

# SEQUENCE LISTING

<110> Tenaya Therapeutics  
 Tenaya Therapeutics Inc.

<120> GENE VECTOR CONTROL BY CARDIOMYOCYTE-EXPRESSED MICRORNAS

<130> TENA-017/01WO 334682-2118

<150> US 62/984,183  
 <151> 2020-03-02

<160> 166

<170> PatentIn version 3.5

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Ser Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala Pro  
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Gln Leu Arg Pro Ala Ala Asp Gly Gln Pro Ser Gly Gly Gly His Lys  
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Ser Ala Pro Lys Gln Val Lys Arg Gln Arg Ser Ser Ser Pro Glu Leu  
 85 90 95

Met Arg Cys Lys Arg Arg Leu Asn Phe Ser Gly Phe Gly Tyr Ser Leu  
 100 105 110

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

Asn Arg Val Lys Leu Val Asn Leu Gly Phe Ala Thr Leu Arg Glu His  
130 135 140

Val Pro Asn Gly Ala Ala Asn Lys Lys Met Ser Lys Val Glu Thr Leu  
145 150 155 160

Arg Ser Ala Val Glu Tyr Ile Arg Ala Leu Gln Gln Leu Leu Asp Glu  
165 170 175

His Asp Ala Val Ser Ala Ala Phe Gln Ala Gly Val Leu Ser Pro Thr  
180 185 190

Ile Ser Pro Asn Tyr Ser Asn Asp Leu Asn Ser Met Ala Gly Ser Pro  
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gcagccgccg cagcggcagc gcagagcgcg cagcagcagc agcagcagca gcagcagcag 180  
cagcaggcgc cgcagctgag accggcggcc gacggccagc cctcaggggg cggtcacaag 240  
tcagcgccca agcaagtcaa gcgacagcgc tcgtcttcgc ccgaactgat gcgctgcaaa 300  
cgccggctca acttcagcgg ctttggttac agcctgccgc agcagcagcc ggccgccgtg 360

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| cttcgggagc | acgtcccca  | cggcgcggcc | aacaagaaga | tgagtaaggt | ggagacactg | 480 |
| cgctcggcgg | tcgagtacat | ccgcgcgctg | cagcagctgc | tggacgagca | tgacgcggtg | 540 |
| agcgccgcct | tccaggcagg | cgctctgtcg | cccaccatct | cccccaacta | ctccaacgac | 600 |
| ttgaactcca | tggccggctc | gccggtctca | tcctactcgt | cggacgaggg | ctcttacgac | 660 |
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Leu Ala Asn Gln Gly Ile Ile Pro Pro Leu Lys Arg Pro Ala Glu Phe  
35 40 45

His Glu Gln Arg Lys His Leu Asp Ser Asp Lys Ala Lys Asn Ser Leu  
50 55 60

Lys Arg Lys Ala Arg Asn Arg Cys Asn Ser Ala Asp Leu Val Asn Met  
65 70 75 80

His Ile Leu Gln Ala Ser Thr Ala Glu Arg Ser Ile Pro Thr Ala Gln  
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Met Lys Leu Lys Arg Ala Arg Leu Ala Asp Asp Leu Asn Glu Lys Ile  
100 105 110

Ala Leu Arg Pro Gly Pro Leu Glu Leu Val Glu Lys Asn Ile Leu Pro

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Val Asp Ser Ala Val Lys Glu Ala Ile Lys Gly Asn Gln Val Ser Phe  
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Ser Lys Ser Thr Asp Ala Phe Ala Phe Glu Glu Asp Ser Ser Ser Asp  
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Gly Leu Ser Pro Asp Gln Thr Arg Ser Glu Asp Pro Gln Asn Ser Ala  
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Gly Ser Pro Pro Asp Ala Lys Ala Ser Asp Thr Pro Ser Thr Gly Ser  
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Leu Gly Thr Asn Gln Asp Leu Ala Ser Gly Ser Glu Asn Asp Arg Asn  
 195 200 205

Asp Ser Ala Ser Gln Pro Ser His Gln Ser Asp Ala Gly Lys Gln Gly  
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Leu Gly Pro Pro Ser Thr Pro Ile Ala Val His Ala Ala Val Lys Ser  
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Lys Ser Leu Gly Asp Ser Lys Asn Arg His Lys Lys Pro Lys Asp Pro  
 245 250 255

Lys Pro Lys Val Lys Lys Leu Lys Tyr His Gln Tyr Ile Pro Pro Asp  
 260 265 270

Gln Lys Ala Glu Lys Ser Pro Pro Pro Met Asp Ser Ala Tyr Ala Arg  
 275 280 285

Leu Leu Gln Gln Gln Gln Leu Phe Leu Gln Leu Gln Ile Leu Ser Gln  
 290 295 300

Gln Gln Gln Gln Gln Gln His Arg Phe Ser Tyr Leu Gly Met His Gln  
 305 310 315 320

Ala Gln Leu Lys Glu Pro Asn Glu Gln Met Val Arg Asn Pro Asn Ser  
325 330 335

Ser Ser Thr Pro Leu Ser Asn Thr Pro Leu Ser Pro Val Lys Asn Ser  
340 345 350

Phe Ser Gly Gln Thr Gly Val Ser Ser Phe Lys Pro Gly Pro Leu Pro  
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Pro Asn Leu Asp Asp Leu Lys Val Ser Glu Leu Arg Gln Gln Leu Arg  
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Ile Arg Gly Leu Pro Val Ser Gly Thr Lys Thr Ala Leu Met Asp Arg  
385 390 395 400

Leu Arg Pro Phe Gln Asp Cys Ser Gly Asn Pro Val Pro Asn Phe Gly  
405 410 415

Asp Ile Thr Thr Val Thr Phe Pro Val Thr Pro Asn Thr Leu Pro Asn  
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Tyr Gln Ser Ser Ser Ser Thr Ser Ala Leu Ser Asn Gly Phe Tyr His  
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Phe Gly Ser Thr Ser Ser Ser Pro Pro Ile Ser Pro Ala Ser Ser Asp  
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Leu Ser Val Ala Gly Ser Leu Pro Asp Thr Phe Asn Asp Ala Ser Pro  
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Ser Phe Gly Leu His Pro Ser Pro Val His Val Cys Thr Glu Glu Ser  
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Leu Met Ser Ser Leu Asn Gly Gly Ser Val Pro Ser Glu Leu Asp Gly  
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Leu Asp Ser Glu Lys Asp Lys Met Leu Val Glu Lys Gln Lys Val Ile

515

520

525

Asn Glu Leu Thr Trp Lys Leu Gln Gln Glu Gln Arg Gln Val Glu Glu  
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Leu Arg Met Gln Leu Gln Lys Gln Lys Arg Asn Asn Cys Ser Glu Lys  
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Lys Pro Leu Pro Phe Leu Ala Ala Ser Ile Lys Gln Glu Glu Ala Val  
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Ser Ser Cys Pro Phe Ala Ser Gln Val Pro Val Lys Arg Gln Ser Ser  
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Ser Ser Glu Cys His Pro Pro Ala Cys Glu Ala Ala Gln Leu Gln Pro  
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Leu Gly Asn Ala His Cys Val Glu Ser Ser Asp Gln Thr Asn Val Leu  
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Ser Ser Thr Phe Leu Ser Pro Gln Cys Ser Pro Gln His Ser Pro Leu  
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Gly Ala Val Lys Ser Pro Gln His Ile Ser Leu Pro Pro Ser Pro Asn  
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Asn Pro His Phe Leu Pro Ser Ser Ser Gly Ala Gln Gly Glu Gly His  
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Arg Val Ser Ser Pro Ile Ser Ser Gln Val Cys Thr Ala Gln Asn Ser  
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Gly Ala His Asp Gly His Pro Pro Ser Phe Ser Pro His Ser Ser Ser  
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Leu His Pro Pro Phe Ser Gly Ala Gln Ala Asp Ser Ser His Gly Ala  
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Gly Gly Asn Pro Cys Pro Lys Ser Pro Cys Val Gln Gln Lys Met Ala  
725 730 735

Gly Leu His Ser Ser Asp Lys Val Gly Pro Lys Phe Ser Ile Pro Ser  
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Pro Thr Phe Ser Lys Ser Ser Ser Ala Ile Ser Glu Val Thr Gln Pro  
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Pro Ser Tyr Glu Asp Ala Val Lys Gln Gln Met Thr Arg Ser Gln Gln  
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Met Asp Glu Leu Leu Asp Val Leu Ile Glu Ser Gly Glu Met Pro Ala  
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Asp Ala Arg Glu Asp His Ser Cys Leu Gln Lys Val Pro Lys Ile Pro  
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Arg Ser Ser Arg Ser Pro Thr Ala Val Leu Thr Lys Pro Ser Ala Ser  
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Phe Glu Gln Ala Ser Ser Gly Ser Gln Ile Pro Phe Asp Pro Tyr Ala  
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Thr Asp Ser Asp Glu His Leu Glu Val Leu Leu Asn Ser Gln Ser Pro  
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Leu Gly Lys Met Ser Asp Val Thr Leu Leu Lys Ile Gly Ser Glu Glu  
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Pro His Phe Asp Gly Ile Met Asp Gly Phe Ser Gly Lys Ala Ala Glu  
885 890 895

Asp Leu Phe Asn Ala His Glu Ile Leu Pro Gly Pro Leu Ser Pro Met  
900 905 910

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

915

920

925

Ser Phe Thr Glu Ser Pro Trp Glu Thr Met Glu Trp Leu Asp Leu Thr  
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Pro Pro Asn Ser Thr Pro Gly Phe Ser Ala Leu Thr Thr Ser Ser Pro  
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| cattcttcca gcctccacc gcccttctct ggagcccaag cagacagcag tcatggtgcc   | 2160 |
| gggggaaacc cttgtcccaa aagcccatgt gtacagcaaa agatggctgg tttaactct   | 2220 |
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Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe  
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Asn Ser Thr Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys  
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Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr

|                                                                 |     |     |     |     |  |    |
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| Asn Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu Asn Lys Gly Cys | 85  | 90  | 95  |     |  |    |
| Glu Ser Pro Asp Pro Asp Ser Ser Tyr Ala Leu Thr Pro Arg Thr Glu | 100 | 105 | 110 |     |  |    |
| Glu Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Ile Lys Ser | 115 | 120 | 125 |     |  |    |
| His Lys Ile Pro Ala Val Pro Pro Pro Asn Phe Glu Met Pro Val Ser | 130 | 135 | 140 |     |  |    |
| Ile Pro Val Ser Ser His Asn Ser Leu Val Tyr Ser Asn Pro Val Ser | 145 | 150 | 155 | 160 |  |    |
| Ser Leu Gly Asn Pro Asn Leu Leu Pro Leu Ala His Pro Ser Leu Gln | 165 | 170 | 175 |     |  |    |
| Arg Asn Ser Met Ser Pro Gly Val Thr His Arg Pro Pro Ser Ala Gly | 180 | 185 | 190 |     |  |    |
| Asn Thr Gly Gly Leu Met Gly Gly Asp Leu Thr Ser Gly Ala Gly Thr | 195 | 200 | 205 |     |  |    |
| Ser Ala Gly Asn Gly Tyr Gly Asn Pro Arg Asn Ser Pro Gly Leu Leu | 210 | 215 | 220 |     |  |    |
| Val Ser Pro Gly Asn Leu Asn Lys Asn Met Gln Ala Lys Ser Pro Pro | 225 | 230 | 235 | 240 |  |    |
| Pro Met Asn Leu Gly Met Asn Asn Arg Lys Pro Asp Leu Arg Val Leu | 245 | 250 | 255 |     |  |    |
| Ile Pro Pro Gly Ser Lys Asn Thr Met Pro Ser Val Asn Gln Arg Ile | 260 | 265 | 270 |     |  |    |

Asn Asn Ser Gln Ser Ala Gln Ser Leu Ala Thr Pro Val Val Ser Val  
275 280 285

Ala Thr Pro Thr Leu Pro Gly Gln Gly Met Gly Gly Tyr Pro Ser Ala  
290 295 300

Ile Ser Thr Thr Tyr Gly Thr Glu Tyr Ser Leu Ser Ser Ala Asp Leu  
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Ser Ser Leu Ser Gly Phe Asn Thr Ala Ser Ala Leu His Leu Gly Ser  
325 330 335

Val Thr Gly Trp Gln Gln Gln His Leu His Asn Met Pro Pro Ser Ala  
340 345 350

Leu Ser Gln Leu Gly Ala Cys Thr Ser Thr His Leu Ser Gln Ser Ser  
355 360 365

Asn Leu Ser Leu Pro Ser Thr Gln Ser Leu Asn Ile Lys Ser Glu Pro  
370 375 380

Val Ser Pro Pro Arg Asp Arg Thr Thr Thr Pro Ser Arg Tyr Pro Gln  
385 390 395 400

His Thr Arg His Glu Ala Gly Arg Ser Pro Val Asp Ser Leu Ser Ser  
405 410 415

Cys Ser Ser Ser Tyr Asp Gly Ser Asp Arg Glu Asp His Arg Asn Glu  
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Phe His Ser Pro Ile Gly Leu Thr Arg Pro Ser Pro Asp Glu Arg Glu  
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Ser Pro Ser Val Lys Arg Met Arg Leu Ser Glu Gly Trp Ala Thr  
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<212> DNA

<213> Homo sapiens

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| tgtgagattg cgctgatcat cttcaacagc accaacaagc tgttccagta tgccagcacc   | 180  |
| gacatggaca aagtgttctt caagtacacg gagtacaacg agccgcatga gagccggaca   | 240  |
| aactcagaca tcgtggaggc attgaacaag aaagaaaaca aaggctgtga aagccccgat   | 300  |
| cccgactcct cttatgcact caccacacgc actgaagaaa aatacaaaaa aattaatgaa   | 360  |
| gaatttgata atatgatcaa gagtcataaa attcctgctg ttccacctcc caacttcgag   | 420  |
| atgccagtct ccatcccagt gtccagccac aacagtttgg tgtacagcaa ccctgtcagc   | 480  |
| tcactgggaa accccaacct attgccactg gctcaccctt ctctgcagag gaatagtatg   | 540  |
| tctcctgggtg taacacatcg acctccaagt gcaggtaaca cagggtggtct gatgggtgga | 600  |
| gacctcacgt ctggtgcagg caccagtgca gggaacgggt atggcaatcc ccgaaactca   | 660  |
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| ccaatgaatt taggaatgaa taaccgtaaa ccagatctcc gagttcttat tccaccaggc   | 780  |
| agcaagaata cgatgccatc agtgaatcaa aggataaata actcccagtc ggctcagtca   | 840  |
| ttggctaccc cagtggtttc cgtagcaact cctactttac caggacaagg aatgggagga   | 900  |
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| tcattctctgt ctgggtttta caccgccagc gctcttcacc ttggttcagt aactggctgg  | 1020 |
| caacagcaac acctacataa catgccacca tctgccctca gtcagttggg agcttgcaact  | 1080 |
| agcactcatt tatctcagag ttcaaattct tccctgcctt ctactcaaag cctcaacatc   | 1140 |
| aagtcagaac ctgttttctc tcctagagac cgtaccacca ccccttcgag ataccacaa    | 1200 |
| cacacgcgcc acgaggcggg gagatctcct gttgacagct tgagcagctg tagcagttcg   | 1260 |
| tacgacggga gcgaccgaga ggatcaccgg aacgaattcc actccccat tggactcacc    | 1320 |
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<213> Homo sapiens

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Gln Gly Met Glu Gly Ile Lys Val Phe Leu His Glu Arg Glu Leu Trp  
50 55 60

Leu Lys Phe His Glu Val Gly Thr Glu Met Ile Ile Thr Lys Ala Gly  
65 70 75 80

Arg Arg Met Phe Pro Ser Tyr Lys Val Lys Val Thr Gly Leu Asn Pro  
85 90 95

Lys Thr Lys Tyr Ile Leu Leu Met Asp Ile Val Pro Ala Asp Asp His  
100 105 110

Arg Tyr Lys Phe Ala Asp Asn Lys Trp Ser Val Thr Gly Lys Ala Glu  
115 120 125

Pro Ala Met Pro Gly Arg Leu Tyr Val His Pro Asp Ser Pro Ala Thr  
130 135 140

Gly Ala His Trp Met Arg Gln Leu Val Ser Phe Gln Lys Leu Lys Leu  
145 150 155 160

