

eolf-seql
SEQUENCE LISTING

<110> GENOVIS AB
<120> PROTEIN AND METHOD
<130> N.114953A
<150> 1115841.7
<151> 2011-09-13
<160> 19
<170> PatentIn version 3.5
<210> 1
<211> 843
<212> PRT
<213> Streptococcus pyogenes
<400> 1

Met Asp Lys His Leu Leu Val Lys Arg Thr Leu Gly Cys Val Cys Ala
1 5 10 15

Ala Thr Leu Met Gly Ala Ala Leu Ala Thr His His Asp Ser Leu Asn
20 25 30

Thr Val Lys Ala Glu Glu Lys Thr Val Gln Thr Gly Lys Thr Asp Gln
35 40 45

Gln Val Gly Ala Lys Leu Val Gln Glu Ile Arg Glu Gly Lys Arg Gly
50 55 60

Pro Leu Tyr Ala Gly Tyr Phe Arg Thr Trp His Asp Arg Ala Ser Thr
65 70 75 80

Gly Ile Asp Gly Lys Gln Gln His Pro Glu Asn Thr Met Ala Glu Val
85 90 95

Pro Lys Glu Val Asp Ile Leu Phe Val Phe His Asp His Thr Ala Ser
100 105 110

Asp Ser Pro Phe Trp Ser Glu Leu Lys Asp Ser Tyr Val His Lys Leu
115 120 125

His Gln Gln Gly Thr Ala Leu Val Gln Thr Ile Gly Val Asn Glu Leu
130 135 140

Asn Gly Arg Thr Gly Leu Ser Lys Asp Tyr Pro Asp Thr Pro Glu Gly
145 150 155 160

Asn Lys Ala Leu Ala Ala Ala Ile Val Lys Ala Phe Val Thr Asp Arg
165 170 175

Gly Val Asp Gly Leu Asp Ile Asp Ile Glu His Glu Phe Thr Asn Lys
180 185 190

eolf-seql

Arg Thr Pro Glu Glu Asp Ala Arg Ala Leu Asn Val Phe Lys Glu Ile
195 200 205

Ala Gln Leu Ile Gly Lys Asn Gly Ser Asp Lys Ser Lys Leu Leu Ile
210 215 220

Met Asp Thr Thr Leu Ser Val Glu Asn Asn Pro Ile Phe Lys Gly Ile
225 230 235 240

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

Gly Glu Ala Glu Val Asp Thr Ile Asn Ser Asp Trp Asn Gln Tyr Gln
260 265 270

Asn Tyr Ile Asp Ala Ser Gln Phe Met Ile Gly Phe Ser Phe Phe Glu
275 280 285

Glu Ser Ala Ser Lys Gly Asn Leu Trp Phe Asp Val Asn Glu Tyr Asp
290 295 300

Pro Asn Asn Pro Glu Lys Gly Lys Asp Ile Glu Gly Thr Arg Ala Lys
305 310 315 320

Lys Tyr Ala Glu Trp Gln Pro Ser Thr Gly Gly Leu Lys Ala Gly Ile
325 330 335

Phe Ser Tyr Ala Ile Asp Arg Asp Gly Val Ala His Val Pro Ser Thr
340 345 350

