

SEQUENCE LISTING

<110> Seikagaku Corporation

<120> Horseshoe crab factor B variant

<130> F201805-8009

<150> JP2017-038692

<151> 2017-03-01

<160> 42

<170> PatentIn version 3.5

<210> 1

<211> 1203

<212> DNA

<213> Tachypleus tridentatus

<220>

<223> Tachypleus tridentatus factor B

<400> 1

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<211> 400

<212> PRT

<213> Tachypleus tridentatus

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<400> 2

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Asn Asp Asn Glu Cys Thr Ala Arg Gly Gly Leu Lys Gly Ser Cys Lys
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Ser Leu Ile Asp Cys Pro Ser Val Leu Ala Thr Leu Lys Asp Ser Phe
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Pro Val Val Cys Ser Trp Asn Gly Arg Phe Gln Pro Ile Val Cys Cys
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 Ser Pro Ile Leu Pro Pro Ile Ser Thr Pro Gln Asn Ser Thr Gly Gly
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 Arg Gly Ile Ile Ala Gly Gly Val Glu Ala Lys Ile Gly Ala Trp Pro
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 Trp Met Ala Ala Val Phe Val Lys Asn Phe Gly Ile Gly Arg Phe His
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 Cys Ala Gly Ser Ile Ile Ser Asn Lys Tyr Ile Leu Ser Ala Ala His
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 210 215 220
 Asp Val Ile Ile His Pro His Tyr Val Glu Lys Glu Asn Tyr Asn Asp
 225 230 235 240
 Ile Ala Ile Ile Glu Leu Lys Glu Glu Leu Asn Phe Thr Asp Leu Val
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 260 265 270
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 275 280 285
 Pro Arg Ser Gln Val Leu Arg Glu Val Ser Ile Pro Val Val Pro Val
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 325 330 335
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 340 345 350
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<211> 1203

<212> DNA

<213> *Limulus polyphemus*

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<213> Limulus polyphemus

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<220>
<223> Limulus polyphemus factor B

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35 40 45
Lys Ser Leu Thr Asp Cys Pro Ala Val Leu Ala Thr Leu Lys Asp Ser
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65 70 75 80
Cys Pro Asp Ala Ala Ala Pro Ser Val Thr Thr Thr Val Thr Thr Ile
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Val Pro Thr Lys Glu Thr Lys Ile Pro Arg Leu His Ile Pro Gly Cys
100 105 110
Gly Lys Arg Lys Val Asn Val Asp Ile Thr Thr Ile Gly Arg Ser Gly
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Ser Pro Ile Leu Pro Pro Ile Ser Thr Ser Gln Asp Leu Lys Gly Gly
130 135 140
Arg Gly Ile Ile Ala Gly Gly Val Glu Ala Lys Ile Gly Ala Trp Pro
145 150 155 160
Trp Met Ala Ala Val Phe Val Lys Asn Phe Gly Ile Gly Arg Phe His
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Cys Ala Gly Ser Ile Ile Ser Ser Lys Tyr Ile Leu Ser Ala Ala His
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Ala Phe Leu Ile Gly Gly Arg Lys Leu Thr Pro Thr Arg Leu Ala Val
195 200 205
Arg Val Gly Gly His Tyr Val Lys Met Gly Gln Glu Tyr His Val Glu
210 215 220
Asp Val Ile Ile His Pro Asp Tyr Val Glu Arg Glu Asn Tyr Asn Asp
225 230 235 240
Ile Ala Ile Ile Val Leu Lys Glu Glu Leu Asn Phe Thr Asp Leu Val
245 250 255
Arg Pro Ile Cys Leu Pro Asp Pro Glu Ala Val Thr Asp Ser Leu Lys
260 265 270
Gly Arg Arg Val Thr Val Ala Gly Trp Gly Asp Leu Asp Phe Ala Gly
275 280 285
Pro Arg Ser Gln Val Leu Arg Glu Val Ser Ile Pro Val Val Pro Ile
290 295 300
Gly Asp Cys Asn Lys Ala Tyr Gln Lys Leu Asn Thr Leu Ala Leu Lys
305 310 315 320
Asn Gly Ile Thr Lys Lys Phe Ile Cys Ala Gly Leu Glu Glu Gly Gly
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340 345 350
Asn Ser Ser Trp Ile Val Thr Gly Val Val Ser Phe Gly His Lys Cys
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<211> 1203