Thr Asn Asn His Leu Asp Pro Phe Gly His Ile Ile Leu Asn Ser Met  
165 170 175

His Lys Tyr Gln Pro Arg Leu His Ile Val Lys Ala Asp Glu Asn Asn  
180 185 190

Gly Phe Gly Ser Lys Asn Thr Ala Phe Cys Thr His Val Phe Pro Glu  
195 200 205

Thr Ala Phe Ile Ala Val Thr Ser Tyr Gln Asn His Lys Ile Thr Gln  
210 215 220

Leu Lys Ile Glu Asn Asn Pro Phe Ala Lys Gly Phe Arg Gly Ser Asp  
225 230 235 240

Asp Met Glu Leu His Arg Met Ser Arg Met Gln Ser Lys Glu Tyr Pro  
245 250 255

Val Val Pro Arg Ser Thr Val Arg Gln Lys Val Ala Ser Asn His Ser  
260 265 270

Pro Phe Ser Ser Glu Ser Arg Ala Leu Ser Thr Ser Ser Asn Leu Gly  
275 280 285

Ser Gln Tyr Gln Cys Glu Asn Gly Val Ser Gly Pro Ser Gln Asp Leu  
290 295 300

Leu Pro Pro Pro Asn Pro Tyr Pro Leu Pro Gln Glu His Ser Gln Ile  
305 310 315 320

Tyr His Cys Thr Lys Arg Lys Glu Glu Glu Cys Ser Thr Thr Asp His  
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Pro Tyr Lys Lys Pro Tyr Met Glu Thr Ser Pro Ser Glu Glu Asp Ser  
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Phe Tyr Arg Ser Ser Tyr Pro Gln Gln Gln Gly Leu Gly Ala Ser Tyr

355

360

365

Arg Thr Glu Ser Ala Gln Arg Gln Ala Cys Met Tyr Ala Ser Ser Ala  
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Pro Pro Ser Glu Pro Val Pro Ser Leu Glu Asp Ile Ser Cys Asn Thr  
 385 390 395 400

Trp Pro Ser Met Pro Ser Tyr Ser Ser Cys Thr Val Thr Thr Val Gln  
 405 410 415

Pro Met Asp Arg Leu Pro Tyr Gln His Phe Ser Ala His Phe Thr Ser  
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Gly Pro Leu Val Pro Arg Leu Ala Gly Met Ala Asn His Gly Ser Pro  
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Gln Leu Gly Glu Gly Met Phe Gln His Gln Thr Ser Val Ala His Gln  
 450 455 460

Pro Val Val Arg Gln Cys Gly Pro Gln Thr Gly Leu Gln Ser Pro Gly  
 465 470 475 480

Thr Leu Gln Pro Pro Glu Phe Leu Tyr Ser His Gly Val Pro Arg Thr  
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Leu Ser Pro His Gln Tyr His Ser Val His Gly Val Gly Met Val Pro  
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Glu Trp Ser Asp Asn Ser  
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<212> DNA

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| agagaactgt ggctaaaatt ccacgaagtg ggcacggaaa tgatcataac caaggctgga  | 240  |
| aggcggatgt ttcccagtta caaagtgaag gtgacgggcc ttaatcccaa aacgaagtac  | 300  |
| attcttctca tggacattgt acctgccgac gatcacagat acaaattcgc agataataaa  | 360  |
| tggctctgtga cgggcaaagc tgagcccgcc atgcctggcc gcctgtacgt gcacccagac | 420  |
| tccccgccca ccggggcgca ttggatgagg cagctcgtct ccttcagaa actcaagctc   | 480  |
| accaacaacc acctggaccc atttgggcat attattctaa attccatgca caaataccag  | 540  |
| cctagattac acatcgtgaa agcggatgaa aataatggat ttggctcaaa aaatacagcg  | 600  |
| ttctgcactc acgtctttcc tgagactgcg tttatagcag tgacttccta ccagaaccac  | 660  |
| aagatcacgc aattaaagat tgagaataat ccctttgcca aaggatttcg gggcagtgat  | 720  |
| gacatggagc tgcacagaat gtcaagaatg caaagtaaag aatatcccgt ggtccccagg  | 780  |
| agcaccgtga ggcaaaaagt ggcctccaac cacagtcctt tcagcagcga gtctcgagct  | 840  |
| ctctccacct catccaattt ggggtcccaa taccagtgtg agaatggtgt ttccggcccc  | 900  |
| tcccaggacc tcctgcctcc acccaacca taccactgc cccaggagca tagccaaatt    | 960  |
| taccattgta ccaagaggaa agaggaagaa tgttccacca cagaccatcc ctataagaag  | 1020 |
| ccctacatgg agacatcacc cagtgaagaa gattccttct accgctctag ctatccacag  | 1080 |
| cagcagggcc tgggtgcctc ctacaggaca gagtcggcac agcggcaagc ttgcatgtat  | 1140 |
| gccagctctg cgccccccag cgagcctgtg cccagcctag aggacatcag ctgcaacacg  | 1200 |
| tggccaagca tgccttccta cagcagctgc accgtcacca ccgtgcagcc catggacagg  | 1260 |
| ctaccctacc agcacttctc cgctcacttc acctcggggc ccctgggtccc tcggctggct | 1320 |
| ggcatggcca accatggctc cccacagctg ggagagggaa tgttccagca ccagacctcc  | 1380 |
| gtggcccacc agcctgtggt caggcagtgt gggcctcaga ctggcctgca gtcccctggc  | 1440 |
| acccttcagc cccctgagtt cctctactct catggcgtgc caaggactct atccccctcat | 1500 |
| cagtaccact ctgtgcacgg agttggcatg gtgccagagt ggagcgacaa tagctaa     | 1557 |

<210> 9  
<211> 20  
<212> PRT  
<213> Homo sapiens

<400> 9

Lys Arg Lys Glu Glu Cys Ser Thr Thr Asp His Pro Tyr Lys Lys  
1 5 10 15

Pro Tyr Met Glu  
20

<210> 10  
<211> 409  
<212> PRT  
<213> Homo sapiens

<400> 10

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

Gln Leu Arg Leu Gln Gln Arg Arg Thr Gln Glu Gln Leu Ala Asn Gln  
20 25 30

Gly Ile Ile Pro Pro Leu Lys Arg Pro Ala Glu Phe His Glu Gln Arg  
35 40 45

Lys His Leu Asp Ser Asp Lys Ala Lys Asn Ser Leu Lys Arg Lys Ala  
50 55 60

Arg Asn Arg Cys Asn Ser Ala Asp Leu Val Asn Met His Ile Leu Gln  
65 70 75 80

Ala Ser Thr Ala Glu Arg Ser Ile Pro Thr Ala Gln Met Lys Leu Lys  
85 90 95

Arg Ala Arg Leu Ala Asp Asp Leu Asn Glu Lys Ile Ala Leu Arg Pro  
100 105 110

Gly Pro Leu Glu Leu Val Glu Lys Asn Ile Leu Pro Val Asp Ser Ala  
115 120 125

Val Lys Glu Ala Ile Lys Gly Asn Gln Val Ser Phe Ser Lys Ser Thr  
130 135 140

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

Asp Gln Thr Arg Ser Glu Asp Pro Gln Asn Ser Ala Gly Ser Pro Pro  
165 170 175

Asp Ala Lys Ala Ser Asp Thr Pro Ser Thr Gly Ser Leu Gly Thr Asn  
180 185 190

Gln Asp Leu Ala Ser Gly Ser Glu Asn Asp Arg Asn Asp Ser Ala Ser  
195 200 205

Gln Pro Ser His Gln Ser Asp Ala Gly Lys Gln Gly Leu Gly Pro Pro  
210 215 220

Ser Thr Pro Ile Ala Val His Ala Ala Val Lys Ser Lys Ser Leu Gly  
225 230 235 240

Asp Ser Lys Asn Arg His Lys Lys Pro Lys Asp Pro Lys Pro Lys Val  
245 250 255

Lys Lys Leu Lys Tyr His Gln Tyr Ile Pro Pro Asp Gln Lys Ala Glu  
260 265 270

Lys Ser Pro Pro Pro Met Asp Ser Ala Tyr Ala Arg Leu Leu Gln Gln  
275 280 285

Gln Gln Leu Phe Leu Gln Leu Gln Ile Leu Ser Gln Gln Gln Gln  
290 295 300

Gln Gln His Arg Phe Ser Tyr Leu Gly Met His Gln Ala Gln Leu Lys  
305 310 315 320

Glu Pro Asn Glu Gln Met Val Arg Asn Pro Asn Ser Ser Ser Thr Pro  
325 330 335

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

Thr Gly Val Ser Ser Phe Lys Pro Gly Pro Leu Pro Pro Asn Leu Asp  
355 360 365

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

Pro Val Ser Gly Thr Lys Thr Ala Leu Met Asp Arg Leu Arg Pro Phe  
385 390 395 400

Gln Asp Cys Ser Gly Asn Pro Val Pro  
405

<210> 11  
<211> 223  
<212> PRT  
<213> Homo sapiens

<400> 11

Glu Val Thr Gln Pro Pro Ser Tyr Glu Asp Ala Val Lys Gln Gln Met  
1 5 10 15

Thr Arg Ser Gln Gln Met Asp Glu Leu Leu Asp Val Leu Ile Glu Ser  
20 25 30

Gly Glu Met Pro Ala Asp Ala Arg Glu Asp His Ser Cys Leu Gln Lys  
35 40 45

Val Pro Lys Ile Pro Arg Ser Ser Arg Ser Pro Thr Ala Val Leu Thr  
50 55 60

Lys Pro Ser Ala Ser Phe Glu Gln Ala Ser Ser Gly Ser Gln Ile Pro  
65 70 75 80

Phe Asp Pro Tyr Ala Thr Asp Ser Asp Glu His Leu Glu Val Leu Leu  
85 90 95

Asn Ser Gln Ser Pro Leu Gly Lys Met Ser Asp Val Thr Leu Leu Lys  
100 105 110

Ile Gly Ser Glu Glu Pro His Phe Asp Gly Ile Met Asp Gly Phe Ser  
115 120 125

Gly Lys Ala Ala Glu Asp Leu Phe Asn Ala His Glu Ile Leu Pro Gly  
130 135 140

Pro Leu Ser Pro Met Gln Thr Gln Phe Ser Pro Ser Ser Val Asp Ser  
145 150 155 160

Asn Gly Leu Gln Leu Ser Phe Thr Glu Ser Pro Trp Glu Thr Met Glu  
165 170 175

Trp Leu Asp Leu Thr Pro Pro Asn Ser Thr Pro Gly Phe Ser Ala Leu  
180 185 190

Thr Thr Ser Ser Pro Ser Ile Phe Asn Ile Asp Phe Leu Asp Val Thr  
195 200 205

Asp Leu Asn Leu Asn Ser Ser Met Asp Leu His Leu Gln Gln Trp  
210 215 220

<210> 12  
<211> 434  
<212> PRT  
<213> Homo sapiens

<400> 12

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

Gln Leu Arg Leu Gln Gln Arg Arg Thr Gln Glu Gln Leu Ala Asn Gln  
20 25 30

Gly Ile Ile Pro Pro Leu Lys Arg Pro Ala Glu Phe His Glu Gln Arg  
35 40 45

Lys His Leu Asp Ser Asp Lys Ala Lys Asn Ser Leu Lys Arg Lys Ala  
50 55 60

Arg Asn Arg Cys Asn Ser Ala Asp Leu Val Asn Met His Ile Leu Gln  
65 70 75 80

Ala Ser Thr Ala Glu Arg Ser Ile Pro Thr Ala Gln Met Lys Leu Lys  
85 90 95

Arg Ala Arg Leu Ala Asp Asp Leu Asn Glu Lys Ile Ala Leu Arg Pro  
100 105 110

Gly Pro Leu Glu Leu Val Glu Lys Asn Ile Leu Pro Val Asp Ser Ala  
115 120 125

Val Lys Glu Ala Ile Lys Gly Asn Gln Val Ser Phe Ser Lys Ser Thr  
130 135 140

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

Asp Gln Thr Arg Ser Glu Asp Pro Gln Asn Ser Ala Gly Ser Pro Pro  
165 170 175

Asp Ala Lys Ala Ser Asp Thr Pro Ser Thr Gly Ser Leu Gly Thr Asn  
180 185 190

Gln Asp Leu Ala Ser Gly Ser Glu Asn Asp Arg Asn Asp Ser Ala Ser  
195 200 205

Gln Pro Ser His Gln Ser Asp Ala Gly Lys Gln Gly Leu Gly Pro Pro  
210 215 220

Ser Thr Pro Ile Ala Val His Ala Ala Val Lys Ser Lys Ser Leu Gly  
225 230 235 240

Asp Ser Lys Asn Arg His Lys Lys Pro Lys Asp Pro Lys Pro Lys Val  
245 250 255

Lys Lys Leu Lys Tyr His Gln Tyr Ile Pro Pro Asp Gln Lys Ala Glu  
260 265 270

Lys Ser Pro Pro Pro Met Asp Ser Ala Tyr Ala Arg Leu Leu Gln Gln  
275 280 285

Gln Gln Leu Phe Leu Gln Leu Gln Ile Leu Ser Gln Gln Gln Gln  
290 295 300

Gln Gln His Arg Phe Ser Tyr Leu Gly Met His Gln Ala Gln Leu Lys  
305 310 315 320

Glu Pro Asn Glu Gln Met Val Arg Asn Pro Asn Ser Ser Ser Thr Pro  
325 330 335

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

Thr Gly Val Ser Ser Phe Lys Pro Gly Pro Leu Pro Pro Asn Leu Asp  
355 360 365

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

Pro Val Ser Gly Thr Lys Thr Ala Leu Met Asp Arg Leu Arg Pro Phe  
385 390 395 400

Gln Asp Cys Ser Gly Asn Pro Val Pro Asn Phe Gly Asp Ile Thr Thr  
405 410 415

Val Thr Phe Pro Val Thr Pro Asn Thr Leu Pro Asn Tyr Gln Ser Ser  
420 425 430

Ser Ser

<210> 13  
<211> 555  
<212> PRT  
<213> Homo sapiens

<400> 13

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

Gln Leu Arg Leu Gln Gln Arg Arg Thr Gln Glu Gln Leu Ala Asn Gln  
20 25 30

Gly Ile Ile Pro Pro Leu Lys Arg Pro Ala Glu Phe His Glu Gln Arg  
35 40 45

Lys His Leu Asp Ser Asp Lys Ala Lys Asn Ser Leu Lys Arg Lys Ala  
50 55 60

Arg Asn Arg Cys Asn Ser Ala Asp Leu Val Asn Met His Ile Leu Gln  
65 70 75 80

Ala Ser Thr Ala Glu Arg Ser Ile Pro Thr Ala Gln Met Lys Leu Lys  
85 90 95

Arg Ala Arg Leu Ala Asp Asp Leu Asn Glu Lys Ile Ala Leu Arg Pro  
100 105 110

Gly Pro Leu Glu Leu Val Glu Lys Asn Ile Leu Pro Val Asp Ser Ala  
115 120 125

Val Lys Glu Ala Ile Lys Gly Asn Gln Val Ser Phe Ser Lys Ser Thr

130

135

140

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

Asp Gln Thr Arg Ser Glu Asp Pro Gln Asn Ser Ala Gly Ser Pro Pro  
 165 170 175

Asp Ala Lys Ala Ser Asp Thr Pro Ser Thr Gly Ser Leu Gly Thr Asn  
 180 185 190

Gln Asp Leu Ala Ser Gly Ser Glu Asn Asp Arg Asn Asp Ser Ala Ser  
 195 200 205

Gln Pro Ser His Gln Ser Asp Ala Gly Lys Gln Gly Leu Gly Pro Pro  
 210 215 220

Ser Thr Pro Ile Ala Val His Ala Ala Val Lys Ser Lys Ser Leu Gly  
 225 230 235 240

Asp Ser Lys Asn Arg His Lys Lys Pro Lys Asp Pro Lys Pro Lys Val  
 245 250 255

Lys Lys Leu Lys Tyr His Gln Tyr Ile Pro Pro Asp Gln Lys Ala Glu  
 260 265 270

Lys Ser Pro Pro Pro Met Asp Ser Ala Tyr Ala Arg Leu Leu Gln Gln  
 275 280 285

Gln Gln Leu Phe Leu Gln Leu Gln Ile Leu Ser Gln Gln Gln Gln Gln  
 290 295 300

Gln Gln His Arg Phe Ser Tyr Leu Gly Met His Gln Ala Gln Leu Lys  
 305 310 315 320