Tyr Lys Asn Arg Thr Ser Thr Asn Leu Gln Arg His Glu Val Asp Asn
355 360 365

Ile Ser His Thr Asp Tyr Thr Val Ser Arg Lys Leu Lys Thr Leu Met
370 375 380

Thr Glu Asp Lys Arg Tyr Asp Val Ile Asp Gln Lys Asp Ile Pro Asp
385 390 395 400

Pro Ala Leu Arg Glu Gln Ile Ile Gln Gln Val Gly Gln Tyr Lys Gly
405 410 415

Asp Leu Glu Arg Tyr Asn Lys Thr Leu Val Leu Thr Gly Asp Lys Ile
420 425 430

Gln Asn Leu Lys Gly Leu Glu Lys Leu Ser Lys Leu Gln Lys Leu Glu
435 440 445

Leu Arg Gln Leu Ser Asn Val Lys Glu Ile Thr Pro Glu Leu Leu Pro
450 455 460

eolf-seql

Glu Ser Met Lys Lys Asp Ala Glu Leu Val Met Val Gly Met Thr Gly
 465 470 475 480
 Leu Glu Lys Leu Asn Leu Ser Gly Leu Asn Arg Gln Thr Leu Asp Gly
 485 490 495
 Ile Asp Val Asn Ser Ile Thr His Leu Thr Ser Phe Asp Ile Ser His
 500 505 510
 Asn Ser Leu Asp Leu Ser Glu Lys Ser Glu Asp Arg Lys Leu Leu Met
 515 520 525
 Thr Leu Met Glu Gln Val Ser Asn His Gln Lys Ile Thr Val Lys Asn
 530 535 540
 Thr Ala Phe Glu Asn Gln Lys Pro Lys Gly Tyr Tyr Pro Gln Thr Tyr
 545 550 555 560
 Asp Thr Lys Glu Gly His Tyr Asp Val Asp Asn Ala Glu His Asp Ile
 565 570 575
 Leu Thr Asp Phe Val Phe Gly Thr Val Thr Lys Arg Asn Thr Phe Ile
 580 585 590
 Gly Asp Glu Glu Ala Phe Ala Ile Tyr Lys Glu Gly Ala Val Asp Gly
 595 600 605
 Arg Gln Tyr Val Ser Lys Asp Tyr Thr Tyr Glu Ala Phe Arg Lys Asp
 610 615 620
 Tyr Lys Gly Tyr Lys Val His Leu Thr Ala Ser Asn Leu Gly Glu Thr
 625 630 635 640
 Val Thr Ser Lys Val Thr Ala Thr Thr Asp Glu Thr Tyr Leu Val Asp
 645 650 655
 Val Ser Asp Gly Glu Lys Val Val His His Met Lys Leu Asn Ile Gly
 660 665 670
 Ser Gly Ala Ile Met Met Glu Asn Leu Ala Lys Gly Ala Lys Val Ile
 675 680 685
 Gly Thr Ser Gly Asp Phe Glu Gln Ala Lys Lys Ile Phe Asp Gly Glu
 690 695 700
 Lys Ser Asp Arg Phe Phe Thr Trp Gly Gln Thr Asn Trp Ile Ala Phe
 705 710 715 720
 Asp Leu Gly Glu Ile Asn Leu Ala Lys Glu Trp Arg Leu Phe Asn Ala
 725 730 735

