

# SEQUENCE LISTING

<110> National University of Singapore

<120> RECOMBINANT BACTERIA AND USES THEREOF

<130> 10104SG1252

<150> SG 10201901828T

<151> 2019-02-28

<160> 13

<170> PatentIn version 3.5

<210> 1

<211> 1449

<212> DNA

<213> Artificial Sequence

<220>

<223> DUSP10

<400> 1

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| caggatctca acctttgttt agactctagt taccttggct ctgccaaccc aggcagtaac | 120 |
| agccaccctc ctgtcatcgc caccaccgtt gtgtccctca aggctgcgaa tctgacgtat | 180 |
| atgccctcat ccagcggctc tgcccgtcgt ctgaattgtg gatgcagcag tgccagctgc | 240 |
| tgcactgtgg caacctacga caaggacaat caggcccaaa cccaagccat tgccgctggc | 300 |
| accaccacca ctgccatcgg aacctctacc acctgccctg ctaaccagat ggtcaacaat | 360 |
| aatgagaata caggctctct aagtccatca agtgggggtg gcagccctgt gtcagggacc | 420 |
| cccaagcagc tagccagcat caaaataatc taccccaatg acttggcaaa gaagatgacc | 480 |
| aaatgcagca agagtcacct gccgagtcag ggccctgtca tcattgactg caggcccttc | 540 |
| atggagtaca acaagagtca catccaagga gctgtccaca ttaactgtgc cgataagatc | 600 |
| agccggcgga gactgcagca gggcaagatc actgtcctag acttgatttc ctgtagggaa | 660 |
| ggcaaggact ctttcaagag gatcttttcc aaagaaatta tagtttatga tgagaatacc | 720 |
| aatgaaccaa gccgagtgat gccctcccag ccacttcaca tagtcctcga gtccctgaag | 780 |
| agagaaggca aagaacctct ggtgttgaaa ggtggactta gtagttttaa gcagaacat  | 840 |
| gaaaacctct gtgacaactc cctccagctc caagagtgcc gggaggtggg gggcggcgca | 900 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tccgcggcct cgagcttgct acctcagccc atccccacca cccctgacat cgagaacgct  | 960  |
| gagctcacc ccatcttgcc cttcctgttc cttggcaatg agcaggatgc tcaggacctg   | 1020 |
| gacaccatgc agcggctgaa catcgggtac gtcacaaacg tcaccactca tcttcccctc  | 1080 |
| taccactatg agaaaggcct gttcaactac aagcggctgc cagccactga cagcaacaag  | 1140 |
| cagaacctgc ggcagtactt tgaagaggct tttgagttca ttgaggaagc tcaccagtgt  | 1200 |
| gggaaggggc ttctcatcca ctgccaggct ggggtgtccc gctccgccac catcgatcatc | 1260 |
| gcttacttga tgaagcacac tcggatgacc atgactgatg cttataaatt tgtcaaaggc  | 1320 |
| aaacgaccaa ttatctcccc aaaccttaac ttcattggggc agttgctaga gttcgaggaa | 1380 |
| gacctaaaca acggtgtgac accgagaatc cttacaccaa agctgatggg cgtggagacg  | 1440 |
| gttgtgtga                                                          | 1449 |

<210> 2  
 <211> 129  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PH promoter

|                                                                   |     |
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| gtaacagttt tgtaataaaa aaacctataa atattccgga ttattcatac cgtcccacca | 120 |
| tcgggcgcg                                                         | 129 |

<210> 3  
 <211> 576  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> CMV promoter

|                                                                    |     |
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| <400> 3                                                            |     |
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| cttacggtaa atggcccgcc tggctgaccg cccaacgacc cccgcccatt gacgtcaata  | 120 |
| atgacgtatg ttcccatagt aacgccaata gggactttcc attgacgtca atgggtggag  | 180 |
| tatttacggg aaactgcca cttggcagta catcaagtgt atcatatgcc aagtacgccc   | 240 |

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| cctattgacg tcaatgacgg taaatggccc gcctggcatt atgcccagta catgacctta  | 300 |
| tgggactttc ctacttggca gtacatctac gtattagtca tcgctattac catggtgatg  | 360 |
| cggtttttggc agtacatcaa tgggcgtgga tagcggtttg actcacgggg atttccaagt | 420 |
| ctccacccca ttgacgtcaa tgggagtttg ttttggcacc aaaatcaacg ggactttcca  | 480 |
| aaatgtcgta acaactccgc cccattgacg caaatgggcg gtaggcgtgt acggtgggag  | 540 |
| gtctatataa gcagagctgg tttagtgaac cgtcag                            | 576 |

<210> 4  
 <211> 345  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> SV40 promoter

|                                                                    |     |
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| atgcaaagca tgcattctaa ttagtcagca accaggtgtg gaaagtcccc aggctcccca  | 120 |
| gcaggcagaa gtatgcaaag catgcatctc aattagtcag caaccatagt cccgccctta  | 180 |
| actccgcca tcccgccctt aactccgcc agttccgcc attctccgcc ccatggctga     | 240 |
| ctaatttttt ttatttatgc agaggccgag gccgcctctg cctctgagct attccagaag  | 300 |
| tagtgaggag gcttttttgg aggcctaggc ttttgcaaaa agctc                  | 345 |

