

N3355PCT_sequence listing.txt
SEQUENCE LISTING

<110> Max-Delbrück-Centrum für Molekulare Medizin (MDC) Berlin-Buch
 <120> Transposon-mediated mutagenesis in spermatogonial stem cells
 <130> N3355 PCT
 <150> EP 07 02 3771.4
 <151> 2007-12-07
 <150> US 61/012,267
 <151> 2007-12-07
 <160> 13
 <170> PatentIn version 3.3
 <210> 1
 <211> 340
 <212> PRT
 <213> artificial sequence
 <220>
 <221> source
 <223> /note="Description of artificial sequence: consensus sequence
 reconstructed from several fish species"
 <400> 1

Met Gly Lys Ser Lys Glu Ile Ser Gln Asp Leu Arg Lys Lys Ile Val
 1 5 10 15

Asp Leu His Lys Ser Gly Ser Ser Leu Gly Ala Ile Ser Lys Arg Leu
 20 25 30

Lys Val Pro Arg Ser Ser Val Gln Thr Ile Val Arg Lys Tyr Lys His
 35 40 45

His Gly Thr Thr Gln Pro Ser Tyr Arg Ser Gly Arg Arg Arg Val Leu
 50 55 60

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

Arg Thr Thr Ala Lys Asp Leu Val Lys Met Leu Glu Glu Thr Gly Thr
 85 90 95

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

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

Lys Ala Arg Leu Arg Phe Ala Thr Ala His Gly Asp Lys Asp Arg Thr
 130 135 140

Phe Trp Arg Asn Val Leu Trp Ser Asp Glu Thr Lys Ile Glu Leu Phe
 145 150 155 160
 1

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Gly His Asn Asp His Arg Tyr Val Trp Arg Lys Lys Gly Glu Ala Cys
165 170 175

Lys Pro Lys Asn Thr Ile Pro Thr Val Lys His Gly Gly Gly Ser Ile
180 185 190

Met Leu Trp Gly Cys Phe Ala Ala Gly Gly Thr Gly Ala Leu His Lys
195 200 205

Ile Asp Gly Ile Met Arg Lys Glu Asn Tyr Val Asp Ile Leu Lys Gln
210 215 220

His Leu Lys Thr Ser Val Arg Lys Leu Lys Leu Gly Arg Lys Trp Val
225 230 235 240

Phe Gln Met Asp Asn Asp Pro Lys His Thr Ser Lys Val Val Ala Lys
245 250 255

Trp Leu Lys Asp Asn Lys Val Lys Val Leu Glu Trp Pro Ser Gln Ser
260 265 270

Pro Asp Leu Asn Pro Ile Glu Asn Leu Trp Ala Glu Leu Lys Lys Arg
275 280 285

Val Arg Ala Arg Arg Pro Thr Asn Leu Thr Gln Leu His Gln Leu Cys
290 295 300

Gln Glu Glu Trp Ala Lys Ile His Pro Thr Tyr Cys Gly Lys Leu Val
305 310 315 320

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

Ala Thr Lys Tyr
340

<210> 2
<211> 225
<212> DNA
<213> Tanichthys albonubes

<400> 2
cagttgaagt cggaagttta catacactta agttggagtc attaaaactc gtttttcaac 60
tacaccacaa atttcttggt aacaacaat agttttggca agtcagttag gacatctact 120
ttgtgcatga cacaagtcatt ttttccaaca attggtttaca gacagattat ttcacttata 180
attcactgta tcacaattcc agtgggtcag aagttttacat acact 225

<210> 3
<211> 226
<212> DNA

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<213> Tanichthys albonubes

<400> 3
 agtgtatggt aacttctgac ccactgggaa tgtgatgaaa gaaataaaag ctgaaatgaa 60
 tcattctctc tactattatt ctgatatttc acattcttaa aataaagtgg tgatcctaac 120
 tgaccttaag acaggggaatc ttactcggga ttaaatgtca ggaattgtga aaaagtgagt 180
 ttaaatgtat ttggctaagg tgtatgtaaa cttccgactt caactg 226

