

eolf-seql (5)
SEQUENCE LISTING

<110> von Pawel-Rammingen, Ulrich
Spoerry, Christian

<120> NEW STREPTOCOCCAL PROTEASES

<130> N410149W0

<150> SE1630021-2

<151> 2016-02-04

<160> 22

<170> PatentIn version 3.5

<210> 1

<211> 1084

<212> PRT

<213> Streptococcus suis

<400> 1

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35 40 45

Gly Thr Leu Ser Thr Arg Glu Glu Leu Glu Glu Phe Gly Lys Asn Asn
50 55 60

Asn Phe Leu Val Ile Asn Gly Lys Val Thr Gln Asn Ile His Asp Phe
65 70 75 80

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

Glu Asp Tyr His Asn Gln Met Arg Glu Leu Arg Phe Ser Gly Asn Gly

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100

105

110

Asp Leu His Asn Ser Met Glu Pro Lys Arg Ile His Ala Leu Phe Lys
115 120 125

Ile Glu Leu Asp Ser Asn Lys Arg Gln Leu Leu Asn Ala Ala Gly Leu
130 135 140

Gly Thr Ala Glu Asn Ser Leu Lys Asn Ile Asn Gly Met Thr Ile Tyr
145 150 155 160

Ser His Gly Leu Thr Val Asp Asn Lys Tyr Tyr Glu Asp Tyr Ser Lys
165 170 175

Tyr Thr His Asn Ser Val Lys Asn Ile Asn Val Thr Lys Glu Arg Phe
180 185 190

Ile Ala Asn Asp Asp Leu Ile His Lys Leu Ile Glu Ser Ser Glu Ala
195 200 205

Met Lys Gln Ser Ser Glu Arg Asp Lys Val Lys Ala Phe Val Gln Tyr
210 215 220

Val Ala Asn His Thr Thr Tyr Asp Trp Glu Ala Ala Asn Lys Ala Val
225 230 235 240

Gln Asn Tyr Ala Asp Ile Asn Tyr Tyr Leu Gly Ser Asp Leu Phe Ala
245 250 255

Val Thr Glu Arg Gln Lys Ala Met Cys Val Gly Phe Ser Thr Thr Ala
260 265 270

Ala Arg Ala Phe Asn Met Leu Gly Leu Pro Ala Tyr Val Val Val Gly
275 280 285

Lys Asn Ala Glu Gly Val Pro His Ala Thr Ala Arg Val Tyr Tyr Asp

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290

295

300

Lys Lys Trp His Thr Ile Asp Gly Thr Gly Phe Ile Thr Gly Asn Lys
305 310 315 320

His Gln Arg Ser Ala Lys Tyr Ser Glu Lys His Phe Ser Thr Ile Gly
325 330 335

Glu Asp Ser Tyr Asp Val Val Glu Ala Gly Gln Glu Pro Lys Ala Glu
340 345 350

Arg Asn Tyr Met Ile Ile Asp Ser Asn Tyr Glu Ser Trp Ala Met Lys
355 360 365

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

Gly Leu Asp Tyr Ile Ala Tyr Val Glu Pro Thr Tyr Ile Thr Glu Asn
385 390 395 400

Lys Lys Asn His Leu Leu Asp Ile Tyr Lys Ala Leu Lys Arg Lys Val
405 410 415

Glu Glu Thr Lys Ala Thr Asp Lys Asp Asp Lys Asp Asp Lys Gln Glu
420 425 430

Gly Tyr Asp Arg Val Leu Gln Phe Val Asn Ser Asp Ile Asp Lys Leu
435 440 445

Ser Ala Leu Ser Lys Ile Thr Glu Glu Glu Phe Lys Ala Leu Glu Asn
450 455 460

Ser Met Asp Leu Ala Arg Val Phe Leu Gly Gln Met Asn Ala Lys Ala
465 470 475 480

Gly Lys Glu Phe Ser Glu Gly Glu Thr Tyr Gln Ser Tyr Leu Lys Asn

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485

490

495

Arg Gln Lys Asn Asn Thr Asn Ser Asp Asp Asp Arg Asn Arg Asn Glu
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Leu Gln Glu Asn Gln Ala Asn Ser Asp Glu Val Ser Gln Asn Ser Lys
515 520 525

Asp Ala Ser Ala Pro Ser Val Asn Ser Ala Gln Gln Ser Glu Glu Leu
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Glu Gly Thr Pro Ser Thr Gln Glu Thr Ile Ser Ala Ala Pro Ser Gln
545 550 555 560

