

02159303
SEQUENCE LISTING

<110> University of Bologna
 <120> TATk-CDKL5 FUSION PROTEINS, COMPOSITONS, FORMULATIONS, AND USE
 <130> 221006-1020
 <150> US 61/946,280
 <151> 2014-02-28
 <160> 16
 <170> PatentIn version 3.5
 <210> 1
 <211> 727
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CDKL5
 <400> 1
 gtgagcaagg gcgaggagct gttcaccggg gtggtgccca tcctggtcga gctggacggc 60
 gacgtaaacg gccacaagtt cagcgtgtcc ggcgagggcg agggcgatgc cacctacggc 120
 aagctgaccc tgaagttcat ctgcaccacc ggcaagctgc ccgtgccctg gcccaccctc 180
 gtgaccaccc tgacctacgg cgtgcagtgc ttcagccgct accccgacca catgaagcag 240
 cacgacttct tcaagtccgc catgcccga ggtctacgtcc aggagcgcac catcttcttc 300
 aaggacgacg gcaactacaa gaccgcgcc gaggtgaagt tcgagggcga caccctggtg 360
 aaccgcatcg agctgaaggg catcgacttc aaggaggacg gcaacatcct ggggcacaag 420
 ctggagtaca actacaacag ccacaacgtc tatatcatgg ccgacaagca gaagaacggc 480
 atcaaggtga acttcaagat ccgccacaac atcgaggacg gcagcgtgca gctcgccgac 540
 cactaccagc agaacacccc catcggcgac ggccccgtgc tgctgcccga caaccactac 600
 ctgagcaccc agtccgccct gagcaaagac cccaacgaga agcgcgatca catggtcctg 660
 ctggagtctg tgaccgccgc cgggatcact ctcggcatgg acgagctgta caagtccgga 720
 ctcatg 727

<210> 2
 <211> 1029
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDKL5

<400> 2

Lys Ile Pro Asn Ile Gly Asn Val Met Asn Lys Phe Glu Ile Leu Gly
 1 5 10 15

Val Val Gly Glu Gly Ala Tyr Gly Val Val Leu Lys Cys Arg His Lys
 20 25 30

02159303

Glu Thr His Glu Ile Val Ala Ile Lys Lys Phe Lys Asp Ser Glu Glu
35 40 45

Asn Glu Glu Val Lys Glu Thr Thr Leu Arg Glu Leu Lys Met Leu Arg
50 55 60

Thr Leu Lys Gln Glu Asn Ile Val Glu Leu Lys Glu Ala Phe Arg Arg
65 70 75 80

Arg Gly Lys Leu Tyr Leu Val Phe Glu Tyr Val Glu Lys Asn Met Leu
85 90 95

Glu Leu Leu Glu Glu Met Pro Asn Gly Val Pro Pro Glu Lys Val Lys
100 105 110

Ser Tyr Ile Tyr Gln Leu Ile Lys Ala Ile His Trp Cys His Lys Asn
115 120 125

Asp Ile Val His Arg Asp Ile Lys Pro Glu Asn Leu Leu Ile Ser His
130 135 140

Asn Asp Val Leu Lys Leu Cys Asp Phe Gly Phe Ala Arg Asn Leu Ser
145 150 155 160

Glu Gly Asn Asn Ala Asn Tyr Thr Glu Tyr Val Ala Thr Arg Trp Tyr
165 170 175

Arg Ser Pro Glu Leu Leu Leu Gly Ala Pro Tyr Gly Lys Ser Val Asp
180 185 190

Met Trp Ser Val Gly Cys Ile Leu Gly Glu Leu Ser Asp Gly Gln Pro
195 200 205

Leu Phe Pro Gly Glu Ser Glu Ile Asp Gln Leu Phe Thr Ile Gln Lys
210 215 220

Val Leu Gly Pro Leu Pro Ser Glu Gln Met Lys Leu Phe Tyr Ser Asn
225 230 235 240

Pro Arg Phe His Gly Leu Arg Phe Pro Ala Val Asn His Pro Gln Ser
245 250 255

Leu Glu Arg Arg Tyr Leu Gly Ile Leu Asn Ser Val Leu Leu Asp Leu
260 265 270

Met Lys Asn Leu Leu Lys Leu Asp Pro Ala Asp Arg Tyr Leu Thr Glu
275 280 285

Gln Cys Leu Asn His Pro Thr Phe Gln Thr Gln Arg Leu Leu Asp Arg
290 295 300

02159303

Ser Pro Ser Arg Ser Ala Lys Arg Lys Pro Tyr His Val Glu Ser Ser
305 310 315 320

Thr Leu Ser Asn Arg Asn Gln Ala Gly Lys Ser Thr Ala Leu Gln Ser
325 330 335

His His Arg Ser Asn Ser Lys Asp Ile Gln Asn Leu Ser Val Gly Leu
340 345 350

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

Asn Leu Ala Gly Ala Ser Leu Ser Pro Leu His Thr Lys Thr Tyr Gln
370 375 380

Ala Ser Ser Gln Pro Gly Ser Thr Ser Lys Asp Leu Thr Asn Asn Asn
385 390 395 400

Ile Pro His Leu Leu Ser Pro Lys Glu Ala Lys Ser Lys Thr Glu Phe
405 410 415

Asp Phe Asn Ile Asp Pro Lys Pro Ser Glu Gly Pro Gly Thr Lys Tyr
420 425 430

Leu Lys Ser Asn Ser Arg Ser Gln Gln Asn Arg His Ser Phe Met Glu
435 440 445

Ser Ser Gln Ser Lys Ala Gly Thr Leu Gln Pro Asn Glu Lys Gln Ser
450 455 460

Arg His Ser Tyr Ile Asp Thr Ile Pro Gln Ser Ser Arg Ser Pro Ser
465 470 475 480

Tyr Arg Thr Lys Ala Lys Ser His Gly Ala Leu Ser Asp Ser Lys Ser
485 490 495

Val Ser Asn Leu Ser Glu Ala Arg Ala Gln Ile Ala Glu Pro Ser Thr
500 505 510

Ser Arg Tyr Phe Pro Ser Ser Cys Leu Asp Leu Asn Ser Pro Thr Ser
515 520 525

Pro Thr Pro Thr Arg His Ser Asp Thr Arg Thr Leu Leu Ser Pro Ser
530 535 540

Gly Arg Asn Asn Arg Asn Glu Gly Thr Leu Asp Ser Arg Arg Thr Thr
545 550 555 560

Thr Arg His Ser Lys Thr Met Glu Glu Leu Lys Leu Pro Glu His Met
565 570 575

02159303

Asp Ser Ser His Ser His Ser Leu Ser Ala Pro His Glu Ser Phe Ser
580 585 590

Tyr Gly Leu Gly Tyr Thr Ser Pro Phe Ser Ser Gln Gln Arg Pro His
595 600 605

Arg His Ser Met Tyr Val Thr Arg Asp Lys Val Arg Ala Lys Gly Leu
610 615 620

Asp Gly Ser Leu Ser Ile Gly Gln Gly Met Ala Ala Arg Ala Asn Ser
625 630 635 640

Leu Gln Leu Leu Ser Pro Gln Pro Gly Glu Gln Leu Pro Pro Glu Met
645 650 655

Thr Val Ala Arg Ser Ser Val Lys Glu Thr Ser Arg Glu Gly Thr Ser
660 665 670

Ser Phe His Thr Arg Gln Lys Ser Glu Gly Gly Val Tyr His Asp Pro
675 680 685

His Ser Asp Asp Gly Thr Ala Pro Lys Glu Asn Arg His Leu Tyr Asn
690 695 700

Asp Pro Val Pro Arg Arg Val Gly Ser Phe Tyr Arg Val Pro Ser Pro
705 710 715 720

Arg Pro Asp Asn Ser Phe His Glu Asn Asn Val Ser Thr Arg Val Ser
725 730 735

Ser Leu Pro Ser Glu Ser Ser Ser Gly Thr Asn His Ser Lys Arg Gln
740 745 750

Pro Ala Phe Asp Pro Trp Lys Ser Pro Glu Asn Ile Ser His Ser Glu
755 760 765

Gln Leu Lys Glu Lys Glu Lys Gln Gly Phe Phe Arg Ser Met Lys Lys
770 775 780

Lys Lys Lys Lys Ser Gln Thr Val Pro Asn Ser Asp Ser Pro Asp Leu
785 790 795 800

Leu Thr Leu Gln Lys Ser Ile His Ser Ala Ser Thr Pro Ser Ser Arg
805 810 815

Pro Lys Glu Trp Arg Pro Glu Lys Ile Ser Asp Leu Gln Thr Gln Ser
820 825 830

Gln Pro Leu Lys Ser Leu Arg Lys Leu Leu His Leu Ser Ser Ala Ser
835 840 845

02159303

Asn His Pro Ala Ser Ser Asp Pro Arg Phe Gln Pro Leu Thr Ala Gln
850 855 860

Gln Thr Lys Asn Ser Phe Ser Glu Ile Arg Ile His Pro Leu Ser Gln
865 870 875 880

Ala Ser Gly Gly Ser Ser Asn Ile Arg Gln Glu Pro Ala Pro Lys Gly
885 890 895

Arg Pro Ala Leu Gln Leu Pro Asp Gly Gly Cys Asp Gly Arg Arg Gln
900 905 910

Arg His His Ser Gly Pro Gln Asp Arg Arg Phe Met Leu Arg Thr Thr
915 920 925

Glu Gln Gln Gly Glu Tyr Phe Cys Cys Gly Asp Pro Lys Lys Pro His
930 935 940

Thr Pro Cys Val Pro Asn Arg Ala Leu His Arg Pro Ile Ser Ser Pro
945 950 955 960

Ala Pro Tyr Pro Val Leu Gln Val Arg Gly Thr Ser Met Cys Pro Thr
965 970 975

Leu Gln Val Arg Gly Thr Asp Ala Phe Ser Cys Pro Thr Gln Gln Ser
980 985 990

Gly Phe Ser Phe Phe Val Arg His Val Met Arg Glu Ala Leu Ile His
995 1000 1005

Arg Ala Gln Val Asn Gln Ala Ala Leu Leu Thr Tyr His Glu Asn
1010 1015 1020

Ala Ala Leu Thr Gly Lys
1025

<210> 3
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> TATk

<400> 3
tacgccagaa aggccgccag gcaggccagg gca

33

<210> 4
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> TATk

02159303

<400> 4

Tyr Ala Arg Lys Ala Ala Arg Gln Ala Arg Ala
1 5 10

<210> 5
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Igk-chain leader sequence

<400> 5
atggagacag acacactcct gctatgggta ctgctgctct gggttccagg ttccactggt 60

<210> 6
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Igk-chain leder sequence