<212> DNA

<213> Artificial Sequence

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<223> Tachypleus tridentatus factor B variant

<400> 5

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<223> Tachypleus tridentatus factor B variant

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 <213> Artificial Sequence

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 <223> Tachypleus tridentatus factor B variant

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

<210> 8
 <211> 1203
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Limulus polyphemus factor B variant

<400> 8

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<223> Limulus polyphemus factor B variant

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<213> Artificial Sequence

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<223> Limulus polyphemus factor B variant

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 35 40 45
 Lys Ser Leu Thr Asp Cys Pro Ala Val Leu Ala Thr Leu Lys Asp Ser
 50 55 60
 Phe Pro Val Val Cys Ser Trp Asn Gly Arg Phe Gln Pro Ile Val Cys
 65 70 75 80
 Cys Pro Asp Ala Ala Ala Pro Ser Val Thr Thr Thr Val Thr Thr Ile
 85 90 95
 Val Pro Thr Lys Glu Thr Lys Ile Pro Arg Leu His Ile Pro Gly Cys
 100 105 110
 Gly Lys Arg Lys Val Asn Val Asp Ile Thr Thr Ile Gly Arg Ser Gly
 115 120 125
 Ser Pro Ile Leu Pro Pro Ile Ser Thr Ser Gln Asp Leu Lys Gly Gly
 130 135 140
 Arg Gly Ile Ile Ala Gly Gly Val Glu Ala Lys Ile Gly Ala Trp Pro
 145 150 155 160
 Trp Met Ala Ala Val Phe Val Lys Asn Phe Gly Ile Gly Arg Phe His
 165 170 175
 Cys Ala Gly Ser Ile Ile Ser Ser Lys Tyr Ile Leu Ser Ala Ala His
 180 185 190
 Cys Phe Leu Ile Gly Gly Arg Lys Leu Thr Pro Thr Arg Leu Ala Val
 195 200 205
 Arg Val Gly Gly His Tyr Val Lys Met Gly Gln Glu Tyr His Val Glu
 210 215 220
 Asp Val Ile Ile His Pro Asp Tyr Val Glu Arg Glu Asn Tyr Asn Asp
 225 230 235 240
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 260 265 270
 Gly Arg Arg Val Thr Val Ala Gly Trp Gly Asp Leu Asp Phe Ala Gly
 275 280 285
 Pro Arg Ser Gln Val Leu Arg Glu Val Ser Ile Pro Val Val Pro Ile
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 Gly Asp Cys Asn Lys Ala Tyr Gln Lys Leu Asn Thr Leu Ala Leu Lys
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 Asn Gly Ile Thr Lys Lys Phe Ile Cys Ala Gly Leu Glu Glu Gly Gly
 325 330 335
 Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Leu Val Asn
 340 345 350
 Asn Ser Ser Trp Ile Val Thr Gly Val Val Ser Phe Gly His Lys Cys
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<212> DNA