Glu Pro Asn Glu Gln Met Val Arg Asn Pro Asn Ser Ser Ser Thr Pro  
 325 330 335

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

Thr Gly Val Ser Ser Phe Lys Pro Gly Pro Leu Pro Pro Asn Leu Asp  
355 360 365

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

Pro Val Ser Gly Thr Lys Thr Ala Leu Met Asp Arg Leu Arg Pro Phe  
385 390 395 400

Gln Asp Cys Ser Gly Asn Pro Val Pro Asn Phe Gly Asp Ile Thr Thr  
405 410 415

Val Thr Phe Pro Val Thr Pro Asn Thr Leu Pro Asn Tyr Gln Ser Ser  
420 425 430

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

Ser Ser Ser Pro Pro Ile Ser Pro Ala Ser Ser Asp Leu Ser Val Ala  
450 455 460

Gly Ser Leu Pro Asp Thr Phe Asn Asp Ala Ser Pro Ser Phe Gly Leu  
465 470 475 480

His Pro Ser Pro Val His Val Cys Thr Glu Glu Ser Leu Met Ser Ser  
485 490 495

Leu Asn Gly Gly Ser Val Pro Ser Glu Leu Asp Gly Leu Asp Ser Glu  
500 505 510

Lys Asp Lys Met Leu Val Glu Lys Gln Lys Val Ile Asn Glu Leu Thr  
515 520 525

Trp Lys Leu Gln Gln Glu Gln Arg Gln Val Glu Glu Leu Arg Met Gln

530

535

540

Leu Gln Lys Gln Lys Arg Asn Asn Cys Ser Glu  
 545 550 555

&lt;210&gt; 14

&lt;211&gt; 636

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in Lab - Engineered MYOCD protein

&lt;400&gt; 14

Met Thr Leu Leu Gly Ser Glu His Ser Leu Leu Ile Arg Ser Lys Phe  
 1 5 10 15

Arg Ser Val Leu Gln Leu Arg Leu Gln Gln Arg Arg Thr Gln Glu Gln  
 20 25 30

Leu Ala Asn Gln Gly Ile Ile Pro Pro Leu Lys Arg Pro Ala Glu Phe  
 35 40 45

His Glu Gln Arg Lys His Leu Asp Ser Asp Lys Ala Lys Asn Ser Leu  
 50 55 60

Lys Arg Lys Ala Arg Asn Arg Cys Asn Ser Ala Asp Leu Val Asn Met  
 65 70 75 80

His Ile Leu Gln Ala Ser Thr Ala Glu Arg Ser Ile Pro Thr Ala Gln  
 85 90 95

Met Lys Leu Lys Arg Ala Arg Leu Ala Asp Asp Leu Asn Glu Lys Ile  
 100 105 110

Ala Leu Arg Pro Gly Pro Leu Glu Leu Val Glu Lys Asn Ile Leu Pro  
 115 120 125

Val Asp Ser Ala Val Lys Glu Ala Ile Lys Gly Asn Gln Val Ser Phe

130

135

140

Ser Lys Ser Thr Asp Ala Phe Ala Phe Glu Glu Asp Ser Ser Ser Asp  
 145 150 155 160

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

Gly Ser Pro Pro Asp Ala Lys Ala Ser Asp Thr Pro Ser Thr Gly Ser  
 180 185 190

Leu Gly Thr Asn Gln Asp Leu Ala Ser Gly Ser Glu Asn Asp Arg Asn  
 195 200 205

Asp Ser Ala Ser Gln Pro Ser His Gln Ser Asp Ala Gly Lys Gln Gly  
 210 215 220

Leu Gly Pro Pro Ser Thr Pro Ile Ala Val His Ala Ala Val Lys Ser  
 225 230 235 240

Lys Ser Leu Gly Asp Ser Lys Asn Arg His Lys Lys Pro Lys Asp Pro  
 245 250 255

Lys Pro Lys Val Lys Lys Leu Lys Tyr His Gln Tyr Ile Pro Pro Asp  
 260 265 270

Gln Lys Ala Glu Lys Ser Pro Pro Pro Met Asp Ser Ala Tyr Ala Arg  
 275 280 285

Leu Leu Gln Gln Gln Gln Leu Phe Leu Gln Leu Gln Ile Leu Ser Gln  
 290 295 300

Gln Gln Gln Gln Gln Gln His Arg Phe Ser Tyr Leu Gly Met His Gln  
 305 310 315 320

Ala Gln Leu Lys Glu Pro Asn Glu Gln Met Val Arg Asn Pro Asn Ser  
 325 330 335

Ser Ser Thr Pro Leu Ser Asn Thr Pro Leu Ser Pro Val Lys Asn Ser  
340 345 350

Phe Ser Gly Gln Thr Gly Val Ser Ser Phe Lys Pro Gly Pro Leu Pro  
355 360 365

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

Ile Arg Gly Leu Pro Val Ser Gly Thr Lys Thr Ala Leu Met Asp Arg  
385 390 395 400

Leu Arg Pro Phe Gln Asp Cys Ser Gly Asn Pro Val Pro Glu Val Thr  
405 410 415

Gln Pro Pro Ser Tyr Glu Asp Ala Val Lys Gln Gln Met Thr Arg Ser  
420 425 430

Gln Gln Met Asp Glu Leu Leu Asp Val Leu Ile Glu Ser Gly Glu Met  
435 440 445

Pro Ala Asp Ala Arg Glu Asp His Ser Cys Leu Gln Lys Val Pro Lys  
450 455 460

Ile Pro Arg Ser Ser Arg Ser Pro Thr Ala Val Leu Thr Lys Pro Ser  
465 470 475 480

Ala Ser Phe Glu Gln Ala Ser Ser Gly Ser Gln Ile Pro Phe Asp Pro  
485 490 495

Tyr Ala Thr Asp Ser Asp Glu His Leu Glu Val Leu Leu Asn Ser Gln  
500 505 510

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

Glu Glu Pro His Phe Asp Gly Ile Met Asp Gly Phe Ser Gly Lys Ala

530

535

540

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

Pro Met Gln Thr Gln Phe Ser Pro Ser Ser Val Asp Ser Asn Gly Leu  
 565 570 575

Gln Leu Ser Phe Thr Glu Ser Pro Trp Glu Thr Met Glu Trp Leu Asp  
 580 585 590

Leu Thr Pro Pro Asn Ser Thr Pro Gly Phe Ser Ala Leu Thr Thr Ser  
 595 600 605

Ser Pro Ser Ile Phe Asn Ile Asp Phe Leu Asp Val Thr Asp Leu Asn  
 610 615 620

Leu Asn Ser Ser Met Asp Leu His Leu Gln Gln Trp  
 625 630 635

&lt;210&gt; 15

&lt;211&gt; 661

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in Lab - Engineered MYOCD protein

&lt;400&gt; 15

Met Thr Leu Leu Gly Ser Glu His Ser Leu Leu Ile Arg Ser Lys Phe  
 1 5 10 15

Arg Ser Val Leu Gln Leu Arg Leu Gln Gln Arg Arg Thr Gln Glu Gln  
 20 25 30

Leu Ala Asn Gln Gly Ile Ile Pro Pro Leu Lys Arg Pro Ala Glu Phe  
 35 40 45

His Glu Gln Arg Lys His Leu Asp Ser Asp Lys Ala Lys Asn Ser Leu

50

55

60

Lys Arg Lys Ala Arg Asn Arg Cys Asn Ser Ala Asp Leu Val Asn Met  
 65 70 75 80

His Ile Leu Gln Ala Ser Thr Ala Glu Arg Ser Ile Pro Thr Ala Gln  
 85 90 95

Met Lys Leu Lys Arg Ala Arg Leu Ala Asp Asp Leu Asn Glu Lys Ile  
 100 105 110

Ala Leu Arg Pro Gly Pro Leu Glu Leu Val Glu Lys Asn Ile Leu Pro  
 115 120 125

Val Asp Ser Ala Val Lys Glu Ala Ile Lys Gly Asn Gln Val Ser Phe  
 130 135 140

Ser Lys Ser Thr Asp Ala Phe Ala Phe Glu Glu Asp Ser Ser Ser Asp  
 145 150 155 160

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

Gly Ser Pro Pro Asp Ala Lys Ala Ser Asp Thr Pro Ser Thr Gly Ser  
 180 185 190

Leu Gly Thr Asn Gln Asp Leu Ala Ser Gly Ser Glu Asn Asp Arg Asn  
 195 200 205

Asp Ser Ala Ser Gln Pro Ser His Gln Ser Asp Ala Gly Lys Gln Gly  
 210 215 220

Leu Gly Pro Pro Ser Thr Pro Ile Ala Val His Ala Ala Val Lys Ser  
 225 230 235 240

Lys Ser Leu Gly Asp Ser Lys Asn Arg His Lys Lys Pro Lys Asp Pro  
 245 250 255

Lys Pro Lys Val Lys Lys Leu Lys Tyr His Gln Tyr Ile Pro Pro Asp  
260 265 270

Gln Lys Ala Glu Lys Ser Pro Pro Pro Met Asp Ser Ala Tyr Ala Arg  
275 280 285

Leu Leu Gln Gln Gln Gln Leu Phe Leu Gln Leu Gln Ile Leu Ser Gln  
290 295 300

Gln Gln Gln Gln Gln Gln His Arg Phe Ser Tyr Leu Gly Met His Gln  
305 310 315 320

Ala Gln Leu Lys Glu Pro Asn Glu Gln Met Val Arg Asn Pro Asn Ser  
325 330 335

Ser Ser Thr Pro Leu Ser Asn Thr Pro Leu Ser Pro Val Lys Asn Ser  
340 345 350

Phe Ser Gly Gln Thr Gly Val Ser Ser Phe Lys Pro Gly Pro Leu Pro  
355 360 365

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

Ile Arg Gly Leu Pro Val Ser Gly Thr Lys Thr Ala Leu Met Asp Arg  
385 390 395 400

Leu Arg Pro Phe Gln Asp Cys Ser Gly Asn Pro Val Pro Asn Phe Gly  
405 410 415

Asp Ile Thr Thr Val Thr Phe Pro Val Thr Pro Asn Thr Leu Pro Asn  
420 425 430

Tyr Gln Ser Ser Ser Ser Glu Val Thr Gln Pro Pro Ser Tyr Glu Asp  
435 440 445

Ala Val Lys Gln Gln Met Thr Arg Ser Gln Gln Met Asp Glu Leu Leu

450

455

460

Asp Val Leu Ile Glu Ser Gly Glu Met Pro Ala Asp Ala Arg Glu Asp  
465 470 475 480

His Ser Cys Leu Gln Lys Val Pro Lys Ile Pro Arg Ser Ser Arg Ser  
485 490 495

Pro Thr Ala Val Leu Thr Lys Pro Ser Ala Ser Phe Glu Gln Ala Ser  
500 505 510

Ser Gly Ser Gln Ile Pro Phe Asp Pro Tyr Ala Thr Asp Ser Asp Glu  
515 520 525

His Leu Glu Val Leu Leu Asn Ser Gln Ser Pro Leu Gly Lys Met Ser  
530 535 540

Asp Val Thr Leu Leu Lys Ile Gly Ser Glu Glu Pro His Phe Asp Gly  
545 550 555 560

Ile Met Asp Gly Phe Ser Gly Lys Ala Ala Glu Asp Leu Phe Asn Ala  
565 570 575

His Glu Ile Leu Pro Gly Pro Leu Ser Pro Met Gln Thr Gln Phe Ser  
580 585 590

Pro Ser Ser Val Asp Ser Asn Gly Leu Gln Leu Ser Phe Thr Glu Ser  
595 600 605

Pro Trp Glu Thr Met Glu Trp Leu Asp Leu Thr Pro Pro Asn Ser Thr  
610 615 620

Pro Gly Phe Ser Ala Leu Thr Thr Ser Ser Pro Ser Ile Phe Asn Ile  
625 630 635 640

Asp Phe Leu Asp Val Thr Asp Leu Asn Leu Asn Ser Ser Met Asp Leu  
645 650 655

His Leu Gln Gln Trp  
660

<210> 16  
<211> 782  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in Lab - Engineered MYOCD protein

<400> 16

Met Thr Leu Leu Gly Ser Glu His Ser Leu Leu Ile Arg Ser Lys Phe  
1 5 10 15

Arg Ser Val Leu Gln Leu Arg Leu Gln Gln Arg Arg Thr Gln Glu Gln  
20 25 30

Leu Ala Asn Gln Gly Ile Ile Pro Pro Leu Lys Arg Pro Ala Glu Phe  
35 40 45

His Glu Gln Arg Lys His Leu Asp Ser Asp Lys Ala Lys Asn Ser Leu  
50 55 60

Lys Arg Lys Ala Arg Asn Arg Cys Asn Ser Ala Asp Leu Val Asn Met  
65 70 75 80

His Ile Leu Gln Ala Ser Thr Ala Glu Arg Ser Ile Pro Thr Ala Gln  
85 90 95

Met Lys Leu Lys Arg Ala Arg Leu Ala Asp Asp Leu Asn Glu Lys Ile  
100 105 110

Ala Leu Arg Pro Gly Pro Leu Glu Leu Val Glu Lys Asn Ile Leu Pro  
115 120 125

Val Asp Ser Ala Val Lys Glu Ala Ile Lys Gly Asn Gln Val Ser Phe  
130 135 140

Ser Lys Ser Thr Asp Ala Phe Ala Phe Glu Glu Asp Ser Ser Ser Asp  
145 150 155 160

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

Gly Ser Pro Pro Asp Ala Lys Ala Ser Asp Thr Pro Ser Thr Gly Ser  
180 185 190

Leu Gly Thr Asn Gln Asp Leu Ala Ser Gly Ser Glu Asn Asp Arg Asn  
195 200 205

Asp Ser Ala Ser Gln Pro Ser His Gln Ser Asp Ala Gly Lys Gln Gly  
210 215 220

Leu Gly Pro Pro Ser Thr Pro Ile Ala Val His Ala Ala Val Lys Ser  
225 230 235 240

Lys Ser Leu Gly Asp Ser Lys Asn Arg His Lys Lys Pro Lys Asp Pro  
245 250 255

Lys Pro Lys Val Lys Lys Leu Lys Tyr His Gln Tyr Ile Pro Pro Asp  
260 265 270

Gln Lys Ala Glu Lys Ser Pro Pro Pro Met Asp Ser Ala Tyr Ala Arg  
275 280 285

Leu Leu Gln Gln Gln Gln Leu Phe Leu Gln Leu Gln Ile Leu Ser Gln  
290 295 300

Gln Gln Gln Gln Gln Gln His Arg Phe Ser Tyr Leu Gly Met His Gln  
305 310 315 320

Ala Gln Leu Lys Glu Pro Asn Glu Gln Met Val Arg Asn Pro Asn Ser  
325 330 335

Ser Ser Thr Pro Leu Ser Asn Thr Pro Leu Ser Pro Val Lys Asn Ser

340

345

350

Phe Ser Gly Gln Thr Gly Val Ser Ser Phe Lys Pro Gly Pro Leu Pro  
 355 360 365

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

Ile Arg Gly Leu Pro Val Ser Gly Thr Lys Thr Ala Leu Met Asp Arg  
 385 390 395 400

Leu Arg Pro Phe Gln Asp Cys Ser Gly Asn Pro Val Pro Asn Phe Gly  
 405 410 415

Asp Ile Thr Thr Val Thr Phe Pro Val Thr Pro Asn Thr Leu Pro Asn  
 420 425 430

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

Phe Gly Ser Thr Ser Ser Ser Pro Pro Ile Ser Pro Ala Ser Ser Asp  
 450 455 460

Leu Ser Val Ala Gly Ser Leu Pro Asp Thr Phe Asn Asp Ala Ser Pro  
 465 470 475 480

Ser Phe Gly Leu His Pro Ser Pro Val His Val Cys Thr Glu Glu Ser  
 485 490 495

Leu Met Ser Ser Leu Asn Gly Gly Ser Val Pro Ser Glu Leu Asp Gly  
 500 505 510

Leu Asp Ser Glu Lys Asp Lys Met Leu Val Glu Lys Gln Lys Val Ile  
 515 520 525

Asn Glu Leu Thr Trp Lys Leu Gln Gln Glu Gln Arg Gln Val Glu Glu  
 530 535 540

Leu Arg Met Gln Leu Gln Lys Gln Lys Arg Asn Asn Cys Ser Glu Glu  
545 550 555 560