<400> 6
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly
20

<210> 7
<211> 3318
<212> DNA
<213> Artificial Sequence

<220>
<223> TATk-CDKL5 fusion protein cDNA

<400> 7
atggagacag acacactcct gctatgggta ctgctgctct gggttccagg ttccactggt 60
gacgcggccc agccggccag gcgcgcgcgc cgtacgaagc ttgcggccta cgccagaaaag 120
gccgccaggc aggccagggc accggtgaag attcctaaca ttggtaatgt gatgaataaa 180
tttgagatcc ttgggggttgt aggtgaagga gcctatggag ttgtacttaa atgcagacac 240
aaggaaacac atgaaattgt ggcgatcaag aaattcaagg acagtgaaga aaatgaagaa 300
gtcaaagaaa cgactttacg agagcttaaa atgcttcgga ctctcaagca ggaaaacatt 360
gtggagtiga aggaagcatt tcgtcggagg ggaaagtgtt acttgggtgtt tgagtatgtt 420
gaaaaaaata tgctcgaatt gctggaagaa atgccaaatg gaggttccacc tgagaaagta 480
aaaagctaca tctatcagct aatcaaggct attcactggt gccataagaa tgatattgtc 540
catcgagata taaaaccaga aaatctctta atcagccaca atgatgtcct aaaactgtgt 600
gactttggtt ttgctcgtaa tctgtcagaa ggcaataatg ctaattacac agagtacgtt 660

02159303

gccaccagat	ggtatcgggtc	cccagaactc	ttacttggcg	ctccctatgg	aaagtccgtg	720
gacatgtggt	cggtgggctg	tattcttggg	gagcttagcg	atggacagcc	tttatttcct	780
ggagaaagtg	aaattgacca	actttttact	attcagaagg	tgctaggacc	acttccatct	840
gagcagatga	agctttttcta	cagtaatcct	cgcttccatg	ggctccggtt	tccagctgtt	900
aaccatcctc	agtccttgga	aagaagatac	cttgggaattt	tgaatagtgt	tctacttgac	960
ctaatgaaga	atttactgaa	gttggaccca	gctgacagat	acttgacaga	acagtgtttg	1020
aatcaccccta	catttcaaac	ccagagactt	ctggatcggt	ctccttcaag	gtcagcaaaa	1080
agaaaacctt	accatgtgga	aagcagcaca	ttgtctaata	gaaaccaagc	cggcaaaagt	1140
actgctttgc	agtctcacca	cagatctaac	agcaaggaca	tccagaacct	gagtgtaggc	1200
ctgccccggg	ctgacgaagg	tctccctgcc	aatgaaaagct	tcctaaatgg	aaaccttgct	1260
ggagctagtc	ttagtccact	gcacaccaaa	acctaccaag	caagcagcca	gcctgggtct	1320
accagcaaag	atctcaccaa	caacaacata	ccacaccttc	ttagcccaaa	agaagccaag	1380
tcaaaaacag	agtttgattt	taatattgac	ccaaagcctt	cagaaggccc	agggacaaag	1440
tacctcaagt	caaacagcag	atctcagcag	aaccgccact	cattcatgga	aagctctcaa	1500
agcaaagctg	ggacactgca	gcccfaatga	aagcagagtc	ggcatagcta	tattgacaca	1560
attccccagt	cctctaggag	tccctcctac	aggaccaagg	ccaaaagcca	tggggcactg	1620
agtgactcca	agtctgtgag	caacctttct	gaagccaggg	cccaaattgc	ggagcccagt	1680
accagtaggt	acttcccata	tagctgctta	gacttgaatt	ctcccaccag	cccaaccccc	1740
accagacaca	gtgacacgag	aactttgctc	agcccttctg	gaagaaataa	ccgaaatgag	1800
ggaacgctgg	actcacgtcg	aaccacaacc	agacattcta	agacgatgga	ggaattgaag	1860
ctgccggagc	acatggacag	tagccattcc	cattcactgt	ctgcacctca	cgaatctttt	1920
tcttatggac	tgggctacac	cagccccttt	tcttcccagc	aacgtcctca	taggcattct	1980
atgtatgtga	cccgtgacaa	agtgagagcc	aagggcttgg	atggaagctt	gagcataggg	2040
caagggatgg	cagctagagc	caacagcctg	caactcttgt	caccccagcc	tggagaacag	2100
ctccctccag	agatgactgt	ggcaagatct	tcgggtcaaag	agacctccag	agaaggcacc	2160
tcttccttcc	atacacgcca	gaagtctgag	ggtggagtgt	atcatgaccc	acactctgat	2220
gatggcacag	cccccaaaga	aaatagacac	ctatacaatg	atcctgtgcc	aaggagagtt	2280
ggtagctttt	acagagtgcc	atctccacgt	ccagacaatt	ctttccatga	aaataatgtg	2340
tcaactagag	tttcttctct	accatcagag	agcagttctg	gaaccaacca	ctcaaaaaga	2400
caaccagcat	tcgatccatg	gaaaagtcct	gaaaatatta	gtcattcaga	gcaactcaag	2460
gaaaaagaga	agcaaggatt	tttcagggtca	atgaaaaaga	aaaagaagaa	atctcaaaca	2520
gtacccaatt	ccgacagccc	tgatcttctg	acgttgcaga	aatccattca	ttctgctagc	2580
actccaagca	gcagaccaaa	ggagtggcgc	cccgagaaga	tctcagatct	gcagacccaa	2640
agccagccat	taaaatcact	gcgcaagttg	ttacatctct	cttcggcctc	aaatcacccg	2700

02159303

gcttcctcag atccccgctt ccagccctta acagctcaac aaaccaaaaa ttccttctca	2760
gaaattcgga ttcaccccct gagccaggcc tctggcggga gcagcaacat ccggcaggaa	2820
cccgaccga agggcaggcc agccctccag ctgccagacg gtggatgtga tggcagaaga	2880
cagagacacc attctggacc ccaagataga cgcttcatgt taaggacgac agaacaacaa	2940
ggagaatact tctgctgtgg tgacccaaag aagcctcaca ctccgtgcgt cccaaaccga	3000
gcccttcacg gtccaatctc cagtctgtct ccctatccag tactccaggt ccgaggcact	3060
tccatgtgcc cgacactcca ggtccgaggc actgatgctt tcagctgccc aaccagcaa	3120
tccgggttct ctttcttcgt gagacacgtt atgagggaaag ccctgattca cagggcccag	3180
gtaaaccaag ctgcgctcct gacataccat gagaatgcgg cactgacggg caagtccgct	3240
cgaggagggc ccgaacaaaa actcatctca gaagaggatc tgaatagcgc cgtcgaccat	3300
catcatcatc atcattga	3318

<210> 8
 <211> 1105
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> TATk-CDKL5 fusion protein polypeptide
 <400> 8

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro
1				5					10					15	
Gly	Ser	Thr	Gly	Asp	Ala	Ala	Gln	Pro	Ala	Arg	Arg	Ala	Arg	Arg	Thr
			20					25					30		
Lys	Leu	Ala	Ala	Tyr	Ala	Arg	Lys	Ala	Ala	Arg	Gln	Ala	Arg	Ala	Pro
		35					40					45			
Val	Lys	Ile	Pro	Asn	Ile	Gly	Asn	Val	Met	Asn	Lys	Phe	Glu	Ile	Leu
	50					55					60				
Gly	Val	Val	Gly	Glu	Gly	Ala	Tyr	Gly	Val	Val	Leu	Lys	Cys	Arg	His
65					70					75					80
Lys	Glu	Thr	His	Glu	Ile	Val	Ala	Ile	Lys	Lys	Phe	Lys	Asp	Ser	Glu
				85					90					95	
Glu	Asn	Glu	Glu	Val	Lys	Glu	Thr	Thr	Leu	Arg	Glu	Leu	Lys	Met	Leu
			100					105					110		
Arg	Thr	Leu	Lys	Gln	Glu	Asn	Ile	Val	Glu	Leu	Lys	Glu	Ala	Phe	Arg
		115					120					125			
Arg	Arg	Gly	Lys	Leu	Tyr	Leu	Val	Phe	Glu	Tyr	Val	Glu	Lys	Asn	Met
	130					135					140				

02159303

Leu 145	Glu	Leu	Leu	Glu	Glu 150	Met	Pro	Asn	Gly	Val 155	Pro	Pro	Glu	Lys	Val 160
Lys	Ser	Tyr	Ile	Tyr 165	Gln	Leu	Ile	Lys	Ala 170	Ile	His	Trp	Cys	His 175	Lys
Asn	Asp	Ile	Val 180	His	Arg	Asp	Ile	Lys 185	Pro	Glu	Asn	Leu	Leu 190	Ile	Ser
His	Asn	Asp 195	Val	Leu	Lys	Leu	Cys 200	Asp	Phe	Gly	Phe	Ala 205	Arg	Asn	Leu
Ser	Glu 210	Gly	Asn	Asn	Ala	Asn 215	Tyr	Thr	Glu	Tyr	Val 220	Ala	Thr	Arg	Trp
Tyr 225	Arg	Ser	Pro	Glu	Leu 230	Leu	Leu	Gly	Ala	Pro 235	Tyr	Gly	Lys	Ser	Val 240
Asp	Met	Trp	Ser	Val 245	Gly	Cys	Ile	Leu	Gly 250	Glu	Leu	Ser	Asp	Gly 255	Gln
Pro	Leu	Phe	Pro 260	Gly	Glu	Ser	Glu	Ile 265	Asp	Gln	Leu	Phe	Thr 270	Ile	Gln
Lys	Val	Leu 275	Gly	Pro	Leu	Pro	Ser 280	Glu	Gln	Met	Lys	Leu 285	Phe	Tyr	Ser
Asn 290	Pro	Arg	Phe	His	Gly	Leu 295	Arg	Phe	Pro	Ala	Val 300	Asn	His	Pro	Gln
Ser 305	Leu	Glu	Arg	Arg	Tyr 310	Leu	Gly	Ile	Leu	Asn 315	Ser	Val	Leu	Leu	Asp 320
Leu	Met	Lys	Asn	Leu 325	Leu	Lys	Leu	Asp	Pro 330	Ala	Asp	Arg	Tyr	Leu 335	Thr
Glu	Gln	Cys	Leu 340	Asn	His	Pro	Thr	Phe 345	Gln	Thr	Gln	Arg	Leu 350	Leu	Asp
Arg	Ser	Pro 355	Ser	Arg	Ser	Ala	Lys 360	Arg	Lys	Pro	Tyr	His 365	Val	Glu	Ser
Ser	Thr 370	Leu	Ser	Asn	Arg	Asn 375	Gln	Ala	Gly	Lys	Ser 380	Thr	Ala	Leu	Gln
Ser 385	His	His	Arg	Ser	Asn 390	Ser	Lys	Asp	Ile	Gln 395	Asn	Leu	Ser	Val	Gly 400
Leu	Pro	Arg	Ala	Asp 405	Glu	Gly	Leu	Pro	Ala 410	Asn	Glu	Ser	Phe	Leu 415	Asn