<210> 5  
 <211> 753  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> TK promoter

|                                                                    |     |
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| <400> 5                                                            |     |
| aaatgagtct tcggacctcg cgggggccgc ttaagcgggtg gttagggttt gtctgacgcg | 60  |
| gggggagggg gaaggaacga aacactctca ttcggaggcg gctcgggggtt tggcttttgt | 120 |
| ggccacgggc acgcagaaga gcgccgcat cctcttaagc accccccgc cctccgtgga    | 180 |
| ggcgggggtt tggtcggcgg gtggtaactg gcgggccgct gactcgggcg ggtcgcgcgc  | 240 |
| cccagagtgt gaccttttcg gtctgctcgc agacccccgg gcggcgccgc cgcggcggcg  | 300 |

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| acgggctcgc tgggtcctag gtcctatggg gaccgtatac gtggacaggc tctggagcat  | 360 |
| ccgcacgact gcggtgatat taccggagac cttctgcggg acgagccggg tcacgcggct  | 420 |
| gacgcggagc gtccgttggg cgacaaacac caggacgggg cacaggtaca ctatcttgtc  | 480 |
| acccggaggc gcgagggact gcaggagctt caggagtggt cgagctgct tcatccccgt   | 540 |
| ggcccgttgc tcgcttttgc tggcgggtgc cccggaagaa atatatttgc atgtcttttag | 600 |
| ttctatgatg acacaaaccc cgcccagcgt cttgtcattg gcgaattcga acacgcagat  | 660 |
| gcagtcgggg cggcgcgggtc ccaggtccac ttcgcatatt aaggtgacgc gtgtggcctc | 720 |
| gaacaccgag cgaccctgca gcgacccgct taa                               | 753 |

<210> 6  
 <211> 633  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> LTR promoter

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 6                                                            |     |
| tggaagggt aattcactcc caacgaagac aagatatact tgatctgtgg atctaccaca   | 60  |
| cacaaggcta cttccctgat tagcagaact acacaccagg gccagggatc agatatccac  | 120 |
| tgaccttttg atggtgctac aagctagtac cagttgagcc agagaagtta gaagaagcca  | 180 |
| acaaaggaga gaacaccagc ttgttacacc ctgtgagcct gcatggaatg gatgacccgg  | 240 |
| agagagaagt gttagagtgg aggtttgaca gccgcctagc atttcatcac atggcccagag | 300 |
| agctgcatcc ggagtacttc aagaactgct gacatcgagc ttgctacaag ggactttccg  | 360 |
| ctggggactt tccagggagg cgtggcctgg gcgggactgg ggagtggcga gccctcagat  | 420 |
| cctgcatata agcagctgct ttttgcctgt actgggtctc tctggttaga ccagatctga  | 480 |
| gcctgggagc tctctggcta actaggggaac ccactgctta agcctcaata aagcttgcct | 540 |
| tgagtgcctc aagtagtgtg tgcccgtctg ttgtgtgact ctggttaacta gagatccctc | 600 |
| agaccctttt agtcagtgtg gaaaatctct agc                               | 633 |

<210> 7  
 <211> 3280  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Fibronectin binding protein A