eolf-seql

Glu Thr Asn Thr Glu Ile Lys Thr Asp Ser Ser Leu Asn Val Ala Lys
740 745 750

Gly Arg Leu Gln Ile Leu Lys Asp Thr Thr Ile Asp Leu Glu Lys Met
755 760 765

Asp Ile Lys Asn Arg Lys Glu Tyr Leu Ser Asn Asp Glu Asn Trp Thr
770 775 780

Asp Val Ala Gln Met Asp Asp Ala Lys Ala Ile Phe Asn Ser Lys Leu
785 790 795 800

Ser Asn Val Leu Ser Arg Tyr Trp Arg Phe Cys Val Asp Gly Gly Ala
805 810 815

Ser Ser Tyr Tyr Pro Gln Tyr Thr Glu Leu Gln Ile Leu Gly Gln Arg
820 825 830

Leu Ser Asn Asp Val Ala Asn Thr Leu Lys Asp
835 840

<210> 2
<211> 843
<212> PRT
<213> Streptococcus pyogenes
<400> 2

Met Asp Lys His Leu Leu Val Lys Arg Thr Leu Gly Cys Val Cys Ala
1 5 10 15

Ala Thr Leu Met Gly Ala Ala Leu Ala Thr His His Asp Ser Leu Asn
20 25 30

Thr Val Lys Ala Glu Glu Lys Thr Val Gln Thr Gly Lys Thr Asp Gln
35 40 45

Gln Val Gly Ala Lys Leu Val Gln Glu Ile Arg Glu Gly Lys Arg Gly
50 55 60

Pro Leu Tyr Ala Gly Tyr Phe Arg Thr Trp His Asp Arg Ala Ser Thr
65 70 75 80

Gly Ile Asp Gly Lys Gln Gln His Pro Glu Asn Thr Met Ala Glu Val
85 90 95

Pro Lys Glu Val Asp Ile Leu Phe Val Phe His Asp His Thr Ala Ser
100 105 110

Asp Ser Pro Phe Trp Ser Glu Leu Lys Asp Ser Tyr Val His Lys Leu
115 120 125

eolf-seql

His Gln Gln Gly Thr Ala Leu Val Gln Thr Ile Gly Val Asn Glu Leu
130 135 140

Asn Gly Arg Thr Gly Leu Ser Lys Asp Tyr Pro Asp Thr Pro Glu Gly
145 150 155 160

Asn Lys Ala Leu Ala Ala Ala Ile Val Lys Ala Phe Val Thr Asp Arg
165 170 175

Gly Val Asp Gly Leu Asp Ile Asp Ile Leu His Glu Phe Thr Asn Lys
180 185 190

Arg Thr Pro Glu Glu Asp Ala Arg Ala Leu Asn Val Phe Lys Glu Ile
195 200 205

Ala Gln Leu Ile Gly Lys Asn Gly Ser Asp Lys Ser Lys Leu Leu Ile
210 215 220

Met Asp Thr Thr Leu Ser Val Glu Asn Asn Pro Ile Phe Lys Gly Ile
225 230 235 240

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

Gly Glu Ala Glu Val Asp Thr Ile Asn Ser Asp Trp Asn Gln Tyr Gln
260 265 270

Asn Tyr Ile Asp Ala Ser Gln Phe Met Ile Gly Phe Ser Phe Phe Glu
275 280 285

Glu Ser Ala Ser Lys Gly Asn Leu Trp Phe Asp Val Asn Glu Tyr Asp
290 295 300

Pro Asn Asn Pro Glu Lys Gly Lys Asp Ile Glu Gly Thr Arg Ala Lys
305 310 315 320

Lys Tyr Ala Glu Trp Gln Pro Ser Thr Gly Gly Leu Lys Ala Gly Ile
325 330 335

Phe Ser Tyr Ala Ile Asp Arg Asp Gly Val Ala His Val Pro Ser Thr
340 345 350

Tyr Lys Asn Arg Thr Ser Thr Asn Leu Gln Arg His Glu Val Asp Asn
355 360 365

Ile Ser His Thr Asp Tyr Thr Val Ser Arg Lys Leu Lys Thr Leu Met
370 375 380

Thr Glu Asp Lys Arg Tyr Asp Val Ile Asp Gln Lys Asp Ile Pro Asp
385 390 395 400

eolf-seql

Pro Ala Leu Arg Glu Gln Ile Ile Gln Gln Val Gly Gln Tyr Lys Gly
405 410 415

Asp Leu Glu Arg Tyr Asn Lys Thr Leu Val Leu Thr Gly Asp Lys Ile