02159303

Gly Asn Leu Ala Gly Ala Ser Leu Ser Pro Leu His Thr Lys Thr Tyr
420 425 430

Gln Ala Ser Ser Gln Pro Gly Ser Thr Ser Lys Asp Leu Thr Asn Asn
435 440 445

Asn Ile Pro His Leu Leu Ser Pro Lys Glu Ala Lys Ser Lys Thr Glu
450 455 460

Phe Asp Phe Asn Ile Asp Pro Lys Pro Ser Glu Gly Pro Gly Thr Lys
465 470 475 480

Tyr Leu Lys Ser Asn Ser Arg Ser Gln Gln Asn Arg His Ser Phe Met
485 490 495

Glu Ser Ser Gln Ser Lys Ala Gly Thr Leu Gln Pro Asn Glu Lys Gln
500 505 510

Ser Arg His Ser Tyr Ile Asp Thr Ile Pro Gln Ser Ser Arg Ser Pro
515 520 525

Ser Tyr Arg Thr Lys Ala Lys Ser His Gly Ala Leu Ser Asp Ser Lys
530 535 540

Ser Val Ser Asn Leu Ser Glu Ala Arg Ala Gln Ile Ala Glu Pro Ser
545 550 555 560

Thr Ser Arg Tyr Phe Pro Ser Ser Cys Leu Asp Leu Asn Ser Pro Thr
565 570 575

Ser Pro Thr Pro Thr Arg His Ser Asp Thr Arg Thr Leu Leu Ser Pro
580 585 590

Ser Gly Arg Asn Asn Arg Asn Glu Gly Thr Leu Asp Ser Arg Arg Thr
595 600 605

Thr Thr Arg His Ser Lys Thr Met Glu Glu Leu Lys Leu Pro Glu His
610 615 620

Met Asp Ser Ser His Ser His Ser Leu Ser Ala Pro His Glu Ser Phe
625 630 635 640

Ser Tyr Gly Leu Gly Tyr Thr Ser Pro Phe Ser Ser Gln Gln Arg Pro
645 650 655

His Arg His Ser Met Tyr Val Thr Arg Asp Lys Val Arg Ala Lys Gly
660 665 670

Leu Asp Gly Ser Leu Ser Ile Gly Gln Gly Met Ala Ala Arg Ala Asn
675 680 685

02159303

Ser Leu Gln Leu Leu Ser Pro Gln Pro Gly Glu Gln Leu Pro Pro Glu
690 695 700

Met Thr Val Ala Arg Ser Ser Val Lys Glu Thr Ser Arg Glu Gly Thr
705 710 715 720

Ser Ser Phe His Thr Arg Gln Lys Ser Glu Gly Gly Val Tyr His Asp
725 730 735

Pro His Ser Asp Asp Gly Thr Ala Pro Lys Glu Asn Arg His Leu Tyr
740 745 750

Asn Asp Pro Val Pro Arg Arg Val Gly Ser Phe Tyr Arg Val Pro Ser
755 760 765

Pro Arg Pro Asp Asn Ser Phe His Glu Asn Asn Val Ser Thr Arg Val
770 775 780

Ser Ser Leu Pro Ser Glu Ser Ser Ser Gly Thr Asn His Ser Lys Arg
785 790 795 800

Gln Pro Ala Phe Asp Pro Trp Lys Ser Pro Glu Asn Ile Ser His Ser
805 810 815

Glu Gln Leu Lys Glu Lys Glu Lys Gln Gly Phe Phe Arg Ser Met Lys
820 825 830

Lys Lys Lys Lys Lys Ser Gln Thr Val Pro Asn Ser Asp Ser Pro Asp
835 840 845

Leu Leu Thr Leu Gln Lys Ser Ile His Ser Ala Ser Thr Pro Ser Ser
850 855 860

Arg Pro Lys Glu Trp Arg Pro Glu Lys Ile Ser Asp Leu Gln Thr Gln
865 870 875 880

Ser Gln Pro Leu Lys Ser Leu Arg Lys Leu Leu His Leu Ser Ser Ala
885 890 895

Ser Asn His Pro Ala Ser Ser Asp Pro Arg Phe Gln Pro Leu Thr Ala
900 905 910

Gln Gln Thr Lys Asn Ser Phe Ser Glu Ile Arg Ile His Pro Leu Ser
915 920 925

Gln Ala Ser Gly Gly Ser Ser Asn Ile Arg Gln Glu Pro Ala Pro Lys
930 935 940

Gly Arg Pro Ala Leu Gln Leu Pro Asp Gly Gly Cys Asp Gly Arg Arg
945 950 955 960

02159303

Gln Arg His His Ser Gly Pro Gln Asp Arg Arg Phe Met Leu Arg Thr
965 970 975

Thr Glu Gln Gln Gly Glu Tyr Phe Cys Cys Gly Asp Pro Lys Lys Pro
980 985 990

His Thr Pro Cys Val Pro Asn Arg Ala Leu His Arg Pro Ile Ser Ser
995 1000 1005

Pro Ala Pro Tyr Pro Val Leu Gln Val Arg Gly Thr Ser Met Cys
1010 1015 1020

Pro Thr Leu Gln Val Arg Gly Thr Asp Ala Phe Ser Cys Pro Thr
1025 1030 1035

Gln Gln Ser Gly Phe Ser Phe Phe Val Arg His Val Met Arg Glu
1040 1045 1050

Ala Leu Ile His Arg Ala Gln Val Asn Gln Ala Ala Leu Leu Thr
1055 1060 1065

Tyr His Glu Asn Ala Ala Leu Thr Gly Lys Ser Ala Arg Gly Gly
1070 1075 1080

Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val
1085 1090 1095

Asp His His His His His His
1100 1105

<210> 9
<211> 4068
<212> DNA
<213> Artificial Sequence

<220>
<223> TATK-CDKL5 fusion protein cDNA

<400> 9
gctagccacc atggagacag acacactcct gctatgggta ctgctgctct gggttccagg 60
ttccactggt gacgcggccc agccggccag gcgcgcgcgc cgtacgaagc ttgcggccta 120
cgccagaaag gccgccaggc aggccagggc acggtcgcca ccatggtgag caagggcgag 180
gagctgttca ccgggggtggt gcccatcctg gtcgagctgg acggcgacgt aaacggccac 240
aagttcagcg tgtccggcga gggcgagggc gatgccacct acggcaagct gaccctgaag 300
ttcatctgca ccaccggcaa gctgcccgtg ccctggccca ccctcgtgac caccctgacc 360
tacggcgtgc agtgcttcag ccgctacccc gaccacatga agcagcacga cttcttcaag 420
tccgccatgc ccgaaggcta cgtccaggag cgcaccatct tcttcaagga cgacggcaac 480
tacaagaccc gcgccgaggt gaagttcgag ggcgacaccc tggatgaacc catcgagctg 540

02159303

aagggcatcg	acttcaagga	ggacggcaac	atcctggggc	acaagctgga	gtacaactac	600
aacagccaca	acgtctatat	catggccgac	aagcagaaga	acggcatcaa	ggtgaacttc	660
aagatccgcc	acaacatcga	ggacggcagc	gtgcagctcg	ccgaccacta	ccagcagaac	720
acccccatcg	gcgacggccc	cgtgctgctg	cccgacaacc	actacctgag	cacccagtcc	780
gccctgagca	aagaccccaa	cgagaagcgc	gatcacatgg	tcctgctgga	gttcgtgacc	840
gccgccggga	tcactctcgg	catggacgag	ctgtacaagt	ccggactcag	atctcgagcg	900
aagattccta	acattggtaa	tgtgatgaat	aaatttgaga	tccttggggg	tgtagggtgaa	960
ggagcctatg	gagttgtact	taaatgcaga	cacaaggaaa	cacatgaaat	tgtggcgatc	1020
aagaaattca	aggacagtga	agaaaatgaa	gaagtcaaa	aaacgacttt	acgagagctt	1080
aaaatgcttc	ggactctcaa	gcaggaaaac	attgtggagt	tgaaggaagc	atttcgtcgg	1140
aggggaaagt	tgtacttggg	gtttgagtat	gttgaaaaaa	atatgctcga	attgctggaa	1200
gaaatgccaa	atggagttcc	acctgagaaa	gtaaaaagct	acatctatca	gctaataaag	1260
gctattcact	ggtgcctaag	aatgatattg	tccatcgaga	tataaaaacca	gaaaatctct	1320
taatcagcca	caatgatgtc	ctaaaactgt	gtgactttgg	ttttgctcgt	aatctgtcag	1380
aaggcaataa	tgctaattac	acagagtacg	ttgccaccag	atgggtatcg	tccccagaac	1440
tcttacttgg	cgctccctat	ggaaagtccg	tggacatgtg	gtcgggtggg	tgtattcttg	1500
gggagcttag	cgatggacag	cctttatttc	ctggagaaaag	tgaaattgac	caacttttta	1560
ctattcagaa	ggtgctagga	ccacttccat	ctgagcagat	gaagcttttc	tacagtaatc	1620
ctcgcttcca	tgggctccgg	tttccagctg	ttaaccatcc	tcagtccttg	gaaagaagat	1680
accttggaat	tttgaatagt	gttctacttg	acctaataaa	gaatttactg	aagttggacc	1740
cagctgacag	atacttgaca	gaacagtgtt	tgaatcacc	tacatttcaa	accagagac	1800
ttctggatcg	ttctccttca	aggtcagcaa	aaagaaaacc	ttacatgtg	gaaagcagca	1860
cattgtctaa	tagaaaccaa	gccggcaaaa	gtactgcttt	gcagtctcac	cacagatcta	1920
acagcaagga	catccagaac	ctgagtgtag	gcctgccccg	ggctgacgaa	ggtctccctg	1980
ccaatgaaag	cttcctaaat	ggaaaccttg	ctggagctag	tcttagtcca	ctgcacacca	2040
aaacctacca	agcaagcagc	cagcctgggt	ctaccagcaa	agatctcacc	aacaacaaca	2100
taccacacct	tcttagccca	aaagaagcca	agtcaaaaac	agagtttgat	tttaatatg	2160
acccaaagcc	ttcagaaggc	ccagggacaa	agtacctcaa	gtcaaacagc	agatctcagc	2220
agaaccgcca	ctcattcatg	gaaagctctc	aaagcaaagc	tgggacactg	cagcccaatg	2280
aaaagcagag	tcggcatagc	tatattgaca	caattcccca	gtcctctagg	agtccctcct	2340
acaggaccaa	ggccaaaagc	catggggcac	tgagtgactc	caagtctgtg	agcaaccttt	2400
ctgaagccag	ggcccaaatt	gcggagccca	gtaccagtag	gtacttccca	tctagctgct	2460
tagacttgaa	ttctcccacc	agcccaaccc	ccaccagaca	cagtgcacag	agaactttgc	2520
tcagcccttc	tggaagaaat	aaccgaaatg	agggaaacgct	ggactcacgt	cgaaccacaa	2580

