

SHK-HTB-023PC_-_SequenceListing.txt
SEQUENCE LISTING

<110> Heat Biologics, Inc.

<120> COMPOSITIONS AND METHODS FOR ADJOINING TYPE I AND TYPE II
EXTRACELLULAR DOMAINS AS HETEROLOGOUS CHIMERIC PROTEINS

<130> SHK-HTB-023PC

<150> US 62/235,727

<151> 2015-10-01

<150> US 62/263,313

<151> 2015-12-04

<150> US 62/372,574

<151> 2016-08-09

<160> 78

<170> PatentIn version 3.5

<210> 1

<211> 1605

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic sequence

<400> 1

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ctgctcgtgg tgaccgaagg ggacaacgcc accttcacct gcagcttctc caacacatcg	180
gagagcttcg tgctaaactg gtaccgcatg agccccagca accagacgga caagctggcc	240
gccttccccg aggaccgcag ccagcccggc caggactgcc gcttccgtgt cacacaactg	300
cccaacgggc gtgacttcca catgagcgtg gtcagggccc ggcgcaatga cagcggcacc	360
tacctctgtg gggccatctc cctggcccc aaggcgcaga tcaaagagag cctgcgggca	420
gagctcaggg tgacagagag aagggcagaa gtgcccacag cccaccccag cccctcacc	480
aggccagccg gccagttcca atctaagtac ggccctccct gccctagctg tccgcccct	540
gaatttctgg gcggaccctc cgtgtttctg ttcccccaa agcccaagga caccctgatg	600

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gaggaacagt tcaacagcac ctaccgggtg gtgtctgtgc tgaccgtgct gcaccaggat      780
tggctgagcg gcaaagagta caagtgaag gtgtccagca agggcctgcc cagcagcatc      840
gaaaagacca tcagcaacgc caccggccag cccagggaac cccagggtga cacactgccc      900
cctagccagg aagagatgac caagaaccag gtgtccctga catgcctcgt gaagggttc      960
taccctccg atatcgccgt ggaatgggag agcaacggcc agccagagaa caactacaag     1020
accaccccc cagtgtgga cagcgacggc tcattcttcc tgtactcccg gctgacagt      1080
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aacaactcag tcatcatcaa ctgtgatggg ttttatctca tctccctgaa gggctacttc     1380
tcccaggaag tcaacattag ctttcattac cagaaggatg aggagcccct cttccaactg     1440
aagaaggatc ggtctgtcaa ctcttgatg gtggcctctc tgacttaca agacaaagtc     1500
tacttgaatg tgaccactga caatacctcc ctggatgact tccatgtgaa tggcggagaa     1560
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<210> 2
 <211> 534
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic sequence

<400> 2

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Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
 20 25 30

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Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp
35 40 45

Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
50 55 60

Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65 70 75 80

Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
85 90 95

Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
100 105 110

Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
115 120 125

Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
130 135 140

Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
145 150 155 160

Arg Pro Ala Gly Gln Phe Gln Ser Lys Tyr Gly Pro Pro Cys Pro Ser
165 170 175

Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
180 185 190

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
195 200 205

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
210 215 220

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

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Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
245 250 255

Leu His Gln Asp Trp Leu Ser Gly Lys Glu Tyr Lys Cys Lys Val Ser
260 265 270

Ser Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Asn Ala Thr
275 280 285

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
290 295 300

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
305 310 315 320

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
325 330 335

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
340 345 350

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Ser Trp Gln Glu Gly
355 360 365

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
370 375 380

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Ile Glu Gly Arg Met
385 390 395 400

Asp Gln Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val Gln
405 410 415

Phe Thr Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys
420 425 430

Glu Asp Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn Cys
435 440 445

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Asp Gly Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val
450 455 460

Asn Ile Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu
465 470 475 480

Lys Lys Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr Tyr
485 490 495

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

Asp Phe His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro
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Gly Glu Phe Cys Val Leu
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<210> 3
<211> 1782
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence

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ctgctgggtc tgaccgaggg cgacaatgcc accttcacct gtagcttcag caacaccagc 180
gagagcttcg tgctgaactg gtacagaatg agccccagca accagaccga caagctggcc 240
gccttccccg aggatagatc tcagcccggc caggactgcc gggtcagagt gaccagctg 300
cccaacggcc gggacttcca catgtctgtc gtgcgggcca gacggaacga cagcggcaca 360
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gagctgagag tgaccgagag aagggccgaa gtgcctaccg cccaccctag cccatctcca 480
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gaattttctgg gcggaaccag cgtgttcctg ttccccccaa agcccaagga caccctgatg	600
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gtgcagttca attggtacgt ggacggcgtg gaagtgcaca acgccaagac caagcccaga	720
gaggaacagt tcaacagcac ctaccgggtg gtgtccgtgc tgaccgtgct gcaccaggat	780
tggctgagcg gcaaagagta caagtgaag gtgtccagca agggcctgcc cagcagcatc	840
gagaaaacca tcagcaacgc caccggccag cccagggaac cccagggtgta cacactgccc	900
cctagccagg aagagatgac caagaaccag gtgtccctga cctgtctcgt gaagggttc	960
taccctccg atatcgccgt ggaatgggag agcaacggcc agcctgagaa caactacaag	1020
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gacaagagca gctggcagga aggcaacgtg ttcagctgct ccgtgatgca cgaggccctg	1140
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tgggagcacg agctgggcct ggccttcacc aagaacagaa tgaactacac caacaagttt	1440
ctgctgatcc ccgagagcgg cgactacttc atctacagcc aagtgacctt ccggggcatg	1500
accagcgagt gcagcgagat cagacaggcc ggcagacctt acaagcccga cagcatcacc	1560
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aagagcgtgt gcgaagtggg cagcaactgg ttccagccca tctacctggg cgccatgttc	1680
agtctgcaag agggcgataa gctgatggtc aacgtgtccg acatctccct ggtggattac	1740
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<210> 4
 <211> 1782
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic sequence

 <400> 4

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gagagcttcg tgctaaactg gtaccgcatg agccccagca accagacgga caagctggcc	240
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taccctccg atatcgccgt ggaatgggag agcaacggcc agccagagaa caactacaag	1020
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gacaagagca gctggcagga aggcaacgtg ttcagctgca gcgtgatgca cgaagccctg	1140
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gtgggtcatca ccaaggtaac agacagctac cctgagccaa cccagctcct catggggacc 1620
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acaaaagaag ataaaacctt ctttgagacc ttcttactat ag 1782

<210> 5
<211> 593
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 5

Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
1 5 10 15

Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
20 25 30

Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp
35 40 45

Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
50 55 60

Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65 70 75 80

Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
85 90 95

Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
100 105 110

Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
115 120 125

Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val

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130

135

140

Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
 145 150 155 160

Arg Pro Ala Gly Gln Phe Gln Ser Lys Tyr Gly Pro Pro Cys Pro Ser
 165 170 175

Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 180 185 190

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 195 200 205

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
 210 215 220

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

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 245 250 255

Leu His Gln Asp Trp Leu Ser Gly Lys Glu Tyr Lys Cys Lys Val Ser
 260 265 270

Ser Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Asn Ala Thr
 275 280 285

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
 290 295 300

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 305 310 315 320

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 325 330 335

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

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340

345

350

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Ser Trp Gln Glu Gly
355 360 365

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
370 375 380

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Ile Glu Gly Arg Met
385 390 395 400

Asp Arg Ala Gln Gly Glu Ala Cys Val Gln Phe Gln Ala Leu Lys Gly
405 410 415

Gln Glu Phe Ala Pro Ser His Gln Gln Val Tyr Ala Pro Leu Arg Ala
420 425 430

Asp Gly Asp Lys Pro Arg Ala His Leu Thr Val Val Arg Gln Thr Pro
435 440 445

Thr Gln His Phe Lys Asn Gln Phe Pro Ala Leu His Trp Glu His Glu
450 455 460

Leu Gly Leu Ala Phe Thr Lys Asn Arg Met Asn Tyr Thr Asn Lys Phe
465 470 475 480

Leu Leu Ile Pro Glu Ser Gly Asp Tyr Phe Ile Tyr Ser Gln Val Thr
485 490 495

Phe Arg Gly Met Thr Ser Glu Cys Ser Glu Ile Arg Gln Ala Gly Arg
500 505 510

Pro Asn Lys Pro Asp Ser Ile Thr Val Val Ile Thr Lys Val Thr Asp
515 520 525

Ser Tyr Pro Glu Pro Thr Gln Leu Leu Met Gly Thr Lys Ser Val Cys
530 535 540

Glu Val Gly Ser Asn Trp Phe Gln Pro Ile Tyr Leu Gly Ala Met Phe

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545 550 555 560

Ser Leu Gln Glu Gly Asp Lys Leu Met Val Asn Val Ser Asp Ile Ser
565 570 575

Leu Val Asp Tyr Thr Lys Glu Asp Lys Thr Phe Phe Gly Ala Phe Leu
580 585 590

Leu

<210> 6
<211> 1554
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 6
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gatcccaggagg tgcagttcaa ttggtacgtg gacgggggtg aagtgacaaa cgccaagacc 660
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caccaggatt ggctgagcgg caaagagtac aagtgaagg tgtccagcaa gggcctgccc 780
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aactacaaga ccaccccccc agtgctggac agcgacggct cattcttcct gtactcccgg     1020
ctgacagtgg acaagagcag ctggcaggaa ggcaacgtgt tcagctgcag cgtgatgcac     1080
gaagccctgc acaaccacta caccagaag tccctgagcc tgtccctggg caaaatagag     1140
ggacgaatgg accaggtatc acatcggtat cctcgaattc aaagtatcaa agtacaattt     1200
accgaatata agaaggagaa aggtttcatc ctcaattccc aaaaggagga tgaaatcatg     1260
aaggtgcaga acaactcagt catcatcaac tgtgatgggt tttatctcat ctccctgaag     1320
ggctacttct ccaggaagt caacattagc cttcattacc agaaggatga ggagcccctc     1380
ttccaactga agaaggtcag gtctgtcaac tccttgatgg tggcctctct gacttacaaa     1440
gacaaagtct acttgaatgt gaccactgac aatacctccc tggatgactt ccatgtgaat     1500
ggcggagaac tgattcttat ccatcaaaat cctggatgaat tctgtgtcct ttga         1554

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<210> 7
 <211> 517
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic sequence

<400> 7

Met	Lys	Thr	Leu	Pro	Ala	Met	Leu	Gly	Thr	Gly	Lys	Leu	Phe	Trp	Val
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Phe	Phe	Leu	Ile	Pro	Tyr	Leu	Asp	Ile	Trp	Asn	Ile	His	Gly	Lys	Glu
		20						25					30		