Val Thr Gln Pro Pro Ser Tyr Glu Asp Ala Val Lys Gln Gln Met Thr  
565 570 575

Arg Ser Gln Gln Met Asp Glu Leu Leu Asp Val Leu Ile Glu Ser Gly  
580 585 590

Glu Met Pro Ala Asp Ala Arg Glu Asp His Ser Cys Leu Gln Lys Val  
595 600 605

Pro Lys Ile Pro Arg Ser Ser Arg Ser Pro Thr Ala Val Leu Thr Lys  
610 615 620

Pro Ser Ala Ser Phe Glu Gln Ala Ser Ser Gly Ser Gln Ile Pro Phe  
625 630 635 640

Asp Pro Tyr Ala Thr Asp Ser Asp Glu His Leu Glu Val Leu Leu Asn  
645 650 655

Ser Gln Ser Pro Leu Gly Lys Met Ser Asp Val Thr Leu Leu Lys Ile  
660 665 670

Gly Ser Glu Glu Pro His Phe Asp Gly Ile Met Asp Gly Phe Ser Gly  
675 680 685

Lys Ala Ala Glu Asp Leu Phe Asn Ala His Glu Ile Leu Pro Gly Pro  
690 695 700

Leu Ser Pro Met Gln Thr Gln Phe Ser Pro Ser Ser Val Asp Ser Asn  
705 710 715 720

Gly Leu Gln Leu Ser Phe Thr Glu Ser Pro Trp Glu Thr Met Glu Trp  
725 730 735

Leu Asp Leu Thr Pro Pro Asn Ser Thr Pro Gly Phe Ser Ala Leu Thr

740

745

750

Thr Ser Ser Pro Ser Ile Phe Asn Ile Asp Phe Leu Asp Val Thr Asp  
 755 760 765

Leu Asn Leu Asn Ser Ser Met Asp Leu His Leu Gln Gln Trp  
 770 775 780

<210> 17  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 17

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

Gln Leu Arg Leu Gln Gln Arg Arg Thr Gln Glu Gln Leu Ala Asn Gln  
 20 25 30

Gly Ile Ile Pro Pro Leu Lys Arg Pro Ala Glu Phe His Glu Gln Arg  
 35 40 45

Lys His Leu Asp Ser Asp Lys Ala Lys Asn Ser Leu Lys Arg Lys Ala  
 50 55 60

Arg Asn Arg Cys Asn Ser Ala Asp Leu Val Asn Met His Ile Leu Gln  
 65 70 75 80

Ala Ser Thr Ala Glu Arg Ser Ile Pro Thr Ala Gln Met Lys Leu Lys  
 85 90 95

Arg Ala Arg Leu Ala Asp Asp Leu Asn Glu Lys Ile Ala Leu Arg Pro  
 100 105 110

Gly Pro Leu Glu  
 115

<210> 18  
<211> 111  
<212> PRT  
<213> Homo sapiens

<400> 18

Ser Ala Ser Gln Pro Ser His Gln Ser Asp Ala Gly Lys Gln Gly Leu  
1 5 10 15

Gly Pro Pro Ser Thr Pro Ile Ala Val His Ala Ala Val Lys Ser Lys  
20 25 30

Ser Leu Gly Asp Ser Lys Asn Arg His Lys Lys Pro Lys Asp Pro Lys  
35 40 45

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

Lys Ala Glu Lys Ser Pro Pro Pro Met Asp Ser Ala Tyr Ala Arg Leu  
65 70 75 80

Leu Gln Gln Gln Gln Leu Phe Leu Gln Leu Gln Ile Leu Ser Gln Gln  
85 90 95

Gln Gln Gln Gln Gln His Arg Phe Ser Tyr Leu Gly Met His Gln  
100 105 110

<210> 19  
<211> 54  
<212> PRT  
<213> Homo sapiens

<400> 19

Ser Ser Phe Lys Pro Gly Pro Leu Pro Pro Asn Leu Asp Asp Leu Lys  
1 5 10 15

Val Ser Glu Leu Arg Gln Gln Leu Arg Ile Arg Gly Leu Pro Val Ser  
20 25 30

Gly Thr Lys Thr Ala Leu Met Asp Arg Leu Arg Pro Phe Gln Asp Cys  
35 40 45

Ser Gly Asn Pro Val Pro  
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<210> 20  
<211> 41  
<212> PRT  
<213> Homo sapiens

<400> 20

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

Lys Val Ile Asn Glu Leu Thr Trp Lys Leu Gln Gln Glu Gln Arg Gln  
20 25 30

Val Glu Glu Leu Arg Met Gln Leu Gln  
35 40

<210> 21  
<211> 57  
<212> DNA  
<213> Porcine teschovirus-1

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<210> 22  
<211> 57  
<212> DNA  
<213> Porcine teschovirus-1

<400> 22  
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<210> 23  
<211> 19  
<212> PRT  
<213> Porcine teschovirus-1

<400> 23

Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn  
1 5 10 15

Pro Gly Pro

<210> 24

<211> 54

<212> DNA

<213> Thoseaasigna virus

<400> 24

gagggcagag gaagtctgct aacatgcggt gacgtcgagg agaadcctgg acct 54

<210> 25

<211> 18

<212> PRT

<213> Thoseaasigna virus

<400> 25

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro  
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Gly Pro

<210> 26

<211> 60

<212> DNA

<213> Equine rhinitis A virus

<400> 26

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<210> 27

<211> 20

<212> PRT

<213> Equine rhinitis A virus

<400> 27

Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp Cys Glu Ser  
1 5 10 15

Asn Pro Gly Pro  
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<210> 28  
<211> 66  
<212> DNA  
<213> Foot-and-mouth disease virus

<400> 28  
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ggacct 66

<210> 29  
<211> 22  
<212> PRT  
<213> Foot-and-mouth disease virus

<400> 29

Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val  
1 5 10 15

Glu Ser Asn Pro Gly Pro  
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<210> 30  
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<220>  
<223> Made in Lab - linker peptide

<400> 30

Gly Gly Ser Gly Gly Ser  
1 5

<210> 31  
<211> 6

<212> PRT  
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<220>  
<223> Made in Lab - linker peptide

<400> 31

Gly Ser Ser Gly Gly Ser  
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<210> 32  
<211> 6  
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<220>  
<223> Made in Lab - linker peptide

<400> 32

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<210> 33  
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<212> PRT  
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<220>  
<223> Made in Lab - linker peptide

<400> 33

Gly Gly Ser Gly Gly Ser Gly Gly Ser  
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<210> 34  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in Lab - linker peptide

<400> 34

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser  
 1 5 10

<210> 35  
 <211> 3726  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Made in Lab - synthesized MYOCD-2A-ASCL1 construct

<400> 35  
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 ccactgaaac gtccagctga attccatgag caaagaaaaac atttggatag tgacaaggct 180  
 aaaaattccc tgaagcgcaa agccagaaac aggtgcaaca gtgccgactt ggtaatatg 240  
 cacatactcc aagcttccac tgcagagagg tccattccaa ctgctcagat gaagctgaaa 300  
 agagcccgac tcgccgatga tctcaatgaa aaaattgctc tacgaccagg cccactggag 360  
 ctggtggaac aaaacattct tcctgtggat tctgctgtga aagaggccat aaaaggtaac 420  
 caggtagatt tctccaaatc cacggatgct ttgctcttg aagaggacag cagcagcgat 480  
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 gggaagcagg ggcttggccc cccagcacc cccatagccg tgcattgctg tgtaaagtcc 720  
 aaatccttgg gtgacagtaa gaaccgccac aaaaagccca aggaccccaa gccaaagggtg 780  
 aagaagctta aatatcacca gtacattccc ccagaccaga aggcagagaa gtcccctcca 840  
 cctatggact cagcctacgc tcggctgctc cagcaacagc agctgttcct gcagctccaa 900  
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 tctttcaaac caggccact cccacctaac ctggatgatc tgaaggctct tgaattaaga 1140

|                                                                    |      |
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| caacagcttc gaattcgggg cttgcctgtg tcaggcacca aaacggctct catggaccgg  | 1200 |
| cttcgaccct tccaggactg ctctggcaac ccagtgccga actttgggga tataacgact  | 1260 |
| gtcacttttc ctgtcacacc caacacgctg cccaattacc agtcttcctc ttctaccagt  | 1320 |
| gccctgtcca acggcttcta ccactttggc agcaccagct ccagcccccc gatctcccca  | 1380 |
| gcctcctctg acctgtcagt cgctgggtcc ctgccggaca ctttcaatga tgcctcccc   | 1440 |
| tccttcggcc tgcacccgtc cccagtccac gtgtgcacgg aggaaagtct catgagcagc  | 1500 |
| ctgaatgggg gctctgttcc ttctgagctg gatgggctgg actccgagaa ggacaagatg  | 1560 |
| ctgggtggaga agcagaaggt gatcaatgaa ctcacctgga aactccagca agagcagagg | 1620 |
| cagggtggagg agctgaggat gcagcttcag aagcagaaaa ggaataactg ttcagagaag | 1680 |
| aagccgctgc ctttcctggc tgcctccatc aagcaggaag aggctgtctc cagctgtcct  | 1740 |
| tttgcatccc aagtacctgt gaaaagacaa agcagcagct cagagtgtca cccaccggct  | 1800 |
| tgtgaagctg ctcaactcca gcctcttggg aatgctcatt gtgtggagtc ctcagatcaa  | 1860 |
| accaatgtac tttcttcac atttctcagc cccagtggt cccctcagca ttcaccgctg    | 1920 |
| ggggctgtga aaagcccaca gcacatcagt ttgccccat cacccaacaa ccctcacttt   | 1980 |
| ctgccctcat cctccggggc ccaggagaa gggcacaggg tctcctcgcc catcagcagc   | 2040 |
| cagggtgtgca ctgcacagaa ctcaggagca cacgatggcc atcctccaag cttctctccc | 2100 |
| cattcttcca gcctccaccc gcccttctct ggagcccaag cagacagcag tcatggtgcc  | 2160 |
| gggggaaacc cttgtccaa aagcccatgt gtacagcaaa agatggctgg ttacactct    | 2220 |
| tctgataagg tggggccaaa gttttcaatt ccatcccaa ctttttctaa gtcaagttca   | 2280 |
| gcaatttcag aggtaacaca gcctccatcc tatgaagatg ccgtaaagca gcaaatgacc  | 2340 |
| cggagtcagc agatggatga actcctggac gtgcttattg aaagcggaga aatgccagca  | 2400 |
| gacgctagag aggatcactc atgtcttcaa aaagtcccaa agatacccag atcttcccga  | 2460 |
| agtccaactg ctgtcctcac caagccctcg gcttcctttg aacaagcctc ttcaggcagc  | 2520 |
| cagatcccct ttgatcccta tgccaccgac agtgatgagc atcttgaagt cttattaaat  | 2580 |
| tcccagagcc ccctaggaaa gatgagtgat gtcacccttc taaaaattgg gagcgaagag  | 2640 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| cctcactttg atgggataat ggatggattc tctgggaagg ctgcagaaga cctcttcaat  | 2700 |
| gcacatgaga tcttgccagg cccctctct ccaatgcaga cacagttttc accctcttct   | 2760 |
| gtggacagca atgggctgca gttaagcttc actgaatctc cctgggaaac catggagtgg  | 2820 |
| ctggacctca ctccgcaaaa ttccacacca ggcttttagcg ccctcaccac cagcagcccc | 2880 |
| agcatcttca acatcgattt cctggatgtc actgatctca atttgaattc ttccatggac  | 2940 |
| cttcacttgc agcagtgggc cacgaacttc tctctgttaa agcaagcagg agacgtggaa  | 3000 |
| gaaaaccccg gtcctatgga aagctctgcc aagatggaga gcggcggcgc cggccagcag  | 3060 |
| ccccagccgc agccccagca gcccttcctg ccgcccgcag cctgtttctt tgccacggcc  | 3120 |
| gcagccgcgg cggccgcagc cgccgcagcg gcagcgcaga gcgcgcagca gcagcagcag  | 3180 |
| cagcagcagc agcagcagca ggccgcccag ctgagaccgg cggccgacgg ccagccctca  | 3240 |
| gggggcggtc acaagtcagc gccaagcaa gtcaagcgac agcgctcgtc ttcgcccga    | 3300 |
| ctgatgcgct gcaaacgccg gctcaacttc agcggctttg gctacagcct gccgcagcag  | 3360 |
| cagccggccg ccgtggcgcg ccgcaacgag cgcgagcgca accgctcaa gttggtcaac   | 3420 |
| ctgggctttg ccaccttcg ggagcacgtc cccaacggcg cggccaacaa gaagatgagt   | 3480 |
| aagggtggaga cactgcgctc ggcggtcgag tacatccgcg cgctgcagca gctgctggac | 3540 |
| gagcatgacg cggtagcgc gccttccag gcaggcgtcc tgctgcccac catctcccc     | 3600 |
| aactactcca acgacttgaa ctccatggcc ggctcgccgg tctcatccta ctcgtcggac  | 3660 |
| gagggtcttt acgaccgct cagccccgag gagcaggagc ttctcgactt caccaactgg   | 3720 |
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<210> 36

<211> 3744

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - synthesized MYOCD-2A-MYF6 construct

<400> 36

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|-------------------------------------------------------------------|----|