02159303

ccagacattc taagacgatg gaggaattga agctgccgga gcacatggac agtagccatt	2640
cccattcact gtctgcacct cacgaatctt tttcttatgg actgggctac accagcccct	2700
tttcttccca gcaacgtcct cataggcatt ctatgtatgt gacccgtgac aaagtgagag	2760
ccaagggctt ggatggaagc ttgagcatag ggcaagggat ggcagctaga gccaacagcc	2820
tgcaactctt gtcaccccag cctggagaac agctccctcc agagatgact gtggcaagat	2880
cttcggtcaa agagacctcc agagaaggca cctcttcctt ccatacacgc cagaagtctg	2940
aggggtggagt gtatcatgac ccacactctg atgatggcac agccccaaa gaaaatagac	3000
acctatacaa tgatcctgtg ccaaggagag ttggtagctt ttacagagtg ccatctccac	3060
gtccagacaa ttctttccat gaaaataatg tgtcaactag agtttcttct ctaccatcag	3120
agagcagttc tggaaccaac cactcaaaaa gacaaccagc attcgatcca tggaaaagtc	3180
ctgaaaatat tagtcattca gagcaactca aggaaaaaga gaagcaagga tttttcaggt	3240
caatgaaaaa gaaaaagaag aaatctcaaa cagtacccaa ttccgacagc cctgatcttc	3300
tgacgttgca gaaatccatt cattctgcta gcactccaag cagcagacca aaggagtggc	3360
gccccggaag atctcagatc tgcagaccca aagccagcca ttaaaatcac tgcgcaagtt	3420
gttacatctc tcttcggcct caaatcaccg ggcttcctca gtccccgctt ccagccctta	3480
acagctcaac aaaccaaaaa ttctttctca gaaattcgga ttcaccccct gagccaggcc	3540
tctggcggga gcagcaacat ccggcaggaa cccgcaccga agggcaggcc agccctccag	3600
ctgccagacg gtggatgtga tggcagaaga cagagacacc attctggacc ccaagataga	3660
cgcttcatgt taaggacgac agaacaacaa ggagaatact tctgctgtgg tgacccaaag	3720
aagcctcaca ctccgtgcgt cccaaaccga gcccttcatc gtccaatctc cagtctgtct	3780
ccctatccag tactccaggt ccgaggcact tccatgtgcc cgacactcca ggtccgaggc	3840
actgatgctt tcagctgccc aaccagcaa tccgggttct ctttcttcgt gagacacgtt	3900
atgaggggaag ccctgattca cagggccccag gtaaaccaag ctgcgctcct gacataccat	3960
gagaatgcgg cactgacggg caagtccgct cgaggagggc ccgaacaaaa actcatctca	4020
gaagaggatc tgaatagcgc cgtcgaccat catcatcatc atcattga	4068

<210> 10
 <211> 1353
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> TATk-CDKL5 fusion protein polypeptide

 <400> 10

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15

Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Arg Arg Ala Arg Arg Thr
 20 25 30

02159303

Lys Leu Ala Ala Tyr Ala Arg Lys Ala Ala Arg Gln Ala Arg Ala Pro
35 40 45

Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
50 55 60

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

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
85 90 95

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
100 105 110

Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp
115 120 125

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
130 135 140

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
145 150 155 160

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
165 170 175

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
180 185 190

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

Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
210 215 220

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
225 230 235 240

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
245 250 255

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
260 265 270

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
275 280 285

Tyr Lys Ser Gly Leu Arg Ser Arg Ala Lys Ile Pro Asn Ile Gly Asn
290 295 300

02159303

Val 305	Met	Asn	Lys	Phe	Glu 310	Ile	Leu	Gly	Val	Val 315	Gly	Glu	Gly	Ala	Tyr 320
Gly	Val	Val	Leu	Lys 325	Cys	Arg	His	Lys	Glu 330	Thr	His	Glu	Ile	Val 335	Ala
Ile	Lys	Lys	Phe 340	Lys	Asp	Ser	Glu	Glu 345	Asn	Glu	Glu	Val	Lys 350	Glu	Thr
Thr	Leu	Arg 355	Glu	Leu	Lys	Met	Leu	Arg 360	Thr	Leu	Lys	Gln 365	Glu	Asn	Ile
Val	Glu 370	Leu	Lys	Glu	Ala	Phe 375	Arg	Arg	Arg	Gly	Lys 380	Leu	Tyr	Leu	Val
Phe 385	Glu	Tyr	Val	Glu	Lys 390	Asn	Met	Leu	Glu	Leu 395	Leu	Glu	Glu	Met	Pro 400
Asn	Gly	Val	Pro	Pro 405	Glu	Lys	Val	Lys	Ser 410	Tyr	Ile	Tyr	Gln	Leu 415	Ile
Lys	Ala	Ile	His 420	Trp	Cys	His	Lys	Asn 425	Asp	Ile	Val	His	Arg 430	Asp	Ile
Lys	Pro	Glu 435	Asn	Leu	Leu	Ile	Ser 440	His	Asn	Asp	Val	Leu 445	Lys	Leu	Cys
Asp	Phe 450	Gly	Phe	Ala	Arg	Asn 455	Leu	Ser	Glu	Gly	Asn 460	Asn	Ala	Asn	Tyr
Thr 465	Glu	Tyr	Val	Ala	Thr 470	Arg	Trp	Tyr	Arg	Ser 475	Pro	Glu	Leu	Leu	Leu 480
Gly	Ala	Pro	Tyr	Gly 485	Lys	Ser	Val	Asp	Met 490	Trp	Ser	Val	Gly	Cys 495	Ile
Leu	Gly	Glu	Leu 500	Ser	Asp	Gly	Gln	Pro 505	Leu	Phe	Pro	Gly	Glu 510	Ser	Glu
Ile	Asp	Gln 515	Leu	Phe	Thr	Ile	Gln 520	Lys	Val	Leu	Gly	Pro 525	Leu	Pro	Ser
Glu	Gln 530	Met	Lys	Leu	Phe	Tyr 535	Ser	Asn	Pro	Arg	Phe 540	His	Gly	Leu	Arg
Phe 545	Pro	Ala	Val	Asn	His 550	Pro	Gln	Ser	Leu	Glu 555	Arg	Arg	Tyr	Leu	Gly 560
Ile	Leu	Asn	Ser	Val 565	Leu	Leu	Asp	Leu	Met 570	Lys	Asn	Leu	Leu	Lys 575	Leu

02159303

Asp Pro Ala Asp Arg Tyr Leu Thr Glu Gln Cys Leu Asn His Pro Thr
580 585 590

Phe Gln Thr Gln Arg Leu Leu Asp Arg Ser Pro Ser Arg Ser Ala Lys
595 600 605

Arg Lys Pro Tyr His Val Glu Ser Ser Thr Leu Ser Asn Arg Asn Gln
610 615 620

Ala Gly Lys Ser Thr Ala Leu Gln Ser His His Arg Ser Asn Ser Lys
625 630 635 640

Asp Ile Gln Asn Leu Ser Val Gly Leu Pro Arg Ala Asp Glu Gly Leu
645 650 655

Pro Ala Asn Glu Ser Phe Leu Asn Gly Asn Leu Ala Gly Ala Ser Leu
660 665 670

Ser Pro Leu His Thr Lys Thr Tyr Gln Ala Ser Ser Gln Pro Gly Ser
675 680 685

Thr Ser Lys Asp Leu Thr Asn Asn Asn Ile Pro His Leu Leu Ser Pro
690 695 700

Lys Glu Ala Lys Ser Lys Thr Glu Phe Asp Phe Asn Ile Asp Pro Lys
705 710 715 720

Pro Ser Glu Gly Pro Gly Thr Lys Tyr Leu Lys Ser Asn Ser Arg Ser
725 730 735

Gln Gln Asn Arg His Ser Phe Met Glu Ser Ser Gln Ser Lys Ala Gly
740 745 750

Thr Leu Gln Pro Asn Glu Lys Gln Ser Arg His Ser Tyr Ile Asp Thr
755 760 765

Ile Pro Gln Ser Ser Arg Ser Pro Ser Tyr Arg Thr Lys Ala Lys Ser
770 775 780

His Gly Ala Leu Ser Asp Ser Lys Ser Val Ser Asn Leu Ser Glu Ala
785 790 795 800

Arg Ala Gln Ile Ala Glu Pro Ser Thr Ser Arg Tyr Phe Pro Ser Ser
805 810 815

Cys Leu Asp Leu Asn Ser Pro Thr Ser Pro Thr Pro Thr Arg His Ser
820 825 830

Asp Thr Arg Thr Leu Leu Ser Pro Ser Gly Arg Asn Asn Arg Asn Glu
835 840 845

02159303

Gly Thr Leu Asp Ser Arg Arg Thr Thr Thr Arg His Ser Lys Thr Met
850 855 860

Glu Glu Leu Lys Leu Pro Glu His Met Asp Ser Ser His Ser His Ser
865 870 875 880

Leu Ser Ala Pro His Glu Ser Phe Ser Tyr Gly Leu Gly Tyr Thr Ser
885 890 895

Pro Phe Ser Ser Gln Gln Arg Pro His Arg His Ser Met Tyr Val Thr
900 905 910

Arg Asp Lys Val Arg Ala Lys Gly Leu Asp Gly Ser Leu Ser Ile Gly
915 920 925

Gln Gly Met Ala Ala Arg Ala Asn Ser Leu Gln Leu Leu Ser Pro Gln
930 935 940

Pro Gly Glu Gln Leu Pro Pro Glu Met Thr Val Ala Arg Ser Ser Val
945 950 955 960

Lys Glu Thr Ser Arg Glu Gly Thr Ser Ser Phe His Thr Arg Gln Lys
965 970 975

Ser Glu Gly Gly Val Tyr His Asp Pro His Ser Asp Asp Gly Thr Ala
980 985 990

Pro Lys Glu Asn Arg His Leu Tyr Asn Asp Pro Val Pro Arg Arg Val
995 1000 1005

Gly Ser Phe Tyr Arg Val Pro Ser Pro Arg Pro Asp Asn Ser Phe
1010 1015 1020

His Glu Asn Asn Val Ser Thr Arg Val Ser Ser Leu Pro Ser Glu
1025 1030 1035

Ser Ser Ser Gly Thr Asn His Ser Lys Arg Gln Pro Ala Phe Asp
1040 1045 1050

Pro Trp Lys Ser Pro Glu Asn Ile Ser His Ser Glu Gln Leu Lys
1055 1060 1065

Glu Lys Glu Lys Gln Gly Phe Phe Arg Ser Met Lys Lys Lys Lys
1070 1075 1080

Lys Lys Ser Gln Thr Val Pro Asn Ser Asp Ser Pro Asp Leu Leu
1085 1090 1095

Thr Leu Gln Lys Ser Ile His Ser Ala Ser Thr Pro Ser Ser Arg
1100 1105 1110

02159303

Pro	Lys	Glu	Trp	Arg	Pro	Glu	Lys	Ile	Ser	Asp	Leu	Gln	Thr	Gln
	1115					1120					1125			
Ser	Gln	Pro	Leu	Lys	Ser	Leu	Arg	Lys	Leu	Leu	His	Leu	Ser	Ser
	1130					1135					1140			
Ala	Ser	Asn	His	Pro	Ala	Ser	Ser	Asp	Pro	Arg	Phe	Gln	Pro	Leu
	1145					1150					1155			
Thr	Ala	Gln	Gln	Thr	Lys	Asn	Ser	Phe	Ser	Glu	Ile	Arg	Ile	His
	1160					1165					1170			
Pro	Leu	Ser	Gln	Ala	Ser	Gly	Gly	Ser	Ser	Asn	Ile	Arg	Gln	Glu
	1175					1180					1185			
Pro	Ala	Pro	Lys	Gly	Arg	Pro	Ala	Leu	Gln	Leu	Pro	Asp	Gly	Gly
	1190					1195					1200			
Cys	Asp	Gly	Arg	Arg	Gln	Arg	His	His	Ser	Gly	Pro	Gln	Asp	Arg
	1205					1210					1215			
Arg	Phe	Met	Leu	Arg	Thr	Thr	Glu	Gln	Gln	Gly	Glu	Tyr	Phe	Cys
	1220					1225					1230			
Cys	Gly	Asp	Pro	Lys	Lys	Pro	His	Thr	Pro	Cys	Val	Pro	Asn	Arg
	1235					1240					1245			
Ala	Leu	His	Arg	Pro	Ile	Ser	Ser	Pro	Ala	Pro	Tyr	Pro	Val	Leu
	1250					1255					1260			
Gln	Val	Arg	Gly	Thr	Ser	Met	Cys	Pro	Thr	Leu	Gln	Val	Arg	Gly
	1265					1270					1275			
Thr	Asp	Ala	Phe	Ser	Cys	Pro	Thr	Gln	Gln	Ser	Gly	Phe	Ser	Phe
	1280					1285					1290			
Phe	Val	Arg	His	Val	Met	Arg	Glu	Ala	Leu	Ile	His	Arg	Ala	Gln
	1295					1300					1305			
Val	Asn	Gln	Ala	Ala	Leu	Leu	Thr	Tyr	His	Glu	Asn	Ala	Ala	Leu
	1310					1315					1320			
Thr	Gly	Lys	Ser	Ala	Arg	Gly	Gly	Pro	Glu	Gln	Lys	Leu	Ile	Ser
	1325					1330					1335			
Glu	Glu	Asp	Leu	Asn	Ser	Ala	Val	Asp	His	His	His	His	His	His
	1340					1345					1350			