<213> Tachypleus tridentatus

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Val	Tyr	Val	Thr	Ser	Lys	Gln	Arg	Ala	Trp	Glu	Arg	Ala	Gln	Gly	Val
	450					455					460				
Cys	Thr	Asn	Met	Ala	Ala	Arg	Leu	Ala	Val	Leu	Asp	Lys	Asp	Val	Ile
	465				470					475					480
Pro	Ser	Ser	Leu	Thr	Glu	Thr	Leu	Arg	Gly	Lys	Gly	Leu	Ala	Thr	Thr
				485					490					495	
Trp	Ile	Gly	Leu	His	Arg	Leu	Asp	Ala	Asp	Asn	His	Phe	Ile	Trp	Glu
		500						505					510		
Leu	Met	Asp	Arg	Ser	Ser	Val	Ala	Leu	Asn	Asp	Ser	Leu	Thr	Phe	Trp
		515					520					525			
Ala	Pro	Gly	Glu	Pro	Gly	Asn	Glu	Thr	Asn	Cys	Val	Tyr	Leu	Asp	Ile
	530					535					540				
Gln	Asp	Gln	Leu	Gln	Pro	Val	Trp	Lys	Thr	Lys	Ser	Cys	Phe	Gln	Pro

<220>

<223> Carcinoscorpius rotundicauda factor C

<400> 15

atggtcttag	cgctcgtttt	ggtgtctggt	ttagttctag	ggctactagc	ccaaaaaatg	60
cgcccagttc	agtcctaaagg	agtagatcta	ggcttggtg	atgaaacgag	gttcgagtgt	120
aagtgtggcg	atccaggcta	tgtgttcaac	attccagtga	aacaatgtac	atacttttat	180
cgatggaggc	cgtattgtaa	accatgtgat	gacctggagg	ctaaggatat	ttgtccaaag	240
tacaaacgat	gtcaagagtg	taaggctggt	cttgatagtt	gtgttacttg	tccacctaac	300
aaatatggta	cttgggtgtag	cggtgaatgt	cagtgtgaaga	atggagggtat	ctgtgaccag	360
aggacaggag	cttgtgcatg	tcgtgacaga	tatgaagggg	tgcaactgtga	aattctcaaa	420
ggttgtcctc	ttcttccatc	ggattctcag	gttcagggaag	tcagaaatcc	accagataat	480
ccccaaacta	ttagctacag	ctgttcacca	gggttcaagc	ttaagggtat	ggcacgaatt	540
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atggtttcat	ctccagaaca	tgggaaagtg	aatgctctta	gtgggtgat	gatagaaggg	660
gctactttac	ggttctcatg	ttagatgtcc	tactacttga	ttggtcaaga	aacattaacc	720
tgtcagggtg	atggtcagtg	gaatggacag	ataccacaat	gtaagaactt	ggtcttctgt	780
cctgacctgg	atcctgtaaa	ccatgctgaa	cacaagggtta	aaattgggtg	ggaacaaaaa	840
tatggtcagt	ttcctcaagg	cactgaagtg	acctatacgt	gttcgggtaa	ctacttcttg	900
atgggttttg	acaccttaaa	atgtaaccct	gatgggtctt	ggtcaggatc	acagccatcc	960
tgtgttaaag	tggcagacag	agaggtcgac	tgtgacagta	aagctgtaga	cttcttggat	1020
gatgttgggt	aacctgtcag	gctccactgt	cctgctggct	gttctttgac	agctgggtact	1080
gtgtggggta	cagccatata	ccatgaactt	tcctcagtg	gtcgtgcagc	catccatgct	1140
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tttctgggta	gtgacctgaa	tgggataaaa	tcggaagagt	tgaagtctct	tgcccgaggt	1260
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caaggtgtgt	gtaccaatat	ggctgtcctg	cttgtctgtg	tggacaaaaga	tgtaatcca	1440
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tcactggaaa	atggacacgc	cacacttcat	ggacaaaagta	ttgatgggtt	ctatgctggt	1800
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tgtacaacaa	atggcacatg	gagtgtcctt	aaacctcgat	gtatcaaaagt	catcacctgc	1920
caaaaccccc	ctgtaccatc	atatggttct	gtggaaatca	aacccccaa	tcggacaaac	1980
tcgataaagt	gtgttgggtc	acctttcttg	aggttgccac	ggttaccctt	cccattagct	2040
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tctaaagtta	aactacctga	aggtcattac	cgggtagggt	ctcgagccat	ctacacgtgc	2160
gagtcgagat	actacgaact	acttggatct	caaggcagaa	gatgtgactc	taatggaac	2220
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ccttttatct	ggaatgggaa	ttctacagaa	ataggtcagt	ggccgtggca	ggcaggaatc	2340
tctagatggc	ttgcagacca	caatatgtgg	tttctccagt	gtggaggatc	tctattgaat	2400
gagaaatgga	tcgtcactgc	tgcccactgt	gtcacctact	ctgctactgc	tgagattatt	2460
gacccaatc	agtttaaaat	gtatctgggc	aagtactacc	gtgatgacag	tagagacgat	2520
gactatgtac	aagtaagaga	ggctcttgag	atccacgtga	atcctaacta	cgaccccggc	2580
aatctcaact	ttgacatagc	cctaattcaa	ctgaaaactc	ctgttacttt	gacaacacga	2640
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ttagcagtg	tgacaggttg	gggtttgaat	gaaaacaaca	cctattcaga	gacgattcaa	2760
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ttaccactga	cagtaacaga	gaacatgttc	tgtgcaggtt	acaagaaggg	acgttatgat	2880
gcctgcagt	gggacagtg	aggaccttta	gtgtttgctg	atgattccc	taccgaaagg	2940
cgggtgggtct	tgggaaggat	tgtcagctgg	ggcagtcaca	gtggatgtgg	caaggcgaac	3000
cagtacgggg	gcttactaa	agttaacgtt	ttcctgtcat	ggattaggca	gttcatttga	3060

