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 <120> New proteins for use in human and animal Staphylococcus infections
 <130> PRO-028 PCT
 <140> unknown
 <141> 2008-08-19
 <150> EP 07 114 785.4
 <151> 2007-08-22
 <150> EP 08 152 096.7
 <151> 2008-02-28
 <150> US 60/957 351
 <151> 2007-08-22
 <150> US 61/032 211
 <151> 2008-02-28
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 35 40 45
 Trp Lys Val Leu Phe Gly Leu Leu Lys Gly Leu Gly Ala Lys Asp
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 65 70 75 80
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 Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr
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 Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp
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 130 135 140
 Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn Phe
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 165 170 175
 Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile


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<213> unknown

<220>
<223> prophage SA2USA

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35          40          45
Pro Asn Asn Thr Thr Ile Thr Tyr Asp Gly Ala Tyr Cys Ile Asn Gly
50          55          60
Tyr Arg Trp Ile Thr Tyr Ile Ala Asn Ser Gly Gln Arg Arg Tyr Ile
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<212> DNA
<213> unknown

<220>
<223> prophage SA2USA

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tgtattaatg gttatagatg gattacttat attgctaata gtggacaacg tcgctatatt 240
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 <213> unknown

<220>
 <223> pittti20

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 35 40 45
 Val Thr Pro Asn Gln Lys Met Thr Phe Asp Tyr Leu Ala Gln Gln Asp
 50 55 60
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<220>
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 <211> 496
 <212> PRT
 <213> artificial sequence

<220>
 <223> pittti26-prophage SA2USA

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 20 25 30
 Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala Gly
 35 40 45
 Trp Lys Val Leu Phe Gly Leu Leu Lys Gly Leu Gly Ala Lys Asp
 50 55 60
 Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn
 65 70 75 80

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<211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> pittti26-prophage SA2USA

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<210> 9
<211> 506
<212> PRT
<213> artificial sequence

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<220>
<223> pittti26-prophage SA2USA

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Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala Gly
35 40 45
Trp Lys Val Leu Phe Gly Leu Leu Lys Gly Leu Gly Ala Lys Asp
50 55 60
Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn
65 70 75 80
Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser
85 90 95
Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr
100 105 110
Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp
115 120 125
Thr Asp Arg Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg
130 135 140
Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn Phe
145 150 155 160
Lys Ser Glu Thr Ala Pro Arg Ser Ile Gln Ser Pro Thr Gln Ala Ser
165 170 175
Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile

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<210> 11
<211> 491
<212> PRT
<213> artificial sequence

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<220>
<223> pittti26-pittti20

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20          25          30
Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala Gly
35          40          45
Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly Ala Lys Asp
50          55          60
Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn
65          70          75          80
Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser
85          90          95
Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr
100         105         110
Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp
115         120         125
Thr Asp Arg Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg
130         135         140
Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn Phe
145         150         155         160
Lys Ser Glu Thr Ala Pro Arg Ser Ile Gln Ser Pro Thr Gln Ala Ser
165         170         175
Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile
180         185         190
Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly Gly Asn
195         200         205
Pro Lys Gly Ile Val Ile His Asn Asp Ala Gly Ser Lys Gly Ala Thr
210         215         220
Ala Glu Ala Tyr Arg Asn Gly Leu Val Asn Ala Pro Ser Ser Arg Leu
225         230         235         240
Glu Ala Gly Ile Ala His Ser Tyr Val Ser Gly Asn Thr Val Trp Gln
245         250         255
Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Leu Gly

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<210> 13
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<212> PRT
<213> artificial sequence

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<220>
<223> pittti26-pittti20

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35 40 45
Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly Ala Lys Asp
50 55 60
Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn
65 70 75 80
Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser
85 90 95
Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr
100 105 110
Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp
115 120 125
Thr Asp Arg Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg
130 135 140
Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn Phe
145 150 155 160
Lys Ser Glu Thr Ala Pro Arg Ser Ile Gln Ser Pro Thr Gln Ala Ser
165 170 175
Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile
180 185 190
Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly Gly Asn
195 200 205
Pro Lys Gly Ile Val Ile His Asn Asp Ala Gly Ser Lys Gly Ala Thr
210 215 220
Ala Glu Ala Tyr Arg Asn Gly Leu Val Asn Ala Pro Ser Ser Arg Leu
225 230 235 240
Glu Ala Gly Ile Ala His Ser Tyr Val Ser Gly Asn Thr Val Trp Gln
245 250 255
Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Leu Gly
260 265 270
Asn Lys Tyr Tyr Tyr Gly Ile Glu Val Cys Gln Ser Met Gly Ala Asp
275 280 285
Asn Ala Thr Phe Leu Lys Asn Glu Gln Ala Thr Phe Gln Glu Cys Ala
290 295 300
Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile Arg
305 310 315 320
Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser Val
325 330 335
Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu Asp
340 345 350
Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala Tyr
355 360 365

