val Ser Tyr Arg Phe Gly Gln Gly Glu Ala Ala Pro Val Val Ala Pro  
 195 200 205  
 Ala Pro Ala Pro Ala Pro Glu Val Gln Thr Lys His Phe Thr Leu Lys  
 210 215 220  
 Phe Thr Ser Asp Val Leu Phe Asn Phe Asn Lys Ala Thr Leu Lys Pro  
 225 230 235 240  
 Glu Gly Gln Ala Ala Leu Asp Gln Leu Tyr Ser Gln Leu Ser Asn Leu  
 245 250 255  
 Asp Pro Lys Asp Gly Ser Val Val Val Leu Gly Tyr Thr Asp Arg Ile  
 260 265 270  
 Gly Ser Asp Ala Tyr Asn Gln Gly Leu Ser Glu Arg Phe Thr Arg Ala  
 275 280 285  
 Gln Ser Val Val Asp Tyr Leu Ile Ser Lys Gly Ile Pro Ala Asp Lys  
 290 295 300  
 Ile Ser Ala Arg Gly Met Gly Glu Ser Asn Pro Val Thr Gly Asn Thr  
 305 310 315 320

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Cys Asp Asn Val Lys Gln Arg Ala Ala Leu Ile Asp Cys Leu Ala Pro  
325 330 335

Asp Arg Arg Val Glu Ile Glu Val Phe Thr Lys Gly Ile Lys Asp Val  
340 345 350

Val Thr Gln Pro Gln Ala  
355

<210> 4  
<211> 20  
<212> DNA  
<213> artificial sequence

<220>  
<223> oligonucleotide

<400> 4  
aaagccacgt tgtgtctcaa 20

<210> 5  
<211> 20  
<212> DNA  
<213> artificial sequence

<220>  
<223> oligonucleotide

<400> 5  
ttagaaaaac tcatcgagca 20

<210> 6  
<211> 67  
<212> DNA  
<213> artificial sequence

<220>  
<223> oligonucleotide

<400> 6  
aaaggcaaaa aaaaccccg c agcggggttt ttctaccaga cgagaactta gaaaaactca 60  
tcgagca 67

<210> 7  
<211> 70  
<212> DNA  
<213> artificial sequence

<220>  
<223> oligonucleotide

<400> 7  
ctcgttggag atattcatgg cgtatatttg atgataacga ggcgcaaaaa aaagccacgt 60  
tgtgtctcaa 70

<210> 8  
<211> 20

<212> DNA  
<213> artificial sequence

<220>  
<223> oligonucleotide

<400> 8  
ggagccggag caactactgg 20

<210> 9  
<211> 20  
<212> DNA  
<213> artificial sequence

<220>  
<223> oligonucleotide

<400> 9  
acgacaccgg cgtttctccg 20

<210> 10  
<211> 20  
<212> DNA  
<213> artificial sequence

<220>  
<223> oligonucleotide

<400> 10  
gcaggcattg ctgggtaagg 20

<210> 11  
<211> 21  
<212> DNA  
<213> artificial sequence

<220>  
<223> oligonucleotide

<400> 11  
aatattgagc agatcccccg g 21

<210> 12  
<211> 30  
<212> DNA  
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<220>  
<223> oligonucleotide

<400> 12  
acgcgtcgac cgttggagat attcatggcg 30

<210> 13  
<211> 32  
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<220>  
<223> oligonucleotide

<400> 13  
cccaagcttg ggagacgaga acttaagcct gc 32



<210> 14  
<211> 20  
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<220>  
<223> oligonucleotide

<400> 14  
gggtgtggtg gactcagatg

20

<210> 15  
<211> 20  
<212> DNA  
<213> artificial sequence

<220>  
<223> oligonucleotide

<400> 15  
gttgccagac catccgtact

20