<210> 16

<211> 1019

<212> PRT

<213> Carcinoscorpius rotundicauda

<220>

<223> Carcinoscorpius rotundicauda factor C

<400> 16

Met Val Leu Ala Ser Phe Leu Val Ser Gly Leu Val Leu Gly Leu Leu
 1 5 10 15
 Ala Gln Lys Met Arg Pro Val Gln Ser Lys Gly Val Asp Leu Gly Leu
 20 25 30
 Cys Asp Glu Thr Arg Phe Glu Cys Lys Cys Gly Asp Pro Gly Tyr Val
 35 40 45
 Phe Asn Ile Pro Val Lys Gln Cys Thr Tyr Phe Tyr Arg Trp Arg Pro
 50 55 60
 Tyr Cys Lys Pro Cys Asp Asp Leu Glu Ala Lys Asp Ile Cys Pro Lys
 65 70 75 80
 Tyr Lys Arg Cys Gln Glu Cys Lys Ala Gly Leu Asp Ser Cys Val Thr
 85 90 95
 Cys Pro Pro Asn Lys Tyr Gly Thr Trp Cys Ser Gly Glu Cys Gln Cys
 100 105 110
 Lys Asn Gly Gly Ile Cys Asp Gln Arg Thr Gly Ala Cys Ala Cys Arg
 115 120 125
 Asp Arg Tyr Glu Gly Val His Cys Glu Ile Leu Lys Gly Cys Pro Leu
 130 135 140
 Leu Pro Ser Asp Ser Gln Val Gln Glu Val Arg Asn Pro Pro Asp Asn
 145 150 155 160
 Pro Gln Thr Ile Asp Tyr Ser Cys Ser Pro Gly Phe Lys Leu Lys Gly
 165 170 175
 Met Ala Arg Ile Ser Cys Leu Pro Asn Gly Gln Trp Ser Asn Phe Pro
 180 185 190
 Pro Lys Cys Ile Arg Glu Cys Ala Met Val Ser Ser Pro Glu His Gly
 195 200 205
 Lys Val Asn Ala Leu Ser Gly Asp Met Ile Glu Gly Ala Thr Leu Arg
 210 215 220
 Phe Ser Cys Asp Ser Pro Tyr Tyr Leu Ile Gly Gln Glu Thr Leu Thr
 225 230 235 240
 Cys Gln Gly Asn Gly Gln Trp Asn Gly Gln Ile Pro Gln Cys Lys Asn
 245 250 255
 Leu Val Phe Cys Pro Asp Leu Asp Pro Val Asn His Ala Glu His Lys
 260 265 270
 Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr
 275 280 285
 Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Gly Phe Asp
 290 295 300
 Thr Leu Lys Cys Asn Pro Asp Gly Ser Trp Ser Gly Ser Gln Pro Ser
 305 310 315 320
 Cys Val Lys Val Ala Asp Arg Glu Val Asp Cys Asp Ser Lys Ala Val
 325 330 335
 Asp Phe Leu Asp Asp Val Gly Glu Pro Val Arg Ile His Cys Pro Ala
 340 345 350
 Gly Cys Ser Leu Thr Ala Gly Thr Val Trp Gly Thr Ala Ile Tyr His
 355 360 365
 Glu Leu Ser Ser Val Cys Arg Ala Ala Ile His Ala Gly Lys Leu Pro
 370 375 380
 Asn Ser Gly Gly Ala Val His Val Val Asn Asn Gly Pro Tyr Ser Asp
 385 390 395 400
 Phe Leu Gly Ser Asp Leu Asn Gly Ile Lys Ser Glu Glu Leu Lys Ser
 405 410 415
 Leu Ala Arg Ser Phe Arg Phe Asp Tyr Val Arg Ser Ser Thr Ala Gly
 420 425 430
 Lys Ser Gly Cys Pro Asp Gly Trp Phe Glu Val Asp Glu Asn Cys Val
 435 440 445
 Tyr Val Thr Ser Lys Gln Arg Ala Trp Glu Arg Ala Gln Gly Val Cys
 450 455 460
 Thr Asn Met Ala Ala Arg Leu Ala Val Leu Asp Lys Asp Val Ile Pro
 465 470 475 480
 Asn Ser Leu Thr Glu Thr Leu Arg Gly Lys Gly Leu Thr Thr Thr Trp
 485 490 495
 Ile Gly Leu His Arg Leu Asp Ala Glu Lys Pro Phe Ile Trp Glu Leu
 500 505 510
 Met Asp Arg Ser Asn Val Val Leu Asn Asp Asn Leu Thr Phe Trp Ala