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Met Asp Gly Lys Ile Pro Val Ala Thr Val Ser Asn Glu Ser Ser Ala
370 375 380
Ser Ser Asn Thr Val Lys Pro Val Ala Glu Leu Met Lys Arg Lys Lys
385 390 395 400
Pro Lys Gly Trp Ser Glu Asn Pro Tyr Gly Thr Tyr Tyr Lys Lys Val
405 410 415
Asp Lys Thr Phe Ile Val Gly Ser Glu Lys Ile Glu Thr Arg Ile Gly
420 425 430
Ser Pro Phe Leu Ser Ala Pro Ser Gly Gly His Val Thr Pro Asn Gln
435 440 445
Lys Met Thr Phe Asp Tyr Leu Ala Gln Gln Asp Gly Tyr Glu Trp Gly
450 455 460
Gln Leu Glu Asn Asn Arg Gly Gln Gln Glu Phe Val Pro Ile Arg Pro
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<210> 14
<211> 1506
<212> DNA
<213> artificial sequence

<220>
<223> pittti26-pittti20

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ttaagtcaaa aagaatattg gggatatttta aaaggatcca gatctcatca ccatcaccat 1500
cactaa 1506

<210> 15
<211> 497
<212> PRT
<213> artificial sequence

<220>

<223> pittti26_prophage SA2 USA

<400> 15

Met	Ala	Ser	Ile	Ile	Met	Glu	Val	Ala	Thr	Met	Gln	Ala	Lys	Leu	Thr
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Lys	Lys	Glu	Phe	Ile	Glu	Trp	Leu	Lys	Thr	Ser	Glu	Gly	Lys	Gln	Phe
			20					25					30		
Asn	Val	Asp	Leu	Trp	Tyr	Gly	Phe	Gln	Cys	Phe	Asp	Tyr	Ala	Asn	Ala
		35					40					45			
Gly	Trp	Lys	Val	Leu	Phe	Gly	His	Thr	Leu	Lys	Gly	Leu	Gly	Ala	Lys
	50					55					60				
Asp	Ile	Pro	Phe	Ala	Asn	Asn	Phe	Asp	Gly	Leu	Ala	Thr	Val	Tyr	Gln
65					70					75				80	
Asn	Thr	Pro	Asp	Phe	Leu	Ala	Gln	Pro	Gly	Asp	Met	Val	Val	Phe	Gly
			85						90					95	
Ser	Asn	Tyr	Gly	Ala	Gly	Tyr	Gly	His	Val	Ala	Trp	Val	Ile	Glu	Ala
			100					105					110		
Thr	Leu	Asp	Tyr	Ile	Ile	Val	Tyr	Glu	Gln	Asn	Trp	Leu	Gly	Gly	Gly
		115					120					125			
Trp	Thr	Asp	Arg	Ile	Glu	Gln	Pro	Gly	Trp	Gly	Trp	Glu	Lys	Val	Thr
	130					135					140				
Arg	Arg	Gln	His	Ala	Tyr	Asp	Phe	Pro	Met	Trp	Phe	Ile	Arg	Pro	Asn
145					150					155				160	
Phe	Lys	Ser	Ala	Thr	Ala	Pro	Ala	Ser	Ile	Gln	Ser	Pro	Thr	Gln	Ala
			165						170					175	
Ser	Lys	Lys	Glu	Thr	Ala	Lys	Pro	Gln	Pro	Lys	Ala	Val	Glu	Leu	Lys
			180					185					190		
Ile	Ile	Lys	Asp	Val	Val	Lys	Gly	His	Asp	Leu	Pro	Lys	Arg	Gly	Gly
	195						200					205			
Asn	Pro	Lys	Gly	Ile	Val	Ile	His	Asn	Asp	Ala	Gly	Ser	Lys	Gly	Ala
	210					215					220				
Thr	Ala	Glu	Ala	Tyr	Arg	Asn	Gly	Leu	Val	Asn	Ala	Pro	Ser	Ser	Arg
225					230					235				240	
Leu	Glu	Ala	Gly	Ile	Ala	His	Ser	Tyr	Val	Ser	Gly	Asn	Thr	Val	Trp
			245						250					255	
Gln	Ala	Leu	Asp	Glu	Ser	Gln	Val	Gly	Trp	His	Thr	Ala	Asn	Gln	Leu
		260						265					270		
Gly	Asn	Lys	Tyr	Tyr	Tyr	Gly	Ile	Glu	Val	Cys	Gln	Ser	Met	Gly	Ala
		275					280					285			
Asp	Asn	Ala	Thr	Phe	Leu	Lys	Asn	Glu	Gln	Ala	Thr	Phe	Gln	Glu	Cys
	290					295					300				
Ala	Arg	Leu	Leu	Lys	Lys	Trp	Gly	Leu	Pro	Ala	Asn	Arg	Asn	Thr	Ile
305					310					315				320	
Arg	Leu	His	Asn	Glu	Phe	Thr	Ser	Thr	Ser	Cys	Pro	His	Arg	Ser	Ser
			325						330					335	
Val	Leu	His	Thr	Gly	Phe	Asp	Pro	Val	Thr	Arg	Gly	Leu	Leu	Pro	Glu
			340					345					350		
Asp	Lys	Arg	Leu	Gln	Leu	Lys	Asp	Tyr	Phe	Ile	Lys	Gln	Ile	Arg	Ala
		355					360					365			
Tyr	Met	Asp	Gly	Lys	Ile	Pro	Val	Ala	Thr	Val	Ser	Asn	Glu	Ser	Ser
	370					375					380				
Ala	Ser	Ser	Asn	Thr	Val	Lys	Pro	Val	Ala	Glu	Leu	Met	Pro	Pro	Val
385					390					395				400	
Pro	Ala	Gly	Tyr	Thr	Leu	Asp	Lys	Asn	Asn	Val	Pro	Tyr	Lys	Lys	Glu
			405						410					415	
Gln	Gly	Asn	Tyr	Thr	Val	Ala	Asn	Val	Lys	Gly	Asn	Asn	Val	Arg	Asp
		420						425					430		
Gly	Tyr	Ser	Thr	Asn	Ser	Arg	Ile	Thr	Gly	Val	Leu	Pro	Asn	Asn	Thr
		435					440						445		

Thr Ile Thr Tyr Asp Gly Ala Tyr Cys Ile Asn Gly Tyr Arg Trp Ile
 450 455 460
 Thr Tyr Ile Ala Asn Ser Gly Gln Arg Arg Tyr Ile Ala Thr Gly Glu
 465 470 475 480
 Val Asp Ile Ala Gly Asn Arg Ile Ser Ser Phe Gly Lys Phe Ser Ala
 485 490 495
 Val