|                                                                    |      |
|--------------------------------------------------------------------|------|
| cagttaagac ttcaacaaag aaggacccag gaacaactgg ctaaccaagg cataatacca  | 120  |
| ccactgaaac gtccagctga attccatgag caaagaaaac atttggatag tgacaaggct  | 180  |
| aaaaattccc tgaagcgcaa agccagaaac aggtgcaaca gtgccgactt ggттаататg  | 240  |
| cacatactcc aagcttccac tgcagagagg tccattccaa ctgctcagat gaagctgaaa  | 300  |
| agagcccgac tcgccgatga tctcaatgaa aaaattgctc tacgaccagg cccactggag  | 360  |
| ctggtggaaa aaaacattct tcctgtggat tctgctgtga aagaggccat aaaaggtaac  | 420  |
| caggtgagtt tctccaaatc cacggatgct tttgcctttg aagaggacag cagcagcgat  | 480  |
| gggctttctc cggatcagac tcgaagtga gacccccaaa actcagcggg atccccgcca   | 540  |
| gacgctaaaag cctcagatac cccttcgaca ggttctctgg ggacaaacca ggatcttgct | 600  |
| tctggctcag aaaatgacag aaatgactca gcctcacagc ccagccacca gtcagatgcg  | 660  |
| gggaagcagg ggcttggccc cccagcacc cccatagccg tgcattgctgc tgtaaagtcc  | 720  |
| aaatccttgg gtgacagtaa gaaccgccac aaaaagccca aggaccccaa gccaaagggtg | 780  |
| aagaagctta aatatcacca gtacattccc ccagaccaga aggagagaaa gtccccctcca | 840  |
| cctatggact cagcctacgc tcggctgctc cagcaacagc agctgttcct gcagctccaa  | 900  |
| atcctcagcc agcagcagca gcagcagcaa caccgattca gctacctagg gatgcaccaa  | 960  |
| gctcagctta aggaacaaaa tgaacagatg gtcagaaaac caaactcttc ttcaacgcca  | 1020 |
| ctgagcaata ccccttgtc tcctgtcaaa aacagttttt ctggacaaac tgggtgtctct  | 1080 |
| tctttcaaac caggccact cccacctaac ctggatgatc tgaaggctc tgaattaaga    | 1140 |
| caacagcttc gaattcgggg cttgcctgtg tcaggcacca aaacggctct catggaccgg  | 1200 |
| cttcgaccct tccaggactg ctctggcaac ccagtgccga actttgggga tataacgact  | 1260 |
| gtcacttttc ctgtcacacc caacacgctg cccaattacc agtcttcctc ttctaccagt  | 1320 |
| gccctgtcca acggcttcta ccactttggc agcaccagct ccagcccccc gatctcccca  | 1380 |
| gcctcctctg acctgtcagt cgctgggtcc ctgccggaca ccttcaatga tgcctcccc   | 1440 |
| tccttcggcc tgcacccgtc cccagtcac gtgtgcacgg aggaaagtct catgagcagc   | 1500 |
| ctgaatgggg gctctgttcc ttctgagctg gatgggctgg actccgagaa ggacaagatg  | 1560 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ctggtggaga agcagaaggt gatcaatgaa ctcacctgga aactccagca agagcagagg  | 1620 |
| caggtggagg agctgaggat gcagcttcag aagcagaaaa ggaataactg ttcagagaag  | 1680 |
| aagccgctgc ctttcctggc tgcctccatc aagcaggaag aggctgtctc cagctgtcct  | 1740 |
| tttgcacccc aagtacctgt gaaaagacaa agcagcagct cagagtgtca cccaccggct  | 1800 |
| tgtgaagctg ctcaactcca gcctcttgga aatgctcatt gtgtggagtc ctcagatcaa  | 1860 |
| accaatgtac tttcttcac atttctcagc cccagtggtt cccctcagca ttcaccgctg   | 1920 |
| ggggctgtga aaagcccaca gcacatcagt ttgccccat cacccaacaa ccctcacttt   | 1980 |
| ctgccctcat cctccggggc ccaggagaaa gggcacaggg tctcctcgcc catcagcagc  | 2040 |
| caggtgtgca ctgcacagaa ctcaggagca cacgatggcc atcctccaag cttctctccc  | 2100 |
| cattcttcca gcctccacc gcccttctct ggagcccaag cagacagcag tcatggtgcc   | 2160 |
| gggggaaacc cttgtcccaa aagcccatgt gtacagcaaa agatggctgg tttacactct  | 2220 |
| tctgataagg tggggccaaa gttttcaatt ccatcccaa ctttttctaa gtcaagttca   | 2280 |
| gcaatttcag aggtaacaca gcctccatcc tatgaagatg ccgtaaagca gcaaatgacc  | 2340 |
| cggagtcagc agatggatga actcctggac gtgcttattg aaagcggaga aatgccagca  | 2400 |
| gacgctagag aggatcactc atgtcttcaa aaagtcccaa agatacccag atcttcccga  | 2460 |
| agtccaactg ctgtcctcac caagccctcg gcttcctttg aacaagcctc ttcaggcagc  | 2520 |
| cagatcccct ttgatcccta tgccaccgac agtgatgagc atcttgaagt cttattaaat  | 2580 |
| tcccagagcc ccctaggaaa gatgagtgat gtcaccctc taaaaattgg gagcgaagag   | 2640 |
| cctcactttg atgggataat ggatggattc tctgggaagg ctgcagaaga cctcttcaat  | 2700 |
| gcacatgaga tcttgccagg cccctctct ccaatgcaga cacagttttc accctcttct   | 2760 |
| gtggacagca atgggctgca gttaagcttc actgaatctc cctgggaaac catggagtgg  | 2820 |
| ctggacctca ctccgcaaaa ttccacacca ggcttttagcg ccctcaccac cagcagcccc | 2880 |
| agcatcttca acatcgattt cctggatgtc actgatctca atttgaattc ttccatggac  | 2940 |
| cttcacttgc agcagtgggc cacgaacttc tctctgttaa agcaagcagg agacgtggaa  | 3000 |
| gaaaaccccg gtcctatgat gatggacctt ttgaaactg gtcctatatt cttctacttg   | 3060 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| gatggggaaa atgttactct gcagccatta gaagtggcag aaggctctcc tttgtatcca | 3120 |
| gggagtgatg gtaccttgct cccctgccag gaccaaagtc ccccggaagc ggggagcgac | 3180 |
| agcagcggag aggaacatgt cctggcgccc ccgggcctgc agcctccaca ctgccccggc | 3240 |
| cagtgtctga tctgggcttg caagacctgc aagagaaaat ctgccccac tgaccggcga  | 3300 |
| aaagccgcca ccctgcgcga aaggaggagg ctaaagaaaa tcaacgaggc cttcgaggca | 3360 |
| ctgaagcggc gaactgtggc caacccaac cagaggctgc ccaagggtga gattctgcgg  | 3420 |
| agcgccatca gctatatga gcggctgcag gacctgctgc accggctgga tcagcaggag  | 3480 |
| aagatgcagg agctgggggt ggaccccttc agctacagac ccaaacaaga aaatcttgag | 3540 |
| ggtgcggatt tcctgcgcac ctgcagctcc cagtggccaa gtgtttccga tcattccagg | 3600 |
| gggctcgtga taacggctaa ggaaggagga gcaagtattg attcgtcagc ctcgagtagc | 3660 |
| cttcgatgcc tttcttccat cgtggacagt atttcctcgg aggaacgcaa actcccctgc | 3720 |
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<210> 37

<211> 3114

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - synthesized MyDelta3-2A-ASCL1 construct

<400> 37

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| ccactgaaac gtccagctga attccatgag caaagaaaac atttgatag tgacaaggct   | 180 |
| aaaaattccc tgaagcgcaa agccagaaac aggtgcaaca gtgccgactt ggtaatatg   | 240 |
| cacatactcc aagcttcac tgcagagagg tccattccaa ctgctcagat gaagctgaaa   | 300 |
| agagcccgac tcgccgatga tctcaatgaa aaaattgctc tacgaccagg cccactggag  | 360 |
| ctgggtgaaa aaaacattct tcctgtggat tctgctgtga aagaggccat aaaaggtaac  | 420 |
| caggtgagtt tctcaaatac cacggatgct tttgcctttg aagaggacag cagcagcgat  | 480 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gggctttctc cggatcagac tcgaagtga gacccccaaa actcagcggg atccccgcca   | 540  |
| gacgctaaag cctcagatac cccttcgaca ggttctctgg ggacaaacca ggatcttgct  | 600  |
| tctggctcag aaaatgacag aaatgactca gcctcacagc ccagccacca gtcagatgcg  | 660  |
| gggaagcagg ggcttggccc ccccagcacc cccatagccg tgcattgctgc tgtaaagtcc | 720  |
| aaatccttgg gtgacagtaa gaaccgccac aaaaagccca aggaccccaa gccaaagggtg | 780  |
| aagaagctta aatatcacca gtacattccc ccagaccaga aggagagaaa gtccccctcca | 840  |
| cctatggact cagcctacgc tcggctgctc cagcaacagc agctgttcct gcagctccaa  | 900  |
| atcctcagcc agcagcagca gcagcagcaa caccgattca gctacctagg gatgcaccaa  | 960  |
| gctcagctta aggaacaaaa tgaacagatg gtcagaaaac caaactcttc ttcaacgcca  | 1020 |
| ctgagcaata cccccttgct tcctgtcaaa aacagttttt ctggacaaac tgggtgtctct | 1080 |
| tctttcaaac caggcccact cccacctaac ctggatgatc tgaaggctctc tgaattaaga | 1140 |
| caacagcttc gaattcgggg cttgcctgtg tcaggcacca aaacggctct catggaccgg  | 1200 |
| cttcgaccct tccaggactg ctctggcaac ccagtgccga actttgggga tataacgact  | 1260 |
| gtcacttttc ctgtcacacc caacacgctg cccaattacc agtcttcctc ttctaccagt  | 1320 |
| gccctgtcca acggcttcta ccactttggc agcaccagct ccagcccccc gatctcccca  | 1380 |
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| cagggtggagg agctgaggat gcagcttcag aagcagaaaa ggaataactg ttcagaggag | 1680 |
| gtaacacagc ctccatccta tgaagatgcc gtaaagcagc aaatgacccg gagtcagcag  | 1740 |
| atggatgaac tcctggacgt gcttattgaa agcggagaaa tgccagcaga cgctagagag  | 1800 |
| gatcactcat gtcttcaaaa agtcccaaag ataccagat cttcccgaag tccaactgct   | 1860 |
| gtcctcacca agccctcggc ttcttttgaa caagcctctt caggcagcca gatccccctt  | 1920 |
| gatccctatg ccaccgacag tgatgagcat cttgaagtct tattaaattc ccagagcccc  | 1980 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| ctaggaaaga tgagtgatgt cacccttcta aaaattggga gcgaagagcc tcactttgat | 2040 |
| gggataatgg atggattctc tgggaaggct gcagaagacc tcttcaatgc acatgagatc | 2100 |
| ttgccaggcc ccctctctcc aatgcagaca cagttttcac cctcttctgt ggacagcaat | 2160 |
| gggctgcagt taagcttcac tgaatctccc tgggaaacca tggagtggct ggacctcact | 2220 |
| ccgccaaatt ccacaccagg ctttagcgcc ctcaccacca gcagccccag catcttcaac | 2280 |
| atcgatttcc tggatgtcac tgatctcaat ttgaattctt ccatggacct tcacttgcag | 2340 |
| cagtgggcca cgaacttctc tctgttaaag caagcaggag acgtggaaga aaaccccggt | 2400 |
| cctatggaaa gctctgccaa gatggagagc ggcgggcgcc gccagcagcc ccagccgcag | 2460 |
| ccccagcagc ctttctgcc gcccgagcc tgtttctttg ccacggccgc agccgcggcg   | 2520 |
| gccgcagccg ccgcagcggc agcgagagc gcgcagcagc agcagcagca gcagcagcag  | 2580 |
| cagcagcagg cgccgcagct gagaccggcg gccgacggcc agccctcagg gggcggtcac | 2640 |
| aagtcagcgc ccaagcaagt caagcgacag cgctcgtctt cgcccgaact gatgcgctgc | 2700 |
| aaacgccggc tcaacttcag cggctttggc tacagcctgc cgcagcagca gccggccgcc | 2760 |
| gtggcgcgcc gcaacgagcg cgagcgcaac cgctcaagt tggtaacct gggctttgcc   | 2820 |
| acccttcggg agcacgtccc caacggcgcg gccacaaga agatgagtaa ggtggagaca  | 2880 |
| ctgcgctcgg cggctgagta catccgcgcg ctgcagcagc tgctggacga gcatgacgcg | 2940 |
| gtgagcgccg cttccaggc aggcgtcctg tcgcccacca tctccccaa ctactccaac   | 3000 |
| gacttgaact ccatggccgg ctcgccggtc tcacctact cgtcggacga gggctcttac  | 3060 |
| gacccgctca gccccgagga gcaggagctt ctcgacttca ccaactggtt ctga       | 3114 |

<210> 38

<211> 3132

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - Synthesized MyDelta3-2A-MYF6 construct

<400> 38

|                                                                    |    |
|--------------------------------------------------------------------|----|
| atgacactcc tggggctctga gcattccttg ctgattagga gcaagttcag atcagtttta | 60 |
|--------------------------------------------------------------------|----|

|                                                                    |      |
|--------------------------------------------------------------------|------|
| cagttaagac ttcaacaaag aaggacccag gaacaactgg ctaaccaagg cataatacca  | 120  |
| ccactgaaac gtccagctga attccatgag caaagaaaac atttggatag tgacaaggct  | 180  |
| aaaaattccc tgaagcgcaa agccagaaac aggtgcaaca gtgccgactt ggттаататg  | 240  |
| cacatactcc aagcttccac tgcagagagg tccattccaa ctgctcagat gaagctgaaa  | 300  |
| agagcccgac tcgccgatga tctcaatgaa aaaattgctc tacgaccagg cccactggag  | 360  |
| ctggtggaaa aaaacattct tcctgtggat tctgctgtga aagaggccat aaaaggtaac  | 420  |
| caggtgagtt tctccaaatc cacggatgct tttgcctttg aagaggacag cagcagcgat  | 480  |
| gggctttctc cggatcagac tcgaagtga gacccccaaa actcagcggg atccccgcca   | 540  |
| gacgctaaag cctcagatac cccttcgaca ggttctctgg ggacaaacca ggatcttgct  | 600  |
| tctggctcag aaaatgacag aaatgactca gcctcacagc ccagccacca gtcagatgcg  | 660  |
| gggaagcagg ggcttggccc cccagcacc cccatagccg tgcattgctgc tgtaaagtcc  | 720  |
| aaatccttgg gtgacagtaa gaaccgccac aaaaagccca aggaccccaa gccaaagggtg | 780  |
| aagaagctta aatatcacca gtacattccc ccagaccaga aggagagaaa gtccccctcca | 840  |
| cctatggact cagcctacgc tcggctgctc cagcaacagc agctgttcct gcagctccaa  | 900  |
| atcctcagcc agcagcagca gcagcagcaa caccgattca gctacctagg gatgcaccaa  | 960  |
| gctcagctta aggaacaaaa tgaacagatg gtcagaaaac caaactcttc ttcaacgcca  | 1020 |
| ctgagcaata ccccttgtc tcctgtcaaa aacagttttt ctggacaaac tgggtgtctct  | 1080 |
| tctttcaaac caggccact cccacctaac ctggatgatc tgaaggctc tgaattaaga    | 1140 |
| caacagcttc gaattcgggg cttgcctgtg tcaggcacca aaacggctct catggaccgg  | 1200 |
| cttcgaccct tccaggactg ctctggcaac ccagtgccga actttgggga tataacgact  | 1260 |
| gtcacttttc ctgtcacacc caacacgctg cccaattacc agtcttcctc ttctaccagt  | 1320 |
| gccctgtcca acggcttcta ccactttggc agcaccagct ccagcccccc gatctcccca  | 1380 |
| gcctcctctg acctgtcagt cgctgggtcc ctgccggaca cttcaatga tgcctcccc    | 1440 |
| tccttcggcc tgcacccgtc cccagtcac gtgtgcacgg aggaaagtct catgagcagc   | 1500 |
| ctgaatgggg gctctgttcc ttctgagctg gatgggctgg actccgagaa ggacaagatg  | 1560 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ctggtggaga agcagaaggt gatcaatgaa ctcacctgga aactccagca agagcagagg  | 1620 |
| caggtggagg agctgaggat gcagcttcag aagcagaaaa ggaataactg ttcagaggag  | 1680 |
| gtaacacagc ctccatccta tgaagatgcc gtaaagcagc aaatgacccg gagtcagcag  | 1740 |
| atggatgaac tcctggacgt gcttattgaa agcggagaaa tgccagcaga cgctagagag  | 1800 |
| gatcactcat gtcttcaaaa agtcccaaag atacccagat cttcccgaag tccaactgct  | 1860 |
| gtcctcacca agccctcggc ttcctttgaa caagcctctt caggcagcca gatccccctt  | 1920 |
| gatccctatg ccaccgacag tgatgagcat cttgaagtct tattaaattc ccagagcccc  | 1980 |
| ctaggaaaga tgagtgatgt cacccttcta aaaattggga gcgaagagcc tcactttgat  | 2040 |
| gggataatgg atggattctc tgggaaggct gcagaagacc tcttcaatgc acatgagatc  | 2100 |
| ttgccaggcc ccctctctcc aatgcagaca cagttttcac cctcttctgt ggacagcaat  | 2160 |
| gggctgcagt taagcttcac tgaatctccc tgggaaacca tggagtggct ggacctcact  | 2220 |
| ccgccaaatt ccacaccagg cttagcgcc ctcaccacca gcagccccag catcttcaac   | 2280 |
| atcgatttcc tggatgtcac tgatctcaat ttgaattctt ccatggacct tcacttgcag  | 2340 |
| cagtgggcca cgaacttctc tctgttaaag caagcaggag acgtggaaga aaaccccggt  | 2400 |
| cctatgatga tggacctttt tgaaactggc tcctatttct tctacttggga tggggaaaat | 2460 |
| gttactctgc agccattaga agtggcagaa ggctctcctt tgtatccagg gagtgatggt  | 2520 |
| accttgtccc cctgccagga ccaaatgccc ccggaagcgg ggagcgacag cagcggagag  | 2580 |
| gaacatgtcc tggcgcccc gggcctgcag cctccacact gccccggcca gtgtctgac    | 2640 |
| tgggcttgca agacctgcaa gagaaaaatct gccccactg accggcgaaa agccgccacc  | 2700 |
| ctgcgcgaaa ggaggaggct aaagaaaaatc aacgaggcct tcgaggcact gaagcggcga | 2760 |
| actgtggcca accccaacca gaggctgccc aaggtggaga ttctgcggag cgccatcagc  | 2820 |
| tatattgagc ggctgcagga cctgctgcac cggctggatc agcaggagaa gatgcaggag  | 2880 |
| ctgggggtgg accccttcag ctacagaccc aaacaagaaa atcttgaggg tgcggatttc  | 2940 |
| ctgcgcacct gcagctccca gtggccaagt gtttccgac attccagggg gctcgtgata   | 3000 |
| acggctaagg aaggaggagc aagtattgat tcgtcagcct cgagtagcct tcgatgcctt  | 3060 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| tcttccatcg tggacagtat ttcctcggag gaacgcaaac tcccctgcgt ggaggaagtg | 3120 |
| gtggagaagt aa                                                     | 3132 |