Ser	Cys	Asp	Val	Gln	Leu	Tyr	Ile	Lys	Arg	Gln	Ser	Glu	His	Ser	Ile
		35					40					45			

Leu	Ala	Gly	Asp	Pro	Phe	Glu	Leu	Glu	Cys	Pro	Val	Lys	Tyr	Cys	Ala
	50					55					60				

Asn	Arg	Pro	His	Val	Thr	Trp	Cys	Lys	Leu	Asn	Gly	Thr	Thr	Cys	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu

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275

280

285

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
290 295 300

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
305 310 315 320

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
325 330 335

Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Ser Trp Gln Glu Gly Asn
340 345 350

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
355 360 365

Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Ile Glu Gly Arg Met Asp
370 375 380

Gln Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val Gln Phe
385 390 395 400

Thr Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys Glu
405 410 415

Asp Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn Cys Asp
420 425 430

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

Ile Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys
450 455 460

Lys Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr Tyr Lys
465 470 475 480

Asp Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu Asp Asp

Phe His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly
 500 505 510

Glu Phe Cys Val Leu
 515

<210> 8
 <211> 1527
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic sequence

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 atcatcttac aatgtcacct ctctccacc acggcacaag tgacccagggt caactgggag 180
 cagcaggacc agcttctggc catttgtaat gctgacttgg ggtggcacat ctccccatcc 240
 ttcaaggatc gagtggcccc aggtcccggc ctgggcctca ccctccagtc gctgaccgtg 300
 aacgatacag gggagtactt ctgcatctat cacacctacc ctgatgggac gtacactggg 360
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aagtcctga gcctgtccct gggcaaaata gagggacgaa tggaccaggt atcacatcgg 1140
tattctcgaa ttcaaagtat caaagtacaa tttaccgaat ataagaagga gaaaggtttc 1200
atcctcactt cccaaaagga ggatgaaatc atgaagggtgc agaacaactc agtcatcatc 1260
aactgtgatg ggttttatct catctccctg aagggtact tctcccagga agtcaacatt 1320
agccttcatt accagaagga tgaggagccc ctctccaac tgaagaaggt caggtctgtc 1380
aactccttga tgggtggcctc tctgacttac aaagacaaag tctacttgaa tgtgaccact 1440
gacaatacct ccctggatga cttccatgtg aatggcggag aactgattct tatccatcaa 1500
aatcctgggtg aattctgtgt cctttga 1527

<210> 9
<211> 508
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 9

Met Arg Trp Cys Leu Leu Leu Ile Trp Ala Gln Gly Leu Arg Gln Ala
1 5 10 15

Pro Leu Ala Ser Gly Met Met Thr Gly Thr Ile Glu Thr Thr Gly Asn
20 25 30

Ile Ser Ala Glu Lys Gly Gly Ser Ile Ile Leu Gln Cys His Leu Ser
35 40 45

Ser Thr Thr Ala Gln Val Thr Gln Val Asn Trp Glu Gln Gln Asp Gln
50 55 60

Leu Leu Ala Ile Cys Asn Ala Asp Leu Gly Trp His Ile Ser Pro Ser
65 70 75 80

Phe Lys Asp Arg Val Ala Pro Gly Pro Gly Leu Gly Leu Thr Leu Gln

85

90

95

Ser Leu Thr Val Asn Asp Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr
 100 105 110

Tyr Pro Asp Gly Thr Tyr Thr Gly Arg Ile Phe Leu Glu Val Leu Glu
 115 120 125

Ser Ser Val Ala Glu His Gly Ala Arg Phe Gln Ile Pro Ser Lys Tyr
 130 135 140

Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
 145 150 155 160

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 165 170 175

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
 180 185 190

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 195 200 205

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
 210 215 220

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Ser Gly Lys Glu
 225 230 235 240

Tyr Lys Cys Lys Val Ser Ser Lys Gly Leu Pro Ser Ser Ile Glu Lys
 245 250 255

Thr Ile Ser Asn Ala Thr Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 260 265 270

Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
 275 280 285

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu

SHK-HTB-023PC_-_SequenceListing.txt

290

295

300

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 305 310 315 320

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
 325 330 335

Ser Ser Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 340 345 350

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
 355 360 365

Lys Ile Glu Gly Arg Met Asp Gln Val Ser His Arg Tyr Pro Arg Ile
 370 375 380

Gln Ser Ile Lys Val Gln Phe Thr Glu Tyr Lys Lys Glu Lys Gly Phe
 385 390 395 400

Ile Leu Thr Ser Gln Lys Glu Asp Glu Ile Met Lys Val Gln Asn Asn
 405 410 415

Ser Val Ile Ile Asn Cys Asp Gly Phe Tyr Leu Ile Ser Leu Lys Gly
 420 425 430

Tyr Phe Ser Gln Glu Val Asn Ile Ser Leu His Tyr Gln Lys Asp Glu
 435 440 445

Glu Pro Leu Phe Gln Leu Lys Lys Val Arg Ser Val Asn Ser Leu Met
 450 455 460

Val Ala Ser Leu Thr Tyr Lys Asp Lys Val Tyr Leu Asn Val Thr Thr
 465 470 475 480

Asp Asn Thr Ser Leu Asp Asp Phe His Val Asn Gly Gly Glu Leu Ile
 485 490 495

Leu Ile His Gln Asn Pro Gly Glu Phe Cys Val Leu

<210> 10
 <211> 1710
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic sequence

<400> 10
 atgtttttcac atcttccctt tgactgtgtc ctgctgctgc tgctgctact acttacaagg 60
 tcctcagaag tggaatacag agcggaggtc ggtcagaatg cctatctgcc ctgcttctac 120
 accccagccg ccccagggaa cctcgtgccc gtctgtctggg gcaaaggagc ctgtcctgtg 180
 tttgaatgtg gcaacgtggt gctcaggact gatgaaaggg atgtgaatta ttggacatcc 240
 agatactggc taaatgggga tttccgcaaa ggagatgtgt ccctgaccat agagaatgtg 300
 actctagcag acagtgggat ctactgctgc cggatccaaa tcccaggcat aatgaatgat 360
 gaaaaattta acctgaagtt ggtcatcaaa ccagccaagg tcacccctgc accgactcgg 420
 cagagagact tcaactgcagc ctttccaagg atgcttacca ccaggggaca tggcccagca 480
 gagacacaga cactgggggag cctccctgat ataaatctaa cacaaatatc cacattggcc 540
 aatgagttac gggactctag attggccaat gacttacggg actctggagc aaccatcaga 600
 ataggctcta agtacggccc tccctgccct agctgtcccg cccctgaatt tctgggcgga 660
 ccctccgtgt ttctgttccc cccaaagccc aaggacaccc tgatgatcag ccggaccccc 720
 gaagtgcact gtgtgggtgtt ggatgtgtcc caggaagatc ccgagggtgca gttcaattgg 780
 tacgtggacg ggggtggaagt gcacaacgcc aagaccaagc ccagagagga acagttcaac 840
 agcacctacc ggggtggtgtc tgtgctgacc gtgctgcacc aggattggct gagcggcaaa 900
 gagtacaagt gcaagggtgtc cagcaagggc ctgcccagca gcatcgaaaa gaccatcagc 960
 aacgccaccg gccagcccag ggaaccccag gtgtacacac tgccccctag ccaggaagag 1020
 atgaccaaga accaggtgtc cctgacatgc ctctgtgaagg gcttctaccc ctccgatatc 1080
 gccgtggaat gggagagcaa cggccagcca gagaacaact acaagaccac cccccagtg 1140
 ctggacagcg acggctcatt cttcctgtac tcccggctga cagtggacaa gagcagctgg 1200

SHK-HTB-023PC_-_SequenceListing.txt

caggaaggca acgtgttcag ctgcagcgtg atgcacgaag ccctgcacaa ccactacacc 1260
cagaagtccc tgagcctgtc cctgggcaaa atagaggggac gaatggacca ggtatcacat 1320
cggatcctc gaattcaaag tatcaaagta caatttaccg aatataagaa ggagaaaggt 1380
ttcatcctca cttcccaaaa ggaggatgaa atcatgaagg tgcagaacaa ctcagtcatc 1440
atcaactgtg atgggtttta tctcatctcc ctgaagggtt acttctccca ggaagtcaac 1500
attagccttc attaccagaa ggatgaggag cccctcttcc aactgaagaa ggtcagggtc 1560
gtcaactcct tgatgggtggc ctctctgact tacaagaca aagtctactt gaatgtgacc 1620
actgacaata cctccctgga tgacttccat gtgaatggcg gagaactgat tcttatccat 1680
caaaatcctg gtgaattctg tgcctttga 1710

<210> 11
<211> 569
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 11

Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu
1 5 10 15

Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
20 25 30

Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
35 40 45

Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
50 55 60

Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
65 70 75 80

Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
85 90 95

SHK-HTB-023PC_-_SequenceListing.txt

Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
100 105 110

Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
115 120 125

Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Arg Gln Arg Asp Phe
130 135 140

Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
145 150 155 160

Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
165 170 175

Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
180 185 190

Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly Ser Lys Tyr Gly Pro Pro
195 200 205

Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
210 215 220

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
225 230 235 240

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
245 250 255

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
260 265 270

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
275 280 285

Leu Thr Val Leu His Gln Asp Trp Leu Ser Gly Lys Glu Tyr Lys Cys
290 295 300

SHK-HTB-023PC_-_SequenceListing.txt

Lys Val Ser Ser Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
305 310 315 320

Asn Ala Thr Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
325 330 335

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
340 345 350

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
355 360 365

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
370 375 380

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Ser Trp
385 390 395 400

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
405 410 415

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Ile Glu
420 425 430

Gly Arg Met Asp Gln Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile
435 440 445

Lys Val Gln Phe Thr Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr
450 455 460

Ser Gln Lys Glu Asp Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile
465 470 475 480

Ile Asn Cys Asp Gly Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser
485 490 495

Gln Glu Val Asn Ile Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu
500 505 510

SHK-HTB-023PC_-_SequenceListing.txt

Phe Gln Leu Lys Lys Val Arg Ser Val Asn Ser Leu Met Val Ala Ser
515 520 525

Leu Thr Tyr Lys Asp Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr
530 535 540