<210> 16
 <211> 1491
 <212> DNA
 <213> artificial sequence

<220>
 <223> pittti26_prophage SA2 USA

<400> 16
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 caatgctttg attatgccaa tgctgggttg aaagttttgt ttggacatac actgaaaggt 180
 ttaggtgcaa aagatatacc atttgcaaac aatttcgatg gactagctac tgtataccaa 240
 aatacaccgg actttttggc acaaccggc gacatgggtg tattcggtag caattacggg 300
 gcaggatacg gacacgtagc atgggtaatt gaagcaactt tagattatat cattgtatat 360
 gagcagaatt ggctaggcgg tggctggact gacagaatcg aacaaccggg ctgggggttg 420
 gaaaaagtta caagacgaca acatgcttac gatttcccta tgtggtttat ccgtcctaac 480
 ttcaaaagcg ctacagctcc agcttcaata caatctccta cgcaagcatc taaaaaggaa 540
 acagctaagc cacaacctaa agcggtagaa cttaaaatta tcaaagatgt gggttaaagg 600
 catgaccttc ctaaacgtgg tggtaatcct aagggtatag ttattcataa cgacgcagga 660
 agcaaagggg caacagcaga agcgtatcga aacggattag ttaacgcacc ttcatacaaga 720
 ttagaagcgg gtattgcgca tagttatgta tcaggtaaca cagtgtggca agctttagat 780
 gaatcgcaag taggttggca tactgctaac caattaggca ataaatatta ttacggtatt 840
 gaagtgtgtc aatcaatggg agcgggataat gcgacgtttt taaaaaatga acaggcgact 900
 ttccaagaat gcgctagatt gttgaaaaaa tggggattac cagcaaacag aaatacaatc 960
 agattacaca acgaattcac ttcaacatca tgcccacaca gaagctcagt attgcacact 1020
 ggttttgacc cagtaactcg cggctctattg ccagaagaca agcggttgca acttaaagac 1080
 tactttatca agcagattag ggcgtacatg gatggtaaaa taccggttgca cactgtctct 1140
 aatgagtcaa gcgcttcaag taatacagtt aaaccagttg cagagctcat gccaccagt 1200
 ccagcaggtt atacactcga taagaataat gtcccttata aaaaagaaca aggcaattac 1260
 acagtagcta atgttaaagg taataatgta agagacgggtt attcaactaa ttcaagaatt 1320
 acaggggtat taccacaaca cacaacaatt acgtatgacg gtgcatattg tattaatgg 1380
 tatagatgga ttacttatat tgctaatagt ggacaacgct gctatattgc gaccggagag 1440
 gtagacatag caggcaaccg aataagcagt tttggttaagt ttagtgcatg t 1491

<210> 17
 <211> 1491
 <212> DNA
 <213> artificial sequence

<220>
 <223> pittti26_prophage SA2 USA

<400> 17
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 atcgaatggc tgaaaaccag cgaaggcaaa cagttaaacy tggatctgtg gtatggcttt 120
 cagtgtcttg attatgcgaa cgcgggctgg aaagtgtgtt ttggccatac cctgaaaggc 180
 ctggggcgca aagatattcc gtttgcgaaat aactttgatg gcctggccac cgtgtatcag 240
 aacaccccg attttctggc ccagccgggc gatatgggtg tgtttggcag caactatggc 300
 gcgggttatg gccatgtggc gtgggtgatt gaagcgaccc tggattatat catcgtgtac 360

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gaacagaact ggctgggagg tggctggacc gatcgtattg aacagccggg ctggggctgg 420
gaaaaagtga cccgtcgta gcatgcgtac gattttccga tgtggtttat tgcgccgaac 480
tttaaactctg cgacggcccc ggcgagcatt cagagcccga cccaggcgag caaaaaagaa 540
accgcgaaac cgcagccgaa agcgggtggaa ctgaaaatca tcaaagatgt ggtgaaaggc 600
catgatctgc cgaaacgtgg cggcaatccg aaaggcattg tgattcataa cgatgcgggc 660
agcaaaggtg cgaccgcgga agcgtatcgt aacggcctgg tgaacgcgcc gagcagccgt 720
ctggaagcgg gcattgcgca tagctatgtg agcggcaaca ccgtgtggca ggcgctggat 780
gaaagccagg tgggctggca taccgcgaac cagctgggca acaaatatta ttacggcatc 840
gaagtgtgcc agagcatggg cgcggataac gcgacctttc tgaaaaacga acaggcgacc 900
tttcaggaat gcgcgcgtct gctgaaaaaa tggggcctgc cggcgaaccg taacaccatt 960
cgtctgcata acgaatttac cagcaccagc tgcccgcata gtagcagcgt gctgcatacc 1020
ggctttgatc cggtgaccgg tggcctgctg ccggaagata aacgtctgca gctgaaagat 1080
tatttcatca aacaaatccg cgcgtatatg gatggcaaaa ttccggtggc gaccgtgagc 1140
aacgaaagca gcgcgagcag caataccgtg aaaccggtgg cggaaactgat gccgccggtt 1200
ccggccggtt ataccctgga taaaaacaac gtgccgtata aaaaagaaca gggcaactat 1260
accgtggcga acgtgaaagg caacaacgtg cgtgatggct atagcaccaa cagccgtatt 1320
accgcgtgc tgcggaacaa caccaccatt acctatgatg gcgcgtattg cattaacggc 1380
tatcgctgga ttacctatat cgcgaacagc ggccagcgtc gttatattgc gaccggcgaa 1440
gtggatattg cgggcaaccg tattagcagc tttggtaaat ttagcgcggt g 1491