<400> 7

|                                                                     |      |
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| attgggagca gcatcagtat tcttaggaac aatgatcggt gttgggatgg gacaagataa   | 120  |
| agaagctgca gcatcagaac aaaagacaac tacagtagaa gaaaatggga attcagctac   | 180  |
| tgataataaa gtaaacgaaa cacaacaac tacaactaac gttaatacta tagatgaaac    | 240  |
| acaatcatal agcgcaacag caacagaaca accgtcaaac gcaacacaag taacaactga   | 300  |
| aaaagcacca aaagcagtag aagcaccaca aactgcacaa ccagcaaag tagaaacagt    | 360  |
| taaagaagag gtagttaagg aagaagcgaa ccctcaagtt aaggaaacga cacaatctca   | 420  |
| agacaatagc ggagatcaaa gacaagtaga tttaacacct aaaaaggcta caaaaatca    | 480  |
| agcagcagaa acacaagttg aagtggcaca gccagaacg gtatcagaaa gtaaaccacg    | 540  |
| tgtgacaaga tcagcagatg tagcggaagc taaggaagct agtgacgcga aagtggaaac   | 600  |
| gggtacagat gtgacaagta aagttacagt ggaaagtggg tctattgagg cacctcaagg   | 660  |
| aaataaagta gagccacatg ctggtcaacg tgctgtactg aaatacaaat tgaaattcga   | 720  |
| aaagggttta cacaaggag attatthttga tttcaccttg tctaataatg taaatactta   | 780  |
| tggagthttca acagctagaa aagtaccaga aatcaaaaat ggthtcagtcg taatggcgac | 840  |
| aggtcaactt cttggaaatg ggaaaattag gtatacattt acagactata ttgattataa   | 900  |
| agtaaatgtg actgctgatt tagaaatcaa thtattthatt gatcctaaaa ctgtacaaag  | 960  |
| caatggacaa caaacaataa cttcaacgtt gaatgataag gaaacaaaaa acacattgcc   | 1020 |
| aatagaatat aatccaggag taagtaatag ctatgctaath gtaaatggat ctattgaaac  | 1080 |
| thttgataaa gggaacaata aattcactca tgtagcttac ataaaaccac aaaatgggca   | 1140 |
| taaatcagat agcgtthtcaa ttactggtac actaactcaa ggtagcaaag ctaatggaaa  | 1200 |
| tgthccaact gtaaaagtat atgaagtctt aaaggatgct aaagaattac cagaaagtgt   | 1260 |
| atatgcaaac atatcagact ctacaatgtt taaagatgta actcaggaaa tgaaagataa   | 1320 |
| attaaaagta gaaaataatg ggagttataa attagacatt gagaaattag aaaaaagtta   | 1380 |
| tgthatacac tatgatggtg aatacttaag tggthtcagat caagtgaatt ttagaacgca  | 1440 |
| tatgthttgga tatccagaac agcagtataa gtactactat actcattthg gataccaact  | 1500 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tacatgggat aatggattag ttttatatag taacaaagca aaaggtgatg gaacgaatgg  | 1560 |
| aacaataaca gaatcgaata atatgacatt tgatgaagaa tatggaactg gagttattac  | 1620 |
| aggtcaatat gataagaatt tagtaactac tgttgaagaa gaatatgatt cttcaactct  | 1680 |
| tgacattgat taccacacag ctatagatgg tgaaggtggt tatgttgatg gatacattga  | 1740 |
| aacaatagaa gaaacggatt catcagctat tgatatcgat taccatactg ctgtggatag  | 1800 |
| cgaagcgggt cacgttggag gatacactga gtcctctgag gaatcaaatc caattgactt  | 1860 |
| tgaagaatct acgcatgaaa attcaaaaca tcacgctgat gttgttgaat atgaagagga  | 1920 |
| tacaaacca ggtggtggtc aggttactac tgagtctaac ttagttgaat ttgacgaaga   | 1980 |
| gtctacaaaa ggtattgtaa ctggcgcagt gagcgaccat acaacaattg aagatacgaa  | 2040 |
| agaatataca actgaaagta atctgattga actagtagat gaactacctg aagaacatgg  | 2100 |
| tcaagcacia ggaccaatcg aggaaattac tgaaaacaat catcatattt ctcattctgg  | 2160 |
| tttaggaact gaaaatggtc acggtaatta tgggtgtgatt gaagaaatcg aagaaaatag | 2220 |
| ccatgttgat attaagagtg aattaggtta tgaaggtggc caaaatagcg gtaaccagtc  | 2280 |
| attcgaggaa gacacagaag aagataaacc taaatatgaa caaggtggca atatcgtaga  | 2340 |
| tatcgatttc gatagtgtac ctcaaattca tgggtcaaaat aaaggtgatc agtcattcga | 2400 |
| agaagataca gagaaagaca aacctaagta tgaacaaggt ggtaatatca ttgatatcga  | 2460 |
| cttcgacagt gtgccacaaa ttcatggatt caataagcat aatgaaatta ttgaagaaga  | 2520 |
| tacaaacaaa gataaaccaa attatcaatt cgggtggacac aacattgttg attttgaaga | 2580 |
| agatacactt ccgaaagtaa gcggtcaaaa tgaaggtcaa caaacgattg aagaagatac  | 2640 |
| aacgccgcca acgccaccga caccagaagt accgagtgag ccggaaacac caacaccacc  | 2700 |
| gacgccggaa gtaccgagtg agccagaaac accaacgcca ccgacaccag aagtaccaag  | 2760 |
| tgagccggaa acaccaacac cgccaacacc agaggtacca agtgagccgg aaacaccaac  | 2820 |
| accgccaaca ccagaggtac cagttgaacc tggtaaacca gtaccacctg ctaaagaaga  | 2880 |
| acctaaaaaa ctttctaaac cagtggaaca aggtaaagta gtaacacctg ttattgaaat  | 2940 |
| caatgaaaag gttaaagcag tggcaccaac taaacaaaaa caatctaaga aatctgaact  | 3000 |
| acctgaaaca ggtggagaag aatcaacaaa caaaggtatg ttgttcggcg gattattcag  | 3060 |
| cattctaggt ttagcgttat tacgtagaaa taaaaagaat aacaaagcat aattaacaaa  | 3120 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| aattgacggg tttatttcat aaattacatg aagtaagcct gtttttttta tattaaatca  | 3180 |
| aatttttaaat agaaaattag agtgttttct gattgcttca ttggtttatg tctgatgatt | 3240 |
| gataacgaac tgagagataa agttagaatt ttaaactagt                        | 3280 |

<210> 8  
 <211> 559  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> erm promoter

|                                                                    |     |
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| atagcgacag agaaggcgaa aacattgcct ggtcgatcat tcataaagca aatgcctttt  | 180 |
| ctaaagataa aacgtataaa agactatgga tcaatagttt agaaaaagat gtgatccgta  | 240 |
| gcggttttca aaatttgcaa ccaggaatga attactatcc cttttatcaa gaagcgcaca  | 300 |
| aaaagaaaaa cgaaatgata caccaatcag tgcaaaaaaa gatataatgg gagataagac  | 360 |
| ggttcgtgtt cgtgctgact tgcaccatat cataaaaaatc gaaacagcaa agaatggcgg | 420 |
| aaacgtaaaa gaagttatgg aaataagact tagaagcaaa cttagagtg tgttgatagt   | 480 |
| gcagtatctt aaaattttgt ataataggaa ttgaagttaa attagatgct aaaaatttgt  | 540 |
| aattaagaag gagtgaatt                                               | 559 |

<210> 9  
 <211> 309  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> nisin promoter

|                                                                   |     |
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| <400> 9                                                           |     |
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| aatctttctt cgaaacagat accaaatcca agctaaaatc ttttgtactc attttgagtg | 120 |
| cctccttata atttattttg tagttccttc gaacgaaatc attgtatcta acaaacttca | 180 |
| gaatttaatc agagccggtt attatgctcg cgttatcgac aataatatta ttaccaatac | 240 |

tttctcaaga tagaattaag actgttttag atttgtaaatt gtttctattg tcagtatatg 300  
tataagact 309

<210> 10  
<211> 482  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> DUSP10