<210> 11
 <211> 3852
 <212> DNA

<213> Artificial Sequence

<220>

<223> TATk-CDKL5 Fusion protein cDNA

<400> 11

```

atggagacag acacactcct gctatgggta ctgctgctct gggttccagg ttccactgg      60
gacgcggccc agccggccag gcgcgcgcgc cgtacgaagc ttgcggccta cgccagaaag      120
gccgccaggc aggccagggc accggtcgcc accatgggta gcaagggcga ggagctgttc      180
accgggggtg tgcccatcct ggtcgagctg gacggcgacg taaacggcca caagttcagc      240
gtgtccggcg agggcgaggg cgatgccacc tacggcaagc tgaccctgaa gttcatctgc      300
accaccggca agctgcccgt gccctggccc accctcgtga ccaccctgac ctacggcgctg      360
cagtgtttca gccgtaccc cgaccacatg aagcagcacg acttcttcaa gtccgccatg      420
cccgaaggct acgtccagga gcgcaccatc ttcttcaagg acgacggcaa ctacaagacc      480
cgcgccgagg tgaagttcga gggcgacacc ctgggtgaacc gcatcgagct gaagggcatc      540
gacttcaagg aggacggcaa catcctgggg cacaagctgg agtacaacta caacagccac      600
aacgtctata tcatggccga caagcagaag aacggcatca aggtgaactt caagatccgc      660
cacaacatcg aggacggcag cgtgcagctc gccgaccact accagcagaa caccctcatc      720
ggcgacggcc ccgtgctgct gcccgacaac cactacctga gcaccagtc cgccctgagc      780
aaagacccca acgagaagcg cgatcacatg gtcctgctgg agttcgtgac cgccgccggg      840
atcactctcg gcatggacga gctgtacaag tccggactca gatctcgagc gaagattcct      900
aacattggta atgtgatgaa taaatttgag atccttgggg ttgtaggtga aggagcctat      960
ggagttgtac ttaaatgcag acacaaggaa acacatgaaa ttgtggcgat caagaaattc     1020
aaggacagtg aagaaaatga agaagtcaaa gaaacgactt tacgagagct taaaatgctt     1080
cggactctca agcaggaaaa cattgtggag ttgaaggaag catttcgtcg gaggggaaaag     1140
ttgtacttgg tgtttgagta tgttgaaaaa aatatgctcg aattgctgga agaaatgcca     1200
aatggagttc cacctgagaa agtaaaaagc tacatctatc agctaataa ggctattcac     1260
tggtgccata agaatgatat tgtccatcga gatataaaac cagaaaatct cttaatcagc     1320
cacaatgatg tcctaaaact gtgtgacttt ggttttgctc gtaatctgtc agaaggcaat     1380
aatgctaatt acacagagta cgttgccacc agatgggtatc ggtcccaga actcttactt     1440
ggcgctccct atggaaagtc cgtggacatg tggtcggtgg gctgtattct tggggagctt     1500
agcgatggac agcctttatt tcctggagaa agtgaaaattg accaactttt tactattcag     1560
aagggtgctag gaccacttcc atctgagcag atgaagcttt tctacagtaa tcctcgcttc     1620
catgggctcc ggtttccagc tgtaaccat cctcagtcct tggaaagaag ataccttgga     1680
attttgaata gtgttctact tgacctaatg aagaatttac tgaagttgga ccagctgac     1740
agatacttga cagaacagtg tttgaatcac cctacatttc aaaccagag acttctggat     1800
cgttctcctt caaggtcagc aaaaagaaaa ccttaccatg tggaaagcag cacattgtct     1860

```

02159303

aatagaaacc	aagccggcaa	aagtactgct	ttgcagttctc	accacagatc	taacagcaag	1920
gacatccaga	acctgagtgt	aggcctgccc	cgggctgacg	aaggtctccc	tgccaatgaa	1980
agcttcctaa	atggaaacct	tgctggagct	agtcttagtc	cactgcacac	caaaacctac	2040
caagcaagca	gccagcctgg	gtctaccagc	aaagatctca	ccaacaacaa	cataccacac	2100
cttcttagcc	caaaagaagc	caagtcaaaa	acagagtttg	attttaatat	tgacccaaag	2160
ccttcagaag	gccaggggac	aaagtacctc	aagtcaaaca	gcagatctca	gcagaaccgc	2220
cactcattca	tggaaagctc	tcaaagcaaa	gctgggacac	tgagcccaa	tgaaaagcag	2280
agtcggcata	gctatatattga	cacaattccc	cagtcctcta	ggagtccctc	ctacaggacc	2340
aaggccaaaa	gccatggggc	actgagtgac	tccaagtctg	tgagcaacct	ttctgaagcc	2400
agggcccaaa	ttgcggagcc	cagtaccagt	aggtaacttc	catctagctg	cttagacttg	2460
aattctccca	ccagcccaac	ccccaccaga	cacagtgcac	cgagaacttt	gctcagccct	2520
tctggaagaa	ataaccgaaa	tgagggaacg	ctggactcac	gtcgaaccac	aaccagacat	2580
tctaagacga	tggaggaatt	gaagctgccg	gagcacatgg	acagtagcca	ttcccattca	2640
ctgtctgcac	ctcacgaatc	tttttcttat	ggactgggct	acaccagccc	cttttcttcc	2700
cagcaacgtc	ctcataggca	ttctatgtat	gtgaccctg	acaaagttag	agccaagggc	2760
ttggatggaa	gcttgagcat	agggcaaggg	atggcagcta	gagccaacag	cctgcaactc	2820
ttgtcacccc	agcctggaga	acagctccct	ccagagatga	ctgtggcaag	atcttcggtc	2880
aaagagacct	ccagagaagg	cacctcttcc	ttccatacac	gccagaagtc	tgagggtgga	2940
gtgtatcatg	acccacactc	tgatgatggc	acagccccc	aagaaaatag	acacctatac	3000
aatgatcctg	tgccaaggag	agttggtagc	ttttacagag	tgccatctcc	acgtccagac	3060
aattctttcc	atgaaaataa	tgtgtcaact	agagtttctt	ctctaccatc	agagagcagt	3120
tctggaacca	accactcaaa	aagacaacca	gcattcgatc	catggaaaag	tcctgaaaat	3180
attagtcatt	cagagcaact	caaggaaaaa	gagaagcaag	gattttttcag	gtcaatgaaa	3240
aagaaaaaga	agaaatctca	aacagtaccc	aattccgaca	gccctgatct	tctgacgttg	3300
cagaaatcca	ttcattctgc	tagcactcca	agcagcagac	caaaggagtg	gcgccccgag	3360
aagatctcag	atctgcagac	ccaaagccag	ccattaaaaat	cactgcgcaa	gttggttacat	3420
ctctcttcgg	cctcaaatca	cccggcttcc	tcagatcccc	gcttccagcc	cttaacagct	3480
caacaaacca	aaaattcctt	ctcagaaatt	cggattcacc	ccctgagcca	ggcctctggc	3540
gggagcagca	acatccggca	ggaacccgca	ccgaaggggca	ggccagccct	ccagctgcca	3600
ggtcagatgg	atcctgggtg	gcatgtgtcc	tctgtgacca	ggagtgccac	agagggccct	3660
tcctactctg	aacagctggg	tgccaaaagt	gggccaaatg	ggcacccta	taacagaaca	3720
aatcgctcac	gaatgccaaa	tctgaatgat	ttaaaagaga	cagccttgct	cgctcgagga	3780
gggcccgaac	aaaaactcat	ctcagaagag	gatctgaata	gcgccgtcga	ccatcatcat	3840
catcatcatt	ga					3852

02159303

<210> 12
<211> 1283
<212> PRT
<213> Artificial Sequence

<220>
<223> TATk-CDKL5 Fusion protein polypeptide

<400> 12

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Arg Arg Ala Arg Arg Thr
20 25 30

Lys Leu Ala Ala Tyr Ala Arg Lys Ala Ala Arg Gln Ala Arg Ala Pro
35 40 45

Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
50 55 60

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

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
85 90 95

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
100 105 110

Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp
115 120 125

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
130 135 140

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
145 150 155 160

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
165 170 175

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
180 185 190

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

Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
210 215 220

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
Page 22

02159303															
225				230				235				240			
Gly	Asp	Gly	Pro	Val 245	Leu	Leu	Pro	Asp	Asn 250	His	Tyr	Leu	Ser	Thr 255	Gln
Ser	Ala	Leu	Ser 260	Lys	Asp	Pro	Asn	Glu 265	Lys	Arg	Asp	His	Met 270	Val	Leu
Leu	Glu	Phe 275	Val	Thr	Ala	Ala	Gly 280	Ile	Thr	Leu	Gly	Met 285	Asp	Glu	Leu
Tyr	Lys 290	Ser	Gly	Leu	Arg	Ser 295	Arg	Ala	Lys	Ile	Pro 300	Asn	Ile	Gly	Asn
Val 305	Met	Asn	Lys	Phe	Glu 310	Ile	Leu	Gly	Val	Val 315	Gly	Glu	Gly	Ala	Tyr 320
Gly	Val	Val	Leu	Lys 325	Cys	Arg	His	Lys	Glu 330	Thr	His	Glu	Ile	Val 335	Ala
Ile	Lys	Lys	Phe 340	Lys	Asp	Ser	Glu	Glu 345	Asn	Glu	Glu	Val	Lys 350	Glu	Thr
Thr	Leu	Arg 355	Glu	Leu	Lys	Met	Leu 360	Arg	Thr	Leu	Lys	Gln 365	Glu	Asn	Ile
Val	Glu 370	Leu	Lys	Glu	Ala	Phe 375	Arg	Arg	Arg	Gly	Lys 380	Leu	Tyr	Leu	Val
Phe 385	Glu	Tyr	Val	Glu	Lys 390	Asn	Met	Leu	Glu	Leu 395	Leu	Glu	Glu	Met	Pro 400
Asn	Gly	Val	Pro	Pro 405	Glu	Lys	Val	Lys	Ser 410	Tyr	Ile	Tyr	Gln	Leu 415	Ile
Lys	Ala	Ile	His 420	Trp	Cys	His	Lys	Asn 425	Asp	Ile	Val	His	Arg 430	Asp	Ile
Lys	Pro	Glu 435	Asn	Leu	Leu	Ile	Ser 440	His	Asn	Asp	Val	Leu 445	Lys	Leu	Cys
Asp	Phe 450	Gly	Phe	Ala	Arg	Asn 455	Leu	Ser	Glu	Gly	Asn 460	Asn	Ala	Asn	Tyr
Thr 465	Glu	Tyr	Val	Ala	Thr 470	Arg	Trp	Tyr	Arg	Ser 475	Pro	Glu	Leu	Leu	Leu 480
Gly	Ala	Pro	Tyr	Gly 485	Lys	Ser	Val	Asp	Met 490	Trp	Ser	Val	Gly	Cys 495	Ile
Leu	Gly	Glu	Leu	Ser	Asp	Gly	Gln	Pro	Leu	Phe	Pro	Gly	Glu	Ser	Glu