Gln Thr Pro Ala Ala Pro Lys Ala Leu Gln Ala Lys Thr Glu Leu Glu
565 570 575

Asp Lys Thr Glu Thr Ser Ser Leu Gly Asn Thr Glu Met Val Ser Pro
580 585 590

Ser Ser Glu Thr Ala Gln Asn Thr Val Asp Ser Lys Glu Glu Ser Asp
595 600 605

Ala Lys Leu Pro Tyr Val Glu Pro Ser Ser Lys Glu Ser Ser Glu Ala
610 615 620

Gln Val Asn Thr Val Ser Ser Pro Gln Val Ser Ser Ala Ser Pro Thr
625 630 635 640

Ser Ser Glu Thr Ile Ser Thr Asp Thr Val Thr Ala Ser Gln Glu Lys
645 650 655

Ala Glu Ser Arg Val Ser Ala Pro Gln Val Ile Ser Ala Ser Gln Thr
660 665 670

Ser Pro Glu Thr Asn Ser Ala Glu Val Val Thr Thr Ser Gln Glu Val

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675

680

685

Ala Lys Ala Pro Val Ser Ala Pro Gln Val Ser Ser Glu Ile Gln Thr
690 695 700

Leu Ser Glu Thr Ala Pro Thr Glu Val Ala Thr Glu Ala Pro Glu Leu
705 710 715 720

Ser Ala Leu Glu Ser Asn Pro Ala Pro Gln Thr Ser Leu Glu Thr Thr
725 730 735

Pro Thr Glu Glu Val Thr Glu Thr Pro Glu Pro Ser Val Val Glu Ser
740 745 750

Asn Ser Ala Ser Pro Thr Ser Pro Glu Thr Asn Ser Ala Glu Ala Val
755 760 765

Thr Thr Ser Gln Glu Met Ala Glu Pro Ser Val Ser Val Pro Gln Val
770 775 780

Ser Ser Glu Ile Pro Thr Ser Ser Glu Thr Ala Pro Ala Glu Val Ala
785 790 795 800

Thr Glu Val Ser Glu Glu Ser Ser Ser Ala Ser Gln Pro Ser Pro Glu
805 810 815

Thr Thr Pro Thr Glu Thr Val Thr Thr Ser Gln Glu Val Ala Glu Ala
820 825 830

Pro Val Ser Ala Pro Gln Val Ser Ser Glu Ile Pro Thr Ser Pro Glu
835 840 845

Thr Ala Ser Thr Glu Val Val Val Ala Lys Gln Glu Val Ala Asp Ser
850 855 860

Pro Val Ser Ala Pro Gln Val Ile Ser Glu Ile Pro Thr Ser Ser Glu

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865		870		875		880									
Thr	Ala	Pro	Ala	Glu	Val	Ala	Thr	Glu	Val	Thr	Glu	Pro	Ser	Val	Val
				885					890					895	
Ala	Ser	Ser	Ser	Ala	Ser	Pro	Thr	Ser	Pro	Glu	Ala	Asn	Ser	Thr	Glu
			900					905					910		
Val	Val	Val	Ala	Lys	Gln	Glu	Val	Ala	Asp	Pro	Leu	Val	Ser	Ala	Pro
		915					920					925			
Gln	Thr	Ser	Ser	Ala	Ser	Leu	Thr	Leu	Glu	Val	Pro	Lys	Asn	Glu	His
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Leu	Asp	Glu	Lys	Ala	Asp	Ala	Thr	Thr	Pro	Asn	Gly	Val	Glu	Ala	Asn
945					950					955					960
Thr	His	Glu	Ala	Val	Ser	Val	Pro	Thr	Ser	Asp	Ile	Arg	Val	Gln	Asp
			965					970						975	
Ala	Gly	Ser	Asp	Thr	Val	Pro	Gln	Pro	Tyr	Ser	Leu	Ser	Ala	Thr	Leu
			980					985					990		
Phe	Glu	Glu	Ala	Ile	Ser	Thr	Val	Glu	Pro	Val	Gly	Val	Ala	Thr	Ser
	995						1000					1005			
Ser	Gln	Glu	Arg	Ser	Ala	Val	Ala	Gly	Lys	Val	Lys	Val	Pro	Thr	
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Ile	Leu	Thr	Ser	Glu	Asn	Val	Leu	Asn	Ser	Leu	Val	Thr	Ile	Trp	

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1055

1060

1065

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<210> 2

<211> 3255

<212> DNA

<213> Streptococcus suis

<400> 2

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ggtaaaaaca acaatttttt ggtaatcaat ggtaaagtta ctcaaaatat tcatgacttt      240
ccacatatcc ttgttatgaa caagggtgat gttattgctc ataatgagga agattatcat      300
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<210> 3