<210> 4
 <211> 340
 <212> PRT
 <213> Rana pipiens

<400> 4
 Met Pro Arg Pro Lys Glu Ile Gln Glu Gln Leu Arg Lys Lys Val Ile
 1 5 10 15
 Glu Ile Tyr Gln Ser Gly Lys Gly Tyr Lys Ala Ile Ser Lys Ala Leu
 20 25 30
 Gly Ile Gln Arg Thr Thr Val Arg Ala Ile Ile His Lys Trp Arg Arg
 35 40 45
 His Gly Thr Val Val Asn Leu Pro Arg Ser Gly Arg Pro Pro Lys Ile
 50 55 60
 Thr Pro Arg Ala Gln Arg Arg Leu Ile Gln Glu Val Thr Lys Asp Pro
 65 70 75 80
 Thr Thr Thr Ser Lys Glu Leu Gln Ala Ser Leu Ala Ser Val Lys Val
 85 90 95
 Ser Val His Ala Ser Thr Ile Arg Lys Arg Leu Gly Lys Asn Gly Leu
 100 105 110
 His Gly Arg Val Pro Arg Arg Lys Pro Leu Leu Ser Lys Lys Asn Ile
 115 120 125
 Lys Ala Arg Leu Asn Phe Ser Thr Thr His Leu Asp Asp Pro Gln Asp
 130 135 140
 Phe Trp Asp Asn Ile Leu Trp Thr Asp Glu Thr Lys Val Glu Leu Phe
 145 150 155 160
 Gly Arg Cys Val Ser Lys Tyr Ile Trp Arg Arg Arg Asn Thr Ala Phe
 165 170 175
 His Lys Lys Asn Ile Ile Pro Thr Val Lys Tyr Gly Gly Gly Ser Val
 180 185 190
 Met Val Trp Gly Cys Phe Ala Ala Ser Gly Pro Gly Arg Leu Ala Val
 3

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195

200

205

Ile Lys Gly Thr Met Asn Ser Ala Val Tyr Gln Glu Ile Leu Lys Glu
210 215 220

Asn Val Arg Pro Ser Val Arg Val Leu Lys Leu Lys Arg Thr Trp Val
225 230 235 240

Leu Gln Gln Asp Asn Asp Pro Lys His Thr Ser Lys Ser Thr Thr Glu
245 250 255

Trp Leu Lys Lys Asn Lys Met Lys Thr Leu Glu Trp Pro Ser Gln Ser
260 265 270

Pro Asp Leu Asn Pro Ile Glu Met Leu Trp Tyr Asp Leu Lys Lys Ala
275 280 285

Val His Ala Arg Lys Pro Ser Asn Val Thr Glu Leu Gly Gln Phe Cys
290 295 300

Lys Asp Glu Trp Ala Lys Ile Pro Pro Gly Arg Cys Lys Ser Leu Ile
305 310 315 320

Ala Arg Tyr Arg Lys Arg Leu Val Ala Val Val Ala Ala Lys Gly Gly
325 330 335

Pro Thr Ser Tyr
340

<210> 5
<211> 214
<212> DNA
<213> Rana pipiens

<400> 5
cagtgggtgtg aaaaagtgtt tgcccccttc ctcatttcct gttcctttgc atgtttgtca 60
cacttaagtg tttcgggaaca tcaaaccaat ttaaacaata gtcaaggaca acacaagtaa 120
acacaaaatg caatttgtaa atgaaggtgt ttattattaa aggtgaaaaa aaatccaaac 180
catcatggcc ctgtgtgaaa aagtgattgc cccc 214

<210> 6
<211> 214
<212> DNA
<213> Rana pipiens

<400> 6
gggggcaatc actttttcac acagggccat gatggtttgg attttttttc acctttaata 60
ataaacacct tcattttaca attgcatttt gtgtttactt gtgttgctct tgactattgt 120
ttaaattggt ttgatgttcc gaaacactta agtgtgacaa acatgcaaag gaacaggaaa 180
tgaggaaggg ggcaaact ttttcacacc actg 214

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<210> 7
 <211> 649
 <212> PRT
 <213> Oryzias latipes