<210> 39  
 <211> 3726  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Made in Lab - synthesized ASCL1-2A-MYOC construct

|                                                                     |      |
|---------------------------------------------------------------------|------|
| <400> 39                                                            |      |
| atggaaaagct ctgccaagat ggagagcggc ggcgccggcc agcagcccca gccgcagccc  | 60   |
| cagcagcccct tcctgccgcc cgcagcctgt ttctttgccca cggccgcagc cgcggcggcc | 120  |
| gcagccgccg cagcggcagc gcagagcgcg cagcagcagc agcagcagca gcagcagcag   | 180  |
| cagcaggcgc cgcagctgag accggcggcc gacggccagc cctcaggggg cggtcacaag   | 240  |
| tcagcgccca agcaagtcaa gcgacagcgc tcgtcttcgc ccgaactgat gcgctgcaaa   | 300  |
| cgccgggtca acttcagcgg ctttggttac agcctgccgc agcagcagcc ggccgccgtg   | 360  |
| gcgcgccgca acgagcgcga gcgcaaccgc gtcaagttgg tcaacctggg ctttgccacc   | 420  |
| cttcgggagc acgtcccca cggcgcggcc aacaagaaga tgagtaaggt ggagacactg    | 480  |
| cgctcggcgg tcgagtacat ccgcgcgctg cagcagctgc tggacgagca tgacgcggtg   | 540  |
| agcgccgcct tccaggcagg cgtcctgtcg cccaccatct cccccaacta ctccaacgac   | 600  |
| ttgaactcca tggccggctc gccggtctca tcctactcgt cggacgaggg ctcttacgac   | 660  |
| ccgctcagcc ccgaggagca ggagcttctc gacttcacca actggttcgc cacgaacttc   | 720  |
| tctctgttaa agcaagcagg agacgtggaa gaaaaccccg gtcctatgac actcctgggg   | 780  |
| tctgagcatt ccttgctgat taggagcaag ttcagatcag ttttacagtt aagacttcaa   | 840  |
| caaagaagga cccaggaaca actggctaac caaggcataa taccaccact gaaacgtcca   | 900  |
| gctgaattcc atgagcaaag aaaacatttg gatagtgaca aggctaaaaa ttccctgaag   | 960  |
| cgcaaagcca gaaacaggtg caacagtgcc gacttggtta atatgcacat actccaagct   | 1020 |
| tccactgcag agagggtccat tccaactgct cagatgaagc tgaaaagagc ccgactcgcc  | 1080 |

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gatgatctca atgaaaaaat tgctctacga ccaggcccac tggagctggt ggaaaaaac    | 1140 |
| attcttcctg tggattctgc tgtgaaagag gccataaaag gtaaccaggt gagtttctcc   | 1200 |
| aatccacgg atgcttttgc ctttgaagag gacagcagca gcgatgggct ttctccggat    | 1260 |
| cagactcgaa gtgaagaccc caaaaactca gcgggatccc cgccagacgc taaagcctca   | 1320 |
| gatacccctt cgacagggtt tctggggaca aaccaggatc ttgcttctgg ctcaaaaaat   | 1380 |
| gacagaaatg actcagcctc acagcccagc caccagtcag atgcggggaa gcaggggctt   | 1440 |
| ggcccccca gcacccccat agccgtgcat gctgctgtaa agtccaaatc cttgggtgac    | 1500 |
| agtaagaacc gccacaaaaa gccaaggac cccaagccaa aggtgaagaa gcttaaatat    | 1560 |
| caccagtaca ttccccaga ccagaaggca gagaagtccc ctccacctat ggactcagcc    | 1620 |
| tacgctcggc tgctccagca acagcagctg ttcctgcagc tccaaatcct cagccagcag   | 1680 |
| cagcagcagc agcaacaccg attcagctac ctagggatgc accaagctca gcttaaggaa   | 1740 |
| ccaaatgaac agatggtcag aaatccaaac tcttcttcaa cgccactgag caatacccc    | 1800 |
| ttgtctcctg tcaaaaacag ttttctgga caaactgggt tctcttctt caaaccaggc     | 1860 |
| ccactcccac ctaacctgga tgatctgaag gtctctgaat taagacaaca gcttcgaatt   | 1920 |
| cggggcttgc ctgtgtcagg caccaaaacg gctctcatgg accggcttcg acccttccag   | 1980 |
| gactgctctg gcaaccaggt gccgaacttt ggggatataa cgactgtcac ttttctgtc    | 2040 |
| acaccaaca cgctgccccaa ttaccagtct tcctcttcta ccagtgccct gtccaacggc   | 2100 |
| ttctaccact ttggcagcac cagctccagc ccccgatct cccagcctc ctctgacctg     | 2160 |
| tcagtcgctg ggtccctgcc ggacacctc aatgatgcct cccctcctt cggcctgcac     | 2220 |
| ccgtccccag tccacgtgtg cacggaggaa agtctcatga gcagcctgaa tgggggctct   | 2280 |
| gttccttctg agctggatgg gctggactcc gagaaggaca agatgctggt ggagaagcag   | 2340 |
| aaggatgatca atgaactcac ctggaaaactc cagcaagagc agaggcaggt ggaggagctg | 2400 |
| aggatgcagc ttcagaagca gaaaaggaat aactgttcag agaagaagcc gctgcctttc   | 2460 |
| ctggctgcct ccatcaagca ggaagaggct gtctccagct gtccttttgc atcccaagta   | 2520 |
| cctgtgaaaa gacaaagcag cagctcagag tgtcaccac cggttgtga agctgctcaa     | 2580 |

|                                                                      |      |
|----------------------------------------------------------------------|------|
| ctccagcctc ttggaaatgc tcattgtgtg gaggcctcag atcaaaccacaa tgtactttct  | 2640 |
| tccacatttc tcagcccccga gtgttccccct cagcattcac cgctggggggc tgtgaaaagc | 2700 |
| ccacagcaca tcagtttgcc cccatcaccc aacaaccctc actttctgcc ctcacctcc     | 2760 |
| ggggcccagg gagaaggga cagggtctcc tcgcccacac gcagccagggt gtgcactgca    | 2820 |
| cagaactcag gagcacacga tggccatcct ccaagcttct ctccccattc ttccagcctc    | 2880 |
| cacccgccct tctctggagc ccaagcagac agcagtcacg gtgccggggg aaacccttgt    | 2940 |
| cccaaaagcc catgtgtaca gcaaaagatg gctgggtttac actcttctga taagggtggg   | 3000 |
| ccaaagtgtt caattccatc cccaactttt tctaagtcaa gttcagcaat ttcagaggta    | 3060 |
| acacagcctc catcctatga agatgccgta aagcagcaaa tgacccggag tcagcagatg    | 3120 |
| gatgaactcc tggacgtgct tattgaaagc ggagaaatgc cagcagacgc tagagaggat    | 3180 |
| cactcatgtc ttcaaaaagt ccaaaagata cccagatctt cccgaagtcc aactgctgtc    | 3240 |
| ctcaccaagc cctcggcttc ctttgaacaa gcctcttcag gcagccagat cccctttgat    | 3300 |
| ccctatgccca ccgacagtga tgagcatctt gaagtcttat taaattccca gagcccccta   | 3360 |
| ggaaagatga gtgatgtcac ctttctaaaa attgggagcg aagagcctca ctttgatggg    | 3420 |
| ataatggatg gattctctgg gaaggctgca gaagacctct tcaatgcaca tgagatcttg    | 3480 |
| ccaggcccc tctctccaat gcagacacag ttttcaccct cttctgtgga cagcaatggg     | 3540 |
| ctgcagttaa gcttcactga atctccctgg gaaaccatgg agtggctgga cctcactccg    | 3600 |
| ccaaattcca caccaggctt tagcgccctc accaccagca gcccagcat cttcaacatc     | 3660 |
| gatttcctgg atgtcactga tctcaatttg aattcttcca tggaccttca cttgcagcag    | 3720 |
| tggtag                                                               | 3726 |

<210> 40

<211> 3744

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - synthesized MYF6-2A-MYOC construct

<400> 40

|                                                                     |      |
|---------------------------------------------------------------------|------|
| atgatgatgg accctttttga aactggctcc tatttcttct acttggatgg ggaaaatgtt  | 60   |
| actctgcagc cattagaagt ggcagaaggc tctcctttgt atccagggag tgatggtacc   | 120  |
| ttgtccccct gccaggacca aatgcccccg gaagcgggga gcgacagcag cggagaggaa   | 180  |
| catgtcctgg cgccccggg cctgcagcct ccacactgcc ccggccagtg tctgatctgg    | 240  |
| gcttgcaaga cctgcaagag aaaatctgcc cccactgacc ggcgaaaagc cgccaccctg   | 300  |
| cgcgaaagga ggaggctaaa gaaaatcaac gaggccttcg aggcactgaa gcggcgaaact  | 360  |
| gtggccaacc ccaaccagag gctgccaag gtggagattc tgcggagcgc catcagctat    | 420  |
| attgagcggc tgcaggacct gctgcaccgg ctggatcagc aggagaagat gcaggagctg   | 480  |
| ggggtggacc ccttcagcta cagacccaaa caagaaaatc ttgagggtgc ggatttcctg   | 540  |
| cgcacctgca gctcccagtg gccaagtgtt tccgatcatt ccagggggct cgtgataacg   | 600  |
| gctaaggaag gaggagcaag tattgattcg tcagcctcga gtagccttcg atgcctttct   | 660  |
| tccatcgtgg acagtatttc ctcggaggaa cgcaaaactcc cctgcgtgga ggaagtgggtg | 720  |
| gagaaggcca cgaacttctc tctgttaaag caagcaggag acgtggaaga aaaccccggt   | 780  |
| cctatgacac tcctggggtc tgagcattcc ttgctgatta ggagcaagtt cagatcagtt   | 840  |
| ttacagttaa gacttcaaca aagaaggacc caggaacaac tggctaacca aggcataata   | 900  |
| ccaccactga aacgtccagc tgaattccat gagcaaagaa aacatttgga tagtgacaag   | 960  |
| gctaaaaatt ccctgaagcg caaagccaga aacagggtgca acagtgccga cttggttaat  | 1020 |
| atgcacatac tccaagcttc cactgcagag aggtccattc caactgctca gatgaagctg   | 1080 |
| aaaagagccc gactcgccga tgatctcaat gaaaaaattg ctctacgacc aggccactg    | 1140 |
| gagctggtgg aaaaaaacat tcttcctgtg gattctgctg tgaaaagggc cataaaaggt   | 1200 |
| aaccagggtga gtttctccaa atccacggat gcttttgcct ttgaagagga cagcagcagc  | 1260 |
| gatgggcttt ctccggatca gactcgaagt gaagaccccc aaaactcagc gggatccccg   | 1320 |
| ccagacgcta aagcctcaga tacccttcg acaggttctc tggggacaaa ccaggatctt    | 1380 |
| gcttctggct cagaaaatga cagaaatgac tcagcctcac agcccagcca ccagtcagat   | 1440 |
| gcggggaagc aggggcttgg cccccccagc acccccatag ccgtgcatgc tgctgtaaag   | 1500 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tccaaatcct tgggtgacag taagaaccgc cacaaaaagc ccaaggaccc caagccaaag  | 1560 |
| gtgaagaagc ttaaatatca ccagtacatt ccccccagacc agaaggcaga gaagtcccct | 1620 |
| ccacctatgg actcagccta cgctcggctg ctccagcaac agcagctgtt cctgcagctc  | 1680 |
| caaatcctca gccagcagca gcagcagcag caacaccgat tcagctacct agggatgcac  | 1740 |
| caagctcagc ttaaggaacc aaatgaacag atggtcagaa atccaaactc ttcttcaacg  | 1800 |
| ccactgagca atacccccctt gtctcctgtc aaaaacagtt tttctggaca aactggtgtc | 1860 |
| tcttctttca aaccaggccc actcccacct aacctggatg atctgaaggc ctctgaatta  | 1920 |
| agacaacagc ttcgaattcg gggcttgctt gtgtcaggca ccaaaacggc tctcatggac  | 1980 |
| cggcttcgac ccttccagga ctgctctggc aaccagtgac cgaactttgg ggatataacg  | 2040 |
| actgtcactt ttcctgtcac acccaacacg ctgcccatt accagtcctt ctcttctacc   | 2100 |
| agtgccctgt ccaacggctt ctaccacttt ggcagcacca gctccagccc cccgatctcc  | 2160 |
| ccagcctcct ctgacctgtc agtcgctggg tccctgccgg acaccttcaa tgatgcctcc  | 2220 |
| ccctccttcg gcctgcaccc gtccccagtc cacgtgtgca cggaggaaaag tctcatgagc | 2280 |
| agcctgaatg ggggctctgt tccttctgag ctggatgggc tggactccga gaaggacaag  | 2340 |
| atgctggtgg agaagcagaa ggtgatcaat gaactcacct ggaaaactcca gcaagagcag | 2400 |
| aggcaggtgg aggagctgag gatgcagctt cagaagcaga aaaggaataa ctgttcagag  | 2460 |
| aagaagccgc tgcctttcct ggctgcctcc atcaagcagg aagaggctgt ctccagctgt  | 2520 |
| ccttttgcat cccaagtacc tgtgaaaaga caaagcagca gctcagagtg tcaccaccg   | 2580 |
| gcttgtgaag ctgctcaact ccagcctctt ggaaatgctc attgtgtgga gtcctcagat  | 2640 |
| caaaccaatg tactttcttc cacatttctc agccccagc gttccccctca gcattcaccg  | 2700 |
| ctgggggctg tgaaaagccc acagcacatc agtttgcccc catcacccaa caaccctcac  | 2760 |
| tttctgccct catcctccgg ggcccaggga gaagggcaca gggctctctc gcccatcagc  | 2820 |
| agccaggtgt gactgcaca gaactcagga gcacacgatg gccatcctcc aagcttctct   | 2880 |
| ccccattctt ccagcctcca cccgcccttc tctggagccc aagcagacag cagtcatggt  | 2940 |
| gccgggggaa acccttgtcc caaaagccca tgtgtacagc aaaagatggc tggtttacac  | 3000 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| tcttctgata aggtggggcc aaagttttca attccatccc caactttttc taagtcaagt | 3060 |
| tcagcaattt cagaggtaac acagcctcca tcctatgaag atgccgtaaa gcagcaaatg | 3120 |
| acccggagtc agcagatgga tgaactcctg gacgtgctta ttgaaagcgg agaaatgcca | 3180 |
| gcagacgcta gagaggatca ctcatgtctt caaaaagtcc caaagatacc cagatcttcc | 3240 |
| cgaagtccaa ctgctgtcct caccaagccc tcggcttcct ttgaacaagc ctcttcaggc | 3300 |
| agccagatcc cctttgatcc ctatgccacc gacagtgatg agcatcttga agtcttatta | 3360 |
| aattcccaga gccccctagg aaagatgagt gatgtcaccc ttctaataat tgggagcgaa | 3420 |
| gagcctcact ttgatgggat aatggatgga ttctctggga aggctgcaga agacctcttc | 3480 |
| aatgcacatg agatcttgcc aggccccctc tctccaatgc agacacagtt ttcaccctct | 3540 |
| tctgtggaca gcaatgggct gcagttaagc ttactgaat ctccctggga aaccatggag  | 3600 |
| tggctggacc tactccgcc aaattccaca ccaggcttta gcgccctcac caccagcagc  | 3660 |
| cccagcatct tcaacatcga tttcctggat gtcactgatc tcaatttgaa ttcttccatg | 3720 |
| gaccttcact tgcagcagtg gtag                                        | 3744 |

<210> 41  
 <211> 3114  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Made in Lab - synthesized ASCL1-2A-MyDelta3