<211> 586

<212> PRT

<213> Streptococcus agalactiae

<400> 3

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			20					25					30		

Phe	Lys	Gly	Phe	Asn	Val	Trp	Ile	Leu	Gly	Asp	Lys	Gly	Tyr	Tyr	Lys
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eolf-seql (5)

35

40

45

Asn Leu Ile Asn Leu Glu Glu Ile Lys Asn Ile Gln Ala Thr Leu Lys
50 55 60

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

Ala His Asp Thr Thr Val Phe Leu Met Asn Lys Lys His Lys Leu Leu
85 90 95

Lys Asn Ile Glu Glu Phe Lys Thr Ile Thr Gln Lys Arg Leu Thr Glu
100 105 110

Arg Gly Lys Phe Pro Tyr Asp Thr Val His Ser Thr Phe Glu Ile Lys
115 120 125

Asp Glu Asn Phe Ile Met Glu Arg Leu Lys Ser Ser Gly Leu Ser Met
130 135 140

Gly Lys Pro Val Asp Tyr Met Gly Val Asn Gly Ile Pro Ile Tyr Thr
145 150 155 160

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

Asp Ser Ser Tyr Ser Ser Asn Ile Asn Ile Ser Glu Asp Lys Ile Lys
180 185 190

Glu Asn Asp Gln Lys Ile Leu Asp Leu Ile Val Lys Ser Gly Ala Asn
195 200 205

Asn Gln Asn Leu Thr Asp Glu Glu Lys Val Ile Ala Phe Thr Lys Tyr
210 215 220

Ile Gly Glu Ile Thr Asn Tyr Asp Asn Glu Ala Tyr Arg Ala Arg Asn

eolf-seql (5)

225		230		235		240
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						255
Arg	Lys	Leu	Ala	Met	Cys	Val
		260				265
						270
Phe	Asn	Ile	Met	Gly	Ile	Pro
	275					280
						285
Gln	Gly	Ile	Ser	His	Ala	Ala
	290				295	
						300
His	Ile	Ile	Asp	Ile	Thr	Ala
305					310	
						315
						320
Lys	Thr	Thr	Tyr	Ser	Asp	Phe
				325		
						330
						335
Asp	Val	Tyr	Asp	Pro	Ala	Lys
			340			
						345
						350
Met	Glu	Ser	Asn	Glu	Ala	Phe
	355					
						360
						365
Lys	Ser	Met	Leu	Phe	Ile	Asn
	370					375
						380
Pro	Lys	Asp	Asp	Phe	Val	Pro
385					390	
						395
						400
Ile	Asp	Lys	Tyr	Lys	Lys	Leu
				405		
						410
						415
Asn	Pro	Gly	Glu	Lys	Asn	Ile
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						Asp
						Tyr
						Leu
						Lys
						Asn
						Glu
						Tyr
						Glu

eolf-seql (5)

420

425

430

Glu Ile Leu Lys Lys Asp Asn Leu Phe Glu His Glu His Ala Glu Phe
435 440 445

Lys Glu Ser Leu Asn Leu Asn Glu Ser Phe Tyr Leu Gln Leu Lys Lys
450 455 460

Glu Glu Lys Lys Pro Ser Asp Asn Leu Lys Lys Glu Glu Lys Pro Arg
465 470 475 480

Glu Asn Ser Val Lys Glu Arg Glu Thr Pro Ala Glu Asn Asn Asp Phe
485 490 495

Val Ser Val Thr Glu Lys Asn Asn Leu Ile Asp Lys Tyr Lys Glu Leu
500 505 510

Leu Ser Lys Ile Pro Glu Asn Thr Gln Asn Pro Gly Glu Lys Asn Ile
515 520 525

Arg Asn Tyr Leu Glu Lys Glu Tyr Glu Glu Leu Leu Gln Lys Asp Lys
530 535 540

Leu Phe Lys His Glu Tyr Thr Glu Phe Thr Lys Ser Leu Asn Leu Asn
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Glu Thr Phe Tyr Ser Gln Leu Lys Glu Gly Glu Met Lys Leu Ser Glu
565 570 575

Asn Pro Glu Lys Gly Glu Thr Asn Thr Asn
580 585

<210> 4

<211> 1761

<212> DNA

<213> Streptococcus agalactiae

eolf-seql (5)

<400> 4

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gaatttaaga cgataaccca aaaaaggcta actgagagag gaaagttccc atatgatacc	360
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<210> 5

<211> 493

<212> PRT

<213> Streptococcus porcinus

<400> 5

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Lys Glu Glu Ile Ser Glu Asn Gln Gln Phe His Val Phe Lys Leu Gly
35 40 45