Ser Leu Asp Asp Phe His Val Asn Gly Gly Glu Leu Ile Leu Ile His
545 550 555 560

Gln Asn Pro Gly Glu Phe Cys Val Leu
565

<210> 12
<211> 2223
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 12
atggagcccc cccgcccggc ccccggccgc ctcgggcccgc tgctctgcct gctgctcgcc 60
gcgtcctgcg cctggtcagg agtggcgggt gaggaggagc tgcaggtgat tcagcctgac 120
aagtccgtgt tggttgcagc tggagagaca gccactctgc gctgcactgc gacctctctg 180
atccctgtgg ggcccatcca gtggttcaga ggagctggac caggccggga attaatctac 240
aatcaaaaag aaggccactt cccccgggta acaactgttt cagacctcac aaagagaaac 300
aacatggact tttccatccg catcggtaac atcacccag cagatgccgg cacctactac 360
tgtgtgaagt tccggaaagg gagccccgat gacgtggagt ttaagtctgg agcaggcact 420
gagctgtctg tgcgcgcaa accctctgcc cccgtgggtat cgggccctgc ggcgagggcc 480
acacctcagc acacagtgag cttcacctgc gagtccacg gcttctcacc cagagacatc 540
accctgaaat ggttcaaaaa tgggaatgag ctctcagact tccagaccaa cgtggacccc 600
gtaggagaga gcgtgtccta cagcatccac agcacagcca aggtggtgct gacccgcgag 660
gacgttcact ctcaagtcac ctgcgagggtg gcccacgtca ccttgagggg ggacctctt 720
cgtgggactg ccaacttgtc tgagaccatc cgagttccac ccaccttgga ggttactcaa 780

SHK-HTB-023PC_-_SequenceListing.txt

cagcccgtga gggcagagaa ccaggtgaat gtcacctgcc aggtgaggaa gttctacccc	840
cagagactac agctgacctg gttggagaat ggaaacgtgt cccggacaga aacggcctca	900
accgttacag agaacaagga tggtagctac aactggatga gctggctcct ggtgaatgta	960
tctgcccaca gggatgatgt gaagctcacc tgccaggtgg agcatgacgg gcagccagcg	1020
gtcagcaaaa gccatgacct gaaggtctca gcccacccga aggagcaggg ctcaaatacc	1080
gccgctgaga aactggatc taatgaacgg aacatctatt ctaagtacgg ccctccctgc	1140
cctagctgtc ccgcccctga atttctgggc ggaccctccg tgtttctgtt cccccaaag	1200
cccaaggaca ccctgatgat cagccggacc cccgaagtga cctgtgtggt ggtggatgtg	1260
tcccaggaag atcccaggt gcagttcaat tggtagctgg acggggtgga agtgacacaac	1320
gccaagacca agcccagaga ggaacagttc aacagcacct accgggtggt gtctgtgctg	1380
accgtgctgc accaggattg gctgagcggc aaagagtaca agtgcaagg gtccagcaag	1440
ggcctgcccga gcagcatcga aaagaccatc agcaacgccca ccggccagcc cagggaaccc	1500
caggtgtaca cactgcccc tagccaggaa gagatgacca agaaccagggt gtccctgaca	1560
tgccctgtga agggcttcta cccctccgat atcgccgtgg aatgggagag caacggccag	1620
ccagagaaca actacaagac cccccccca gtgctggaca gcgacggctc attcttcctg	1680
tactcccggc tgacagtgga caagagcagc tggcaggaag gcaacgtgtt cagctgcagc	1740
gtgatgcacg aagccctgca caaccactac acccagaagt ccctgagcct gtccctgggc	1800
aaaatagagg gacgaatgga ccaggtatca catcggatc ctcgaattca aagtatcaaa	1860
gtacaattta ccgaatataa gaaggagaaa ggtttcatcc tcaattccca aaaggaggat	1920
gaaatcatga aggtgcagaa caactcagtc atcatcaact gtgatgggtt ttatctcatc	1980
tccctgaagg gctacttctc ccaggaagtc aacattagcc ttattacca gaaggatgag	2040
gagcccctct tccaactgaa gaaggtcagg tctgtcaact ccttgatggt ggctctctg	2100
acttacaag acaaagtcta cttgaatgtg accactgaca atacctccct ggatgacttc	2160
catgtgaatg gcggagaact gattcttata catcaaaatc ctggtgaatt ctgtgtcctt	2220
tga	2223

SHK-HTB-023PC_-_SequenceListing.txt

<211> 740

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence

<400> 13

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30

Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala Ala Gly
35 40 45

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly
50 55 60

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr
65 70 75 80

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
85 90 95

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125

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

Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala
145 150 155 160

Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser
165 170 175

SHK-HTB-023PC_-_SequenceListing.txt

Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser
180 185 190

Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser
195 200 205

Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser
210 215 220

Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu
225 230 235 240

Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu
245 250 255

Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr
260 265 270

Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu
275 280 285

Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu
290 295 300

Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val
305 310 315 320

Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp
325 330 335

Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His
340 345 350

Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn
355 360 365

Glu Arg Asn Ile Tyr Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro
370 375 380

SHK-HTB-023PC_-_SequenceListing.txt

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
385 390 395 400

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
405 410 415

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
420 425 430

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
435 440 445

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
450 455 460

Gln Asp Trp Leu Ser Gly Lys Glu Tyr Lys Cys Lys Val Ser Ser Lys
465 470 475 480

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Asn Ala Thr Gly Gln
485 490 495

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
500 505 510

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
515 520 525

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
530 535 540

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
545 550 555 560

Tyr Ser Arg Leu Thr Val Asp Lys Ser Ser Trp Gln Glu Gly Asn Val
565 570 575

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
580 585 590

SHK-HTB-023PC_-_SequenceListing.txt

Lys Ser Leu Ser Leu Ser Leu Gly Lys Ile Glu Gly Arg Met Asp Gln
595 600 605

Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val Gln Phe Thr
610 615 620

Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys Glu Asp
625 630 635 640

Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn Cys Asp Gly
645 650 655

Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val Asn Ile
660 665 670

Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys Lys
675 680 685

Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr Tyr Lys Asp
690 695 700

Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu Asp Asp Phe
705 710 715 720

His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly Glu
725 730 735

Phe Cys Val Leu
740

<210> 14
<211> 1554
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 14
atgggggtccc cgggcatggt gctgggcctc ctggtgcaga tctgggccct gcaagaagcc

60

SHK-HTB-023PC_-_SequenceListing.txt

tcaagcctga gcggtgcagca ggggcccac ttgctgcagg tgaggcaggg cagtcaggcg	120
accctggtct gccaggtgga ccaggccaca gcctgggaac ggctccgtgt taagtggaca	180
aaggatgggg ccatcctgtg tcaaccgtac atcaccaacg gcagcctcag cctgggggtc	240
tgcgggcccc agggacggct ctcttgagc gcacccagcc atctcacctt gcagctggac	300
cctgtgagcc tcaaccacag cggggcgtag gtgtgctggg cggccgtaga gattcctgag	360
ttggaggagg ctgagggcaa cataacaagg ctctttgtgg acccagatga cccacacag	420
aacagaaacc ggatcgcaag cttcccagga tctaagtacg gccctccctg ccctagctgt	480
cccggccctg aatttctggg cggaccctcc gtgtttctgt tcccccaaa gcccaaggac	540
accctgatga tcagccggac cccgaagtg acctgtgtgg tggaggatgt gtcccaggaa	600
gatcccgagg tgcagttcaa ttggtacgtg gacgggggtg aagtgacaa cgccaagacc	660
aagcccagag aggaacagtt caacagcacc taccgggtgg tgtctgtgct gaccgtgctg	720
caccaggatt ggctgagcgg caaagagtag aagtgcagg tgtccagcaa gggcctgccc	780
agcagcatcg aaaagaccat cagcaacgcc accggccagc ccagggaacc ccaggtgtac	840
acactgcccc ctagccagga agagatgacc aagaaccagg tgtccctgac atgcctcgtg	900
aagggtttct acccctccga tatcgccgtg gaatgggaga gcaacggcca gccagagaac	960
aactacaaga ccaccccccc agtgctggac agcgacggct cattcttcct gtactcccgg	1020
ctgacagtgg acaagagcag ctggcaggaa ggcaacgtgt tcagctgcag cgtgatgcac	1080
gaagccctgc acaaccacta caccagaag tccctgagcc tgtccctggg caaaatagag	1140
ggacgaatgg accaggtatc acatcggtat cctcgaattc aaagtatcaa agtacaattt	1200
accgaatata agaaggagaa aggtttcatc ctacttccc aaaaggagga tgaaatcatg	1260
aaggtgcaga acaactcagt catcatcaac tgtgatgggt tttatctcat ctccctgaag	1320
ggctacttct cccagggaagt caacattagc cttcattacc agaaggatga ggagcccctc	1380
ttccaactga agaaggtcag gtctgtcaac tccttgatgg tggcctctct gacttacaaa	1440
gacaaagtct acttgaatgt gaccactgac aatacctccc tggatgactt ccatgtgaat	1500
ggcgggagaac tgattcttat ccatcaaaat cctggtgaat tctgtgtcct ttga	1554

SHK-HTB-023PC_-_SequenceListing.txt

<211> 517

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence

<400> 15

Met Gly Ser Pro Gly Met Val Leu Gly Leu Leu Val Gln Ile Trp Ala
1 5 10 15

Leu Gln Glu Ala Ser Ser Leu Ser Val Gln Gln Gly Pro Asn Leu Leu
20 25 30

Gln Val Arg Gln Gly Ser Gln Ala Thr Leu Val Cys Gln Val Asp Gln
35 40 45

Ala Thr Ala Trp Glu Arg Leu Arg Val Lys Trp Thr Lys Asp Gly Ala
50 55 60

Ile Leu Cys Gln Pro Tyr Ile Thr Asn Gly Ser Leu Ser Leu Gly Val
65 70 75 80

Cys Gly Pro Gln Gly Arg Leu Ser Trp Gln Ala Pro Ser His Leu Thr
85 90 95

Leu Gln Leu Asp Pro Val Ser Leu Asn His Ser Gly Ala Tyr Val Cys
100 105 110

Trp Ala Ala Val Glu Ile Pro Glu Leu Glu Glu Ala Glu Gly Asn Ile
115 120 125

Thr Arg Leu Phe Val Asp Pro Asp Asp Pro Thr Gln Asn Arg Asn Arg
130 135 140

Ile Ala Ser Phe Pro Gly Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys
145 150 155 160

Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
165 170 175

SHK-HTB-023PC_-_SequenceListing.txt

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
180 185 190

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
195 200 205

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
210 215 220

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
225 230 235 240

His Gln Asp Trp Leu Ser Gly Lys Glu Tyr Lys Cys Lys Val Ser Ser
245 250 255

Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Asn Ala Thr Gly
260 265 270

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu
275 280 285

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
290 295 300

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
305 310 315 320

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
325 330 335

Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Ser Trp Gln Glu Gly Asn
340 345 350

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
355 360 365

Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Ile Glu Gly Arg Met Asp
370 375 380