<211> 1128
 <212> DNA
 <213> Tachypleus tridentatus

<220>
 <223> Tachypleus tridentatus pro-clotting enzyme

<400> 17
 atgttgggtga ataacgtggtt ttcactactg tgtttccac tcttgatgtc tgttggttaga 60
 tgcagtactc tcagcagaca gcgtagacag tttgttttcc ctgacgagga agaactttgc 120
 tcaaaccgat ttactgaaga aggaacatgc aaaaatgtct tggattgtag aatactttta 180
 caaaaaaatg attataattht actcaaagaa tcaatatgct gctttgaagg cataacaccc 240
 aaagtttgtt gtccgaaatc aagccatgta atttcaagta cacaggcacc tccagaaacc 300
 actacgactg aacgccacc aaaacagata ccaccaatc ttcctgaagt gtgtggaatt 360
 cacaatacta caactaccag gattattgga ggctgggaag cacctattgg agcctggccg 420
 tggatgactg ctgtctacat aaaacaagga ggaatcagaa gtgttcagtg tgggtggcgca 480
 cttgtcacta acaggcagct gattacagct tcgcactgtg ttgtaaacag tgcaggaaca 540
 gatgtgatgc cagctgatgt attctcggtt cgtctgggtg aacacaattt atacagtacc 600
 gatgacgatt cgaatccaat agattttgca gttacgtcgg tgaacatca cgaacacttt 660
 gtactcgcga cgtatttgaa tgacatcgca attctaactg taaatgacac agttacgttt 720
 acagacagaa ttcgaccat ttgtctacct tatcgttaagt tgagatacga tgatctagca 780
 atgagaaaaa cgtttatcac tggatgggga acaacagcat ttaacggccc atctagtga 840
 gtgttgagag aagtacagtt accaatatgg gaacacgagg cctgtagaca ggcctacgag 900
 aaggatttaa atattacaa cgtgtatatg tgtgctggct ttgcagatgg cgggaaggat 960
 gcttgccagg gtgattctgg aggtccaatg atgttcctg ttaaaaccgg agagttttat 1020
 ctcatgggaa ttgtgtcttt cggaaagaaa tgcgcattgc ctggatttcc tgggggtttac 1080
 acaaaagtga cagagttttt agattggatt gcagaacata tgggtgtag 1128