<400> 10

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Pro Val Arg Pro Gln Asp Leu Asn Leu Cys Leu Asp Ser Ser Tyr Leu  
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Gly Ser Ala Asn Pro Gly Ser Asn Ser His Pro Pro Val Ile Ala Thr  
35 40 45

Thr Val Val Ser Leu Lys Ala Ala Asn Leu Thr Tyr Met Pro Ser Ser  
50 55 60

Ser Gly Ser Ala Arg Ser Leu Asn Cys Gly Cys Ser Ser Ala Ser Cys  
65 70 75 80

Cys Thr Val Ala Thr Tyr Asp Lys Asp Asn Gln Ala Gln Thr Gln Ala  
85 90 95

Ile Ala Ala Gly Thr Thr Thr Thr Ala Ile Gly Thr Ser Thr Thr Cys  
100 105 110

Pro Ala Asn Gln Met Val Asn Asn Asn Glu Asn Thr Gly Ser Leu Ser  
115 120 125

Pro Ser Ser Gly Val Gly Ser Pro Val Ser Gly Thr Pro Lys Gln Leu  
130 135 140

Ala Ser Ile Lys Ile Ile Tyr Pro Asn Asp Leu Ala Lys Lys Met Thr  
145 150 155 160

Lys Cys Ser Lys Ser His Leu Pro Ser Gln Gly Pro Val Ile Ile Asp  
165 170 175

Cys Arg Pro Phe Met Glu Tyr Asn Lys Ser His Ile Gln Gly Ala Val  
180 185 190

His Ile Asn Cys Ala Asp Lys Ile Ser Arg Arg Arg Leu Gln Gln Gly  
195 200 205

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

Phe Lys Arg Ile Phe Ser Lys Glu Ile Ile Val Tyr Asp Glu Asn Thr  
225 230 235 240

Asn Glu Pro Ser Arg Val Met Pro Ser Gln Pro Leu His Ile Val Leu  
245 250 255

Glu Ser Leu Lys Arg Glu Gly Lys Glu Pro Leu Val Leu Lys Gly Gly  
260 265 270

Leu Ser Ser Phe Lys Gln Asn His Glu Asn Leu Cys Asp Asn Ser Leu  
275 280 285

Gln Leu Gln Glu Cys Arg Glu Val Gly Gly Gly Ala Ser Ala Ala Ser  
290 295 300

Ser Leu Leu Pro Gln Pro Ile Pro Thr Thr Pro Asp Ile Glu Asn Ala  
305 310 315 320

Glu Leu Thr Pro Ile Leu Pro Phe Leu Phe Leu Gly Asn Glu Gln Asp  
325 330 335

Ala Gln Asp Leu Asp Thr Met Gln Arg Leu Asn Ile Gly Tyr Val Ile  
340 345 350

Asn Val Thr Thr His Leu Pro Leu Tyr His Tyr Glu Lys Gly Leu Phe  
355 360 365

Asn Tyr Lys Arg Leu Pro Ala Thr Asp Ser Asn Lys Gln Asn Leu Arg

370

375

380

Gln Tyr Phe Glu Glu Ala Phe Glu Phe Ile Glu Glu Ala His Gln Cys  
 385 390 395 400

Gly Lys Gly Leu Leu Ile His Cys Gln Ala Gly Val Ser Arg Ser Ala  
 405 410 415

Thr Ile Val Ile Ala Tyr Leu Met Lys His Thr Arg Met Thr Met Thr  
 420 425 430

Asp Ala Tyr Lys Phe Val Lys Gly Lys Arg Pro Ile Ile Ser Pro Asn  
 435 440 445

Leu Asn Phe Met Gly Gln Leu Leu Glu Phe Glu Glu Asp Leu Asn Asn  
 450 455 460

Gly Val Thr Pro Arg Ile Leu Thr Pro Lys Leu Met Gly Val Glu Thr  
 465 470 475 480

Val Val

<210> 11

<211> 2823

<212> DNA

<213> Artificial Sequence

<220>

<223> Fibronectin binding protein B

<400> 11

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ttaggaacaa tgatcgttgt tggaatggga caagaaaaag aagctgcagc atcggaaacaa 120