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<210> 18
<211> 497
<212> PRT
<213> artificial sequence

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<220>
<223> pitt26_prophage SA2 USA

```

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<400> 18
Met Ala Ser Ile Ile Met Glu Val Ala Thr Met Gln Ala Lys Leu Thr
1          5          10          15
Lys Lys Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys Gln Phe
20          25          30
Asn Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala
35          40          45
Gly Trp Lys Val Leu Phe Gly His Thr Leu Lys Gly Leu Gly Ala Lys
50          55          60
Asp Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln
65          70          75          80
Asn Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly
85          90          95
Ser Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala
100         105         110
Thr Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly
115         120         125
Trp Thr Asp Arg Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr
130         135         140
Arg Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn
145         150         155         160
Phe Lys Ser Ala Thr Ala Pro Ala Ser Ile Gln Ser Pro Thr Gln Ala
165         170         175
Ser Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys
180         185         190
Ile Ile Lys Asp Val Val Lys Gly His Asp Leu Pro Lys Arg Gly Gly
195         200         205
Asn Pro Lys Gly Ile Val Ile His Asn Asp Ala Gly Ser Lys Gly Ala
210         215         220
Thr Ala Glu Ala Tyr Arg Asn Gly Leu Val Asn Ala Pro Leu Ser Arg
225         230         235         240
Leu Glu Ala Gly Ile Ala His Ser Tyr Val Ser Gly Asn Thr Val Trp