420 425 430

Gln Asn Leu Lys Gly Leu Glu Lys Leu Ser Lys Leu Gln Lys Leu Glu
435 440 445

Leu Arg Gln Leu Ser Asn Val Lys Glu Ile Thr Pro Glu Leu Leu Pro
450 455 460

Glu Ser Met Lys Lys Asp Ala Glu Leu Val Met Val Gly Met Thr Gly
465 470 475 480

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

Ile Asp Val Asn Ser Ile Thr His Leu Thr Ser Phe Asp Ile Ser His
500 505 510

Asn Ser Leu Asp Leu Ser Glu Lys Ser Glu Asp Arg Lys Leu Leu Met
515 520 525

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

Thr Ala Phe Glu Asn Gln Lys Pro Lys Gly Tyr Tyr Pro Gln Thr Tyr
545 550 555 560

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

Leu Thr Asp Phe Val Phe Gly Thr Val Thr Lys Arg Asn Thr Phe Ile
580 585 590

Gly Asp Glu Glu Ala Phe Ala Ile Tyr Lys Glu Gly Ala Val Asp Gly
595 600 605

Arg Gln Tyr Val Ser Lys Asp Tyr Thr Tyr Glu Ala Phe Arg Lys Asp
610 615 620

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

Val Thr Ser Lys Val Thr Ala Thr Thr Asp Glu Thr Tyr Leu Val Asp
645 650 655

Val Ser Asp Gly Glu Lys Val Val His His Met Lys Leu Asn Ile Gly
660 665 670

eolf-seql

Ser Gly Ala Ile Met Met Glu Asn Leu Ala Lys Gly Ala Lys Val Ile
675 680 685

Gly Thr Ser Gly Asp Phe Glu Gln Ala Lys Lys Ile Phe Asp Gly Glu
690 695 700

Lys Ser Asp Arg Phe Phe Thr Trp Gly Gln Thr Asn Trp Ile Ala Phe
705 710 715 720

Asp Leu Gly Glu Ile Asn Leu Ala Lys Glu Trp Arg Leu Phe Asn Ala
725 730 735

Glu Thr Asn Thr Glu Ile Lys Thr Asp Ser Ser Leu Asn Val Ala Lys
740 745 750

Gly Arg Leu Gln Ile Leu Lys Asp Thr Thr Ile Asp Leu Glu Lys Met
755 760 765

Asp Ile Lys Asn Arg Lys Glu Tyr Leu Ser Asn Asp Glu Asn Trp Thr
770 775 780

Asp Val Ala Gln Met Asp Asp Ala Lys Ala Ile Phe Asn Ser Lys Leu
785 790 795 800

Ser Asn Val Leu Ser Arg Tyr Trp Arg Phe Cys Val Asp Gly Gly Ala
805 810 815

Ser Ser Tyr Tyr Pro Gln Tyr Thr Glu Leu Gln Ile Leu Gly Gln Arg
820 825 830

Leu Ser Asn Asp Val Ala Asn Thr Leu Lys Asp
835 840

<210> 3
<211> 2532
<212> DNA
<213> Streptococcus pyogenes

<400> 3
atggataaac atttgttggg aaaaagaaca ctaggggtgtg tttgtgctgc aacgttgatg 60
ggagctgcct tagcgacca ccatgattca ctcaatactg taaaagcgga ggagaagact 120
gttcaaacag gaaagacaga tcagcagggtt ggtgctaaat tggtagagga aatccgtgaa 180
ggaaaacgag gaccactata tgctgggttat ttaggacat ggcattgatc tgcttcaaca 240
ggaatagatg gtaaacagca acatccagaa aatactatgg ctgaggtccc aaaagaagtt 300
gatattcttat ttgtttttca tgaccataca gcttcagata gtccattttg gtctgaatta 360
aaggacagtt atgtccataa attacatcaa cagggaacgg cacttgttca gacaattggt 420
gttaacgaat taaatggacg tacagggtta tctaaagatt atcctgatac tcctgagggg 480
aacaaagctt tagcagcagc cattgtcaag gcatttgtaa ctgatcgtgg tgtcgatgga 540