<400> 7

Met Glu Glu Val Cys Asp Ser Ser Ala Ala Ala Ser Ser Thr Val Gln
 1 5 10 15

Asn Gln Pro Gln Asp Gln Glu His Pro Trp Pro Tyr Leu Arg Glu Phe
 20 25 30

Phe Ser Leu Ser Gly Val Asn Lys Asp Ser Phe Lys Met Lys Cys Val
 35 40 45

Leu Cys Leu Pro Leu Asn Lys Glu Ile Ser Ala Phe Lys Ser Ser Pro
 50 55 60

Ser Asn Leu Arg Lys His Ile Glu Arg Met His Pro Asn Tyr Leu Lys
 65 70 75 80

Asn Tyr Ser Lys Leu Thr Ala Gln Lys Arg Lys Ile Gly Thr Ser Thr
 85 90 95

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

Lys His Val Ser Pro Val Thr Val Asn Lys Ala Ile Leu Arg Tyr Ile
 115 120 125

Ile Gln Gly Leu His Pro Phe Ser Thr Val Asp Leu Pro Ser Phe Lys
 130 135 140

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

Thr Leu Arg Ser Lys Ile Ala Glu Ala Ala Leu Ile Met Lys Gln Lys
 165 170 175

Val Thr Ala Ala Met Ser Glu Val Glu Trp Ile Ala Thr Thr Thr Asp
 180 185 190

Cys Trp Thr Ala Arg Arg Lys Ser Phe Ile Gly Val Thr Ala His Trp
 195 200 205

Ile Asn Pro Gly Ser Leu Glu Arg His Ser Ala Ala Leu Ala Cys Lys
 210 215 220

Arg Leu Met Gly Ser His Thr Phe Glu Val Leu Ala Ser Ala Met Asn
 225 230 235 240

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Asp Ile His Ser Glu Tyr Glu Ile Arg Asp Lys Val Val Cys Thr Thr
245 250 255

Thr Asp Ser Gly Ser Asn Phe Met Lys Ala Phe Arg Val Phe Gly Val
260 265 270

Glu Asn Asn Asp Ile Glu Thr Glu Ala Arg Arg Cys Glu Ser Asp Asp
275 280 285

Thr Asp Ser Glu Gly Cys Gly Glu Gly Ser Asp Gly Val Glu Phe Gln
290 295 300

Asp Ala Ser Arg Val Leu Asp Gln Asp Asp Gly Phe Glu Phe Gln Leu
305 310 315 320

Pro Lys His Gln Lys Cys Ala Cys His Leu Leu Asn Leu Val Ser Ser
325 330 335

Val Asp Ala Gln Lys Ala Leu Ser Asn Glu His Tyr Lys Lys Leu Tyr
340 345 350

Arg Ser Val Phe Gly Lys Cys Gln Ala Leu Trp Asn Lys Ser Ser Arg
355 360 365

Ser Ala Leu Ala Ala Glu Ala Val Glu Ser Glu Ser Arg Leu Gln Leu
370 375 380

Leu Arg Pro Asn Gln Thr Arg Trp Asn Ser Thr Phe Met Ala Val Asp
385 390 395 400

Arg Ile Leu Gln Ile Cys Lys Glu Ala Gly Glu Gly Ala Leu Arg Asn
405 410 415

Ile Cys Thr Ser Leu Glu Val Pro Met Phe Asn Pro Ala Glu Met Leu
420 425 430

Phe Leu Thr Glu Trp Ala Asn Thr Met Arg Pro Val Ala Lys Val Leu
435 440 445

Asp Ile Leu Gln Ala Glu Thr Asn Thr Gln Leu Gly Trp Leu Leu Pro
450 455 460

Ser Val His Gln Leu Ser Leu Lys Leu Gln Arg Leu His His Ser Leu
465 470 475 480

Arg Tyr Cys Asp Pro Leu Val Asp Ala Leu Gln Gln Gly Ile Gln Thr
485 490 495

Arg Phe Lys His Met Phe Glu Asp Pro Glu Ile Ile Ala Ala Ala Ile
500 505 510

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Leu Leu Pro Lys Phe Arg Thr Ser Trp Thr Asn Asp Glu Thr Ile Ile
515 520 525

Lys Arg Gly Met Asp Tyr Ile Arg Val His Leu Glu Pro Leu Asp His
530 535 540

Lys Lys Glu Leu Ala Asn Ser Ser Ser Asp Asp Glu Asp Phe Phe Ala
545 550 555 560

Ser Leu Lys Pro Thr Thr His Glu Ala Ser Lys Glu Leu Asp Gly Tyr
565 570 575

Leu Ala Cys Val Ser Asp Thr Arg Glu Ser Leu Leu Thr Phe Pro Ala
580 585 590

Ile Cys Ser Leu Ser Ile Lys Thr Asn Thr Pro Leu Pro Ala Ser Ala
595 600 605

Ala Cys Glu Arg Leu Phe Ser Thr Ala Gly Leu Leu Phe Ser Pro Lys
610 615 620

Arg Ala Arg Leu Asp Thr Asn Asn Phe Glu Asn Gln Leu Leu Leu Lys
625 630 635 640

Leu Asn Leu Arg Phe Tyr Asn Phe Glu
645

<210> 8
<211> 150
<212> DNA
<213> Oryzias latipes

<400> 8
cagaggtgta aaaagtactc aaaaatttta ctcaagtga agtacaagta cttagggaaa 60
attttactca attaaaagta aaagtatctg gctagaatct tacttgagta aaagtaaaaa 120
agtactccat taaaattgta cttgagtatt 150