aacaatacta cagtagagga aagtgggagt tcagctactg aaagtaaagc aagcgaaaca 180

caaacaacta caaataacgt taataacaata gatgaaacac aatcatacag cgcgacatca 240

actgagcaac catcacaatc aacacaagta acaacagaag aagcaccgaa aactgtgcaa 300

gcaccaaaaag tagaaacttc gcgagttgat ttgccatcgg aaaaagttgc tgataaggaa 360

actacaggaa ctcaagttga catagctcaa ccaagtaacg tctcagaaat taaaccaaga 420

|                                                                     |      |
|---------------------------------------------------------------------|------|
| atgaaaagat caactgacgt tacagcagtt gcagagaaag aagtagtgga agaaactaaa   | 480  |
| gcgacaggta cagatgtaac aaataaagtg gaagtagaag aaggtagtga aattgtagga   | 540  |
| cataaacaag atacgaatgt tgtaaadcct cataacgcag aaagagtaac cttgaaatat   | 600  |
| aaatggaaat ttggagaagg aattaaggcg ggagattatt ttgatttcac attaagcgat   | 660  |
| aatgttgaaa ctcatggtat ctcaacactg cgtaaagttc cggagataaa aagtacagat   | 720  |
| ggtcaagtta tggcgacagg agaaataatt ggagaaagaa aagttagata tacgtttaaa   | 780  |
| gaatatgtac aagaaaagaa agatttaact gctgaattat ctttaaactct atttattgat  | 840  |
| cctacaacag tgacgcaaaa aggtaaccaa aatgttgaag tttaaattggg tgagactacg  | 900  |
| gtagcaaaa tatttaatat tcaatattta ggtggagtta gagataattg gggagtaaca    | 960  |
| gctaattggc gaattgatac tttaaataaa gtagatggga aatttagtca ttttgcgtac   | 1020 |
| atgaaaccta acaaccagtc gttaagctct gtgacagtaa ctgggtcaagt aactaaagga  | 1080 |
| aataaaccag gggttaataa tccaacagtt aaggtatata aacacattgg ttcagacgat   | 1140 |
| ttagctgaaa gcgtatatgc aaagcttgat gatgtcagca aatttgaaga tgtgactgat   | 1200 |
| aatatgagtt tagattttga tactaatggg ggttattctt taaactttaa taatttagac   | 1260 |
| caaagtaaaa attatgtaat aaaatatgaa ggggtattatg attcaaagtc tagcaactta  | 1320 |
| gaatttcaaa cacacctttt tggatattat aactattatt atacaagtaa tttaacttgg   | 1380 |
| aaaaatggcg ttgcatttta ctctaataac gctcaaggcg acggcaaaga taaactaaag   | 1440 |
| gaacctatta tagaacatag tactcctatc gaacttgaat ttaaatcaga gccgccagtg   | 1500 |
| gagaagcatg aattgactgg tacaatcgaa gaaagtaatg attctaagcc aattgatttt   | 1560 |
| gaatatcata cagctgttga aggtgcagaa ggtcatgcag aaggtaccat tgaaactgaa   | 1620 |
| gaagattcta ttcattgtaga ctttgaagaa tcgacacatg aaaattcaaa acatcatgct  | 1680 |
| gatgttggtg aatatgaaga agatacaaac ccaggtgggtg gtcagggttac tactgagtct | 1740 |
| aacctagttg aatttgacga agattctaca aaaggtattg taactgggtgc tgttagcgat  | 1800 |
| catacaacaa ttgaagatac gaaagaatat acgactgaaa gtaatctgat tgaactagta   | 1860 |
| gatgaactac ctgaagaaca tgggtcaagcg caaggaccaa tcgaggaaat tactgaaaac  | 1920 |
| aatcatcata tttctcattc tgggttagga actgaaaatg gtcacggtaa ttatggcgtg   | 1980 |
| attgaagaaa tcgaagaaaa tagccacgtg gatattaaga gtgaattagg ttacgaaggt   | 2040 |

ggccaaaata gcggtaatca gtcatttgag gaagacacag aagaagataa accgaaatat 2100  
 gaacaagggtg gcaatatcgt agatatcgat ttcgatagtg tacctcaaat tcatgggtcaa 2160  
 aataatggta accaatcatt cgaagaagat acagagaaag acaaacctaa gtatgaacaa 2220  
 ggtggtaata tcattgatat cgacttcgac agtgtgccac atattcacgg attcaataag 2280  
 cacactgaaa ttattgaaga agatacaaat aaagataaac caaattatca attcgggtgga 2340  
 cacaatagtg ttgactttga agaagataca cttccacaag taagtgggtca taatgaagggt 2400  
 caacaaacga ttgaagaaga tacaacacct ccaatcgtgc caccaacgcc accgacacca 2460  
 gaagtaccaa gcgagccgga aacaccaaca ccaccgacac cagaagtacc aagcgagccg 2520  
 gaaacaccaa caccgccaac gccagaggta ccaactgaac ctggttaaacc aataccacct 2580  
 gctaaagaag aacctaataaa accttctaaa ccagtgggaac aaggtaaagt agtaacacct 2640  
 gttattgaaa tcaatgaaaa gggttaaagca gtggtaccaa ctaaaaaagc acaatctaag 2700  
 aaatctgaac tacctgaaac aggtggagaa gaatcaacaa acaacggcat gttgttcggc 2760  
 ggattattta gcattttagg tttagcggtta ttacgcagaa ataaaaagaa tcacaaagca 2820  
 taa 2823

<210> 12  
 <211> 1029  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Fibronectin binding protein A

<400> 12

Met Lys Asn Asn Leu Arg Tyr Gly Ile Arg Lys His Lys Leu Gly Ala  
 1 5 10 15

Ala Ser Val Phe Leu Gly Thr Met Ile Val Val Gly Met Gly Gln Asp  
 20 25 30

Lys Glu Ala Ala Ala Ser Glu Gln Lys Thr Thr Thr Val Glu Glu Asn  
 35 40 45

Gly Asn Ser Ala Thr Asp Asn Lys Val Asn Glu Thr Gln Thr Thr Thr  
 50 55 60

Thr Asn Val Asn Thr Ile Asp Glu Thr Gln Ser Tyr Ser Ala Thr Ala  
65 70 75 80

Thr Glu Gln Pro Ser Asn Ala Thr Gln Val Thr Thr Glu Lys Ala Pro  
85 90 95

Lys Ala Val Gln Ala Pro Gln Thr Ala Gln Pro Ala Asn Val Glu Thr  
100 105 110

Val Lys Glu Glu Val Val Lys Glu Glu Ala Asn Pro Gln Val Lys Glu  
115 120 125

Thr Thr Gln Ser Gln Asp Asn Ser Gly Asp Gln Arg Gln Val Asp Leu  
130 135 140

Thr Pro Lys Lys Ala Thr Gln Asn Gln Ala Ala Glu Thr Gln Val Glu  
145 150 155 160