SHK-HTB-023PC_-_SequenceListing.txt

Gln Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val Gln Phe
385 390 395 400

Thr Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys Glu
405 410 415

Asp Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn Cys Asp
420 425 430

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

Ile Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys
450 455 460

Lys Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr Tyr Lys
465 470 475 480

Asp Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu Asp Asp
485 490 495

Phe His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly
500 505 510

Glu Phe Cys Val Leu
515

<210> 16
<211> 3493
<212> DNA
<213> Homo sapiens

<400> 16
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ccatatcttc atcttccctc taccagatt gtgaagatgg aaagggtcca acccctggaa 180
gagaatgtgg gaaatgcagc caggccaaga ttcgagagga acaagctatt gctggtggcc 240
tctgtaattc agggactggg gctgctcctg tgcttcacct acatctgcct gcacttctct 300

SHK-HTB-023PC_-_SequenceListing.txt

gctcttcagg tatcacatcg gtatcctcga attcaaagta tcaaagtaca atttaccgaa	360
tataagaagg agaaaggttt catcctcact tcccaaaagg aggatgaaat catgaagggtg	420
cagaacaact cagtcatcat caactgtgat gggttttatc tcatctccct gaagggtac	480
ttctcccagg aagtcaacat tagccttcat taccagaagg atgaggagcc cctcttccaa	540
ctgaagaagg tcagggtctgt caactccttg atgggtggcct ctctgactta caaagacaaa	600
gtctacttga atgtgaccac tgacaatacc tccctggatg acttccatgt gaatggcgga	660
gaactgattc ttatccatca aaatcctggg gaattctgtg tcctttgagg ggctgatggc	720
aatatctaaa accaggcacc agcatgaaca ccaagctggg ggtggacagg gcatggattc	780
ttcattgcaa gtgaaggagc ctcccagctc agccacgtgg gatgtgacaa gaagcagatc	840
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agaaatttcc cttcaaagaa ctgtctgggg atgtgatgct ttgaaaaatc taatcagtga	1440
cttaagagag attttcttgt atacagggag agtgagataa cttattgtga agggttagct	1500
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agttattgtg cttatgaaa aataatgatc tctgtctaga aataccatag accatatata	1800
gtctcacatt gataattgaa actagaaggg tctataatca gcctatgcca gggcttcaat	1860

SHK-HTB-023PC_-_SequenceListing.txt

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tctgtgccaa accttttata aacataaatt tttgagatat gtattttaaa attgtagcac	2040
atgtttccct gacattttca atagaggata caacatcaca gaatctttct ggatgattct	2100
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gctgttcgcc cttacactaa atgggtctcag ttggattttt ttttcctggt ttctattttcc	2220
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ggaccaggca ctgggctaaa tacttacatt tacaagaatc attctgagac agatattcaa	2460
tgatatctgg cttcactact cagaagattg tgtgtgtgtt tgtgtgtgtg tgtgtgtgtg	2520
tatttcactt tttgttattg accatgttct gcaaaattgc agttactcag tgagtgatat	2580
ccgaaaaagt aaacgtttat gactataggt aatattttaag aaaatgcatg gttcattttt	2640
aagtttgga tttttatcta tatttctcac agatgtgcag tgcacatgca ggctaagta	2700
tatgttgtgt gtgttgtttg tctttgatgt catgggtcccc tctcttaggt gctcactcgc	2760
tttgggtgca cctggcctgc tcttcccatg ttggcctctg caaccacaca gggatatttc	2820
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ccctgtaagt catgtccttc acaggagaa ttaacccttc gatatacatg gcagagtttt	2940
gtgggaaaag aattgaatga aaagtcagga gatcagaatt ttaaatttga cttagccact	3000
aactagccat gtaaccttgg gaaagtcatt tcccatttct gggctttgct tttctttctg	3060
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tcctttacta tgttgaatgt attttttct ggacaagctt acatcttcct cagccatctt	3240
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ttaagggatt ccaatccga tccaaatcat aatttgttct taagtatact gggcagggtcc	3360
cctattttta gtcataattt tgtatttagt gctttcctgg ctctcagaga gtattaatat	3420

SHK-HTB-023PC_-_SequenceListing.txt

tgatattaat aatatagtta atagtaatat tgctattttac atggaaacaa ataaaagatc 3480

tcagaattca cta 3493

<210> 17

<211> 183

<212> PRT

<213> Homo sapiens

<400> 17

Met Glu Arg Val Gln Pro Leu Glu Glu Asn Val Gly Asn Ala Ala Arg
1 5 10 15

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

Gly Leu Gly Leu Leu Leu Cys Phe Thr Tyr Ile Cys Leu His Phe Ser
35 40 45

Ala Leu Gln Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val
50 55 60

Gln Phe Thr Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln
65 70 75 80

Lys Glu Asp Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn
85 90 95

Cys Asp Gly Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu
100 105 110

Val Asn Ile Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln
115 120 125

Leu Lys Lys Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr
130 135 140

Tyr Lys Asp Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu
145 150 155 160

SHK-HTB-023PC_-_SequenceListing.txt

Asp Asp Phe His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn
165 170 175

Pro Gly Glu Phe Cys Val Leu
180

<210> 18
<211> 684
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 18
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acctgtgtgg tgggtgatgt gtcccaggaa gatcccgagg tgcagttcaa ttggtacgtg 180
gacggggtgg aagtgcacaa cgccaagacc aagcccagag aggaacagtt caacagcacc 240
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aagtgcaagg tgtccagcaa gggcctgccc agcagcatcg aaaagaccat cagcaacgcc 360
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aagaaccagg tgtccctgac atgcctcgtg aagggttctt acccctccga tatcgccgtg 480
gaatgggaga gcaacggcca gccagagaac aactacaaga ccaccccccc agtgctggac 540
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tccctgagcc tgtccctggg caaa 684

<210> 19
<211> 867
<212> DNA
<213> Homo sapiens

<400> 19
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SHK-HTB-023PC_-_SequenceListing.txt

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gagagcttcg tgctaaactg gtaccgcatg agccccagca accagacgga caagctggcc	240
gccttccccg aggaccgcag ccagcccggc caggactgcc gcttccgtgt cacacaactg	300
cccaacgggc gtgacttcca catgagcgtg gtcagggccc ggcgcaatga cagcggcacc	360
tacctctgtg gggccatctc cctggcccc aaggcgcaga tcaaagagag cctgcgggca	420
gagctcaggg tgacagagag aagggcagaa gtgcccacag cccaccccag cccctcacc	480
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ctgggtgtgc tagtctgggt cctggccgtc atctgtctcc gggccgcacg agggacaata	600
ggagccaggc gcaccggcca gcccctgaag gaggaccct cagccgtgcc tgtgttctct	660
gtggactatg gggagctgga tttccagtgg cgagagaaga ccccgagcc ccccggtccc	720
tgtgtccctg agcagacgga gtatgccacc attgtctttc ctagcggaat gggcacctca	780
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gatggacact gctcttggcc cctctga	867

<210> 20
 <211> 1623
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic sequence

<400> 20	
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ttctccccag ccctgctcgt ggtgaccgaa ggggacaacg ccaccttcac ctgcagcttc	180
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gacaagctgg ccgccttccc cgaggaccgc agccagcccg gccaggactg ccgcttccgt	300
gtcacacaac tgcccaacgg gcgtgacttc cacatgagcg tggtcagggc ccggcgcaat	360
gacagcggca cctacctctg tggggccatc tccctggccc ccaaggcgca gatcaaagag	420
agcctgcggg cagagctcag ggtgacagag agaaggcgag aagtgcccac agccccccc	480

SHK-HTB-023PC_-_SequenceListing.txt

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gacaccctga tgatcagccg gacccccgaa gtgacctgtg tgggtggtgga tgtgtcccag	660
gaagatcccg aggtgcagtt caattggtac gtggacgggg tggaaagtga caacgccaaag	720
accaagccca gagaggaaca gttcaacagc acctaccggg tgggtgtctgt gctgaccgtg	780
ctgcaccagg attggctgag cggcaaagag tacaagtga aggtgtccag caagggcctg	840
cccagcagca tcgaaaagac catcagcaac gccaccggcc agcccaggga accccagggtg	900
tacacactgc cccctagcca ggaagagatg accaagaacc aggtgtccct gacatgcctc	960
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aacaactaca agaccacccc cccagtgtg gacagcgacg gctcattctt cctgtactcc	1080
cggctgacag tggacaagag cagctggcag gaaggcaacg tggtcagctg cagcgtgatg	1140
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aaagacaaag tctacttgaa tgtgaccact gacaatacct ccctggatga cttccatgtg	1560
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gac	1623

<210> 21
 <211> 1637
 <212> DNA
 <213> Homo sapiens

<400> 21	
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SHK-HTB-023PC_-_SequenceListing.txt

ccccacctt tagccctgct ctgctggtcg tgaccgaggg cgacaacgcc accttcacct	180
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tgacctaaa ggacaagggtg tacctgaacg tgaccaccga caatacctcc ctggacgact	1560
tccacgtgaa cggcggcgag ctgatcctga tccaccagaa ccctggcgag ttctgcgtgc	1620
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SHK-HTB-023PC_-_SequenceListing.txt

<210> 22
 <211> 534
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic sequence

<400> 22

Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
 1 5 10 15

Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
 20 25 30

Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp
 35 40 45

Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
 50 55 60

Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
 65 70 75 80

Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
 85 90 95

Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
 100 105 110

Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
 115 120 125

Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
 130 135 140

Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
 145 150 155 160

Arg Pro Ala Gly Gln Phe Gln Ser Lys Tyr Gly Pro Pro Cys Pro Ser

SHK-HTB-023PC_-_SequenceListing.txt

165 170 175

Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
180 185 190

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
195 200 205

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
210 215 220

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

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
245 250 255

Leu His Gln Asp Trp Leu Ser Gly Lys Glu Tyr Lys Cys Lys Val Ser
260 265 270

Ser Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Asn Ala Thr
275 280 285

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
290 295 300

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
305 310 315 320

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
325 330 335

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
340 345 350

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Ser Trp Gln Glu Gly
355 360 365

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

SHK-HTB-023PC_-_SequenceListing.txt

370

375

380

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Ile Glu Gly Arg Met
385 390 395 400