<210> 9
<211> 200
<212> DNA
<213> Oryzias latipes

<400> 9
aagtgatctc caaaaaataa gtactttttg actgtaaata aaattgtaag gagtaaaaag 60
tacttttttt tctaaaaaaa tgtaattaag taaaagtaaa agtattgatt tttaattgta 120
ctcaagtaaa gtaaaaatcc ccaaaaaataa tacttaagta cagtaatcaa gtaaaattac 180
tcaagtactt tacacctctg 200

<210> 10
<211> 594
<212> PRT
<213> Trichoplusia ni

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<400> 10

Met Gly Ser Ser Leu Asp Asp Glu His Ile Leu Ser Ala Leu Leu Gln
1 5 10 15

Ser Asp Asp Glu Leu Val Gly Glu Asp Ser Asp Ser Glu Ile Ser Asp
20 25 30

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

Asp Glu Val His Glu Val Gln Pro Thr Ser Ser Gly Ser Glu Ile Leu
50 55 60

Asp Glu Gln Asn Val Ile Glu Gln Pro Gly Ser Ser Leu Ala Ser Asn
65 70 75 80

Arg Ile Leu Thr Leu Pro Gln Arg Thr Ile Arg Gly Lys Asn Lys His
85 90 95

Cys Trp Ser Thr Ser Lys Ser Thr Arg Arg Ser Arg Val Ser Ala Leu
100 105 110

Asn Ile Val Arg Ser Gln Arg Gly Pro Thr Arg Met Cys Arg Asn Ile
115 120 125

Tyr Asp Pro Leu Leu Cys Phe Lys Leu Phe Phe Thr Asp Glu Ile Ile
130 135 140

Ser Glu Ile Val Lys Trp Thr Asn Ala Glu Ile Ser Leu Lys Arg Arg
145 150 155 160

Glu Ser Met Thr Gly Ala Thr Phe Arg Asp Thr Asn Glu Asp Glu Ile
165 170 175

Tyr Ala Phe Phe Gly Ile Leu Val Met Thr Ala Val Arg Lys Asp Asn
180 185 190

His Met Ser Thr Asp Asp Leu Phe Asp Arg Ser Leu Ser Met Val Tyr
195 200 205

Val Ser Val Met Ser Arg Asp Arg Phe Asp Phe Leu Ile Arg Cys Leu
210 215 220

Arg Met Asp Asp Lys Ser Ile Arg Pro Thr Leu Arg Glu Asn Asp Val
225 230 235 240

Phe Thr Pro Val Arg Lys Ile Trp Asp Leu Phe Ile His Gln Cys Ile
245 250 255

Gln Asn Tyr Thr Pro Gly Ala His Leu Thr Ile Asp Glu Gln Leu Leu
8

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260

265

270

Gly Phe Arg Gly Arg Cys Pro Phe Arg Met Tyr Ile Pro Asn Lys Pro
275 280 285

Ser Lys Tyr Gly Ile Lys Ile Leu Met Met Cys Asp Ser Gly Thr Lys
290 295 300

Tyr Met Ile Asn Gly Met Pro Tyr Leu Gly Arg Gly Thr Gln Thr Asn
305 310 315 320

Gly Val Pro Leu Gly Glu Tyr Tyr Val Lys Glu Leu Ser Lys Pro Val
325 330 335

His Gly Ser Cys Arg Asn Ile Thr Cys Asp Asn Trp Phe Thr Ser Ile
340 345 350

Pro Leu Ala Lys Asn Leu Leu Gln Glu Pro Tyr Lys Leu Thr Ile Val
355 360 365

Gly Thr Val Arg Ser Asn Lys Arg Glu Ile Pro Glu Val Leu Lys Asn
370 375 380

Ser Arg Ser Arg Pro Val Gly Thr Ser Met Phe Cys Phe Asp Gly Pro
385 390 395 400

Leu Thr Leu Val Ser Tyr Lys Pro Lys Pro Ala Lys Met Val Tyr Leu
405 410 415

Leu Ser Ser Cys Asp Glu Asp Ala Ser Ile Asn Glu Ser Thr Gly Lys
420 425 430

Pro Gln Met Val Met Tyr Tyr Asn Gln Thr Lys Gly Gly Val Asp Thr
435 440 445

Leu Asp Gln Met Cys Ser Val Met Thr Cys Ser Arg Lys Thr Asn Arg
450 455 460

Trp Pro Met Ala Leu Leu Tyr Gly Met Ile Asn Ile Ala Cys Ile Asn
465 470 475 480

Ser Phe Ile Ile Tyr Ser His Asn Val Ser Ser Lys Gly Glu Lys Val
485 490 495

Gln Ser Arg Lys Lys Phe Met Arg Asn Leu Tyr Met Ser Leu Thr Ser
500 505 510