Val Ala Gln Pro Arg Thr Val Ser Glu Ser Lys Pro Arg Val Thr Arg  
165 170 175

Ser Ala Asp Val Ala Glu Ala Lys Glu Ala Ser Asp Ala Lys Val Glu  
180 185 190

Thr Gly Thr Asp Val Thr Ser Lys Val Thr Val Glu Ser Gly Ser Ile  
195 200 205

Glu Ala Pro Gln Gly Asn Lys Val Glu Pro His Ala Gly Gln Arg Val  
210 215 220

Val Leu Lys Tyr Lys Leu Lys Phe Glu Lys Gly Leu His Lys Gly Asp  
225 230 235 240

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

Thr Ala Arg Lys Val Pro Glu Ile Lys Asn Gly Ser Val Val Met Ala  
260 265 270

Thr Gly Gln Leu Leu Gly Asn Gly Lys Ile Arg Tyr Thr Phe Thr Asp

275

280

285

Tyr Ile Asp Tyr Lys Val Asn Val Thr Ala Asp Leu Glu Ile Asn Leu  
 290 295 300

Phe Ile Asp Pro Lys Thr Val Gln Ser Asn Gly Gln Gln Thr Ile Thr  
 305 310 315 320

Ser Thr Leu Asn Asp Lys Glu Thr Lys Asn Thr Leu Pro Ile Glu Tyr  
 325 330 335

Asn Pro Gly Val Ser Asn Ser Tyr Ala Asn Val Asn Gly Ser Ile Glu  
 340 345 350

Thr Phe Asp Lys Gly Asn Asn Lys Phe Thr His Val Ala Tyr Ile Lys  
 355 360 365

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

Thr Gln Gly Ser Lys Ala Asn Gly Asn Val Pro Thr Val Lys Val Tyr  
 385 390 395 400

Glu Val Leu Lys Asp Ala Lys Glu Leu Pro Glu Ser Val Tyr Ala Asn  
 405 410 415

Ile Ser Asp Ser Thr Met Phe Lys Asp Val Thr Gln Glu Met Lys Asp  
 420 425 430

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

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

Ser Asp Gln Val Asn Phe Arg Thr His Met Phe Gly Tyr Pro Glu Gln  
 465 470 475 480

Gln Tyr Lys Tyr Tyr Thr His Leu Gly Tyr Gln Leu Thr Trp Asp  
 485 490 495

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

Gly Thr Ile Thr Glu Ser Asn Asn Met Thr Phe Asp Glu Glu Tyr Gly  
515 520 525

Thr Gly Val Ile Thr Gly Gln Tyr Asp Lys Asn Leu Val Thr Thr Val  
530 535 540

Glu Glu Glu Tyr Asp Ser Ser Thr Leu Asp Ile Asp Tyr His Thr Ala  
545 550 555 560

Ile Asp Gly Glu Gly Gly Tyr Val Asp Gly Tyr Ile Glu Thr Ile Glu  
565 570 575

Glu Thr Asp Ser Ser Ala Ile Asp Ile Asp Tyr His Thr Ala Val Asp  
580 585 590

Ser Glu Ala Gly His Val Gly Gly Tyr Thr Glu Ser Ser Glu Glu Ser  
595 600 605

Asn Pro Ile Asp Phe Glu Glu Ser Thr His Glu Asn Ser Lys His His  
610 615 620

Ala Asp Val Val Glu Tyr Glu Glu Asp Thr Asn Pro Gly Gly Gly Gln  
625 630 635 640

Val Thr Thr Glu Ser Asn Leu Val Glu Phe Asp Glu Glu Ser Thr Lys  
645 650 655

Gly Ile Val Thr Gly Ala Val Ser Asp His Thr Thr Ile Glu Asp Thr  
660 665 670

Lys Glu Tyr Thr Thr Glu Ser Asn Leu Ile Glu Leu Val Asp Glu Leu  
675 680 685

Pro Glu Glu His Gly Gln Ala Gln Gly Pro Ile Glu Glu Ile Thr Glu  
690 695 700

Asn Asn His His Ile Ser His Ser Gly Leu Gly Thr Glu Asn Gly His

|                                                                 |  |     |  |     |  |     |
|-----------------------------------------------------------------|--|-----|--|-----|--|-----|
| 705                                                             |  | 710 |  | 715 |  | 720 |
| Gly Asn Tyr Gly Val Ile Glu Glu Ile Glu Glu Asn Ser His Val Asp |  |     |  |     |  |     |
|                                                                 |  | 725 |  | 730 |  | 735 |
| Ile Lys Ser Glu Leu Gly Tyr Glu Gly Gly Gln Asn Ser Gly Asn Gln |  |     |  |     |  |     |
|                                                                 |  | 740 |  | 745 |  | 750 |
| Ser Phe Glu Glu Asp Thr Glu Glu Asp Lys Pro Lys Tyr Glu Gln Gly |  |     |  |     |  |     |
|                                                                 |  | 755 |  | 760 |  | 765 |
| Gly Asn Ile Val Asp Ile Asp Phe Asp Ser Val Pro Gln Ile His Gly |  |     |  |     |  |     |
|                                                                 |  | 770 |  | 775 |  | 780 |
| Gln Asn Lys Gly Asp Gln Ser Phe Glu Glu Asp Thr Glu Lys Asp Lys |  |     |  |     |  |     |
|                                                                 |  | 785 |  | 790 |  | 800 |
| Pro Lys Tyr Glu Gln Gly Gly Asn Ile Ile Asp Ile Asp Phe Asp Ser |  |     |  |     |  |     |
|                                                                 |  | 805 |  | 810 |  | 815 |
| Val Pro Gln Ile His Gly Phe Asn Lys His Asn Glu Ile Ile Glu Glu |  |     |  |     |  |     |
|                                                                 |  | 820 |  | 825 |  | 830 |
| Asp Thr Asn Lys Asp Lys Pro Asn Tyr Gln Phe Gly Gly His Asn Ile |  |     |  |     |  |     |
|                                                                 |  | 835 |  | 840 |  | 845 |
| Val Asp Phe Glu Glu Asp Thr Leu Pro Lys Val Ser Gly Gln Asn Glu |  |     |  |     |  |     |
|                                                                 |  | 850 |  | 855 |  | 860 |
| Gly Gln Gln Thr Ile Glu Glu Asp Thr Thr Pro Pro Thr Pro Pro Thr |  |     |  |     |  |     |
|                                                                 |  | 865 |  | 870 |  | 880 |
| Pro Glu Val Pro Ser Glu Pro Glu Thr Pro Thr Pro Pro Thr Pro Glu |  |     |  |     |  |     |
|                                                                 |  | 885 |  | 890 |  | 895 |
| Val Pro Ser Glu Pro Glu Thr Pro Thr Pro Pro Thr Pro Glu Val Pro |  |     |  |     |  |     |
|                                                                 |  | 900 |  | 905 |  | 910 |
| Ser Glu Pro Glu Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu |  |     |  |     |  |     |
|                                                                 |  | 915 |  | 920 |  | 925 |