Asp Gln Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val Gln
405 410 415

Phe Thr Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys
420 425 430

Glu Asp Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn Cys
435 440 445

Asp Gly Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val
450 455 460

Asn Ile Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu
465 470 475 480

Lys Lys Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr Tyr
485 490 495

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

Asp Phe His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro
515 520 525

Gly Glu Phe Cys Val Leu
530

<210> 23

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence

<400> 23

Gly Gly Gly Gly Ser
1 5

<210> 24
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 24

Glu Ala Ala Ala Lys
1 5

<210> 25
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 25

Ala Glu Ala Ala Ala Lys Ala
1 5

<210> 26
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 26

Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
1 5 10

<210> 27
<211> 46
<212> PRT
<213> Artificial sequence

SHK-HTB-023PC_-_SequenceListing.txt

<220>

<223> Synthetic sequence

<400> 27

Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10 15

Glu Ala Ala Ala Lys Ala Leu Glu Ala Glu Ala Ala Ala Lys Glu Ala
20 25 30

Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
35 40 45

<210> 28

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence

<400> 28

Pro Ala Pro Ala Pro
1 5

<210> 29

<211> 18

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence

<400> 29

Lys Glu Ser Gly Ser Val Ser Ser Glu Gln Leu Ala Gln Phe Arg Ser
1 5 10 15

Leu Asp

<210> 30

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence

<400> 30

Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr
1 5 10

<210> 31

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence

<400> 31

Gly Ser Ala Gly Ser Ala Ala Gly Ser Gly Glu Phe
1 5 10

<210> 32

<211> 143

<212> PRT

<213> Homo sapiens

<400> 32

Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala
1 5 10 15

Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe
20 25 30

Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro
35 40 45

Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln
50 55 60

Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg
65 70 75 80

SHK-HTB-023PC_-_SequenceListing.txt

Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr
85 90 95

Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu
100 105 110

Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro
115 120 125

Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Phe Gln
130 135 140

<210> 33
<211> 343
<212> PRT
<213> Homo sapiens

<400> 33

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys
85 90 95

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

Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala

SHK-HTB-023PC_-_SequenceListing.txt

115

120

125

Arg Ala Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly
130 135 140

Phe Ser Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu
145 150 155 160

Leu Ser Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser
165 170 175

Tyr Ser Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val
180 185 190

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
195 200 205

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
210 215 220

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
225 230 235 240

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr
245 250 255

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
260 265 270

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val
275 280 285

Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
290 295 300

His Asp Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser
305 310 315 320

Ala His Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly

325

330

335

Ser Asn Glu Arg Asn Ile Tyr
340

<210> 34
<211> 127
<212> PRT
<213> Homo sapiens

<400> 34

Lys Glu Ser Cys Asp Val Gln Leu Tyr Ile Lys Arg Gln Ser Glu His
1 5 10 15

Ser Ile Leu Ala Gly Asp Pro Phe Glu Leu Glu Cys Pro Val Lys Tyr
20 25 30

Cys Ala Asn Arg Pro His Val Thr Trp Cys Lys Leu Asn Gly Thr Thr
35 40 45

Cys Val Lys Leu Glu Asp Arg Gln Thr Ser Trp Lys Glu Glu Lys Asn
50 55 60

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

Gly Ser Tyr Arg Cys Ser Ala Asn Phe Gln Ser Asn Leu Ile Glu Ser
85 90 95

His Ser Thr Thr Leu Tyr Val Thr Asp Val Lys Ser Ala Ser Glu Arg
100 105 110

Pro Ser Lys Asp Glu Met Ala Ser Arg Pro Trp Leu Leu Tyr Arg
115 120 125

<210> 35
<211> 120
<212> PRT
<213> Homo sapiens

<400> 35

SHK-HTB-023PC_-_SequenceListing.txt

Met Met Thr Gly Thr Ile Glu Thr Thr Gly Asn Ile Ser Ala Glu Lys
1 5 10 15

Gly Gly Ser Ile Ile Leu Gln Cys His Leu Ser Ser Thr Thr Ala Gln
20 25 30

Val Thr Gln Val Asn Trp Glu Gln Gln Asp Gln Leu Leu Ala Ile Cys
35 40 45

Asn Ala Asp Leu Gly Trp His Ile Ser Pro Ser Phe Lys Asp Arg Val
50 55 60

Ala Pro Gly Pro Gly Leu Gly Leu Thr Leu Gln Ser Leu Thr Val Asn
65 70 75 80

Asp Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr Tyr Pro Asp Gly Thr
85 90 95

Tyr Thr Gly Arg Ile Phe Leu Glu Val Leu Glu Ser Ser Val Ala Glu
100 105 110

His Gly Ala Arg Phe Gln Ile Pro
115 120

<210> 36
<211> 181
<212> PRT
<213> Homo sapiens

<400> 36

Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln Asn Ala Tyr Leu Pro
1 5 10 15

Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu Val Pro Val Cys Trp
20 25 30

Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly Asn Val Val Leu Arg
35 40 45

SHK-HTB-023PC_-_SequenceListing.txt

Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser Arg Tyr Trp Leu Asn
50 55 60

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

Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile Gln Ile Pro Gly Ile
85 90 95

Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val Ile Lys Pro Ala Lys
100 105 110

Val Thr Pro Ala Pro Thr Arg Gln Arg Asp Phe Thr Ala Ala Phe Pro
115 120 125

Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala Glu Thr Gln Thr Leu
130 135 140

Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile Ser Thr Leu Ala Asn
145 150 155 160

Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu Arg Asp Ser Gly Ala
165 170 175

Thr Ile Arg Ile Gly
180

<210> 37
<211> 202
<212> PRT
<213> Homo sapiens

<400> 37

Gln Val Gln Val Val Thr Gln Asp Glu Arg Glu Gln Leu Tyr Thr Pro
1 5 10 15

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

Thr Trp Gln Lys Lys Lys Ala Val Ser Pro Glu Asn Met Val Thr Phe

SHK-HTB-023PC_-_SequenceListing.txt

35

40

45

Ser Glu Asn His Gly Val Val Ile Gln Pro Ala Tyr Lys Asp Lys Ile
50 55 60

Asn Ile Thr Gln Leu Gly Leu Gln Asn Ser Thr Ile Thr Phe Trp Asn
65 70 75 80

Ile Thr Leu Glu Asp Glu Gly Cys Tyr Met Cys Leu Phe Asn Thr Phe
85 90 95

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

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

Thr Cys Ser Ala Thr Ala Arg Pro Ala Pro Met Val Phe Trp Lys Val
130 135 140

Pro Arg Ser Gly Ile Glu Asn Ser Thr Val Thr Leu Ser His Pro Asn
145 150 155 160

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

Gln Val Gly Lys Glu Val Ile Cys Gln Val Leu His Leu Gly Thr Val
180 185 190

Thr Asp Phe Lys Gln Thr Val Asn Lys Gly
195 200

<210> 38

<211> 128

<212> PRT

<213> Homo sapiens

<400> 38

Leu Ser Val Gln Gln Gly Pro Asn Leu Leu Gln Val Arg Gln Gly Ser
1 5 10 15

SHK-HTB-023PC_-_SequenceListing.txt

Gln Ala Thr Leu Val Cys Gln Val Asp Gln Ala Thr Ala Trp Glu Arg
20 25 30

Leu Arg Val Lys Trp Thr Lys Asp Gly Ala Ile Leu Cys Gln Pro Tyr
35 40 45

Ile Thr Asn Gly Ser Leu Ser Leu Gly Val Cys Gly Pro Gln Gly Arg
50 55 60

Leu Ser Trp Gln Ala Pro Ser His Leu Thr Leu Gln Leu Asp Pro Val
65 70 75 80

Ser Leu Asn His Ser Gly Ala Tyr Val Cys Trp Ala Ala Val Glu Ile
85 90 95

Pro Glu Leu Glu Glu Ala Glu Gly Asn Ile Thr Arg Leu Phe Val Asp
100 105 110

Pro Asp Asp Pro Thr Gln Asn Arg Asn Arg Ile Ala Ser Phe Pro Gly
115 120 125

<210> 39
<211> 162
<212> PRT
<213> Homo sapiens

<400> 39

Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gly Gln
1 5 10 15

Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly His
20 25 30

Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu Val
35 40 45

Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln Asp
50 55 60

SHK-HTB-023PC_-_SequenceListing.txt

Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser His Asp
65 70 75 80

Leu Ala Gln Arg His Gly Leu Glu Ser Ala Ser Asp His His Gly Asn
85 90 95

Phe Ser Ile Thr Met Arg Asn Leu Thr Leu Leu Asp Ser Gly Leu Tyr
100 105 110

Cys Cys Leu Val Val Glu Ile Arg His His His Ser Glu His Arg Val
115 120 125

His Gly Ala Met Glu Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser
130 135 140

Asn Cys Val Val Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr
145 150 155 160