Met Asn Asn Tyr Tyr Arg Ser Gly Ile Arg Ile Asn Glu Leu Asn Asn
50 55 60

Leu Ala Thr Glu His Asp Phe Ile Leu Val Asn Asp His Ala Ser His
65 70 75 80

Lys Lys Tyr Asp Val Pro His Ile Phe Ile Met Asn Lys Gly Asp Val
85 90 95

Ile Val Pro Ser Lys Glu Lys Tyr Asp Glu Gln Met Arg Glu Val Lys
100 105 110

eolf-seql (5)

Phe Ala Gly Asp Gln Pro Asn Ala Gln Arg Gln Arg Ile His Ala Leu
115 120 125

Phe Glu Ile Gly Leu Asp Ser Asn Lys Arg Gln Leu Leu Asn Ala Ala
130 135 140

Gly Leu Gly Thr Ala Glu Asn Thr Leu Ala Lys Val Asp Gly Phe Thr
145 150 155 160

Ile Tyr Ser His Gly Leu Thr Val Asp Asn Lys Tyr Tyr Glu Asp Tyr
165 170 175

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

Lys Val Gln Thr Asn Asp Arg Asp Lys Val Lys Ala Phe Val Met Tyr
210 215 220

Val Ala Asn His Thr Ile Tyr Asp Trp Ile Ala Ala Asn Asn Ala Val
225 230 235 240

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

Ile Thr Glu Arg Lys Lys Ala Met Cys Val Gly Phe Ser Thr Thr Ala
260 265 270

Ala Arg Ala Phe Asn Met Leu Gly Ile Pro Ala Tyr Val Val Val Gly
275 280 285

Lys Asn Ala Gln Gly Val Asp His Ala Thr Ala Arg Ala Tyr Tyr Asn
290 295 300

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Gly Lys Trp His Thr Ile Asp Gly Thr Gly Phe Ile Asn Asp Lys Ala
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Ser Arg Ser Thr Ile Tyr Ser Glu Asn His Phe Tyr Ser Ile Gly Glu
325 330 335

Asp Ser Tyr Asn Ile Val Asp Val Asn Asp Glu Gln Ile Ala Phe Asp
340 345 350

Lys Asn Tyr Met Lys Ile Asp Lys Val Phe Glu Glu Trp Ala Gln Lys
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Gln Pro Thr Ala Asp Leu Leu Leu Ile Asn Lys Asp Lys Ser Leu Val
370 375 380

Pro Ser Asn Tyr Val Ala Tyr Val Ala Pro Val Ile Val Asp Asn Asn
385 390 395 400

Arg Lys Gly Ser Leu Thr Gln Ile Tyr Gln Asn Leu Lys Gln Val Met
405 410 415

Glu Ser Ser Ser Gln Lys Ala Ser Leu Thr Ser Leu Leu Asn Thr Ala
420 425 430

Thr Ala Asp Ile Ala Lys Leu Gln Thr Ser Ser Gln Leu Thr Gln Glu
435 440 445

Asp Tyr Asn Gln Ile Gln Asn Ser Met Lys Ser Val Leu Ser Phe Phe
450 455 460

Trp Gln Leu Asp Lys Asp Ser Ala Thr Asn Phe Glu Asn Ser Glu Asp
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eolf-seql (5)

<210> 6

<211> 1482

<212> DNA

<213> Streptococcus porcinus

<400> 6

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agtaatatat cagatgtcaa ctactatctt ggctctgatt tgttttcaat tactgaacgt	780
aagaaagcta tgtgtgttgg ttttagtact acagcagctc gtgcttttaa tatgttagga	840
attccagcct acgttgttgt tggaaaaaat gcacaagggtg tagaccatgc tacagctcgc	900
gcttactata acggtaaatg gcacactatt gacgggtactg gttttattaa tgataaagct	960
tctcgctcta ctatttatag cgaaaatcac ttttactcta ttggcgaaga tagctataat	1020
atagttgatg ttaacgatga acaaatagct ttcgacaaaa actatatgaa aattgataag	1080
gtttttgaag aatgggctca aaaacaaccg acagcagact tattattgat taataaagat	1140
aaatcattag tcccttcaaa ttatgtagcc tacgtcgcac cagtaattgt cgataacaat	1200
cgtaaagggtt ctcttacaca aatttatcaa aatttaaaac aagtaatgga atcatcttct	1260

eolf-seql (5)

caaaaggcat ccctaacctc tctctttaaact actgcaacag cagacattgc aaaacttcaa 1320
 actagttctc aacttaccca agaagactat aaccagattc agaattctat gaaatctgtt 1380
 ctctcgtttt tctggcagtt agataaggat tctgctacga attttgaaaa tagcgaagat 1440
 tataaaaaat atctaacaga aacaaagaat gcaggtaact aa 1482