<210> 18
 <211> 375
 <212> PRT
 <213> Tachypleus tridentatus

<220>
 <223> Tachypleus tridentatus pro-clotting enzyme

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

Tyr Leu Asn Asp Ile Ala Ile Leu Thr Leu Asn Asp Thr Val Thr Phe
 225 230 235 240
 Thr Asp Arg Ile Arg Pro Ile Cys Leu Pro Tyr Arg Lys Leu Arg Tyr
 245 250 255
 Asp Asp Leu Ala Met Arg Lys Pro Phe Ile Thr Gly Trp Gly Thr Thr
 260 265 270
 Ala Phe Asn Gly Pro Ser Ser Ala Val Leu Arg Glu Val Gln Leu Pro
 275 280 285
 Ile Trp Glu His Glu Ala Cys Arg Gln Ala Tyr Glu Lys Asp Leu Asn
 290 295 300
 Ile Thr Asn Val Tyr Met Cys Ala Gly Phe Ala Asp Gly Gly Lys Asp
 305 310 315 320
 Ala Cys Gln Gly Asp Ser Gly Gly Pro Met Met Leu Pro Val Lys Thr
 325 330 335
 Gly Glu Phe Tyr Leu Ile Gly Ile Val Ser Phe Gly Lys Lys Cys Ala
 340 345 350
 Leu Pro Gly Phe Pro Gly Val Tyr Thr Lys Val Thr Glu Phe Leu Asp
 355 360 365
 Trp Ile Ala Glu His Met Val
 370 375

<210> 19
 <211> 1128
 <212> DNA
 <213> Limulus polyphemus

<220>
 <223> Limulus polyphemus pro-clotting enzyme

<400> 19
 atgttggtga ataacatggtt ttcattgctg tgtttccac tcctgatgtc tatgttttagc 60
 tgcagtagtc tcggcagaca gcgtagacag tttgttttcc ccgatgatga agaatacatgc 120
 tcaaacgat ttactaacga tggaatatgt aaagatgttt tgaattgtag agatctttta 180
 caaaaaatg attataattt actgaaagaa tcaatatgctg gttttgaagg cataacaccc 240
 aaagtttggt gtccgaaaca aagtattgta aatccaataa cagaagcacc tccaaaaacc 300
 actacaactg aacgaccgcc aatacggata ccatccaatc ttcctaaaca gtgtggaaat 360
 cgtaatatga caactaccag gattattgga gggcaggaag caacacctgg agcctggccc 420
 tggatggctg ctgtctatat caaacaagga ggaatcagaa gtgttcagtg tggagggtgcg 480
 cttgtcacca acaggcacgt gattacagca tcgcactgtg ttgtaaacag tttaggaaca 540
 gatgtgatgc gagctgacgt attctcggtt cgcctagggtg aacacaattt atatagcacc 600
 aatgacagtt cagatccaat tgattttgca gttacgtcag tgaacatca tgaaaacttt 660
 gtgctcgcga cgtatttgaa tgatatgca attctgaagt taaacgacac tgttacgttt 720
 acgcacaaaa ttaaaccaat ttgtctacct tatgaaagct taaggatatga ggatctagca 780
 atgagaaacc cttttgtcgc cggatgggga acaacagcat ttaatggccc atctagtgc 840
 gtattacgag aagtgcagtt accaatatgg ggacacgagc cctgcaggca ggcttacgag 900
 aaggatttaa atattacaaa cgtgtatatg tgtgctgggt atgcagatgg cggtaaagat 960
 gcttgccagg gtgattctgg aggtccaatg atgttgctg ataaaaagcgg gaacttttat 1020
 ctcgttgga ttgtgtcttt cggaaagaaa tgcgcgttgc ctggatttcc tggggtttac 1080
 acaaaagtga ccgaattttt agattggatt gcagtaaata tgggtgtag 1128