500

505

510

Ile Asp Gln Leu Phe Thr Ile Gln Lys Val Leu Gly Pro Leu Pro Ser
515 520 525

Glu Gln Met Lys Leu Phe Tyr Ser Asn Pro Arg Phe His Gly Leu Arg
530 535 540

Phe Pro Ala Val Asn His Pro Gln Ser Leu Glu Arg Arg Tyr Leu Gly
545 550 555 560

Ile Leu Asn Ser Val Leu Leu Asp Leu Met Lys Asn Leu Leu Lys Leu
565 570 575

Asp Pro Ala Asp Arg Tyr Leu Thr Glu Gln Cys Leu Asn His Pro Thr
580 585 590

Phe Gln Thr Gln Arg Leu Leu Asp Arg Ser Pro Ser Arg Ser Ala Lys
595 600 605

Arg Lys Pro Tyr His Val Glu Ser Ser Thr Leu Ser Asn Arg Asn Gln
610 615 620

Ala Gly Lys Ser Thr Ala Leu Gln Ser His His Arg Ser Asn Ser Lys
625 630 635 640

Asp Ile Gln Asn Leu Ser Val Gly Leu Pro Arg Ala Asp Glu Gly Leu
645 650 655

Pro Ala Asn Glu Ser Phe Leu Asn Gly Asn Leu Ala Gly Ala Ser Leu
660 665 670

Ser Pro Leu His Thr Lys Thr Tyr Gln Ala Ser Ser Gln Pro Gly Ser
675 680 685

Thr Ser Lys Asp Leu Thr Asn Asn Asn Ile Pro His Leu Leu Ser Pro
690 695 700

Lys Glu Ala Lys Ser Lys Thr Glu Phe Asp Phe Asn Ile Asp Pro Lys
705 710 715 720

Pro Ser Glu Gly Pro Gly Thr Lys Tyr Leu Lys Ser Asn Ser Arg Ser
725 730 735

Gln Gln Asn Arg His Ser Phe Met Glu Ser Ser Gln Ser Lys Ala Gly
740 745 750

Thr Leu Gln Pro Asn Glu Lys Gln Ser Arg His Ser Tyr Ile Asp Thr
755 760 765

Ile Pro Gln Ser Ser Arg Ser Pro Ser Tyr Arg Thr Lys Ala Lys Ser
Page 24

02159303

770

775

780

His Gly Ala Leu Ser Asp Ser Lys Ser Val Ser Asn Leu Ser Glu Ala
 785 790 795 800

Arg Ala Gln Ile Ala Glu Pro Ser Thr Ser Arg Tyr Phe Pro Ser Ser
 805 810 815

Cys Leu Asp Leu Asn Ser Pro Thr Ser Pro Thr Pro Thr Arg His Ser
 820 825 830

Asp Thr Arg Thr Leu Leu Ser Pro Ser Gly Arg Asn Asn Arg Asn Glu
 835 840 845

Gly Thr Leu Asp Ser Arg Arg Thr Thr Thr Arg His Ser Lys Thr Met
 850 855 860

Glu Glu Leu Lys Leu Pro Glu His Met Asp Ser Ser His Ser His Ser
 865 870 875 880

Leu Ser Ala Pro His Glu Ser Phe Ser Tyr Gly Leu Gly Tyr Thr Ser
 885 890 895

Pro Phe Ser Ser Gln Gln Arg Pro His Arg His Ser Met Tyr Val Thr
 900 905 910

Arg Asp Lys Val Arg Ala Lys Gly Leu Asp Gly Ser Leu Ser Ile Gly
 915 920 925

Gln Gly Met Ala Ala Arg Ala Asn Ser Leu Gln Leu Leu Ser Pro Gln
 930 935 940

Pro Gly Glu Gln Leu Pro Pro Glu Met Thr Val Ala Arg Ser Ser Val
 945 950 955 960

Lys Glu Thr Ser Arg Glu Gly Thr Ser Ser Phe His Thr Arg Gln Lys
 965 970 975

Ser Glu Gly Gly Val Tyr His Asp Pro His Ser Asp Asp Gly Thr Ala
 980 985 990

Pro Lys Glu Asn Arg His Leu Tyr Asn Asp Pro Val Pro Arg Arg Val
 995 1000 1005

Gly Ser Phe Tyr Arg Val Pro Ser Pro Arg Pro Asp Asn Ser Phe
 1010 1015 1020

His Glu Asn Asn Val Ser Thr Arg Val Ser Ser Leu Pro Ser Glu
 1025 1030 1035

Ser Ser Ser Gly Thr Asn His Ser Lys Arg Gln Pro Ala Phe Asp
 Page 25

02159303

1040						1045						1050			
Pro	Trp	Lys	Ser	Pro	Glu	Asn	Ile	Ser	His	Ser	Glu	Gln	Leu	Lys	
	1055					1060					1065				
Glu	Lys	Glu	Lys	Gln	Gly	Phe	Phe	Arg	Ser	Met	Lys	Lys	Lys	Lys	
	1070					1075					1080				
Lys	Lys	Ser	Gln	Thr	Val	Pro	Asn	Ser	Asp	Ser	Pro	Asp	Leu	Leu	
	1085					1090					1095				
Thr	Leu	Gln	Lys	Ser	Ile	His	Ser	Ala	Ser	Thr	Pro	Ser	Ser	Arg	
	1100					1105					1110				
Pro	Lys	Glu	Trp	Arg	Pro	Glu	Lys	Ile	Ser	Asp	Leu	Gln	Thr	Gln	
	1115					1120					1125				
Ser	Gln	Pro	Leu	Lys	Ser	Leu	Arg	Lys	Leu	Leu	His	Leu	Ser	Ser	
	1130					1135					1140				
Ala	Ser	Asn	His	Pro	Ala	Ser	Ser	Asp	Pro	Arg	Phe	Gln	Pro	Leu	
	1145					1150					1155				
Thr	Ala	Gln	Gln	Thr	Lys	Asn	Ser	Phe	Ser	Glu	Ile	Arg	Ile	His	
	1160					1165					1170				
Pro	Leu	Ser	Gln	Ala	Ser	Gly	Gly	Ser	Ser	Asn	Ile	Arg	Gln	Glu	
	1175					1180					1185				
Pro	Ala	Pro	Lys	Gly	Arg	Pro	Ala	Leu	Gln	Leu	Pro	Gly	Gln	Met	
	1190					1195					1200				
Asp	Pro	Gly	Trp	His	Val	Ser	Ser	Val	Thr	Arg	Ser	Ala	Thr	Glu	
	1205					1210					1215				
Gly	Pro	Ser	Tyr	Ser	Glu	Gln	Leu	Gly	Ala	Lys	Ser	Gly	Pro	Asn	
	1220					1225					1230				
Gly	His	Pro	Tyr	Asn	Arg	Thr	Asn	Arg	Ser	Arg	Met	Pro	Asn	Leu	
	1235					1240					1245				
Asn	Asp	Leu	Lys	Glu	Thr	Ala	Leu	Ser	Ala	Arg	Gly	Gly	Pro	Glu	
	1250					1255					1260				
Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Ser	Ala	Val	Asp	His	
	1265					1270					1275				
His	His	His	His	His											
	1280														

<210> 13

<211> 3124
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TATk-CDKL5 fusion protein cDNA

<400> 13
 gctagccacc atggagacag acacactcct gctatgggta ctgctgctct gggttccagg 60
 ttccactgggt gacgcggccc agccggccag gcgcgcgcgc cgtacgaagc ttgcggccta 120
 cgccagaaaag gccgccaggc aggccagggc accgggtgaag attcctaaca ttggtaaatgt 180
 gatgaataaa tttagatatcc ttgggggttgt aggtgaagga gcctatggag ttgtacttaa 240
 atgcagacac aaggaaacac atgaaattgt ggcgatcaag aaattcaagg acagtgaaga 300
 aaatgaagaa gtcaaagaaa cgactttacg agagcttaaa atgcttcgga ctctcaagca 360
 ggaaaacatt gtggagttga aggaagcatt tcgtcggagg ggaaagtgtt acttggtgtt 420
 tgagtatgtt gaaaaaata tgctcgaatt gctggaagaa atgccaaatg gagttccacc 480
 tgagaaagta aaaagctaca tctatcagct aatcaaggct attcactgggt gccataagaa 540
 tgatattgtc catcgagata taaaaccaga aaatctctta atcagccaca atgatgtcct 600
 aaaactgtgt gactttgggt ttgctcgtaa tctgtcagaa ggcaataatg ctaattacac 660
 agagtacgtt gccaccagat ggtatcggtc ccagaaactc ttacttggcg ctccctatgg 720
 aaagtccgtg gacatgttgt cgggtgggctg tattcttggg gagcttagcg atggacagcc 780
 ttattttcct ggagaaagtg aaattgacca actttttact attcagaagg tgctaggacc 840
 acttccatct gagcagatga agcttttcta cagtaatcct cgcttccatg ggctccggtt 900
 tccagctgtt aaccatcctc agtccttgga aagaagatac cttggaattt tgaatagtgt 960
 tctacttgac ctaatgaaga atttactgaa gttggaccca gctgacagat acttgacaga 1020
 acagtgtttg aatcaccccta catttcaaac ccagagactt ctggatcgtt ctccctcaag 1080
 gtcagcaaaa agaaaacctt accatgtgga aagcagcaca ttgtctaata gaaaccaagc 1140
 cggcaaaagt actgctttgc agtctcacca cagatctaac agcaaggaca tccagaacct 1200
 gagtgtaggc ctgccccggg ctgacgaagg tctccctgcc aatgaaagct tcctaaatgg 1260
 aaaccttgct ggagctagtc ttagtccact gcacacaaaa acctaccaag caagcagcca 1320
 gcctgggtct accagcaaag atctcaccaa caacaacata ccacaccttc ttagcccaaa 1380
 agaagccaag tcaaaaacag agtttgattt taatattgac ccaaagcctt cagaaggccc 1440
 agggacaaaag tacctcaagt caaacagcag atctcagcag aaccgccact cattcatgga 1500
 aagctctcaa agcaaagctg ggacactgca gccaatgaa aagcagagtc ggcatagcta 1560
 tattgacaca attccccagt cctctaggag tccctcctac aggaccaagg ccaaaagcca 1620
 tggggcactg agtgactcca agtctgtgag caacctttct gaagccaggg ccaaattgac 1680
 ggagcccagt accagtaggt acttcccatc tagctgctta gacttgaatt ctcccaccag 1740
 cccaaccccc accagacaca gtgacacgag aactttgctc agcccttctg gaagaaataa 1800