```



```

ggctttgatc cggtgacccg tggcctgctg ccggaagata aacagctgca gctgaaagat 1080
tatttcatca aacaaatccg cgtgtatatg gatggcaaaa ttccggtggc gaccgtgagc 1140
aacgaaagca gcgcgagcag caataccgtg aaaccggtgg cggaactgat gccgccggtt 1200
ccggccggtt ataccttgga taaaaacaac gtgccgtata aaaaagaaca gggcaactat 1260
accgtggcga acgtgaaagg caacaacgtg cgtgatggct atagcaccaa cagccgtatt 1320
accggcgtgc tgccgaacaa caccaccatt acctatgatg gcgcgtattg cattaacggc 1380
tatcgctgga ttacctatat cgcgacacgc ggccagcgtc gttatattgc gaccggcgaa 1440
gtggatattg cgggcaaccg tattagcagc tttggtaaat ttagcgcggt gtaataa 1497

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<210> 20
<211> 520
<212> PRT
<213> artificial sequence

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<220>
<223> pittti26 lysostaphin

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<400> 20
Met Ala Ser Ile Ile Met Glu Val Ala Thr Met Gln Ala Lys Leu Thr
1          5          10          15
Lys Lys Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys Gln Phe
20          25          30
Asn Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala
35          40          45
Gly Trp Lys Val Leu Phe Gly His Thr Leu Lys Gly Leu Gly Ala Lys
50          55          60
Asp Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln
65          70          75          80
Asn Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly
85          90          95
Ser Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala
100         105         110
Thr Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly
115         120         125
Trp Thr Asp Arg Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr
130         135         140
Arg Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn
145         150         155         160
Phe Lys Ser Ala Thr Ala Pro Ala Ser Ile Gln Ser Pro Thr Gln Ala
165         170         175
Ser Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys
180         185         190
Ile Ile Lys Asp Val Val Lys Gly His Asp Leu Pro Lys Arg Gly Gly
195         200         205
Asn Pro Lys Gly Ile Val Ile His Asn Asp Ala Gly Ser Lys Gly Ala
210         215         220
Thr Ala Glu Ala Tyr Arg Asn Gly Leu Val Asn Ala Pro Ser Ser Arg
225         230         235         240
Leu Glu Ala Gly Ile Ala His Ser Tyr Val Ser Gly Asn Thr Val Trp
245         250         255
Gln Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Leu
260         265         270
Gly Asn Lys Tyr Tyr Tyr Gly Ile Glu Val Cys Gln Ser Met Gly Ala
275         280         285
Asp Asn Ala Thr Phe Leu Lys Asn Glu Gln Ala Thr Phe Gln Glu Cys
290         295         300
Ala Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile
305         310         315         320
Arg Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser
325         330         335

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Val Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu
340 345 350
Asp Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala
355 360 365
Tyr Met Asp Gly Lys Ile Pro Val Ala Thr Val Ser Asn Glu Ser Ser
370 375 380
Ala Ser Ser Asn Thr Val Lys Pro Val Ala Glu Leu Met Ser Asn Ser
385 390 395 400
Thr Ala Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys
405 410 415
Ala Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn
420 425 430
Lys Tyr Gly Thr Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn
435 440 445
Thr Asp Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met Pro Gln
450 455 460
Ser Gly Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu Val Met
465 470 475 480
Lys Gln Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln
485 490 495
Arg Ile Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu
