

eolf-seq1
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

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Thr Val Lys Ala Glu Glu Lys Thr Val Gln Thr Gly Lys Thr Asp Gln
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Gln Val Gly Ala Lys Leu Val Gln Glu Ile Arg Glu Gly Lys Arg Gly
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Pro Leu Tyr Ala Gly Tyr Phe Arg Thr Trp His Asp Arg Ala Ser Thr
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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
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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
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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
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Gly Val Asp Gly Leu Asp Ile Asp Ile Glu His Glu Phe Thr Asn Lys
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eo1f-seq1

Arg Thr Pro Glu Glu Asp Ala Arg Ala Leu Asn Val Phe Lys Glu Ile
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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
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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-seq1

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
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 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

eo1f-seq1

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
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835 840

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

<400> 2

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Ala Thr Leu Met Gly Ala Ala Leu Ala Thr His His Asp Ser Leu Asn
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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-seq1

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

eo1f-seq1

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
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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
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Tyr Lys Gly Tyr Lys Val His Leu Thr Ala Ser Asn Leu Gly Glu Thr
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Val Thr Ser Lys Val Thr Ala Thr Thr Asp Glu Thr Tyr Leu Val Asp
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Val Ser Asp Gly Glu Lys Val Val His His Met Lys Leu Asn Ile Gly
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eof-seq1

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
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Lys Ser Asp Arg Phe Phe Thr Trp Gly Gln Thr Asn Trp Ile Ala Phe
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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
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<213> Streptococcus pyogenes

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gttcaaacag gaaagacaga tcagcagggtt ggtgctaaat tggtagagga aatccgtgaa 180
ggaaaacgcg gaccactata tgctgggttat tttaggacat ggcattgatcg tgcttcaaca 240
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gatatcttat ttgtttttca tgaccataca gcttcagata gtccattttg gtctgaatta 360
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gttaacgaat taaatggacg tacagggttta tctaaagatt atcctgatac tcctgagggg 480
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660	gctctaata	gttttaaga	gatlgcgag	ttaatagta	aaaatgtag	tgaataaatc
720	aaattgctca	tcatggacac	taccttaagt	gttgaataa	atccaatat	taaaaggata
780	gcggaagatc	tgtattatct	tcttagacaa	tattatggt	caaaaggtgg	agaagctgaa
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1260	ccagcattaa	gagaacaat	cattcaacaa	gttggacagt	ataaaggcga	tttggaaagt
1320	tataacaaga	catltgtgtc	tacaggagat	aagattcca	atcttaagg	actagaaaaa
1380	ttaagcaagt	tacaanaatt	agagtgtgc	cagtatacta	acgtttaaga	aattatctca
1440	gaacttttgc	cggaaagcat	gaaaaaagat	gctgagcttg	ttatgttagg	catgacgtgt
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1560	agtatatacg	atttgacatc	atttgatat	tcacataata	gtttggactt	gtcggaaaaag
1620	agtgaagacc	gtaaacatat	aatgacttg	atggagcagg	tttcaaatca	tcaaaaaata
1680	acgttgaaaa	atacgcttt	tgaanaatca	aaaccggaag	gttatatacc	tcagagcgtat
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1800	gttttttgaa	ctgttaactaa	acgtataacc	tttatgttag	acgaagaa	gc atttgctatc
1860	tataaagag	gagctgtcga	tgttcgacaa	tatgtgtcta	aagactatac	ttatgaagct
1920	tttcgtaag	actataaag	ttacaaggt	catttaactg	cttctaacc	aggaagaaaca
1980	gttaacttcta	aggtaaactgc	tactactgat	gaaacttact	tagtagatgt	ttcctgatgg
2040	gaaaaagttg	ttcacccacat	gaaactcaat	ataggtactg	gtgcccacat	gatggaaaat
2100	ctggcaaaa	gggcataagt	gattgtata	tctgggact	ttgaagcaagc	aaagaagatt
2160	ttcgatgttg	aaaagtcaga	tagattcttc	acttgggac	aaaactaactg	gatagctttt
2220	gatctagggag	aaatatact	tgcgaaggaa	tggcgtttat	ttaatgcaga	gaccaaatact
2280	gaaataaaga	cagatagtag	cttaaacgtg	gctaaggac	gtcttcagat	tttaaaaagat
2340	acaaactatlg	atttagaaaa	aatggacata	aaaaatcgt	aagagtatct	gtcgaatgat
2400	gaaaattgga	ctgatgttgc	tcagatggat	gatgcaaaag	cgatatitaa	tagtaaaata
2460	ttccaatgttt	tatctcggta	tggcggttt	tgttagatg	gtggagctag	ctcttatatc
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<210> 4
 <211> 310
 <212> PRT
 <213> Streptococcus pyogenes

<400> 4

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 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-seq1

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
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Ser Trp Asn Gln Thr Asn
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<210> 8
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<220>
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<400> 8

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 <223> Primer

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 <223> Primer

<400> 11
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 <220>
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 <400> 17
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 <400> 18
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eof-seq1
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<222> (5)..(5)

<223> Xaa refers to an unconserved amino acid

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<222> (7)..(7)

<223> Xaa refers to an unconserved amino acid

<400> 19

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