eolf-seql

ctagatattg	atattgagca	cgaatttacg	aacaaaagaa	cacctgaaga	agatgctcgt	600
gctctaaatg	tttttaaaga	gattgcgag	ttaataggt	aaaatggtag	tgataaatct	660
aaattgctca	tcatggacac	taccctaagt	gttgaaaata	atccaatatt	taaagggata	720
gcggaagatc	ttgattatct	tcttagacaa	tattatgggt	cacaaggtgg	agaagctgaa	780
gtggatacta	taaactctga	ttggaaccaa	tatcagaatt	atattgatgc	tagccagttc	840
atgattggat	tctccttttt	tgaagaatct	gcgtccaaag	ggaatttatg	gtttgatggt	900
aacgaatacg	accctaacaa	tcctgaaaaa	gggaaagata	ttgaaggaac	acgtgctaaa	960
aaatatgcag	agtggcaacc	tagtacaggt	ggtttaaaag	caggtatatt	ctcttatgct	1020
attgatcgtg	atggagtggc	tcatgttcct	tcaacatata	aaaataggac	tagtacaagt	1080
ttacaacggc	atgaagtcga	taatattctca	catactgact	acaccgtatc	tcgaaaatta	1140
aaaacattga	tgaccgaaga	caaacgctat	gatgtcattg	atcaaaaaga	cattcctgac	1200
ccagcattaa	gagaacaaat	cattcaacaa	gttggacagt	ataaaggcga	tttggaacgt	1260
tataacaaga	cattggtgct	tacaggagat	aagattcaaa	atcttaaagg	actagaaaaa	1320
ttaagcaagt	tacaaaaatt	agagttgctg	cagctatcta	acgttaaaga	aattactcca	1380
gaacttttgc	cggaaagcat	gaaaaaagat	gctgagcttg	ttatggtagg	catgactggt	1440
ttagaaaaac	taaaccttag	tggctctaat	cgtcaaactt	tagacgggat	agacgtgaat	1500
agtattacgc	atttgacatc	atttgatatt	tcacataata	gtttggactt	gtcggaaaag	1560
agtgaagacc	gtaaaactatt	aatgactttg	atggagcagg	tttcaaataca	tcaaaaaata	1620
acggtgaaaa	atacggcttt	tgaaaatcaa	aaaccgaaag	gttattatcc	tcagacgtat	1680
gataccaaaag	aaggctatta	tgatgttgat	aatgcagaac	atgatatttt	aactgatttt	1740
gtttttggaa	ctgttactaa	acgtaatacc	tttattggag	acgaagaagc	atttgctatc	1800
tataaagaag	gagctgtcga	tggctgacaa	tatgtgtcta	aagactatac	ttatgaagct	1860
tttcgtaaag	actataaagg	ttacaagggt	catttaactg	cttctaacct	aggagaaaca	1920
gttacttcta	aggtaactgc	tactactgat	gaaacttact	tagtagatgt	ttctgatggg	1980
gaaaaagttg	ttcaccacat	gaaactcaat	ataggatctg	gtgccatcat	gatggaaaat	2040
ctggcaaaaag	gggctaaagt	gattggtaca	tctggggact	ttgagcaagc	aaagaagatt	2100
ttcgatggtg	aaaagtcaga	tagattcttc	acttggggac	aaactaactg	gatagctttt	2160
gatctaggag	aaattaatct	tgcaaggaa	tggcgtttat	ttaatgcaga	gacaaatact	2220
gaaataaaga	cagatagtag	cttaaactg	gctaaaggac	gtcttcagat	tttaaaagat	2280
acaactattg	atttagaaaa	aatggacata	aaaaatcgta	aagagtatct	gtcgaatgat	2340
gaaaatttga	ctgatgttgc	tcagatggat	gatgcaaaaag	cgatatttaa	tagtaaatga	2400
tccaatgttt	tatctcggt	ttggcggttt	tgtgtagatg	gtggagctag	ctcttattac	2460
cctcaatata	ccgaacttca	aatcctcgga	caacgtttat	caaatgatgt	cgctaatacg	2520
ctgaaggatt	ga					2532