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| <400> 41                                                          |     |
| atggaaagct ctgccaagat ggagagcggc ggcgccggcc agcagcccca gccgcagccc | 60  |
| cagcagccct tcctgccgcc cgcagcctgt ttctttgcca cggccgcagc cgcggcggcc | 120 |
| gcagccgccg cagcggcagc gcagagcgcg cagcagcagc agcagcagca gcagcagcag | 180 |
| cagcaggcgc cgcagctgag accggcggcc gacggccagc cctcaggggg cggtcacaag | 240 |
| tcagcgccca agcaagtcaa gcgacagcgc tcgtcttcgc ccgaactgat gcgctgcaaa | 300 |
| cgccggctca acttcagcgg ctttggctac agcctgccgc agcagcagcc ggccgccgtg | 360 |
| gcgcgccgca acgagcgcga gcgcaaccgc gtcaagttgg tcaacctggg ctttgccacc | 420 |

|                        |                        |                        |      |
|------------------------|------------------------|------------------------|------|
| cttcgggagc acgtcccca   | cggcgcggcc aacaagaaga  | tgagtaaggt ggagacactg  | 480  |
| cgctcggcgg tcgagtacat  | ccgcgcgctg cagcagctgc  | tggacgagca tgacgcggtg  | 540  |
| agcgccgcct tccaggcagg  | cgctcctgtcg cccaccatct | cccccaacta ctccaacgac  | 600  |
| ttgaactcca tggccggctc  | gccggtctca tcctactcgt  | cggacgaggg ctcttacgac  | 660  |
| ccgctcagcc ccgaggagca  | ggagcttctc gacttcacca  | actggttcgc cacgaacttc  | 720  |
| tctctgttaa agcaagcagg  | agacgtggaa gaaaaccccg  | gtcctatgac actcctgggg  | 780  |
| tctgagcatt ccttgctgat  | taggagcaag ttcagatcag  | ttttacagtt aagacttcaa  | 840  |
| caaagaagga cccaggaaca  | actggctaac caaggcataa  | taccaccact gaaacgtcca  | 900  |
| gctgaattcc atgagcaaa   | gaaaacatttg gatagtgaca | aggctaaaaa ttccctgaag  | 960  |
| cgcaaagcca gaaacagggt  | caacagtgcc gacttggtta  | atatgcacat actccaagct  | 1020 |
| tccactgcag agagggtccat | tccaactgct cagatgaagc  | tgaaaagagc ccgactcgcc  | 1080 |
| gatgatctca atgaaaaaat  | tgctctacga ccaggccac   | tggagctggg ggaaaaaac   | 1140 |
| attcttcctg tggattctgc  | tgtgaaagag gccataaaag  | gtaaccagggt gagtttctcc | 1200 |
| aaatccacgg atgcttttgc  | ctttgaagag gacagcagca  | gcgatgggct ttctccggat  | 1260 |
| cagactcgaa gtgaagaccc  | ccaaaactca gcgggatccc  | cgccagacgc taaagcctca  | 1320 |
| gatacccctt cgacagggttc | tctggggaca aaccaggatc  | ttgcttctgg ctcagaaaat  | 1380 |
| gacagaaatg actcagcctc  | acagcccagc caccagtcag  | atgcgggggaa gcaggggctt | 1440 |
| ggcccccca gcacccccat   | agccgtgcat gctgctgtaa  | agtccaaatc cttgggtgac  | 1500 |
| agtaagaacc gccacaaaaa  | gccaaggac cccaagccaa   | aggtgaagaa gcttaaatat  | 1560 |
| caccagtaca ttccccaga   | ccagaaggca gagaagtccc  | ctccacctat ggactcagcc  | 1620 |
| tacgctcggc tgctccagca  | acagcagctg ttcctgcagc  | tccaaatcct cagccagcag  | 1680 |
| cagcagcagc agcaacaccg  | attcagctac ctagggatgc  | accaagctca gcttaaggaa  | 1740 |
| ccaaatgaac agatggtcag  | aaatccaaac tcttcttcaa  | cgccactgag caatacccc   | 1800 |
| ttgtctcctg tcaaaaacag  | tttttctgga caaactgggt  | tctcttcttt caaaccaggc  | 1860 |
| ccactcccac ctaacctgga  | tgatctgaag gtctctgaat  | taagacaaca gcttcgaatt  | 1920 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| cggggcttgc ctgtgtcagg caccaaaacg gctctcatgg accggcttcg acccttccag  | 1980 |
| gactgctctg gcaacccagt gccgaacttt ggggatataa cgactgtcac ttttcctgtc  | 2040 |
| acaccaaca cgctgccccaa ttaccagtct tcctcttcta ccagtgccct gtccaacggc  | 2100 |
| ttctaccact ttggcagcac cagctccagc ccccgatct cccagcctc ctctgacctg    | 2160 |
| tcagtgcgtg ggtccctgcc ggacaccttc aatgatgcct cccctcctt cggcctgcac   | 2220 |
| ccgtccccag tccacgtgtg cacggaggaa agtctcatga gcagcctgaa tgggggctct  | 2280 |
| gttccttctg agctggatgg gctggactcc gagaaggaca agatgctggt ggagaagcag  | 2340 |
| aaggtgatca atgaactcac ctggaaaactc cagcaagagc agaggcaggt ggaggagctg | 2400 |
| aggatgcagc ttcagaagca gaaaaggaat aactgttcag aggaggtaac acagcctcca  | 2460 |
| tcctatgaag atgccgtaaa gcagcaaactg acccggagtc agcagatgga tgaactcctg | 2520 |
| gacgtgctta ttgaaagcgg agaaatgcca gcagacgcta gagaggatca ctcatgtctt  | 2580 |
| caaaaagtcc caaagatacc cagatcttcc cgaagtccaa ctgctgtcct caccaagccc  | 2640 |
| tcggcttcct ttgaacaagc ctcttcaggc agccagatcc cctttgatcc ctatgccacc  | 2700 |
| gacagtgatg agcatcttga agtcttatta aattcccaga gccccctagg aaagatgagt  | 2760 |
| gatgtcacc ttctaataaat tgggagcgaa gagcctcact ttgatgggat aatggatgga  | 2820 |
| ttctctggga aggctgcaga agacctcttc aatgcacatg agatcttgcc aggccccctc  | 2880 |
| tctccaatgc agacacagtt ttcacctct tctgtggaca gcaatgggct gcagttaagc   | 2940 |
| ttcactgaat ctccctggga aaccatggag tggctggacc tactccgcc aaattccaca   | 3000 |
| ccaggcttta gcgccctcac caccagcagc cccagcatct tcaacatcga tttcctggat  | 3060 |
| gtcactgatc tcaatttgaa ttcttccatg gaccttcact tgcagcagt gtag         | 3114 |

<210> 42

<211> 3132

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - synthesized MYF6-2A-MyDelta3 construct

<400> 42

|                                                                     |      |
|---------------------------------------------------------------------|------|
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| actctgcagc cattagaagt ggcagaaggc tctcctttgt atccaggaggag tgatggtacc | 120  |
| ttgtccccct gccaggacca aatgcccccg gaagcgggga gcgacagcag cggagaggaa   | 180  |
| catgtcctgg cgccccggg cctgcagcct ccacactgcc ccggccagtg tctgatctgg    | 240  |
| gcttgcaaga cctgcaagag aaaatctgcc cccactgacc ggcgaaaagc cgccaccctg   | 300  |
| cgcgaaagga ggaggctaaa gaaaatcaac gaggccttcg aggcactgaa gcggcgaact   | 360  |
| gtggccaacc ccaaccagag gctgccaag gtggagattc tgcggagcgc catcagctat    | 420  |
| attgagcggc tgcaggacct gctgcaccgg ctggatcagc aggagaagat gcaggagctg   | 480  |
| ggggtggacc ccttcagcta cagacccaaa caagaaaatc ttgagggtgc ggatttcctg   | 540  |
| cgcacctgca gctcccagtg gccaagtgtt tccgatcatt ccagggggct cgtgataacg   | 600  |
| gctaaggaag gaggagcaag tattgattcg tcagcctcga gtagccttcg atgcctttct   | 660  |
| tccatcgtgg acagtatttc ctcggaggaa cgcaaaactcc cctgcgtgga ggaagtgggtg | 720  |
| gagaaggcca cgaacttctc tctgttaaag caagcaggag acgtggaaga aaaccccggt   | 780  |
| cctatgacac tcctggggtc tgagcattcc ttgctgatta ggagcaagtt cagatcagtt   | 840  |
| ttacagttaa gacttcaaca aagaaggacc caggaacaac tggctaacca aggcataata   | 900  |
| ccaccactga aacgtccagc tgaattccat gagcaaagaa aacatttgga tagtgacaag   | 960  |
| gctaaaaatt ccctgaagcg caaagccaga aacagggtgca acagtgccga cttggttaat  | 1020 |
| atgcacatac tccaagcttc cactgcagag aggtccattc caactgctca gatgaagctg   | 1080 |
| aaaagagccc gactcgccga tgatctcaat gaaaaaattg ctctacgacc aggccactg    | 1140 |
| gagctggtgg aaaaaaacat tcttcctgtg gattctgctg tgaaaagggc cataaaaggt   | 1200 |
| aaccagggtga gtttctccaa atccacggat gcttttgcct ttgaagagga cagcagcagc  | 1260 |
| gatgggcttt ctccggatca gactcgaagt gaagaccccc aaaactcagc gggatccccg   | 1320 |
| ccagacgcta aagcctcaga tacccttcg acaggttctc tggggacaaa ccaggatctt    | 1380 |
| gcttctggct cagaaaatga cagaaatgac tcagcctcac agcccagcca ccagtcagat   | 1440 |
| gcggggaagc aggggcttgg cccccccagc acccccatag ccgtgcatgc tgctgtaaag   | 1500 |

|                                                                     |      |
|---------------------------------------------------------------------|------|
| tccaaatcct tgggtgacag taagaaccgc cacaaaaagc ccaaggaccc caagccaaag   | 1560 |
| gtgaagaagc ttaaatatca ccagtacatt ccccccagacc agaaggcaga gaagtcccct  | 1620 |
| ccacctatgg actcagccta cgctcggctg ctccagcaac agcagctgtt cctgcagctc   | 1680 |
| caaatcctca gccagcagca gcagcagcag caacaccgat tcagctacct agggatgcac   | 1740 |
| caagctcagc ttaaggaacc aaatgaacag atggtcagaa atccaaactc ttcttcaacg   | 1800 |
| ccactgagca atacccccctt gtctcctgtc aaaaacagtt tttctggaca aactgggtgtc | 1860 |
| tcttctttca aaccaggccc actcccacct aacctggatg atctgaagggt ctctgaatta  | 1920 |
| agacaacagc ttcgaattcg gggcttgctt gtgtcaggca ccaaaacggc tctcatggac   | 1980 |
| cggcttcgac ccttccagga ctgctctggc aaccagtgct cgaactttgg ggatataacg   | 2040 |
| actgtcactt ttcctgtcac acccaacacg ctgcccatt accagtcttc ctcttctacc    | 2100 |
| agtgccctgt ccaacggctt ctaccacttt ggcagcacca gctccagccc cccgatctcc   | 2160 |
| ccagcctcct ctgacctgtc agtcgctggg tccctgccgg acaccttcaa tgatgcctcc   | 2220 |
| ccctccttcg gcctgcaccc gtccccagtc cacgtgtgca cggaggaaaag tctcatgagc  | 2280 |
| agcctgaatg ggggctctgt tccttctgag ctggatgggc tggactccga gaaggacaag   | 2340 |
| atgctgggtg agaagcagaa ggtgatcaat gaactcacct ggaaaactcca gcaagagcag  | 2400 |
| aggcaggtgg aggagctgag gatgcagctt cagaagcaga aaaggaataa ctgttcagag   | 2460 |
| gaggtaacac agcctccatc ctatgaagat gccgtaaagc agcaaatgac ccggagtcag   | 2520 |
| cagatggatg aactcctgga cgtgcttatt gaaagcggag aaatgccagc agacgctaga   | 2580 |
| gaggatcact catgtcttca aaaagtccca aagataccca gatcttcccg aagtccaact   | 2640 |
| gctgtcctca ccaagccctc ggcttccttt gaacaagcct cttcaggcag ccagatcccc   | 2700 |
| tttgatccct atgccaccga cagtgatgag catcttgaag tcttattaaa ttcccagagc   | 2760 |
| cccctaggaa agatgagtga tgtcacctt ctaaaaaattg ggagcgaaga gcctcacttt   | 2820 |
| gatgggataa tggatggatt ctctgggaag gctgcagaag acctcttcaa tgcacatgag   | 2880 |
| atcttgccag gcccccttc tccaatgcag acacagtttt caccctcttc tgtggacagc    | 2940 |
| aatgggctgc agttaagctt cactgaatct ccctgggaaa ccatggagtg gctggacctc   | 3000 |

actccgccaa attccacacc aggctttagc gccctcacca ccagcagccc cagcatcttc 3060  
aacatcgatt tcctggatgt cactgatctc aatttgaatt cttccatgga ccttcacttg 3120  
cagcagtggg ag 3132

<210> 43  
<211> 287  
<212> PRT  
<213> Homo sapiens  
<400> 43

Met Ser Gly Ser Phe Asp Arg Lys Leu Ser Ser Ile Leu Thr Asp Ile  
1 5 10 15

Ser Ser Ser Leu Ser Cys His Ala Gly Ser Lys Asp Ser Pro Thr Leu  
20 25 30

Pro Glu Ser Ser Val Thr Asp Leu Gly Tyr Tyr Ser Ala Pro Gln His  
35 40 45

Asp Tyr Tyr Ser Gly Gln Pro Tyr Gly Gln Thr Val Asn Pro Tyr Thr  
50 55 60

Tyr His His Gln Phe Asn Leu Asn Gly Leu Ala Gly Thr Gly Ala Tyr  
65 70 75 80

Ser Pro Lys Ser Glu Tyr Thr Tyr Gly Ala Ser Tyr Arg Gln Tyr Gly  
85 90 95

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

Glu Glu Pro Glu Ala Glu Val Arg Met Val Asn Gly Lys Pro Lys Lys  
115 120 125

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

Gln Arg Arg Phe Gln Lys Ala Gln Tyr Leu Ala Leu Pro Glu Arg Ala  
 145 150 155 160

Glu Leu Ala Ala Gln Leu Gly Leu Thr Gln Thr Gln Val Lys Ile Trp  
 165 170 175

Phe Gln Asn Arg Arg Ser Lys Phe Lys Lys Leu Tyr Lys Asn Gly Glu  
 180 185 190

Val Pro Leu Glu His Ser Pro Asn Asn Ser Asp Ser Met Ala Cys Asn  
 195 200 205

Ser Pro Pro Ser Pro Ala Leu Trp Asp Thr Ser Ser His Ser Thr Pro  
 210 215 220

Ala Pro Ala Arg Ser Gln Leu Pro Pro Pro Leu Pro Tyr Ser Ala Ser  
 225 230 235 240

Pro Ser Tyr Leu Asp Asp Pro Thr Asn Ser Trp Tyr His Ala Gln Asn  
 245 250 255

Leu Ser Gly Pro His Leu Gln Gln Gln Pro Pro Gln Pro Ala Thr Leu  
 260 265 270

His His Ala Ser Pro Gly Pro Pro Pro Asn Pro Gly Ala Val Tyr  
 275 280 285

<210> 44  
 <211> 864  
 <212> DNA  
 <213> Homo sapiens

<400> 44  
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 agctgccatg cgggctccaa ggactcgcct accctgcccc agtcttctgt cactgacctg 120  
 ggctactaca gcgctcccca gcacgattac tactcggggc agccctatgg ccagacgggtg 180  
 aaccctaca cctaccacca ccaattcaat ctcaatgggc ttgcaggcac gggcgcttac 240

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| tcgccaagt cggaatatac ctacggagcc tcctaccggc aatacggggc gtatcgggag   | 300 |
| cagccgctgc cagcccagga cccagtgtcg gtgaaggagg agccggaagc agaggtgcgc  | 360 |
| atggtgaatg ggaagcccaa gaaggtccga aagccgcgta cgatctactc cagctaccag  | 420 |
| ctggccgccc tgcagcgccg cttccagaag gcccagtacc tggcgctgcc cgagcgcgcc  | 480 |
| gagctggccg cgcagctggg cctcacgcag acacaggtga aaatctgggtt ccagaaccgc | 540 |
| cgttccaagt tcaagaaact ctacaagaac ggggaggtgc cgctggagca cagtcccaat  | 600 |
| aacagtgatt ccatggcctg caactcacca ccatcaccgc ccctctggga cacctcttcc  | 660 |
| cactccactc cggcccctgc ccgcagtcag ctgccccgc cgctcccata cagtgcctcc   | 720 |
| cccagctacc tggacgaccc caccaactcc tggatatcacg cacagaacct gagtggaccc | 780 |
| cacttacagc agcagccgcc tcagccagcc accctgcacc atgcctctcc cgggcccccg  | 840 |
| cccaaccctg gggctgtgta ctga                                         | 864 |

<210> 45  
 <211> 293  
 <212> PRT  
 <213> Homo sapiens

<400> 45

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Thr | Met | Thr | Thr | Met | Ala | Asp | Gly | Leu | Glu | Gly | Gln | Asp | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Lys | Ser | Ala | Phe | Met | Glu | Phe | Gly | Gln | Gln | Gln | Gln | Gln | Gln | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Gln | Gln | Gln | Gln | Gln | Gln | Gln | Gln | Gln | Gln | Gln | Pro | Pro | Pro | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Pro | Pro | Pro | Pro | Gln | Pro | His | Ser | Gln | Gln | Ser | Ser | Pro | Ala | Met |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gly | Ala | His | Tyr | Pro | Leu | His | Cys | Leu | His | Ser | Ala | Ala | Ala | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