02159303

ccgaaatgag ggaacgctgg actcacgtcg aaccacaacc agacattcta agacgatgga	1860
ggaattgaag ctgccggagc acatggacag tagccattcc cattcactgt ctgcacctca	1920
cgaatctttt tcttatggac tgggctacac cagccccctt tcttcccagc aacgtcctca	1980
taggcattct atgtatgtga cccgtgacaa agtgagagcc aagggcttgg atggaagctt	2040
gagcataggg caagggatgg cagctagagc caacagcctg caactcttgt caccacagcc	2100
tggagaacag ctccctccag agatgactgt ggcaagatct tcggtcaaag agacctccag	2160
agaaggcacc tcttccttcc atacacgcca gaagtctgag ggtggagtgt atcatgaccc	2220
acactctgat gatggcacag cccccaaga aaatagacac ctatacaatg atcctgtgcc	2280
aaggagagtt ggtagctttt acagagtgcc atctccacgt ccagacaatt ctttccatga	2340
aaataatgtg tcaactagag tttcttctct accatcagag agcagttctg gaaccaacca	2400
ctcaaaaaga caaccagcat tcgatccatg gaaaagtcct gaaaatatta gtcattcaga	2460
gcaactcaag gaaaaagaga agcaaggatt ttccaggtca atgaaaaaga aaaagaagaa	2520
atctcaaaca gtacccaatt ccgacagccc tgatcttctg acgttgcaga aatccattca	2580
ttctgctagc actccaagca gcagaccaa ggagtggcgc cccgagaaga tctcagatct	2640
gcagacccaa agccagccat taaaatcact gcgcaagttg ttacatctct cttcggcctc	2700
aaatcacccg gcttcctcag atccccgctt ccagccctta acagctcaac aaaccaaaaa	2760
ttcctttctca gaaattcgga ttcacccccct gagccaggcc tctggcggga gcagcaacat	2820
ccggcaggaa cccgcaccga agggcaggcc agccctccag ctgccaggtc agatggatcc	2880
tggttggcat gtgtcctctg tgaccaggag tgccacagag ggcccttcct actctgaaca	2940
gctgggtgcc aaaagtgggc caaatgggca cccctataac agaacaaatc gctcacgaat	3000
gccaaatctg aatgatttaa aagagacagc cttgtctaga ggatcccggg ctgactacaa	3060
agaccatgac ggtgattata aagatcatga catcgactac aaggatgacg atgacaagta	3120
gtga	3124

<210> 14
 <211> 1036
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TATk-CDKL5 fusion protein polypeptide

<400> 14

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15

Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Arg Arg Ala Arg Arg Thr
 20 25 30

Lys Leu Ala Ala Tyr Ala Arg Lys Ala Ala Arg Gln Ala Arg Ala Pro
 35 40 45

02159303

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

02159303

Leu Met Lys Asn Leu Leu Lys Leu Asp Pro Ala Asp Arg Tyr Leu Thr
325 330 335

Glu Gln Cys Leu Asn His Pro Thr Phe Gln Thr Gln Arg Leu Leu Asp
340 345 350

Arg Ser Pro Ser Arg Ser Ala Lys Arg Lys Pro Tyr His Val Glu Ser
355 360 365

Ser Thr Leu Ser Asn Arg Asn Gln Ala Gly Lys Ser Thr Ala Leu Gln
370 375 380

Ser His His Arg Ser Asn Ser Lys Asp Ile Gln Asn Leu Ser Val Gly
385 390 395 400

Leu Pro Arg Ala Asp Glu Gly Leu Pro Ala Asn Glu Ser Phe Leu Asn
405 410 415

Gly Asn Leu Ala Gly Ala Ser Leu Ser Pro Leu His Thr Lys Thr Tyr
420 425 430

Gln Ala Ser Ser Gln Pro Gly Ser Thr Ser Lys Asp Leu Thr Asn Asn
435 440 445

Asn Ile Pro His Leu Leu Ser Pro Lys Glu Ala Lys Ser Lys Thr Glu
450 455 460

Phe Asp Phe Asn Ile Asp Pro Lys Pro Ser Glu Gly Pro Gly Thr Lys
465 470 475 480

Tyr Leu Lys Ser Asn Ser Arg Ser Gln Gln Asn Arg His Ser Phe Met
485 490 495

Glu Ser Ser Gln Ser Lys Ala Gly Thr Leu Gln Pro Asn Glu Lys Gln
500 505 510

Ser Arg His Ser Tyr Ile Asp Thr Ile Pro Gln Ser Ser Arg Ser Pro
515 520 525

Ser Tyr Arg Thr Lys Ala Lys Ser His Gly Ala Leu Ser Asp Ser Lys
530 535 540

Ser Val Ser Asn Leu Ser Glu Ala Arg Ala Gln Ile Ala Glu Pro Ser
545 550 555 560

Thr Ser Arg Tyr Phe Pro Ser Ser Cys Leu Asp Leu Asn Ser Pro Thr
565 570 575

Ser Pro Thr Pro Thr Arg His Ser Asp Thr Arg Thr Leu Leu Ser Pro
580 585 590

02159303

Ser Gly Arg Asn Asn Arg Asn Glu Gly Thr Leu Asp Ser Arg Arg Thr
595 600 605

Thr Thr Arg His Ser Lys Thr Met Glu Glu Leu Lys Leu Pro Glu His
610 615 620

Met Asp Ser Ser His Ser His Ser Leu Ser Ala Pro His Glu Ser Phe
625 630 635 640

Ser Tyr Gly Leu Gly Tyr Thr Ser Pro Phe Ser Ser Gln Gln Arg Pro
645 650 655

His Arg His Ser Met Tyr Val Thr Arg Asp Lys Val Arg Ala Lys Gly
660 665 670

Leu Asp Gly Ser Leu Ser Ile Gly Gln Gly Met Ala Ala Arg Ala Asn
675 680 685

Ser Leu Gln Leu Leu Ser Pro Gln Pro Gly Glu Gln Leu Pro Pro Glu
690 695 700

Met Thr Val Ala Arg Ser Ser Val Lys Glu Thr Ser Arg Glu Gly Thr
705 710 715 720

Ser Ser Phe His Thr Arg Gln Lys Ser Glu Gly Gly Val Tyr His Asp
725 730 735

Pro His Ser Asp Asp Gly Thr Ala Pro Lys Glu Asn Arg His Leu Tyr
740 745 750

Asn Asp Pro Val Pro Arg Arg Val Gly Ser Phe Tyr Arg Val Pro Ser
755 760 765

Pro Arg Pro Asp Asn Ser Phe His Glu Asn Asn Val Ser Thr Arg Val
770 775 780

Ser Ser Leu Pro Ser Glu Ser Ser Ser Gly Thr Asn His Ser Lys Arg
785 790 795 800

Gln Pro Ala Phe Asp Pro Trp Lys Ser Pro Glu Asn Ile Ser His Ser
805 810 815

Glu Gln Leu Lys Glu Lys Glu Lys Gln Gly Phe Phe Arg Ser Met Lys
820 825 830

Lys Lys Lys Lys Lys Ser Gln Thr Val Pro Asn Ser Asp Ser Pro Asp
835 840 845

Leu Leu Thr Leu Gln Lys Ser Ile His Ser Ala Ser Thr Pro Ser Ser
850 855 860

02159303

Arg Pro Lys Glu Trp Arg Pro Glu Lys Ile Ser Asp Leu Gln Thr Gln
865 870 875 880

Ser Gln Pro Leu Lys Ser Leu Arg Lys Leu Leu His Leu Ser Ser Ala
885 890 895

Ser Asn His Pro Ala Ser Ser Asp Pro Arg Phe Gln Pro Leu Thr Ala
900 905 910

Gln Gln Thr Lys Asn Ser Phe Ser Glu Ile Arg Ile His Pro Leu Ser
915 920 925

Gln Ala Ser Gly Gly Ser Ser Asn Ile Arg Gln Glu Pro Ala Pro Lys
930 935 940

Gly Arg Pro Ala Leu Gln Leu Pro Gly Gln Met Asp Pro Gly Trp His
945 950 955 960

Val Ser Ser Val Thr Arg Ser Ala Thr Glu Gly Pro Ser Tyr Ser Glu
965 970 975

Gln Leu Gly Ala Lys Ser Gly Pro Asn Gly His Pro Tyr Asn Arg Thr
980 985 990

Asn Arg Ser Arg Met Pro Asn Leu Asn Asp Leu Lys Glu Thr Ala Leu
995 1000 1005

Ser Arg Gly Ser Arg Ala Asp Tyr Lys Asp His Asp Gly Asp Tyr
1010 1015 1020

Lys Asp His Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys
1025 1030 1035

<210> 15
<211> 2877
<212> DNA
<213> Artificial Sequence

<220>
<223> CDKL5 (107) cDNA

<400> 15
aagattccta acattggtaa tgtgatgaat aaatttgaga tccttgggggt ttaggtgaa 60
ggagcctatg gagttgtact taaatgcaga cacaaggaaa cacatgaaat tgtggcgatc 120
aagaaattca aggacagtga agaaaatgaa gaagtcaaag aaacgacttt acgagagctt 180
aaaatgcttc ggactctcaa gcaggaaaac attgtggagt tgaaggaagc atttcgtcgg 240
aggggaaagt tgtacttgggt gtttgagtat gttgaaaaaa atatgctcga attgctggaa 300
gaaatgccaa atggagttcc acctgagaaa gtaaaaagct acatctatca gctaataaag 360
gctattcact ggtgccataa gaatgatatt gtccatcgag atataaaacc agaaaatctc 420