Ala Ala

<210> 40

<211> 242

<212> PRT

<213> Homo sapiens

<400> 40

Val Arg Ile Asn Gly Asp Gly Gln Glu Val Leu Tyr Leu Ala Glu Gly
1 5 10 15

Asp Asn Val Arg Leu Gly Cys Pro Tyr Val Leu Asp Pro Glu Asp Tyr
20 25 30

Gly Pro Asn Gly Leu Asp Ile Glu Trp Met Gln Val Asn Ser Asp Pro
35 40 45

Ala His His Arg Glu Asn Val Phe Leu Ser Tyr Gln Asp Lys Arg Ile
50 55 60

SHK-HTB-023PC_-_SequenceListing.txt

Asn His Gly Ser Leu Pro His Leu Gln Gln Arg Val Arg Phe Ala Ala
65 70 75 80

Ser Asp Pro Ser Gln Tyr Asp Ala Ser Ile Asn Leu Met Asn Leu Gln
85 90 95

Val Ser Asp Thr Ala Thr Tyr Glu Cys Arg Val Lys Lys Thr Thr Met
100 105 110

Ala Thr Arg Lys Val Ile Val Thr Val Gln Ala Arg Pro Ala Val Pro
115 120 125

Met Cys Trp Thr Glu Gly His Met Thr Tyr Gly Asn Asp Val Val Leu
130 135 140

Lys Cys Tyr Ala Ser Gly Gly Ser Gln Pro Leu Ser Tyr Lys Trp Ala
145 150 155 160

Lys Ile Ser Gly His His Tyr Pro Tyr Arg Ala Gly Ser Tyr Thr Ser
165 170 175

Gln His Ser Tyr His Ser Glu Leu Ser Tyr Gln Glu Ser Phe His Ser
180 185 190

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

Ser Arg Ala Asp Asp Gly Leu Tyr Gln Cys Thr Val Ala Asn Asn Val
210 215 220

Gly Tyr Ser Val Cys Val Val Glu Val Lys Val Ser Asp Ser Arg Arg
225 230 235 240

Ile Gly

<210> 41

<211> 427

<212> PRT

<213> Homo sapiens

SHK-HTB-023PC_-_SequenceListing.txt

<400> 41

Glu Asp Phe Arg Val Ile Gly Pro Ala His Pro Ile Leu Ala Gly Val
1 5 10 15

Gly Glu Asp Ala Leu Leu Thr Cys Gln Leu Leu Pro Lys Arg Thr Thr
20 25 30

Met His Val Glu Val Arg Trp Tyr Arg Ser Glu Pro Ser Thr Pro Val
35 40 45

Phe Val His Arg Asp Gly Val Glu Val Thr Glu Met Gln Met Glu Glu
50 55 60

Tyr Arg Gly Trp Val Glu Trp Ile Glu Asn Gly Ile Ala Lys Gly Asn
65 70 75 80

Val Ala Leu Lys Ile His Asn Ile Gln Pro Ser Asp Asn Gly Gln Tyr
85 90 95

Trp Cys His Phe Gln Asp Gly Asn Tyr Cys Gly Glu Thr Ser Leu Leu
100 105 110

Leu Lys Val Ala Gly Leu Gly Ser Ala Pro Ser Ile His Met Glu Gly
115 120 125

Pro Gly Glu Ser Gly Val Gln Leu Val Cys Thr Ala Arg Gly Trp Phe
130 135 140

Pro Glu Pro Gln Val Tyr Trp Glu Asp Ile Arg Gly Glu Lys Leu Leu
145 150 155 160

Ala Val Ser Glu His Arg Ile Gln Asp Lys Asp Gly Leu Phe Tyr Ala
165 170 175

Glu Ala Thr Leu Val Val Arg Asn Ala Ser Ala Glu Ser Val Ser Cys
180 185 190

Leu Val His Asn Pro Val Leu Thr Glu Glu Lys Gly Ser Val Ile Ser

SHK-HTB-023PC_-_SequenceListing.txt

195

200

205

Leu Pro Glu Lys Leu Gln Thr Glu Leu Ala Ser Leu Lys Val Asn Gly
 210 215 220

Pro Ser Gln Pro Ile Leu Val Arg Val Gly Glu Asp Ile Gln Leu Thr
 225 230 235 240

Cys Tyr Leu Ser Pro Lys Ala Asn Ala Gln Ser Met Glu Val Arg Trp
 245 250 255

Asp Arg Ser His Arg Tyr Pro Ala Val His Val Tyr Met Asp Gly Asp
 260 265 270

His Val Ala Gly Glu Gln Met Ala Glu Tyr Arg Gly Arg Thr Val Leu
 275 280 285

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

Ala Arg Pro Ser Asp Asp Gly Gln Tyr Arg Cys Leu Phe Glu Lys Asp
 305 310 315 320

Asp Val Tyr Gln Glu Ala Ser Leu Asp Leu Lys Val Val Ser Leu Gly
 325 330 335

Ser Ser Pro Leu Ile Thr Val Glu Gly Gln Glu Asp Gly Glu Met Gln
 340 345 350

Pro Met Cys Ser Ser Asp Gly Trp Phe Pro Gln Pro His Val Pro Trp
 355 360 365

Arg Asp Met Glu Gly Lys Thr Ile Pro Ser Ser Ser Gln Ala Leu Thr
 370 375 380

Gln Gly Ser His Gly Leu Phe His Val Gln Thr Leu Leu Arg Val Thr
 385 390 395 400

Asn Ile Ser Ala Val Asp Val Thr Cys Ser Ile Ser Ile Pro Phe Leu

405

410

415

Gly Glu Glu Lys Ile Ala Thr Phe Ser Leu Ser
 420 425

<210> 42
 <211> 235
 <212> PRT
 <213> Homo sapiens

<400> 42

Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
 1 5 10 15

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
 20 25 30

Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
 35 40 45

Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
 50 55 60

Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
 65 70 75 80

Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
 85 90 95

Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
 100 105 110

Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
 115 120 125

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
 130 135 140

Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
 145 150 155 160

SHK-HTB-023PC_-_SequenceListing.txt

Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
165 170 175

Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
180 185 190

His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr
195 200 205

Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
210 215 220

Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp
225 230 235

<210> 43
<211> 438
<212> PRT
<213> Homo sapiens

<400> 43

Leu Glu Val Gln Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr
1 5 10 15

Asp Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu
20 25 30

Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val
35 40 45

His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg
50 55 60

Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg
65 70 75 80

Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val
85 90 95

SHK-HTB-023PC_-_SequenceListing.txt

Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala
100 105 110

Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg
115 120 125

Pro Gly Asp Thr Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro
130 135 140

Glu Ala Glu Val Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly
145 150 155 160

Asn Val Thr Thr Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val
165 170 175

His Ser Ile Leu Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys
180 185 190

Leu Val Arg Asn Pro Val Leu Gln Gln Asp Ala His Ser Ser Val Thr
195 200 205

Ile Thr Pro Gln Arg Ser Pro Thr Gly Ala Val Glu Val Gln Val Pro
210 215 220

Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu Arg Cys
225 230 235 240

Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile
245 250 255

Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Thr Glu Gly
260 265 270

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

Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val
290 295 300

SHK-HTB-023PC_-_SequenceListing.txt

Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly
305 310 315 320

Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser
325 330 335

Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr
340 345 350

Ile Thr Cys Ser Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe Trp
355 360 365

Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln
370 375 380

Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val
385 390 395 400

Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro Val
405 410 415

Leu Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln Pro Met
420 425 430

Thr Phe Pro Pro Glu Ala
435

<210> 44
<211> 208
<212> PRT
<213> Homo sapiens

<400> 44

Cys Gln Gly Ser Ala Asp His Val Val Ser Ile Ser Gly Val Pro Leu
1 5 10 15

Gln Leu Gln Pro Asn Ser Ile Gln Thr Lys Val Asp Ser Ile Ala Trp
20 25 30

SHK-HTB-023PC_-_SequenceListing.txt

Lys Lys Leu Leu Pro Ser Gln Asn Gly Phe His His Ile Leu Lys Trp
35 40 45

Glu Asn Gly Ser Leu Pro Ser Asn Thr Ser Asn Asp Arg Phe Ser Phe
50 55 60

Ile Val Lys Asn Leu Ser Leu Leu Ile Lys Ala Ala Gln Gln Gln Asp
65 70 75 80

Ser Gly Leu Tyr Cys Leu Glu Val Thr Ser Ile Ser Gly Lys Val Gln
85 90 95

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

Val Glu Lys Pro Arg Leu Gln Gly Gln Gly Lys Ile Leu Asp Arg Gly
115 120 125

Arg Cys Gln Val Ala Leu Ser Cys Leu Val Ser Arg Asp Gly Asn Val
130 135 140

Ser Tyr Ala Trp Tyr Arg Gly Ser Lys Leu Ile Gln Thr Ala Gly Asn
145 150 155 160

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

Thr Cys Asn Val Ser Asn Pro Val Ser Trp Glu Ser His Thr Leu Asn
180 185 190

Leu Thr Gln Asp Cys Gln Asn Ala His Gln Glu Phe Arg Phe Trp Pro
195 200 205

<210> 45

<211> 422

<212> PRT

<213> Homo sapiens

<400> 45

Val Pro Val Val Trp Ala Gln Glu Gly Ala Pro Ala Gln Leu Pro Cys

SHK-HTB-023PC_-_SequenceListing.txt

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

SHK-HTB-023PC_-_SequenceListing.txt

210

215

220

Ile Met Tyr Asn Leu Thr Val Leu Gly Leu Glu Pro Pro Thr Pro Leu
 225 230 235 240

Thr Val Tyr Ala Gly Ala Gly Ser Arg Val Gly Leu Pro Cys Arg Leu
 245 250 255

Pro Ala Gly Val Gly Thr Arg Ser Phe Leu Thr Ala Lys Trp Thr Pro
 260 265 270

Pro Gly Gly Gly Pro Asp Leu Leu Val Thr Gly Asp Asn Gly Asp Phe
 275 280 285

Thr Leu Arg Leu Glu Asp Val Ser Gln Ala Gln Ala Gly Thr Tyr Thr
 290 295 300

Cys His Ile His Leu Gln Glu Gln Gln Leu Asn Ala Thr Val Thr Leu
 305 310 315 320

Ala Ile Ile Thr Val Thr Pro Lys Ser Phe Gly Ser Pro Gly Ser Leu
 325 330 335

Gly Lys Leu Leu Cys Glu Val Thr Pro Val Ser Gly Gln Glu Arg Phe
 340 345 350

Val Trp Ser Ser Leu Asp Thr Pro Ser Gln Arg Ser Phe Ser Gly Pro
 355 360 365

Trp Leu Glu Ala Gln Glu Ala Gln Leu Leu Ser Gln Pro Trp Gln Cys
 370 375 380

Gln Leu Tyr Gln Gly Glu Arg Leu Leu Gly Ala Ala Val Tyr Phe Thr
 385 390 395 400

Glu Leu Ser Ser Pro Gly Ala Gln Arg Ser Gly Arg Ala Pro Gly Ala
 405 410 415

Leu Pro Ala Gly His Leu

SHK-HTB-023PC_-_SequenceListing.txt

420

<210> 46
 <211> 498
 <212> PRT
 <213> Homo sapiens

<400> 46

Ile Pro Val Ile Glu Pro Ser Val Pro Glu Leu Val Val Lys Pro Gly
 1 5 10 15

Ala Thr Val Thr Leu Arg Cys Val Gly Asn Gly Ser Val Glu Trp Asp
 20 25 30

Gly Pro Pro Ser Pro His Trp Thr Leu Tyr Ser Asp Gly Ser Ser Ser
 35 40 45

Ile Leu Ser Thr Asn Asn Ala Thr Phe Gln Asn Thr Gly Thr Tyr Arg
 50 55 60

Cys Thr Glu Pro Gly Asp Pro Leu Gly Gly Ser Ala Ala Ile His Leu
 65 70 75 80

Tyr Val Lys Asp Pro Ala Arg Pro Trp Asn Val Leu Ala Gln Glu Val
 85 90 95

Val Val Phe Glu Asp Gln Asp Ala Leu Leu Pro Cys Leu Leu Thr Asp
 100 105 110

Pro Val Leu Glu Ala Gly Val Ser Leu Val Arg Val Arg Gly Arg Pro
 115 120 125

Leu Met Arg His Thr Asn Tyr Ser Phe Ser Pro Trp His Gly Phe Thr
 130 135 140

Ile His Arg Ala Lys Phe Ile Gln Ser Gln Asp Tyr Gln Cys Ser Ala
 145 150 155 160

Leu Met Gly Gly Arg Lys Val Met Ser Ile Ser Ile Arg Leu Lys Val
 165 170 175

SHK-HTB-023PC_-_SequenceListing.txt

Gln Lys Val Ile Pro Gly Pro Pro Ala Leu Thr Leu Val Pro Ala Glu
180 185 190

Leu Val Arg Ile Arg Gly Glu Ala Ala Gln Ile Val Cys Ser Ala Ser
195 200 205

Ser Val Asp Val Asn Phe Asp Val Phe Leu Gln His Asn Asn Thr Lys
210 215 220

Leu Ala Ile Pro Gln Gln Ser Asp Phe His Asn Asn Arg Tyr Gln Lys
225 230 235 240

Val Leu Thr Leu Asn Leu Asp Gln Val Asp Phe Gln His Ala Gly Asn
245 250 255

Tyr Ser Cys Val Ala Ser Asn Val Gln Gly Lys His Ser Thr Ser Met
260 265 270

Phe Phe Arg Val Val Glu Ser Ala Tyr Leu Asn Leu Ser Ser Glu Gln
275 280 285

Asn Leu Ile Gln Glu Val Thr Val Gly Glu Gly Leu Asn Leu Lys Val
290 295 300

Met Val Glu Ala Tyr Pro Gly Leu Gln Gly Phe Asn Trp Thr Tyr Leu
305 310 315 320

Gly Pro Phe Ser Asp His Gln Pro Glu Pro Lys Leu Ala Asn Ala Thr
325 330 335

Thr Lys Asp Thr Tyr Arg His Thr Phe Thr Leu Ser Leu Pro Arg Leu
340 345 350

Lys Pro Ser Glu Ala Gly Arg Tyr Ser Phe Leu Ala Arg Asn Pro Gly
355 360 365

Gly Trp Arg Ala Leu Thr Phe Glu Leu Thr Leu Arg Tyr Pro Pro Glu
370 375 380

SHK-HTB-023PC_-_SequenceListing.txt

Val Ser Val Ile Trp Thr Phe Ile Asn Gly Ser Gly Thr Leu Leu Cys
385 390 395 400

Ala Ala Ser Gly Tyr Pro Gln Pro Asn Val Thr Trp Leu Gln Cys Ser
405 410 415

Gly His Thr Asp Arg Cys Asp Glu Ala Gln Val Leu Gln Val Trp Asp
420 425 430

Asp Pro Tyr Pro Glu Val Leu Ser Gln Glu Pro Phe His Lys Val Thr
435 440 445

Val Gln Ser Leu Leu Thr Val Glu Thr Leu Glu His Asn Gln Thr Tyr
450 455 460

Glu Cys Arg Ala His Asn Ser Val Gly Ser Gly Ser Trp Ala Phe Ile
465 470 475 480

Pro Ile Ser Ala Gly Ala His Thr His Pro Pro Asp Glu Phe Leu Phe
485 490 495

Thr Pro

<210> 47
<211> 93
<212> PRT
<213> Homo sapiens

<400> 47

Leu Gln Cys Phe Cys His Leu Cys Thr Lys Asp Asn Phe Thr Cys Val
1 5 10 15

Thr Asp Gly Leu Cys Phe Val Ser Val Thr Glu Thr Thr Asp Lys Val
20 25 30

Ile His Asn Ser Met Cys Ile Ala Glu Ile Asp Leu Ile Pro Arg Asp
35 40 45

SHK-HTB-023PC_-_SequenceListing.txt

Arg Pro Phe Val Cys Ala Pro Ser Ser Lys Thr Gly Ser Val Thr Thr
50 55 60

Thr Tyr Cys Cys Asn Gln Asp His Cys Asn Lys Ile Glu Leu Pro Thr
65 70 75 80

Thr Val Lys Ser Ser Pro Gly Leu Gly Pro Val Glu Leu
85 90

<210> 48

<211> 214

<212> PRT

<213> Homo sapiens

<400> 48

His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe Glu Ala Glu
1 5 10 15

Phe Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn Gln Ser Glu
20 25 30

Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile Glu Ser Trp
35 40 45

Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp Leu Thr Ala
50 55 60

Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala Arg Val Arg
65 70 75 80

Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr Asn Thr Arg
85 90 95

Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val Asn Leu Glu
100 105 110

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

SHK-HTB-023PC_-_SequenceListing.txt

Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser His Phe Arg
130 135 140

Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe Thr Phe Thr
145 150 155 160

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

Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala Ser Arg Ser
180 185 190

Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu Thr Arg Gln
195 200 205

Tyr Phe Thr Val Thr Asn
210

<210> 49
<211> 173
<212> PRT
<213> Homo sapiens

<400> 49

Glu Pro Pro Thr Ala Cys Arg Glu Lys Gln Tyr Leu Ile Asn Ser Gln
1 5 10 15

Cys Cys Ser Leu Cys Gln Pro Gly Gln Lys Leu Val Ser Asp Cys Thr
20 25 30

Glu Phe Thr Glu Thr Glu Cys Leu Pro Cys Gly Glu Ser Glu Phe Leu
35 40 45

Asp Thr Trp Asn Arg Glu Thr His Cys His Gln His Lys Tyr Cys Asp
50 55 60

Pro Asn Leu Gly Leu Arg Val Gln Gln Lys Gly Thr Ser Glu Thr Asp
65 70 75 80

Thr Ile Cys Thr Cys Glu Glu Gly Trp His Cys Thr Ser Glu Ala Cys

SHK-HTB-023PC_-_SequenceListing.txt

85 90 95

Glu Ser Cys Val Leu His Arg Ser Cys Ser Pro Gly Phe Gly Val Lys
100 105 110

Gln Ile Ala Thr Gly Val Ser Asp Thr Ile Cys Glu Pro Cys Pro Val
115 120 125

Gly Phe Phe Ser Asn Val Ser Ser Ala Phe Glu Lys Cys His Pro Trp
130 135 140

Thr Ser Cys Glu Thr Lys Asp Leu Val Val Gln Gln Ala Gly Thr Asn
145 150 155 160

Lys Thr Asp Val Val Cys Gly Pro Gln Asp Arg Leu Arg
165 170

<210> 50
<211> 186
<212> PRT
<213> Homo sapiens

<400> 50

Leu His Cys Val Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His
1 5 10 15

Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln
20 25 30

Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val
35 40 45

Ser Ser Lys Pro Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly
50 55 60

Ser Glu Arg Lys Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg
65 70 75 80

Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp
85 90 95

SHK-HTB-023PC_-_SequenceListing.txt

Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala
100 105 110

Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln
115 120 125

Pro Ala Ser Asn Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro
130 135 140

Ala Thr Gln Pro Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr
145 150 155 160

Val Gln Pro Thr Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr
165 170 175

Arg Pro Val Glu Val Pro Gly Gly Arg Ala
180 185

<210> 51
<211> 163
<212> PRT
<213> Homo sapiens

<400> 51

Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
1 5 10 15

Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
20 25 30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
35 40 45

Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
50 55 60

Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu
65 70 75 80

SHK-HTB-023PC_-_SequenceListing.txt

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp
85 90 95

Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro
100 105 110

Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly Thr
115 120 125

Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser Pro
130 135 140

Gly Ala Ser Ser Val Thr Pro Pro Ala Pro Ala Arg Glu Pro Gly His
145 150 155 160

Ser Pro Gln

<210> 52
<211> 126
<212> PRT
<213> Homo sapiens

<400> 52

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

SHK-HTB-023PC_-_SequenceListing.txt

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 53

<211> 220

<212> PRT

<213> Homo sapiens

<400> 53

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys

SHK-HTB-023PC_-_SequenceListing.txt

130

135

140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

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

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 54
<211> 201
<212> PRT
<213> Homo sapiens