<210> 7
 <211> 517
 <212> PRT
 <213> Streptococcus equi

<400> 7

Met Glu Ala Trp Lys His Gly Ser Met Glu Ala Trp Lys His Gly Ser
 1 5 10 15

Met Glu Ala Trp Lys His Gly Arg Thr Leu Cys Lys Gly Leu Leu Leu
 20 25 30

Gly Leu Ala Cys Gly Ala Ile Ser Met Ser Leu Val Val Lys Ser Thr
 35 40 45

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

Leu Asp Asn Thr Val Ser Asn Leu Ile Ser Glu Val Lys Asp Glu Leu
 65 70 75 80

Ala Lys Asn His Gln Asp Ala Leu Glu Ile Tyr Ile Leu Gly Glu Gly
 85 90 95

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

Lys Asp Tyr Lys Pro Val Arg Leu Asn Gly Lys Val Ile His Gly Arg
 115 120 125

eolf-seql (5)

Ala Phe Phe Met Met Lys Lys Glu Asp Gln Leu Ile Ser Thr Lys Glu
130 135 140

Glu Tyr Asp Arg Ile Ile Ala Glu Arg Phe Ser Asn Leu Glu Lys Phe
145 150 155 160

Asp Tyr Pro Thr Ile His Tyr Thr Phe Asn Ala Glu Leu Lys Asp Lys
165 170 175

Tyr Pro Tyr Leu Ser Leu Ile Leu Lys Ala Ser Gly Leu Ser Leu Ser
180 185 190

Asp Ser Ile Asn Leu Gly Ser Thr Leu Gly Ile Asn Gly Val Thr Ile
195 200 205

His Thr Gln His Leu Arg Ile Asp Asn Gln Phe Ala Tyr Arg Tyr Asn
210 215 220

Gly Glu Asp Tyr Lys Gln Asp Ser His Ile Thr Phe Asp Arg Phe Lys
225 230 235 240

Lys Asn Asp Asp Lys Leu Lys Glu Leu Ile Ala Thr Ser Gly Ala Asn
245 250 255

Gln Glu Gly Leu Thr Asp Ala Gln Arg Val Lys Ala Tyr Val Leu Tyr
260 265 270

Met Ala Asn His Val Asp Tyr Asp Trp Asp Ala Thr Arg Tyr Asn Pro
275 280 285

Asp Tyr Leu Ile Phe Cys Gln Ala Ser Asp Leu Phe Ala Leu Thr Glu
290 295 300

Arg Asn Lys Ala Met Cys Ile Gly Phe Ser Thr Ala Ala Ala Arg Gly
305 310 315 320

eolf-seql (5)

Leu Asn Leu Leu Gly Ile Pro Ser Tyr Val Thr Tyr Gly Lys Asn Arg
325 330 335

Asp Gly Val Ala His Ala Thr Ile Arg Ala Phe Tyr Asp Lys Lys Trp
340 345 350

Arg Thr Leu Asp Val Thr Gly Val Gly Arg Gly Lys Tyr Thr Glu Glu
355 360 365

His Tyr Asp Asn Leu Asn Thr His Asp Tyr Lys Ile Phe Asp Leu Thr
370 375 380

Lys Glu Thr Asn Val Asp Leu Asp Arg Gly Tyr Met Glu Ile Tyr Lys
385 390 395 400

Asp Phe Glu Asp Trp Ile Leu Ser His Asn Thr Lys Glu Leu Leu Phe
405 410 415

Ile Asn Gln Asp Ala Asn Ile Arg Asn Lys Val Ala Lys Asp Val Phe
420 425 430

Lys Tyr Ile Gln Glu Ala Glu Lys Gln Ser Leu Ile Asp Lys Tyr Asn
435 440 445

Glu Phe Ile Ile Arg Thr Ser Ala Leu Lys Ala Glu Phe Lys Thr Asp
450 455 460

Arg Leu Lys Glu Ile Val Gly Ser Leu Val Ser Gln Ala Gln Glu Glu
465 470 475 480

Leu Glu Asn Ile Lys His Ile Glu Val Met Thr Glu Asp Glu Lys Asp
485 490 495

Gln Phe Glu Tyr Thr Leu Arg Asn Leu Gly Val Tyr Tyr Ser Gln Cys
500 505 510

eolf-seql (5)