Ser Phe Met Arg Lys Arg Leu Glu Ala Pro Thr Leu Lys Arg Tyr Leu
515 520 525

Arg Asp Asn Ile Ser Asn Ile Leu Pro Asn Glu Val Pro Gly Thr Ser
9

530

Asp Asp Ser Thr Glu Glu Pro Val Met Lys Lys Arg Thr Tyr Cys Thr
545 550 555 560

Tyr Cys Pro Ser Lys Ile Arg Arg Lys Ala Asn Ala Ser Cys Lys Lys
565 570 575

Cys Lys Lys Val Ile Cys Arg Glu His Asn Ile Asp Met Cys Gln Ser
580 585 590

Cys Phe

<210> 11
<211> 306
<212> DNA
<213> Trichoplusia ni

<400> 11
ccctagaaag atagtctgcg taaaattgac gcatgcattc ttgaaatatt gctctctctt 60
tctaaatagc gcgaatccgt cgctgtgcat ttaggacatc tcagtcgccg cttggagctc 120
ccgtgaggcg tgcttgtcaa tgcggtaagt gtcactgatt ttgaactata acgaccgcgt 180
gagtcaaaat gacgcgatgat tatctttttac gtgacttttta agattttaact catacgataa 240
ttatattggtt atttcatggtt ctacttacgt gataacttat tatatatata ttttcttggt 300
atagat 306

<210> 12
<211> 237
<212> DNA
<213> Trichoplusia ni

<400> 12
aaaagttttg ttactttata gaagaaattt tgagtttttg ttttttttta ataaataaat 60
aaacataaat aaattgtttg ttgaatttat tattagtagt taagtgtaaa tataataaaa 120
cttaatatct attcaaatta ataaataaac ctcgatatac agaccgataa aacacatgcg 180
tcaattttac gcatgattat ctttaacgta cgtcacaata tgattatctt tctaggg 237

<210> 13
<211> 340
<212> PRT
<213> artificial sequence

<220>
<221> source
<223> /note="Description of artificial sequence: SB100X"
<400> 13

Met Gly Lys Ser Lys Glu Ile Ser Gln Asp Leu Arg Lys Arg Ile Val
1 5 10 15

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Asp Leu His Lys Ser Gly Ser Ser Leu Gly Ala Ile Ser Lys Arg Leu
20 25 30

Ala Val Pro Arg Ser Ser Val Gln Thr Ile Val Arg Lys Tyr Lys His
35 40 45

His Gly Thr Thr Gln Pro Ser Tyr Arg Ser Gly Arg Arg Arg Val Leu
50 55 60

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

Arg Thr Thr Ala Lys Asp Leu Val Lys Met Leu Glu Glu Thr Gly Thr
85 90 95

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

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

Lys Ala Arg Leu Arg Phe Ala Thr Ala His Gly Asp Lys Asp Arg Thr
130 135 140

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

Gly His Asn Asp His Arg Tyr Val Trp Arg Lys Lys Gly Glu Ala Cys
165 170 175

Lys Pro Lys Asn Thr Ile Pro Thr Val Lys His Gly Gly Gly Ser Ile
180 185 190

Met Leu Trp Gly Cys Phe Ala Ala Gly Gly Thr Gly Ala Leu His Lys
195 200 205

Ile Asp Gly Ile Met Asp Ala Val Gln Tyr Val Asp Ile Leu Lys Gln
210 215 220

His Leu Lys Thr Ser Val Arg Lys Leu Lys Leu Gly Arg Lys Trp Val
225 230 235 240

Phe Gln His Asp Asn Asp Pro Lys His Thr Ser Lys Val Val Ala Lys
245 250 255

Trp Leu Lys Asp Asn Lys Val Lys Val Leu Glu Trp Pro Ser Gln Ser
260 265 270

Pro Asp Leu Asn Pro Ile Glu Asn Leu Trp Ala Glu Leu Lys Lys Arg
275 280 285

N3355PCT_sequence listing.txt

Val Arg Ala Arg Arg Pro Thr Asn Leu Thr Gln Leu His Gln Leu Cys
 290 295 300

Gln Glu Glu Trp Ala Lys Ile His Pro Asn Tyr Cys Gly Lys Leu Val
 305 310 315 320

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

Ala Thr Lys Tyr
 340