500 505 510
Gly Val Leu Trp Gly Thr Ile Lys
515 520

<210> 21
<211> 1563
<212> DNA
<213> artificial sequence

<220>
<223> pittti26 lysostaphin

<400> 21
atggcaagta tcatcatgga ggtggcgaca atgcaagcaa aattaactaa aaaagagttt 60
atagagtggg tgaaaacttc tgagggaaaa caattcaatg tggacttatg gtatggattt 120
caatgctttg attatgccaa tgctggttgg aaagttttgt ttggacatac actgaaaggt 180
ttaggtgcaa agatataacc atttgcaaac aatttcgatg gactagctac tgtataccaa 240
aatacaccgg actttttggc acaaccggcg gacatgggtg tattcggtag caattacggg 300
gcaggatacg gacacgtagc atgggtaatt gaagcaactt tagattatat cattgtatat 360
gagcagaatt ggctaggcgg tggctggact gacagaatcg aacaaccggg ctgggggttg 420
gaaaaagtta caagacgaca acatgcttac gatttcccta tgtggtttat ccgtccctaac 480
ttcaaaagcg ctacagctcc agcttcaata caatctccta cgcaagcatc taaaaaggaa 540
acagctaagc cacaacctaa agcggtagaa cttaaaatta tcaaagatgt ggttaaagggt 600
catgaccttc ctaaaogtgg tggtaatcct aagggtatag ttattcataa cgacgcagga 660
agcaaagggg caacagcaga agcgtatcga aacggattag ttaacgcacc ttcatcaaga 720
ttagaagcgg gtattgcgca tagttatgta tcaggtaaca cagtgtggca agcttttagat 780
gaatcgcaag taggttggca tactgctaac caattaggca ataaatatta ttacggtatt 840
gaagtgtgtc aatcaatggg agcggataat gcgacgtttt taaaaaatga acaggcgact 900
ttccaagaat gcgctagatt gttgaaaaaa tggggattac cagcaaacag aaatacaatc 960
agattacaca acgaattcac ttcaacatca tgcccacaca gaagctcagt attgcacact 1020
ggttttgacc cagtaactcg cggctctattg ccagaagaca agcggttgca acttaaagac 1080
tactttatca agcagattag ggcgtacatg gatggtaaaa taccggttgc cactgtctct 1140
aatgagtcaa gcgcttcaag taatacagtt aaaccagttg cagagctcat gtctaatagc 1200
accgcgcagg acccgatgcc gttcttgaag tcggcgggct atggcaaagc aggcggcacc 1260
gtgactccga ccccgaaacac gggctggaaa accaacaagt acggtactct ttacaaaagc 1320
gagagcgcac cttttacgcc aaacacggac atcatcacgc gcaccaccgg cccatttcgc 1380
agcatgccac agagcggcgt cttgaaaagcg ggccagacca ttactacga tgaagttatg 1440
aaacaggacg gccatgtgtg ggtgggctat accggcaaca gcggccagcg tattttattta 1500
ccggttcgca cctggaataa aagcaccaat accttaggcg tggtatgggg taccattaag 1560

<210> 22
 <211> 521
 <212> PRT
 <213> artificial sequence

<220>
 <223> pittti26 ALE1

<400> 22
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 Lys Lys Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys Gln Phe
 20 25 30
 Asn Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala
 35 40 45
 Gly Trp Lys Val Leu Phe Gly His Thr Leu Lys Gly Leu Gly Ala Lys
 50 55 60
 Asp Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln
 65 70 75 80
 Asn Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly
 85 90 95
 Ser Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala
 100 105 110
 Thr Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly
 115 120 125
 Trp Thr Asp Arg Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr
 130 135 140
 Arg Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn
 145 150 155 160
 Phe Lys Ser Ala Thr Ala Pro Ala Ser Ile Gln Ser Pro Thr Gln Ala
 165 170 175
 Ser Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys
 180 185 190
 Ile Ile Lys Asp Val Val Lys Gly His Asp Leu Pro Lys Arg Gly Gly
 195 200 205
 Asn Pro Lys Gly Ile Val Ile His Asn Asp Ala Gly Ser Lys Gly Ala
 210 215 220
 Thr Ala Glu Ala Tyr Arg Asn Gly Leu Val Asn Ala Pro Ser Ser Arg
 225 230 235 240
 Leu Glu Ala Gly Ile Ala His Ser Tyr Val Ser Gly Asn Thr Val Trp
 245 250 255
 Gln Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Leu
 260 265 270
 Gly Asn Lys Tyr Tyr Tyr Gly Ile Glu Val Cys Gln Ser Met Gly Ala
 275 280 285
 Asp Asn Ala Thr Phe Leu Lys Asn Glu Gln Ala Thr Phe Gln Glu Cys
 290 295 300
 Ala Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile
 305 310 315 320
 Arg Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser
 325 330 335