Pro Glu Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Val Glu Pro Gly  
930 935 940

Lys Pro Val Pro Pro Ala Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro  
945 950 955 960

Val Glu Gln Gly Lys Val Val Thr Pro Val Ile Glu Ile Asn Glu Lys  
965 970 975

Val Lys Ala Val Ala Pro Thr Lys Gln Lys Gln Ser Lys Lys Ser Glu  
980 985 990

Leu Pro Glu Thr Gly Gly Glu Glu Ser Thr Asn Lys Gly Met Leu Phe  
995 1000 1005

Gly Gly Leu Phe Ser Ile Leu Gly Leu Ala Leu Leu Arg Arg Asn  
1010 1015 1020

Lys Lys Asn Asn Lys Ala  
1025

<210> 13  
<211> 940  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fibronectin binding protein B

<400> 13

Met Lys Ser Asn Leu Arg Tyr Gly Ile Arg Lys His Lys Leu Gly Ala  
1 5 10 15

Ala Ser Val Phe Leu Gly Thr Met Ile Val Val Gly Met Gly Gln Glu  
20 25 30

Lys Glu Ala Ala Ala Ser Glu Gln Asn Asn Thr Thr Val Glu Glu Ser  
35 40 45

Gly Ser Ser Ala Thr Glu Ser Lys Ala Ser Glu Thr Gln Thr Thr Thr  
50 55 60

Asn Asn Val Asn Thr Ile Asp Glu Thr Gln Ser Tyr Ser Ala Thr Ser  
65 70 75 80

Thr Glu Gln Pro Ser Gln Ser Thr Gln Val Thr Thr Glu Glu Ala Pro  
85 90 95

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

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

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

Thr Asp Val Thr Ala Val Ala Glu Lys Glu Val Val Glu Glu Thr Lys  
145 150 155 160

Ala Thr Gly Thr Asp Val Thr Asn Lys Val Glu Val Glu Glu Gly Ser  
165 170 175

Glu Ile Val Gly His Lys Gln Asp Thr Asn Val Val Asn Pro His Asn  
180 185 190

Ala Glu Arg Val Thr Leu Lys Tyr Lys Trp Lys Phe Gly Glu Gly Ile  
195 200 205

Lys Ala Gly Asp Tyr Phe Asp Phe Thr Leu Ser Asp Asn Val Glu Thr  
210 215 220

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

Gly Gln Val Met Ala Thr Gly Glu Ile Ile Gly Glu Arg Lys Val Arg  
245 250 255

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

Leu Ser Leu Asn Leu Phe Ile Asp Pro Thr Thr Val Thr Gln Lys Gly

275

280

285

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

Phe Asn Ile Gln Tyr Leu Gly Gly Val Arg Asp Asn Trp Gly Val Thr  
 305 310 315 320

Ala Asn Gly Arg Ile Asp Thr Leu Asn Lys Val Asp Gly Lys Phe Ser  
 325 330 335

His Phe Ala Tyr Met Lys Pro Asn Asn Gln Ser Leu Ser Ser Val Thr  
 340 345 350

Val Thr Gly Gln Val Thr Lys Gly Asn Lys Pro Gly Val Asn Asn Pro  
 355 360 365

Thr Val Lys Val Tyr Lys His Ile Gly Ser Asp Asp Leu Ala Glu Ser  
 370 375 380

Val Tyr Ala Lys Leu Asp Asp Val Ser Lys Phe Glu Asp Val Thr Asp  
 385 390 395 400

Asn Met Ser Leu Asp Phe Asp Thr Asn Gly Gly Tyr Ser Leu Asn Phe  
 405 410 415

Asn Asn Leu Asp Gln Ser Lys Asn Tyr Val Ile Lys Tyr Glu Gly Tyr  
 420 425 430

Tyr Asp Ser Asn Ala Ser Asn Leu Glu Phe Gln Thr His Leu Phe Gly  
 435 440 445

Tyr Tyr Asn Tyr Tyr Tyr Thr Ser Asn Leu Thr Trp Lys Asn Gly Val  
 450 455 460

Ala Phe Tyr Ser Asn Asn Ala Gln Gly Asp Gly Lys Asp Lys Leu Lys  
 465 470 475 480