02159303

ttaatcagcc	acaatgatgt	cctaaaactg	tgtgactttg	gttttgctcg	taatctgtca	480		
gaaggcaata	atgctaatta	cacagagtac	gttgccacca	gatggatatcg	gtccccagaa	540		
ctcttacttg	gcgctcccta	tggaaagtcc	gtggacatgt	ggtcggtggg	ctgtattctt	600		
ggggagctta	gcgatggaca	gcctttat	cctggagaaa	gtgaaattga	ccaacttttt	660		
actattcaga	aggtgctagg	accacttcca	tctgagcaga	tgaagctttt	ctacagtaat	720		
cctcgttcc	atgggctccg	gtttccagct	gttaaccatc	ctcagtcctt	ggaaagaaga	780		
taccttggaa	ttttgaatag	tgttctactt	gacctaatga	agaatttact	gaagttggac	840		
ccagctgaca	gatacttgac	agaacagtgt	ttgaatcacc	ctacatttca	aaccagaga	900		
cttctggatc	gttctccttc	aaggtcagca	aaaagaaaac	cttaccatgt	ggaaagcagc	960		
acattgtcta	atagaaacca	agccggcaaa	agtactgctt	tgcagtctca	ccacagatct	1020		
aacagcaagg	acatccagaa	cctgagtgtg	ggcctgcccc	gggctgacga	aggtctccct	1080		
gccaatgaaa	gcttcctaaa	tggaaacctt	gctggagcta	gtcttagtcc	actgcacacc	1140		
aaaacctacc	aagcaagcag	ccagcctggg	tctaccagca	aagatctcac	caacaacaac	1200		
ataccacacc	ttcttagccc	aaaagaagcc	aagtcaaaaa	cagagtttga	ttttaatatt	1260		
gacccaaagc	cttcagaagg	cccagggaca	aagtacctca	agtcaaacag	cagatctcag	1320		
cagaaccgcc	actcattcat	ggaaagctct	caaagcaaag	ctgggacact	gcagcccaat	1380		
gaaaagcaga	gtcggcatag	ctatat	gtgac	acaattcccc	agtcctctag	gagtccttcc	1440	
tacaggacca	aggccaaaag	ccatggggca	ctgagt	gact	ccaagtctgt	gagcaacctt	1500	
tctgaagcca	gggccc	aaat	tgcggagccc	agtaccagta	ggtacttccc	atctagctgc	1560	
ttagacttga	attctcccac	cagcccaacc	cccaccagac	acagt	gacac	gagaactttg	1620	
ctcagccctt	ctggaagaaa	taaccgaaat	gaggggaacgc	tggactcacg	tcgaaccaca		1680	
accagacatt	ctaagacgat	ggaggaattg	aagctgccgg	agcacatgga	cagtagccat		1740	
tcccattcac	tgtctgcacc	tcacgaatct	ttttcttatg	gactgggcta	caccagcccc		1800	
ttttcttccc	agcaacgtcc	tcatag	gcat	tctatgtatg	tgacctgta	caaagt	gaga	1860
gccaagggct	tggatggaag	cttgagcata	gggcaaggga	tggcagctag	agccaacagc			1920
ctgcaactct	tgtcacccca	gcctggagaa	cagctccctc	cagagatgac	tgtggcaaga			1980
tcttcggtca	aagagacctc	cagagaaggc	acctcttcct	tccatacacg	ccagaagtct			2040
gaggggtggag	tgtatcatga	cccacactct	gatgatggca	cagcccccaa	agaaaataga			2100
cacctataca	atgatcctgt	gccaaggaga	gttggtagct	tttacagagt	gccatctcca			2160
cgtccagaca	attctttcca	tgaaaataat	gtgtcaacta	gagtttcttc	tctaccatca			2220
gagagcagtt	ctggaaccaa	ccactcaaaa	agacaaccag	cattcgatcc	atggaaaagt			2280
cctgaaaata	ttagtcat	tc	agagcaactc	aaggaaaaag	agaagcaagg	atttttcagg		2340
tcaatgaaaa	agaaaaagaa	gaaatctcaa	acagtaccca	attccgacag	ccctgatctt			2400
ctgacgttgc	agaaatccat	tcattctgct	agcactccaa	gcagcagacc	aaaggagtgg			2460

02159303

cgccccgaga agatctcaga tctgcagacc caaagccagc cattaataatc actgcgcaag	2520
ttgttacatc tctcttcggc ctcaaatac ccggttcct cagatccccg cttccagccc	2580
ttaacagctc aacaaaccaa aaattccttc tcagaaattc ggattcaccc cctgagccag	2640
gcctctggcg ggagcagcaa catccggcag gaacccgcac cgaagggcag gccagccctc	2700
cagctgccag gtcagatgga tcctggttgg catgtgtcct ctgtgaccag gagtgccaca	2760
gagggccctt cctactctga acagctgggt gccaaaagtg ggccaaatgg gcaccctat	2820
aacagaacaa atcgctcacg aatgccaaat ctgaatgatt taaaagagac agccttg	2877

<210> 16
 <211> 959
 <212> PRT
 <213> CDKL5 (107) polypeptide
 <400> 16

Lys Ile Pro Asn Ile Gly Asn Val Met Asn Lys Phe Glu Ile Leu Gly
 1 5 10 15

Val Val Gly Glu Gly Ala Tyr Gly Val Val Leu Lys Cys Arg His Lys
 20 25 30

Glu Thr His Glu Ile Val Ala Ile Lys Lys Phe Lys Asp Ser Glu Glu
 35 40 45

Asn Glu Glu Val Lys Glu Thr Thr Leu Arg Glu Leu Lys Met Leu Arg
 50 55 60

Thr Leu Lys Gln Glu Asn Ile Val Glu Leu Lys Glu Ala Phe Arg Arg
 65 70 75 80

Arg Gly Lys Leu Tyr Leu Val Phe Glu Tyr Val Glu Lys Asn Met Leu
 85 90 95

Glu Leu Leu Glu Glu Met Pro Asn Gly Val Pro Pro Glu Lys Val Lys
 100 105 110

Ser Tyr Ile Tyr Gln Leu Ile Lys Ala Ile His Trp Cys His Lys Asn
 115 120 125

Asp Ile Val His Arg Asp Ile Lys Pro Glu Asn Leu Leu Ile Ser His
 130 135 140

Asn Asp Val Leu Lys Leu Cys Asp Phe Gly Phe Ala Arg Asn Leu Ser
 145 150 155 160

Glu Gly Asn Asn Ala Asn Tyr Thr Glu Tyr Val Ala Thr Arg Trp Tyr
 165 170 175

Arg Ser Pro Glu Leu Leu Leu Gly Ala Pro Tyr Gly Lys Ser Val Asp
 180 185 190

02159303

Met Trp Ser Val Gly Cys Ile Leu Gly Glu Leu Ser Asp Gly Gln Pro
195 200 205

Leu Phe Pro Gly Glu Ser Glu Ile Asp Gln Leu Phe Thr Ile Gln Lys
210 215 220

Val Leu Gly Pro Leu Pro Ser Glu Gln Met Lys Leu Phe Tyr Ser Asn
225 230 235 240

Pro Arg Phe His Gly Leu Arg Phe Pro Ala Val Asn His Pro Gln Ser
245 250 255

Leu Glu Arg Arg Tyr Leu Gly Ile Leu Asn Ser Val Leu Leu Asp Leu
260 265 270

Met Lys Asn Leu Leu Lys Leu Asp Pro Ala Asp Arg Tyr Leu Thr Glu
275 280 285

Gln Cys Leu Asn His Pro Thr Phe Gln Thr Gln Arg Leu Leu Asp Arg
290 295 300

Ser Pro Ser Arg Ser Ala Lys Arg Lys Pro Tyr His Val Glu Ser Ser
305 310 315 320

Thr Leu Ser Asn Arg Asn Gln Ala Gly Lys Ser Thr Ala Leu Gln Ser
325 330 335

His His Arg Ser Asn Ser Lys Asp Ile Gln Asn Leu Ser Val Gly Leu
340 345 350

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

Asn Leu Ala Gly Ala Ser Leu Ser Pro Leu His Thr Lys Thr Tyr Gln
370 375 380

Ala Ser Ser Gln Pro Gly Ser Thr Ser Lys Asp Leu Thr Asn Asn Asn
385 390 395 400

Ile Pro His Leu Leu Ser Pro Lys Glu Ala Lys Ser Lys Thr Glu Phe
405 410 415

Asp Phe Asn Ile Asp Pro Lys Pro Ser Glu Gly Pro Gly Thr Lys Tyr
420 425 430

Leu Lys Ser Asn Ser Arg Ser Gln Gln Asn Arg His Ser Phe Met Glu
435 440 445

Ser Ser Gln Ser Lys Ala Gly Thr Leu Gln Pro Asn Glu Lys Gln Ser
450 455 460

02159303

Arg His Ser Tyr Ile Asp Thr Ile Pro Gln Ser Ser Arg Ser Pro Ser
465 470 475 480

Tyr Arg Thr Lys Ala Lys Ser His Gly Ala Leu Ser Asp Ser Lys Ser
485 490 495

Val Ser Asn Leu Ser Glu Ala Arg Ala Gln Ile Ala Glu Pro Ser Thr
500 505 510

Ser Arg Tyr Phe Pro Ser Ser Cys Leu Asp Leu Asn Ser Pro Thr Ser
515 520 525

Pro Thr Pro Thr Arg His Ser Asp Thr Arg Thr Leu Leu Ser Pro Ser
530 535 540

Gly Arg Asn Asn Arg Asn Glu Gly Thr Leu Asp Ser Arg Arg Thr Thr
545 550 555 560

Thr Arg His Ser Lys Thr Met Glu Glu Leu Lys Leu Pro Glu His Met
565 570 575

Asp Ser Ser His Ser His Ser Leu Ser Ala Pro His Glu Ser Phe Ser
580 585 590

Tyr Gly Leu Gly Tyr Thr Ser Pro Phe Ser Ser Gln Gln Arg Pro His
595 600 605

Arg His Ser Met Tyr Val Thr Arg Asp Lys Val Arg Ala Lys Gly Leu
610 615 620

Asp Gly Ser Leu Ser Ile Gly Gln Gly Met Ala Ala Arg Ala Asn Ser
625 630 635 640

Leu Gln Leu Leu Ser Pro Gln Pro Gly Glu Gln Leu Pro Pro Glu Met
645 650 655

Thr Val Ala Arg Ser Ser Val Lys Glu Thr Ser Arg Glu Gly Thr Ser
660 665 670

Ser Phe His Thr Arg Gln Lys Ser Glu Gly Gly Val Tyr His Asp Pro
675 680 685

His Ser Asp Asp Gly Thr Ala Pro Lys Glu Asn Arg His Leu Tyr Asn
690 695 700

Asp Pro Val Pro Arg Arg Val Gly Ser Phe Tyr Arg Val Pro Ser Pro
705 710 715 720

Arg Pro Asp Asn Ser Phe His Glu Asn Asn Val Ser Thr Arg Val Ser
725 730 735

02159303

Ser Leu Pro Ser Glu Ser Ser Ser Gly Thr Asn His Ser Lys Arg Gln
740 745 750

Pro Ala Phe Asp Pro Trp Lys Ser Pro Glu Asn Ile Ser His Ser Glu
755 760 765

Gln Leu Lys Glu Lys Glu Lys Gln Gly Phe Phe Arg Ser Met Lys Lys
770 775 780

Lys Lys Lys Lys Ser Gln Thr Val Pro Asn Ser Asp Ser Pro Asp Leu
785 790 795 800

Leu Thr Leu Gln Lys Ser Ile His Ser Ala Ser Thr Pro Ser Ser Arg
805 810 815

Pro Lys Glu Trp Arg Pro Glu Lys Ile Ser Asp Leu Gln Thr Gln Ser
820 825 830

Gln Pro Leu Lys Ser Leu Arg Lys Leu Leu His Leu Ser Ser Ala Ser
835 840 845

Asn His Pro Ala Ser Ser Asp Pro Arg Phe Gln Pro Leu Thr Ala Gln
850 855 860

Gln Thr Lys Asn Ser Phe Ser Glu Ile Arg Ile His Pro Leu Ser Gln
865 870 875 880

Ala Ser Gly Gly Ser Ser Asn Ile Arg Gln Glu Pro Ala Pro Lys Gly
885 890 895

Arg Pro Ala Leu Gln Leu Pro Gly Gln Met Asp Pro Gly Trp His Val
900 905 910

Ser Ser Val Thr Arg Ser Ala Thr Glu Gly Pro Ser Tyr Ser Glu Gln
915 920 925

Leu Gly Ala Lys Ser Gly Pro Asn Gly His Pro Tyr Asn Arg Thr Asn
930 935 940

Arg Ser Arg Met Pro Asn Leu Asn Asp Leu Lys Glu Thr Ala Leu
945 950 955