eolf-seql

<210> 4
 <211> 310
 <212> PRT
 <213> Streptococcus pyogenes

<400> 4

```

Asp Ser Phe Ser Ala Asn Gln Glu Ile Arg Tyr Ser Glu Val Thr Pro
 1          5          10          15

Tyr His Val Thr Ser Val Trp Thr Lys Gly Val Thr Pro Pro Ala Asn
          20          25          30

Phe Thr Gln Gly Glu Asp Val Phe His Ala Pro Tyr Val Ala Asn Gln
          35          40          45

Gly Trp Tyr Asp Ile Thr Lys Thr Phe Asn Gly Lys Asp Asp Leu Leu
 50          55          60

Cys Gly Ala Ala Thr Ala Gly Asn Met Leu His Trp Trp Phe Asp Gln
65          70          75          80

Asn Lys Asp Gln Ile Lys Arg Tyr Leu Glu Glu His Pro Glu Lys Gln
          85          90          95

Lys Ile Asn Phe Asn Gly Glu Gln Met Phe Asp Val Lys Glu Ala Ile
          100          105          110

Asp Thr Lys Asn His Gln Leu Asp Ser Lys Leu Phe Glu Tyr Phe Lys
          115          120          125

Glu Lys Ala Phe Pro Tyr Leu Ser Thr Lys His Leu Gly Val Phe Pro
          130          135          140

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

Asn His Gly Pro Thr Pro Val Lys Glu Gly Ser Lys Asp Pro Arg Gly
          165          170          175

Gly Ile Phe Asp Ala Val Phe Thr Arg Gly Asp Gln Ser Lys Leu Leu
          180          185          190

Thr Ser Arg His Asp Phe Lys Glu Lys Asn Leu Lys Glu Ile Ser Asp
          195          200          205

Leu Ile Lys Lys Glu Leu Thr Glu Gly Lys Ala Leu Gly Leu Ser His
          210          215          220

Thr Tyr Ala Asn Val Arg Ile Asn His Val Ile Asn Leu Trp Gly Ala
225          230          235          240
    
```

eolf-seql

Asp Phe Asp Ser Asn Gly Asn Leu Lys Ala Ile Tyr Val Thr Asp Ser
245 250 255

Asp Ser Asn Ala Ser Ile Gly Met Lys Lys Tyr Phe Val Gly Val Asn
260 265 270

Ser Ala Gly Lys Val Ala Ile Ser Ala Lys Glu Ile Lys Glu Asp Asn
275 280 285

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

Ser Trp Asn Gln Thr Asn
305 310

<210> 5
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavage product

<400> 5

Gly Pro Ser Val Phe Leu Phe Pro
1 5

<210> 6
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 6
ctgtaaggat ccaggagaag actg

24

<210> 7
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 7
gaaacctcga gtctttgtaa tcgtaggact t

31

<210> 8
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 8

ctagatattg atattcttca cgaatttacg aac eolf-seql 33

<210> 9
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 9
 gttcgtaaat tcgtgaagaa tatcaatatc tag 33

<210> 10
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 10
 atttctcgag ctgaagacgt cctttagcca cg 32

<210> 11
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 11
 taaactcgag ccccatcaga aacatctact aag 33

<210> 12
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 12
 attttctcga ggcattatca acatcataat gacc 34

<210> 13
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 13
 taaactcgag ccagtcatgc ctaccataac aagctcagc 39

<210> 14
 <211> 29
 <212> DNA
 <213> Artificial Sequence

eolf-seql

<220>
 <223> Primer

<400> 14
 atttctcgag ctgtccaact tgttgaatg 29

<210> 15
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 15
 aaaacgcgga ccactatatg c 21

<210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 16
 aaacgttggtc cgaggatttg 20

<210> 17
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 17
 agcccttgat gatgctttg 19

<210> 18
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 18
 aacaattctg ggtgatcgg 19

<210> 19
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> GH18 catalytic motif present from residues 179 to 186 of SEQ ID
 NO: 1

<220>
 <221> MISC_FEATURE
 <222> (2)..(3)

eolf-seql
<223> Xaa refers to an unconserved amino acid

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa refers to an unconserved amino acid

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> Xaa refers to an unconserved amino acid

<400> 19

Asp Xaa Xaa Asp Xaa Asp Xaa Glu

1

5