 Val Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu
 340 345 350
 Asp Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala
 355 360 365
 Tyr Met Asp Gly Lys Ile Pro Val Ala Thr Val Ser Asn Glu Ser Ser
 370 375 380
 Ala Ser Ser Asn Thr Val Lys Pro Val Ala Glu Leu Met Asn Ser Phe

<220>

<223> Lysostaphin

<400> 24

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Ser Asn Ser Thr Ala Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly
1          5          10          15
Tyr Gly Lys Ala Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp
          20          25          30
Lys Thr Asn Lys Tyr Gly Thr Leu Tyr Lys Ser Glu Ser Ala Ser Phe
          35          40          45
Thr Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser
          50          55          60
Met Pro Gln Ser Gly Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp
65          70          75          80
Glu Val Met Lys Gln Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn
          85          90          95
Ser Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr
          100          105          110
Asn Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
          115          120
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<210> 25

<211> 372

<212> DNA

<213> unknown

<220>

<223> Lysostaphin

<400> 25

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tacaaaagcg agagcgcac ttttacgcc aacacggaca tcatcacgcg caccaccggc      180
ccatttcgca gcatgccaca gagcggcgtc ttgaaagcgg gccagaccat tcactacgat      240
gaagttatga aacaggacgg ccatgtgtgg gtgggctata ccggcaacag cggccagcgt      300
atttatttac cggttcgcac ctggaataaa agcaccaata ccttaggcgt gttatgggg      360
accattaagt aa                                     372
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<210> 26

<211> 124

<212> PRT

<213> unknown

<220>

<223> AL1

<400> 26

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Asn Ser Phe Ser Asn Asn Thr Ala Gln Asp Pro Met Pro Phe Leu Lys
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Ser Ala Gly Tyr Gly Ser Asn Ser Thr Ser Ser Ser Asn Asn Asn Gly
          20          25          30
Tyr Lys Thr Asn Lys Tyr Gly Thr Leu Tyr Lys Ser Glu Ser Ala Ser
          35          40          45
Phe Thr Ala Asn Thr Asp Ile Ile Thr Arg Leu Thr Gly Pro Phe Arg
          50          55          60
Ser Met Pro Gln Ser Gly Val Leu Arg Lys Gly Leu Thr Ile Lys Tyr
65          70          75          80
Asp Glu Val Met Lys Gln Asp Gly His Val Trp Val Gly Tyr Asn Thr
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				85						90						95			
Asn	Ser	Gly	Lys	Arg	Val	Tyr	Leu	Pro	Val	Arg	Thr	Trp	Asn	Glu	Ser				
			100					105					110						
Thr	Gly	Glu	Leu	Gly	Pro	Leu	Trp	Gly	Thr	Ile	Lys								
		115					120												

<210> 27
 <211> 375
 <212> DNA
 <213> unknown

<220>
 <223> ALE1

<400> 27
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 ggtagcaaca gcaccagcag cagcaacaat aacggttaca agaccaacaa gtacggcacg 120
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 ggtccgttcc gcagcatgcc gcagagcggg gttttacgca aaggcttaac gattaaatat 240
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 Gly Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly Ala Lys
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 Thr Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly
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 Ser Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys
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 Ile Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly Gly
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 Asn Pro Lys Gly Ile Val Ile His Asn Asp Ala Gly Ser Lys Gly Ala