Glu Ser Ala Asn Gln
515

<210> 8
<211> 1554
<212> DNA
<213> Streptococcus equi

<400> 8
atggaagcat ggaagcatgg aagcatggaa gcatggaagc atggaagcat ggaagcatgg 60
aagcatggaa ggactttgtg taaaggatta ttattaggat tagcatgtgg tgctatatct 120
atgtcttttag tcgtcaagag tacaattgta gttgcggacg atgtaaggct tagcgcagcag 180
tcgacgggtca ttttagataa cactgtgtca aatctgatta gtgagggttaa ggatgagtta 240
gccaaaaatc atcaggacgc attagaaatc tataatcttgg gggagggaag tccaaaatat 300
agtggagtgt ctcctgatcg tcttggtgac tacataaaag attataagcc tgtgcggttg 360
aatgggaagg tgatacatgg aagagcattt ttcattgatga aaaaggaaga tcagctgata 420
tcaactaaag aagaatatga ccgcataata gcagaaagggt tttcaaatct ggaaaaattt 480
gattacccta ctatacacta tacctttaat gcggagctaa aggataaata cccttatctt 540
agtttaatac taaaagcgag tggcttttcc ttgtctgact caataaattt aggctcaaca 600
ctgggtataa atggcggttac tatccataca cagcatttac gtatcgacaa tcagtttgct 660
tatagataca atggagagga ttataaaca gatagtcata taacgtttga ccgttttaag 720
aagaatgatg acaagttaaa ggaattgatt gcaacatctg gagctaataca agaggggctg 780
acagatgctc aacgagtaaa agcctatgtc ttgtatatgg caaacatgt tgattatgat 840
tgggatgcaa caagatataa tcctgattat ttaatatattt gtcaggcctc tgatttatatt 900
gcacttacag agcgaaataa ggccatgtgt ataggcttta gtacagcagc tgcaagaggg 960
ttaaatctat tagggatacc atcttatgtg acctatggta aaaatagaga tggtagtagca 1020
catgcaacga tacgtgcttt ttacgataaa aagtggagaa cactagatgt tacaggagtt 1080
ggtagaggga aatacacaga agaacattat gacaatctca atacgcacga ttataagatt 1140

eolf-seql (5)

```

tttgatttaa ctaaggaaac aaacgttgat ttagatcgtg gctatatgga gatctataag      1200
gattttgaag attggatcct ctacacacaat acgaaagagc tattatttat taatcaagat      1260
gcgaatatac gtaataaggt tgcaaaagat gtttttaa atacatacaaga ggctgagaag      1320
caatcgtaa tagataagta taatgaattc atcataagaa cgagtgcctt aaaggctgag      1380
ttcaaaaactg acagggtaaa agaaatagtc ggaagtctag ttagtcaggc acaggaagaa      1440
ttagaaaata tcaagcatat tgaagttatg acagaagatg aaaaagatca gtttgaatat      1500
acactgagga atttaggagt atattattca caatgtgaaa gcgctaataca ataa          1554

```

```

<210> 9
<211> 497
<212> PRT
<213> Streptococcus pseudoporcinus

```

<400> 9

```

Arg Glu Asn Glu Asn Val Arg Gln Leu Gln Ser Glu Asn Lys Gln Met
1              5              10              15

```

```

Lys Ala Val Asn Leu Gln Glu Phe Ser Glu Lys Leu Lys Gly Glu Ile
20              25              30

```

```

Ala Glu Asn Gln Gln Phe His Ile Phe Lys Leu Gly Leu Asn Asn Tyr
35              40              45

```

```

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

```

```

His Asp Phe Ile Met Ile Asp Asn Arg Ala Thr His Asn Lys Tyr Gly
65              70              75              80

```

```

Val Pro His Ile Ile Ile Met Asn Lys Asp Asp Val Ile Val His Asn
85              90              95

```

```

Gln Glu Asp Tyr Asn Lys Glu Met Ala Glu Leu Thr Phe Ala Gly Asp

```

eolf-seql (5)

100

105

110

Lys Pro Ile Gln Ser Asp Ser Tyr Leu Pro Gln Lys Lys Arg Ile His
115 120 125

Ala Leu Phe Glu Ile Gly Leu Asp Ser Asn Arg Arg Gln Leu Leu Asn
130 135 140

Ala Ala Gly Leu Lys Thr Pro Glu Asn Ser Val Ile Glu Leu Asp Thr
145 150 155 160

Phe Lys Ile Tyr Ser His Gly Leu Ala Val Asp Asn Lys Tyr Tyr Asp
165 170 175

Glu Tyr Ser His Phe Asn Asn Asn Thr Asn Val Asn Ile Thr Lys Gln
180 185 190

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

Thr Ala Lys Asp Gln Pro Thr Asp Arg Asp Lys Val Lys Thr Phe Val
210 215 220

Met Tyr Val Ala Asn His Thr Ile Tyr Asp Trp Asn Ala Ala Asn Asn
225 230 235 240

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

Phe Ser Ile Thr Glu Arg Lys Lys Ala Met Cys Val Gly Phe Ser Thr
260 265 270

Thr Ala Ala Arg Ala Phe Asn Met Leu Gly Ile Pro Ala Tyr Val Val
275 280 285

Glu Gly Lys Asn Ala Gln Gly Val Asp His Ala Thr Ala Arg Val Tyr

eolf-seql (5)