<210> 20
 <211> 375
 <212> PRT
 <213> Limulus polyphemus

<220>
 <223> Limulus polyphemus pro-clotting enzyme

<400> 20
 Met Leu Val Asn Asn Met Phe Ser Leu Leu Cys Phe Pro Leu Leu Met
 1 5 10 15
 Ser Met Phe Ser Cys Ser Ser Leu Gly Arg Gln Arg Arg Gln Phe Val
 20 25 30
 Phe Pro Asp Asp Glu Glu Ser Cys Ser Asn Arg Phe Thr Asn Asp Gly
 35 40 45

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

<210> 21
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> designed primer (primer 1)

<400> 21
 gggaccggta gaggagtaga tctgggc

27

<210> 22
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> designed primer (primer 2)

<400> 22
 gggctcgagt cattaaatga actgcctaatt

30

<210> 23
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> designed primer (primer 3)

 <400> 23
 ggggaattca agcttgccac catggtctta gcgtcgttt 39

 <210> 24
 <211> 49
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> designed primer (primer 4)

 <400> 24
 gccctcgatg tgatggtgat ggtggtggga ctgaactgga cgcatttgt 49

 <210> 25
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> designed primer (primer 5)

 <400> 25
 agaagaggag tagatctggg cttgtgtg 28

 <210> 26
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> designed primer (primer 6)

 <400> 26
 gggaccgggc accaccatca ccatcacatc 30

 <210> 27
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> designed primer (primer 7)

 <400> 27
 tctagattat caaatgaact gcctaattcca 30

 <210> 28
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> BGH reverse primer

 <400> 28
 tagaaggcac agtcgagg 18

<210> 29
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> designed primer (primer 8)

 <400> 29
 agcctctgct aaccatgttc atgc 24

 <210> 30
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> designed primer (primer 9)

 <400> 30
 gggaccggtg tgggggtcct cttcccc 27

 <210> 31
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> designed primer (primer 10)

 <400> 31
 gggctcgagt tagttagtga cggcatgac 30

 <210> 32
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> designed primer (primer 11)

 <400> 32
 cttccttatc ggaggtcgaa agttgacccc aactc 35

 <210> 33
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> designed primer (primer 12)

 <400> 33
 cagtgggcag ctgacaaaat gtacttgta ctgat 35

 <210> 34
 <211> 57
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> designed primer (primer 13)

 <400> 34

gggaccggtc accaccatca ccatcacatc gagggcagaa gaggagtaga tctgggc 57

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

<220>
 <223> designed primer (primer 14)

<400> 35
 gggctcgagt caaatgaact gccgaatcca cgata 35

<210> 36
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> designed primer (primer 15)

<400> 36
 ggggaattca agcttgccac catggcgtgg atttgtgtg 39

<210> 37
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> designed primer (primer 16)

<400> 37
 acctcaatg aggaagcagt gggcagcaga caa 33

<210> 38
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> designed primer (primer 17)

<400> 38
 ttgtctgctg cccactgctt cctcattgga ggt 33

<210> 39
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> designed primer (primer 18)

<400> 39
 gggctcgagt cagttagtga ctgcctggtc taacg 35

<210> 40
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> designed primer (primer 19)

<400> 40	
gggctcgagt cagtgatggt gatggtggtg gttagtgact gcctgggc	48
<210> 41	
<211> 35	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> designed primer (primer 20)	
<400> 41	
gggaccggtg tggggatcat ctttcctaag acaca	35
<210> 42	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> designed primer (primer 21)	
<400> 42	
caccagccac caccttctga tag	23