<400> 54

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly
1 5 10 15

Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn
20 25 30

Leu Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser
35 40 45

Pro His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly
50 55 60

Lys Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

SHK-HTB-023PC_-_SequenceListing.txt

Thr Leu Lys Val Lys Ala Ser Tyr Arg Lys Ile Asn Thr His Ile Leu
100 105 110

Lys Val Pro Glu Thr Asp Glu Val Glu Leu Thr Cys Gln Ala Thr Gly
115 120 125

Tyr Pro Leu Ala Glu Val Ser Trp Pro Asn Val Ser Val Pro Ala Asn
130 135 140

Thr Ser His Ser Arg Thr Pro Glu Gly Leu Tyr Gln Val Thr Ser Val
145 150 155 160

Leu Arg Leu Lys Pro Pro Pro Gly Arg Asn Phe Ser Cys Val Phe Trp
165 170 175

Asn Thr His Val Arg Glu Leu Thr Leu Ala Ser Ile Asp Leu Gln Ser
180 185 190

Gln Met Glu Pro Arg Thr His Pro Thr
195 200

<210> 55
<211> 235
<212> PRT
<213> Homo sapiens

<400> 55

Leu Ile Ile Gly Phe Gly Ile Ser Gly Arg His Ser Ile Thr Val Thr
1 5 10 15

Thr Val Ala Ser Ala Gly Asn Ile Gly Glu Asp Gly Ile Leu Ser Cys
20 25 30

Thr Phe Glu Pro Asp Ile Lys Leu Ser Asp Ile Val Ile Gln Trp Leu
35 40 45

Lys Glu Gly Val Leu Gly Leu Val His Glu Phe Lys Glu Gly Lys Asp
50 55 60

SHK-HTB-023PC_-_SequenceListing.txt

Glu Leu Ser Glu Gln Asp Glu Met Phe Arg Gly Arg Thr Ala Val Phe
65 70 75 80

Ala Asp Gln Val Ile Val Gly Asn Ala Ser Leu Arg Leu Lys Asn Val
85 90 95

Gln Leu Thr Asp Ala Gly Thr Tyr Lys Cys Tyr Ile Ile Thr Ser Lys
100 105 110

Gly Lys Gly Asn Ala Asn Leu Glu Tyr Lys Thr Gly Ala Phe Ser Met
115 120 125

Pro Glu Val Asn Val Asp Tyr Asn Ala Ser Ser Glu Thr Leu Arg Cys
130 135 140

Glu Ala Pro Arg Trp Phe Pro Gln Pro Thr Val Val Trp Ala Ser Gln
145 150 155 160

Val Asp Gln Gly Ala Asn Phe Ser Glu Val Ser Asn Thr Ser Phe Glu
165 170 175

Leu Asn Ser Glu Asn Val Thr Met Lys Val Val Ser Val Leu Tyr Asn
180 185 190

Val Thr Ile Asn Asn Thr Tyr Ser Cys Met Ile Glu Asn Asp Ile Ala
195 200 205

Lys Ala Thr Gly Asp Ile Lys Val Thr Glu Ser Glu Ile Lys Arg Arg
210 215 220

Ser His Leu Gln Leu Leu Asn Ser Lys Ala Ser
225 230 235

<210> 56
<211> 133
<212> PRT
<213> Homo sapiens

<400> 56

SHK-HTB-023PC_-_SequenceListing.txt

Gln Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val Gln Phe
1 5 10 15

Thr Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys Glu
20 25 30

Asp Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn Cys Asp
35 40 45

Gly Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val Asn
50 55 60

Ile Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys
65 70 75 80

Lys Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr Tyr Lys
85 90 95

Asp Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu Asp Asp
100 105 110

Phe His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly
115 120 125

Glu Phe Cys Val Leu
130

<210> 57
<211> 132
<212> PRT
<213> Homo sapiens

<400> 57

Thr Ser Leu Lys Pro Thr Ala Ile Glu Ser Cys Met Val Lys Phe Glu
1 5 10 15

Leu Ser Ser Ser Lys Trp His Met Thr Ser Pro Lys Pro His Cys Val
20 25 30

Asn Thr Thr Ser Asp Gly Lys Leu Lys Ile Leu Gln Ser Gly Thr Tyr

SHK-HTB-023PC_-_SequenceListing.txt

35

40

45

Leu Ile Tyr Gly Gln Val Ile Pro Val Asp Lys Lys Tyr Ile Lys Asp
50 55 60

Asn Ala Pro Phe Val Val Gln Ile Tyr Lys Lys Asn Asp Val Leu Gln
65 70 75 80

Thr Leu Met Asn Asp Phe Gln Ile Leu Pro Ile Gly Gly Val Tyr Glu
85 90 95

Leu His Ala Gly Asp Asn Ile Tyr Leu Lys Phe Asn Ser Lys Asp His
100 105 110

Ile Gln Lys Thr Asn Thr Tyr Trp Gly Ile Ile Leu Met Pro Asp Leu
115 120 125

Pro Phe Ile Ser
130

<210> 58
<211> 205
<212> PRT
<213> Homo sapiens

<400> 58

Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala
1 5 10 15

Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro
20 25 30

Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala
35 40 45

Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro
50 55 60

Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp
65 70 75 80

SHK-HTB-023PC_-_SequenceListing.txt

Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
85 90 95

Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val
100 105 110

Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala
115 120 125

Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg
130 135 140

Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly
145 150 155 160

Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala
165 170 175

Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr
180 185 190

Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
195 200 205

<210> 59
<211> 195
<212> PRT
<213> Homo sapiens

<400> 59

Ser Gln Leu Arg Ala Gln Gly Glu Ala Cys Val Gln Phe Gln Ala Leu
1 5 10 15

Lys Gly Gln Glu Phe Ala Pro Ser His Gln Gln Val Tyr Ala Pro Leu
20 25 30

Arg Ala Asp Gly Asp Lys Pro Arg Ala His Leu Thr Val Val Arg Gln
35 40 45

SHK-HTB-023PC_-_SequenceListing.txt

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

His Glu Leu Gly Leu Ala Phe Thr Lys Asn Arg Met Asn Tyr Thr Asn
65 70 75 80

Lys Phe Leu Leu Ile Pro Glu Ser Gly Asp Tyr Phe Ile Tyr Ser Gln
85 90 95

Val Thr Phe Arg Gly Met Thr Ser Glu Cys Ser Glu Ile Arg Gln Ala
100 105 110

Gly Arg Pro Asn Lys Pro Asp Ser Ile Thr Val Val Ile Thr Lys Val
115 120 125

Thr Asp Ser Tyr Pro Glu Pro Thr Gln Leu Leu Met Gly Thr Lys Ser
130 135 140

Val Cys Glu Val Gly Ser Asn Trp Phe Gln Pro Ile Tyr Leu Gly Ala
145 150 155 160

Met Phe Ser Leu Gln Glu Gly Asp Lys Leu Met Val Asn Val Ser Asp
165 170 175

Ile Ser Leu Val Asp Tyr Thr Lys Glu Asp Lys Thr Phe Phe Gly Ala
180 185 190

Phe Leu Leu
195

<210> 60
<211> 215
<212> PRT
<213> Homo sapiens

<400> 60

His Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp
1 5 10 15

SHK-HTB-023PC_-_SequenceListing.txt

Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser
20 25 30

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

Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser
50 55 60

Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val
65 70 75 80

Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu
85 90 95

Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly
100 105 110

Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln
115 120 125

Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile
130 135 140

Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu
145 150 155 160

Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser
165 170 175

Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe
180 185 190

Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr
195 200 205

Ser Phe Gly Leu Leu Lys Leu
210 215

SHK-HTB-023PC_-_SequenceListing.txt

<210> 61

<211> 172

<212> PRT

<213> Homo sapiens

<400> 61

Gln Arg Thr Asp Ser Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys
1 5 10 15

Gly Gly Asn Cys Ser Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro
20 25 30

Phe Lys Lys Ser Trp Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys
35 40 45

Thr Lys Leu Ser Trp Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr
50 55 60

Gln Asp Gly Asn Leu Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile
65 70 75 80

Cys Gln Leu Gln Phe Leu Val Gln Cys Pro Asn Asn Ser Val Asp Leu
85 90 95

Lys Leu Glu Leu Leu Ile Asn Lys His Ile Lys Lys Gln Ala Leu Val
100 105 110

Thr Val Cys Glu Ser Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu
115 120 125

Ser Gln Phe Leu Leu Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val
130 135 140

Asn Val Asp Thr Phe Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu
145 150 155 160

Asn Val Leu Ser Ile Phe Leu Tyr Ser Asn Ser Asp
165 170

<210> 62

SHK-HTB-023PC_-_SequenceListing.txt

<211> 243

<212> PRT

<213> Homo sapiens

<400> 62

Thr Asn Glu Leu Lys Gln Met Gln Asp Lys Tyr Ser Lys Ser Gly Ile
1 5 10 15

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

Glu Ser Met Asn Ser Pro Cys Trp Gln Val Lys Trp Gln Leu Arg Gln
35 40 45

Leu Val Arg Lys Met Ile Leu Arg Thr Ser Glu Glu Thr Ile Ser Thr
50 55 60

Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly
65 70 75 80

Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn
85 90 95

Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys
100 105 110

Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn
115 120 125

Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr
130 135 140

Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu
145 150 155 160

Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr
165 170 175

Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys
180 185 190

SHK-HTB-023PC_-_SequenceListing.txt

Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly
195 200 205

Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn
210 215 220

Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe
225 230 235 240

Leu Val Gly

<210> 63
<211> 155
<212> PRT
<213> Homo sapiens

<400> 63

Gln Arg Phe Ala Gln Ala Gln Gln Gln Leu Pro Leu Glu Ser Leu Gly
1 5 10 15

Trp Asp Val Ala Glu Leu Gln Leu Asn His Thr Gly Pro Gln Gln Asp
20 25 30

Pro Arg Leu Tyr Trp Gln Gly Gly Pro Ala Leu Gly Arg Ser Phe Leu
35 40 45

His Gly Pro Glu Leu Asp Lys Gly Gln Leu Arg Ile His Arg Asp Gly
50 55 60

Ile Tyr Met Val His Ile Gln Val Thr Leu Ala Ile Cys Ser Ser Thr
65 70 75 80

Thr Ala Ser Arg His His Pro Thr Thr Leu Ala Val Gly Ile Cys Ser
85 90 95

Pro Ala Ser Arg Ser Ile Ser Leu Leu Arg Leu Ser Phe His Gln Gly
100 105 110

SHK-HTB-023PC_-_SequenceListing.txt

Cys Thr Ile Ala Ser Gln Arg Leu Thr Pro Leu Ala Arg Gly Asp Thr
 115 120 125

Leu Cys Thr Asn Leu Thr Gly Thr Leu Leu Pro Ser Arg Asn Thr Asp
 130 135 140

Glu Thr Phe Phe Gly Val Gln Trp Val Arg Pro
 145 150 155

<210> 64
 <211> 0
 <212> PRT
 <213> Homo sapiens

<400> 64
 000
 <210> 65
 <211> 0
 <212> PRT
 <213> Homo sapiens

<400> 65
 000
 <210> 66
 <211> 0
 <212> PRT
 <213> Homo sapiens

<400> 66
 000
 <210> 67
 <211> 0
 <212> PRT
 <213> Homo sapiens

<400> 67
 000
 <210> 68
 <211> 0
 <212> PRT
 <213> Homo sapiens

<400> 68
 000
 <210> 69
 <211> 0
 <212> PRT
 <213> Homo sapiens

SHK-HTB-023PC_-_SequenceListing.txt

<400> 69

000

<210> 70

<211> 217

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence

<400> 70

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Ser Gly Lys Glu Tyr Lys Cys Lys Val Ser Ser Lys
85 90 95

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Asn Ala Thr Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
115 120 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
130 135 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145 150 155 160

SHK-HTB-023PC_-_SequenceListing.txt

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175

Tyr Ser Arg Leu Thr Val Asp Lys Ser Ser Trp Gln Glu Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Leu Gly Lys
210 215

<210> 71

<211> 217

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence

<400> 71

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Ser Gly Lys Glu Tyr Lys Cys Lys Val Ser Ser Lys
85 90 95

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Asn Ala Thr Gly Gln

SHK-HTB-023PC_-_SequenceListing.txt

100

105

110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
115 120 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
130 135 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145 150 155 160

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175

Tyr Ser Arg Leu Thr Val Asp Lys Ser Ser Trp Gln Glu Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Leu Gly Lys
210 215

<210> 72

<211> 217

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence

<400> 72

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15

Pro Lys Asp Gln Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
35 40 45

SHK-HTB-023PC_-_SequenceListing.txt

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Thr Pro His
65 70 75 80

Ser Asp Trp Leu Ser Gly Lys Glu Tyr Lys Cys Lys Val Ser Ser Lys
85 90 95

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Asn Ala Thr Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
115 120 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
130 135 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145 150 155 160

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175

Tyr Ser Arg Leu Thr Val Asp Lys Ser Ser Trp Gln Glu Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Leu Gly Lys
210 215

<210> 73

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence

SHK-HTB-023PC_-_SequenceListing.txt

<400> 73

Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro
1 5 10

<210> 74

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence

<400> 74

Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
1 5 10

<210> 75

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence

<400> 75

Ser Lys Tyr Gly Pro Pro
1 5

<210> 76

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence

<400> 76

Ile Glu Gly Arg Met Asp
1 5

<210> 77

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence

<400> 77

Gly Gly Gly Val Pro Arg Asp Cys Gly
1 5

<210> 78

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence

<400> 78

Ile Glu Gly Arg Met Asp Gly Gly Gly Gly Ala Gly Gly Gly Gly
1 5 10 15