Glu Pro Ile Ile Glu His Ser Thr Pro Ile Glu Leu Glu Phe Lys Ser  
 485 490 495

Glu Pro Pro Val Glu Lys His Glu Leu Thr Gly Thr Ile Glu Glu Ser  
500 505 510

Asn Asp Ser Lys Pro Ile Asp Phe Glu Tyr His Thr Ala Val Glu Gly  
515 520 525

Ala Glu Gly His Ala Glu Gly Thr Ile Glu Thr Glu Glu Asp Ser Ile  
530 535 540

His Val Asp Phe Glu Glu Ser Thr His Glu Asn Ser Lys His His Ala  
545 550 555 560

Asp Val Val Glu Tyr Glu Glu Asp Thr Asn Pro Gly Gly Gly Gln Val  
565 570 575

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

Ile Val Thr Gly Ala Val Ser Asp His Thr Thr Ile Glu Asp Thr Lys  
595 600 605

Glu Tyr Thr Thr Glu Ser Asn Leu Ile Glu Leu Val Asp Glu Leu Pro  
610 615 620

Glu Glu His Gly Gln Ala Gln Gly Pro Ile Glu Glu Ile Thr Glu Asn  
625 630 635 640

Asn His His Ile Ser His Ser Gly Leu Gly Thr Glu Asn Gly His Gly  
645 650 655

Asn Tyr Gly Val Ile Glu Glu Ile Glu Glu Asn Ser His Val Asp Ile  
660 665 670

Lys Ser Glu Leu Gly Tyr Glu Gly Gly Gln Asn Ser Gly Asn Gln Ser  
675 680 685

Phe Glu Glu Asp Thr Glu Glu Asp Lys Pro Lys Tyr Glu Gln Gly Gly  
690 695 700

Asn Ile Val Asp Ile Asp Phe Asp Ser Val Pro Gln Ile His Gly Gln

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 705 |     | 710 |     | 715 |     | 720 |     |     |     |     |     |     |     |     |     |
| Asn | Asn | Gly | Asn | Gln | Ser | Phe | Glu | Glu | Asp | Thr | Glu | Lys | Asp | Lys | Pro |
|     |     |     | 725 |     |     |     |     |     | 730 |     |     |     |     | 735 |     |
| Lys | Tyr | Glu | Gln | Gly | Gly | Asn | Ile | Ile | Asp | Ile | Asp | Phe | Asp | Ser | Val |
|     |     |     | 740 |     |     |     |     | 745 |     |     |     |     | 750 |     |     |
| Pro | His | Ile | His | Gly | Phe | Asn | Lys | His | Thr | Glu | Ile | Ile | Glu | Glu | Asp |
|     |     | 755 |     |     |     |     | 760 |     |     |     |     | 765 |     |     |     |
| Thr | Asn | Lys | Asp | Lys | Pro | Asn | Tyr | Gln | Phe | Gly | Gly | His | Asn | Ser | Val |
|     | 770 |     |     |     |     | 775 |     |     |     |     | 780 |     |     |     |     |
| Asp | Phe | Glu | Glu | Asp | Thr | Leu | Pro | Gln | Val | Ser | Gly | His | Asn | Glu | Gly |
| 785 |     |     |     |     | 790 |     |     |     |     | 795 |     |     |     |     | 800 |
| Gln | Gln | Thr | Ile | Glu | Glu | Asp | Thr | Thr | Pro | Pro | Ile | Val | Pro | Pro | Thr |
|     |     |     |     | 805 |     |     |     |     | 810 |     |     |     |     | 815 |     |
| Pro | Pro | Thr | Pro | Glu | Val | Pro | Ser | Glu | Pro | Glu | Thr | Pro | Thr | Pro | Pro |
|     |     |     | 820 |     |     |     |     | 825 |     |     |     |     | 830 |     |     |
| Thr | Pro | Glu | Val | Pro | Ser | Glu | Pro | Glu | Thr | Pro | Thr | Pro | Pro | Thr | Pro |
|     |     | 835 |     |     |     |     | 840 |     |     |     | 845 |     |     |     |     |
| Glu | Val | Pro | Thr | Glu | Pro | Gly | Lys | Pro | Ile | Pro | Pro | Ala | Lys | Glu | Glu |
|     | 850 |     |     |     |     | 855 |     |     |     |     | 860 |     |     |     |     |
| Pro | Lys | Lys | Pro | Ser | Lys | Pro | Val | Glu | Gln | Gly | Lys | Val | Val | Thr | Pro |
| 865 |     |     |     |     | 870 |     |     |     |     | 875 |     |     |     |     | 880 |
| Val | Ile | Glu | Ile | Asn | Glu | Lys | Val | Lys | Ala | Val | Val | Pro | Thr | Lys | Lys |
|     |     |     |     | 885 |     |     |     |     | 890 |     |     |     |     | 895 |     |
| Ala | Gln | Ser | Lys | Lys | Ser | Glu | Leu | Pro | Glu | Thr | Gly | Gly | Glu | Glu | Ser |
|     |     |     | 900 |     |     |     |     | 905 |     |     |     |     | 910 |     |     |
| Thr | Asn | Asn | Gly | Met | Leu | Phe | Gly | Gly | Leu | Phe | Ser | Ile | Leu | Gly | Leu |
|     |     | 915 |     |     |     |     | 920 |     |     |     |     | 925 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Leu | Leu | Arg | Arg | Asn | Lys | Lys | Asn | His | Lys | Ala |
| 930 |     |     |     |     |     | 935 |     |     |     |     | 940 |