290

295

300

Tyr Asn Gly Lys Trp His Thr Ile Asp Gly Thr Gly Phe Ile Asn Gly
305 310 315 320

Asn Arg Thr Arg Ser Thr Leu Tyr Thr Glu Ser His Phe Arg Ser Val
325 330 335

Gly Glu Asp Ser Tyr Gln Leu Val Gly Leu Asn Glu Asp Ile Pro Phe
340 345 350

Asp Arg Asn Tyr Met Lys Ile Asp Lys Val Tyr Glu Glu Trp Ala Pro
355 360 365

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

Val Gly Leu Asp Arg Val Ala Tyr Val Glu Pro Val Tyr Val Asp Lys
385 390 395 400

Asn Arg Gln Asp Ala Leu Thr Gln Ile Tyr Lys Lys Leu Lys Glu Thr
405 410 415

Met Glu Ser Ser Ser Lys Lys Asn Pro Ser Ser Gly Gly Phe Ser Ser
420 425 430

Leu Leu Gly Ser Ala Ser Ser Asp Ile Ala Lys Leu Glu Gly Ser Ser
435 440 445

Gln Leu Thr Gln Glu Glu Tyr Asp Lys Ile His Arg Ser Met Thr Ser
450 455 460

Ile Leu Thr Phe Phe Ala Gln Leu Asp Lys Asp Ala Ala Glu Ala Phe
465 470 475 480

Glu Lys Gly Asn Asp Tyr Lys Asn Tyr Leu Ala Thr Thr Lys His Ala

Gln

<210> 10
 <211> 1494
 <212> DNA
 <213> Streptococcus pseudoporcinus

<400> 10
 agagaaaatg aaaacgtaag acaattacaa tcagaaaata aacaaatgaa agcagtaaac 60
 ttgcaggaat tttcggagaa attaaaagga gaaattgctg aaaatcaaca atttcatatc 120
 tttaaactag ggttgaataa ttattacata ggaggggtac gcataaatga actgagtgat 180
 ttagcgaaaa accatgattt tatcatgatt gataatcgtg ctaccataa taaatatgga 240
 gtccctcata taattattat gaacaaagat gatgttattg tgcataatca agaagactat 300
 aataaagaaa tggcagagtt aacatttgca ggtgataaac cgatacaatc tgactcttac 360
 cttcccaaaa aaaagagaat ccacgcactg ttgaaattg gtttagattc taatagacga 420
 caattactta acgctgcagg acttaaaaca ccagaaaata gtgtaataga acttgatacc 480
 tttaaaatct atttcatgg tttagcgggt gataataaat attatgacga atatagtcat 540
 tttaataaca acacgaatgt caatattacc aagcagcgct ttactgagaa tgataactta 600
 atccataact taataaccac gtcaacagct aaggatcagc caactgatcg cgacaaagtc 660
 aaaacatttg ttatgtatgt ggctaaccat actatatatg actggaatgc cgcaaataat 720
 gctgtaagta atatttcaga tgtcaactat tatcttggtt ctgatttggt ttccattact 780
 gaacgcaaga aagctatgtg tgtaggcttt agcactacag cagctcgtgc ttttaatatg 840
 ctgggtatcc cagcctatgt ggttgaaggt aaaaacgcgc aagggtgtgga ccatgctact 900
 gctcgtgtct actataatgg aaaatggcat accattgacg ggactggctt tattaacggt 960
 aaccgcactc gctccactct ctataccgaa agccacttta ggtctgttgg agaagatagc 1020
 tatcaactgg ttggtcttaa tgaggacata ccttttgata gaaactatat gaagattgat 1080

eolf-seql (5)

```

aaagtttacg aagaatgggc tcccaaacaa aagacggcag acctactatt agttaacaaa      1140
gataaatcat tagttggcct agaccgtgta gcctatgtcg aacctgtata tgttgacaag      1200
aaccgtcaag atgccctcac acaaatttac aaaaaattaa aagaaacaat ggagtcctct      1260
tctaagaaga atccatcttc tggaggattc tcctctctct taggttctgc aagtagcgat      1320
attgcaaagc tggaaggctc ttctcaactt acacaagaag aatacgataa gattcatcgt      1380
tctatgacat ctattctcac cttttttgca caactagata aagacgccgc cgaagccttt      1440
gaaaagggaa atgattataa gaattattta gcaacaacaa agcatgcaca gtaa              1494

```

```

<210> 11
<211> 432
<212> PRT
<213> Streptococcus suis

```

```

<400> 11

```

```

Asp Glu Asn Ser His Leu Gln Ser Pro Lys Asn Thr Asn Lys Ile Glu
1              5              10              15

```

```

Val Leu Asn Trp Glu Ala Phe Ser Lys Lys Leu Lys Asp Tyr Ser Ser
20              25              30

```

```

Asp Gln Arg Gln Phe His Val Leu Lys Leu Gly Phe Glu Asn Arg Leu
35              40              45

```

```

Gly Thr Leu Ser Thr Arg Glu Glu Leu Glu Glu Phe Gly Lys Asn Asn
50              55              60

```

```

Asn Phe Leu Val Ile Asn Gly Lys Val Thr Gln Asn Ile His Asp Phe
65              70              75              80

```

```

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

```

```

Glu Asp Tyr His Asn Gln Met Arg Glu Leu Arg Phe Ser Gly Asn Gly

```

eolf-seql (5)

100

105

110

Asp Leu His Asn Ser Met Glu Pro Lys Arg Ile His Ala Leu Phe Lys
115 120 125

Ile Glu Leu Asp Ser Asn Lys Arg Gln Leu Leu Asn Ala Ala Gly Leu
130 135 140

Gly Thr Ala Glu Asn Ser Leu Lys Asn Ile Asn Gly Met Thr Ile Tyr
145 150 155 160

Ser His Gly Leu Thr Val Asp Asn Lys Tyr Tyr Glu Asp Tyr Ser Lys
165 170 175

Tyr Thr His Asn Ser Val Lys Asn Ile Asn Val Thr Lys Glu Arg Phe
180 185 190

Ile Ala Asn Asp Asp Leu Ile His Lys Leu Ile Glu Ser Ser Glu Ala
195 200 205

Met Lys Gln Ser Ser Glu Arg Asp Lys Val Lys Ala Phe Val Gln Tyr
210 215 220

Val Ala Asn His Thr Thr Tyr Asp Trp Glu Ala Ala Asn Lys Ala Val
225 230 235 240

Gln Asn Tyr Ala Asp Ile Asn Tyr Tyr Leu Gly Ser Asp Leu Phe Ala
245 250 255

Val Thr Glu Arg Gln Lys Ala Met Cys Val Gly Phe Ser Thr Thr Ala
260 265 270

Ala Arg Ala Phe Asn Met Leu Gly Leu Pro Ala Tyr Val Val Val Gly
275 280 285

Lys Asn Ala Glu Gly Val Pro His Ala Thr Ala Arg Val Tyr Tyr Asp

eolf-seql (5)

290

295

300

Lys Lys Trp His Thr Ile Asp Gly Thr Gly Phe Ile Thr Gly Asn Lys
305 310 315 320

His Gln Arg Ser Ala Lys Tyr Ser Glu Lys His Phe Ser Thr Ile Gly
325 330 335

Glu Asp Ser Tyr Asp Val Val Glu Ala Gly Gln Glu Pro Lys Ala Glu
340 345 350

Arg Asn Tyr Met Ile Ile Asp Ser Asn Tyr Glu Ser Trp Ala Met Lys
355 360 365

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

Gly Leu Asp Tyr Ile Ala Tyr Val Glu Pro Thr Tyr Ile Thr Glu Asn
385 390 395 400

Lys Lys Asn His Leu Leu Asp Ile Tyr Lys Ala Leu Lys Arg Lys Val
405 410 415

Glu Glu Thr Lys Ala Thr Asp Lys Asp Asp Lys Asp Asp Lys Gln Glu
420 425 430

<210> 12

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer/probe

<400> 12

tcactgcagt tttggggagt agg

23

<210> 13

eolf-seql (5)

<211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer/probe

<400> 13
 atggatccca gttcagaacc tc 22

<210> 14
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer/probe

<400> 14
 cgggatccag agaaaaaaga gatcc 25

<210> 15
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer/probe

<400> 15
 aggaattcac cggtattgta gcg 23

<210> 16
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer/probe

<400> 16
 attgtatttg gtggaggag 19

<210> 17

eolf-seql (5)

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

<220>
 <223> Primer/probe

<400> 17
 ttttagcagct aagttgatac c 21

<210> 18
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer/probe

<400> 18
 gtttccatgg atgaaaactc acatttaca tcg 33

<210> 19
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer/probe

<400> 19
 acgtgcggcc gcataagctt cgtac 25

<210> 20
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer/probe

<400> 20
 aacgtcagaa agcgatgagt gtaggtttca gcact 35

<210> 21

eolf-seql (5)

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer/probe

<400> 21

cagaagggtgt cccggctgct acagcgcgtg

30

<210> 22

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer/probe

<400> 22

taaaaagtgg cacaccattg ccggtacagg ttttattaca g

41