Ala Ala Ala Gly Ser His His His His His His Gln His His His His  
85 90 95

Gly Ser Pro Tyr Ala Ser Gly Gly Gly Asn Ser Tyr Asn His Arg Ser  
100 105 110

Leu Ala Ala Tyr Pro Tyr Met Ser His Ser Gln His Ser Pro Tyr Leu  
115 120 125

Gln Ser Tyr His Asn Ser Ser Ala Ala Ala Gln Thr Arg Gly Asp Asp  
130 135 140

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

Asn Gly Lys Gly Lys Lys Ile Arg Lys Pro Arg Thr Ile Tyr Ser Ser  
165 170 175

Leu Gln Leu Gln Ala Leu Asn His Arg Phe Gln Gln Thr Gln Tyr Leu  
180 185 190

Ala Leu Pro Glu Arg Ala Glu Leu Ala Ala Ser Leu Gly Leu Thr Gln  
195 200 205

Thr Gln Val Lys Ile Trp Phe Gln Asn Lys Arg Ser Lys Phe Lys Lys  
210 215 220

Leu Leu Lys Gln Gly Ser Asn Pro His Glu Ser Asp Pro Leu Gln Gly  
225 230 235 240

Ser Ala Ala Leu Ser Pro Arg Ser Pro Ala Leu Pro Pro Val Trp Asp  
245 250 255

Val Ser Ala Ser Ala Lys Gly Val Ser Met Pro Pro Asn Ser Tyr Met  
260 265 270

Pro Gly Tyr Ser His Trp Tyr Ser Ser Pro His Gln Asp Thr Met Gln

275

280

285

Arg Pro Gln Met Met  
290

&lt;210&gt; 46

&lt;211&gt; 882

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 46

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atgatgacca tgactacgat ggctgacggc ttggaaggcc aggactcgtc caaatccgcc      60
ttcatggagt tcgggcagca gcagcagcag cagcagcaac agcagcagca gcagcagcag      120
caacagcaac agccgccgcc gccgccgccg ccgccgccgc agccgcactc gcagcagagc      180
tccccggcca tggcaggcgc gcactaccct ctgcactgcc tgcactcggc ggccggcggcg      240
gcagcggccg gctcgcacca ccaccaccac caccagcacc accaccacgg ctcgccctac      300
gcgtcggggc gaggggaactc ctacaaccac cgctcgctcg ccgcctaccc ctacatgagc      360
cactcgcagc acagccctta cctccagtcc taccacaaca gcagcgcagc cgcccagacg      420
cgagggggacg acacagatca aaaaaaact acagtgattg aaaacgggga aatcagggttc      480
aatggaaaag ggaaaaagat tcggaagcct cggaccattht attccagcct gcagctccag      540
gcttttaaacc atcgctttca gcagacacag tatctggccc ttccagagag agccgaactg      600
gcagcttcct taggactgac acaaacacag gtgaagatat ggtttcagaa caaacgctct      660
aagtttaaga aactgctgaa gcagggcagt aatcctcatg agagcgaccc cctccagggc      720
tcggcggccc tgtcgccacg ctcgccagcg ctgcctccag tctgggacgt ttctgcctcg      780
gccaagggtg tcagtatgcc cccaacagc tacatgcctg gctatttctca ctggtactcc      840
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&lt;210&gt; 47

&lt;211&gt; 458

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 47

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

Glu Glu Glu Leu Leu Cys Arg Met Ser Asn Lys Asp Arg His Ile Asp  
20 25 30

Ser Ser Cys Ser Ser Phe Ile Lys Thr Glu Pro Ser Ser Pro Ala Ser  
35 40 45

Leu Thr Asp Ser Val Asn His His Ser Pro Gly Gly Ser Ser Asp Ala  
50 55 60

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

Ser Pro Pro Leu Tyr Pro Ser Ala Pro Ile Leu Gly Gly Ser Gly Pro  
85 90 95

Val Arg Lys Leu Tyr Asp Asp Cys Ser Ser Thr Ile Val Glu Asp Pro  
100 105 110

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

Leu Val Cys Gly Asp Ile Ala Ser Gly Tyr His Tyr Gly Val Ala Ser  
130 135 140

Cys Glu Ala Cys Lys Ala Phe Phe Lys Arg Thr Ile Gln Gly Asn Ile  
145 150 155 160

Glu Tyr Ser Cys Pro Ala Thr Asn Glu Cys Glu Ile Thr Lys Arg Arg  
165 170 175

Arg Lys Ser Cys Gln Ala Cys Arg Phe Met Lys Cys Leu Lys Val Gly  
180 185 190

Met Leu Lys Glu Gly Val Arg Leu Asp Arg Val Arg Gly Gly Arg Gln

195

200

205

Lys Tyr Lys Arg Arg Ile Asp Ala Glu Asn Ser Pro Tyr Leu Asn Pro  
 210 215 220

Gln Leu Val Gln Pro Ala Lys Lys Pro Tyr Asn Lys Ile Val Ser His  
 225 230 235 240

Leu Leu Val Ala Glu Pro Glu Lys Ile Tyr Ala Met Pro Asp Pro Thr  
 245 250 255

Val Pro Asp Ser Asp Ile Lys Ala Leu Thr Thr Leu Cys Asp Leu Ala  
 260 265 270

Asp Arg Glu Leu Val Val Ile Ile Gly Trp Ala Lys His Ile Pro Gly  
 275 280 285

Phe Ser Thr Leu Ser Leu Ala Asp Gln Met Ser Leu Leu Gln Ser Ala  
 290 295 300

Trp Met Glu Ile Leu Ile Leu Gly Val Val Tyr Arg Ser Leu Ser Phe  
 305 310 315 320

Glu Asp Glu Leu Val Tyr Ala Asp Asp Tyr Ile Met Asp Glu Asp Gln  
 325 330 335

Ser Lys Leu Ala Gly Leu Leu Asp Leu Asn Asn Ala Ile Leu Gln Leu  
 340 345 350

Val Lys Lys Tyr Lys Ser Met Lys Leu Glu Lys Glu Glu Phe Val Thr  
 355 360 365

Leu Lys Ala Ile Ala Leu Ala Asn Ser Asp Ser Met His Ile Glu Asp  
 370 375 380

Val Glu Ala Val Gln Lys Leu Gln Asp Val Leu His Glu Ala Leu Gln  
 385 390 395 400

Asp Tyr Glu Ala Gly Gln His Met Glu Asp Pro Arg Arg Ala Gly Lys  
405 410 415

Met Leu Met Thr Leu Pro Leu Leu Arg Gln Thr Ser Thr Lys Ala Val  
420 425 430

Gln His Phe Tyr Asn Ile Lys Leu Glu Gly Lys Val Pro Met His Lys  
435 440 445

Leu Phe Leu Glu Met Leu Glu Ala Lys Val  
450 455

<210> 48  
<211> 1377  
<212> DNA  
<213> Homo sapiens

<400> 48  
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acggaacctt ccagcccagc ctccctgacg gacagcgtca accaccacag ccctgggtggc 180  
tcttcagacg ccagtgggag ctacagttca accatgaatg gccatcagaa cggacttgac 240  
tcgccacctc tctacccttc tgctcctatc ctgggaggta gtgggcctgt caggaaactg 300  
tatgatgact gctccagcac cattgttgaa gatccccaga ccaagtgtga atacatgctc 360  
aactcgatgc ccaagagact gtgttttagtg tgtgggtgaca tcgcttctgg gtaccactat 420  
ggggtagcat catgtgaagc ctgcaaggca ttcttcaaga ggacaattca aggcaatata 480  
gaatacagct gccctgccac gaatgaatgt gaaatcacaa agcgcagacg taaatcctgc 540  
caggcttgcc gcttcatgaa gtgttttaaaa gtgggcatgc tgaaagaagg ggtgcgtctt 600  
gacagagtac gtggaggctg gcagaagtac aagcgcagga tagatgcgga gaacagccca 660  
tacctgaacc ctgagctggg tcagccagcc aaaaagccat ataacaagat tgtctcacat 720  
ttgttggtgg ctgaaccgga gaagatctat gccatgcctg accctactgt ccccgacagt 780  
gacatcaaag ccctcactac actgtgtgac ttggccgacc gagagtgggt ggttatcatt 840

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ggatgggcga agcatattcc aggcttctcc acgctgtccc tggcggacca gatgagcctt      900
ctgcagagtg cttggatgga aattttgatc cttggtgtcg tataccgggtc tctttcgttt      960
gaggatgaac ttgtctatgc agacgattat ataatggacg aagaccagtc caaattagca      1020
ggccttcttg atctaaataa tgctatcctg cagctggtaa agaaatacaa gagcatgaag      1080
ctggaaaaaag aagaatttgt caccctcaaa gctatagctc ttgctaattc agactccatg      1140
cacatagaag atgttgaagc cgttcagaag cttcaggatg tcttacatga agcgctgcag      1200
gattatgaag ctggccagca catggaagac cctcgtcgag ctggcaagat gctgatgaca      1260
ctgccactcc tgaggcagac ctctaccaag gccgtgcagc atttctacaa catcaaacta      1320
gaaggcaaag tcccaatgca caaacttttt ttggaaatgt tggaggccaa ggtctga      1377

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<210> 49
<211> 480
<212> PRT
<213> Homo sapiens

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<400> 49

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Met Glu Val Ala Pro Glu Gln Pro Arg Trp Met Ala His Pro Ala Val
1           5           10          15

```

```

Leu Asn Ala Gln His Pro Asp Ser His His Pro Gly Leu Ala His Asn
20          25          30

```

```

Tyr Met Glu Pro Ala Gln Leu Leu Pro Pro Asp Glu Val Asp Val Phe
35          40          45

```

```

Phe Asn His Leu Asp Ser Gln Gly Asn Pro Tyr Tyr Ala Asn Pro Ala
50          55          60

```

```

His Ala Arg Ala Arg Val Ser Tyr Ser Pro Ala His Ala Arg Leu Thr
65          70          75          80

```

```

Gly Gly Gln Met Cys Arg Pro His Leu Leu His Ser Pro Gly Leu Pro
85          90          95

```

Trp Leu Asp Gly Gly Lys Ala Ala Leu Ser Ala Ala Ala Ala His His  
100 105 110

His Asn Pro Trp Thr Val Ser Pro Phe Ser Lys Thr Pro Leu His Pro  
115 120 125

Ser Ala Ala Gly Gly Pro Gly Gly Pro Leu Ser Val Tyr Pro Gly Ala  
130 135 140

Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Ser Val Ala Ser Leu Thr  
145 150 155 160

Pro Thr Ala Ala His Ser Gly Ser His Leu Phe Gly Phe Pro Pro Thr  
165 170 175

Pro Pro Lys Glu Val Ser Pro Asp Pro Ser Thr Thr Gly Ala Ala Ser  
180 185 190

Pro Ala Ser Ser Ser Ala Gly Gly Ser Ala Ala Arg Gly Glu Asp Lys  
195 200 205

Asp Gly Val Lys Tyr Gln Val Ser Leu Thr Glu Ser Met Lys Met Glu  
210 215 220

Ser Gly Ser Pro Leu Arg Pro Gly Leu Ala Thr Met Gly Thr Gln Pro  
225 230 235 240

Ala Thr His His Pro Ile Pro Thr Tyr Pro Ser Tyr Val Pro Ala Ala  
245 250 255

Ala His Asp Tyr Ser Ser Gly Leu Phe His Pro Gly Gly Phe Leu Gly  
260 265 270

Gly Pro Ala Ser Ser Phe Thr Pro Lys Gln Arg Ser Lys Ala Arg Ser  
275 280 285

Cys Ser Glu Gly Arg Glu Cys Val Asn Cys Gly Ala Thr Ala Thr Pro

290

295

300

Leu Trp Arg Arg Asp Gly Thr Gly His Tyr Leu Cys Asn Ala Cys Gly  
 305 310 315 320

Leu Tyr His Lys Met Asn Gly Gln Asn Arg Pro Leu Ile Lys Pro Lys  
 325 330 335

Arg Arg Leu Ser Ala Ala Arg Arg Ala Gly Thr Cys Cys Ala Asn Cys  
 340 345 350

Gln Thr Thr Thr Thr Thr Leu Trp Arg Arg Asn Ala Asn Gly Asp Pro  
 355 360 365

Val Cys Asn Ala Cys Gly Leu Tyr Tyr Lys Leu His Asn Val Asn Arg  
 370 375 380

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

Ser Asn Lys Ser Lys Lys Ser Lys Lys Gly Ala Glu Cys Phe Glu Glu  
 405 410 415

Leu Ser Lys Cys Met Gln Glu Lys Ser Ser Pro Phe Ser Ala Ala Ala  
 420 425 430

Leu Ala Gly His Met Ala Pro Val Gly His Leu Pro Pro Phe Ser His  
 435 440 445

Ser Gly His Ile Leu Pro Thr Pro Thr Pro Ile His Pro Ser Ser Ser  
 450 455 460

Leu Ser Phe Gly His Pro His Pro Ser Ser Met Val Thr Ala Met Gly  
 465 470 475 480

&lt;210&gt; 50

&lt;211&gt; 1443

&lt;212&gt; DNA

<213> Homo sapiens

<400> 50

|                                                                    |      |
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| atggaggtgg cgcccagca gccgcgctgg atggcgcacc cggccgtgct gaatgcgcag   | 60   |
| caccccgact cacaccaccc gggcctggcg cacaactaca tggaacccgc gcagctgctg  | 120  |
| cctccagacg aggtggacgt cttcttcaat cacctcgact cgcagggcaa cccctactat  | 180  |
| gccaacccccg ctcacgcgcg ggcgcgcgtc tcctacagcc ccgcgcacgc ccgcctgacc | 240  |
| ggaggccaga tgtgccgccc acacttgttg cacagcccgg gtttgccctg gctggacggg  | 300  |
| ggcaaagcag ccctctctgc cgctgcggcc caccaccaca acccctggac cgtgagcccc  | 360  |
| ttctccaaga cgccactgca cccctcagct gctggaggcc ctggaggccc actctctgtg  | 420  |
| tacccagggg ctgggggtgg gagcggggga ggagcggga gctcagtggc ctccctcacc   | 480  |
| cctacagcag cccactctgg ctcccacctt ttcggcttcc caccacgcc acccaaagaa   | 540  |
| gtgtctcctg accctagcac cacgggggct gcgtctccag cctcatcttc cgcggggggt  | 600  |
| agtgcagccc gaggagagga caaggacggc gtcaagtacc aggtgtcact gacggagagc  | 660  |
| atgaagatgg aaagtggcag tcccctgcgc ccaggcctag ctactatggg caccagcct   | 720  |
| gctacacacc accccatccc cacctacccc tcctatgtgc cggcggctgc ccacgactac  | 780  |
| agcagcggac tcttccaccc cggaggcttc ctggggggac cggcctccag cttcacccct  | 840  |
| aagcagcgca gcaaggctcg ttcctgttca gaaggccggg agtgtgtcaa ctgtggggcc  | 900  |
| acagccaccc ctctctggcg gcgggacggc accggccact acctgtgcaa tgcctgtggc  | 960  |
| ctctaccaca agatgaatgg gcagaaccga ccactcatca agcccaagcg aagactgtcg  | 1020 |
| gccgccagaa gagccggcac ctgttggtgca aattgtcaga cgacaaccac caccttatgg | 1080 |
| cgccgaaacg ccaacgggga ccctgtctgc aacgcctgtg gcctctacta caagctgcac  | 1140 |
| aatgttaaca ggccactgac catgaagaag gaagggatcc agactcggaa ccggaagatg  | 1200 |
| tccaacaagt ccaagaagag caagaaaggg gcggagtgtc tcgaggagct gtcaaagtgc  | 1260 |
| atgcaggaga agtcatcccc cttcagtgc gctgccctgg ctggacacat ggcacctgtg   | 1320 |
| ggccacctcc cgcccttcag ccactccgga cacatcctgc ccactccgac gcccattcac  | 1380 |
| ccctcctcca gcctctcctt cggccacccc caccgtcca gcatggtgac cgccatgggc   | 1440 |

tag

1443

<210> 51  
<211> 443  
<212> PRT  
<213> Homo sapiens

<400> 51

Met Tyr Gln Ser Leu Ala Met Ala Ala Asn His Gly Pro Pro Pro Gly  
1 5 10 15

Ala Tyr Glu Ala Gly Gly Pro Gly Ala Phe Met His Gly Ala Gly Ala  
20 25 30

Ala Ser Ser Pro Val Tyr Val Pro Thr Pro Arg Val Pro Ser Ser Val  
35 40 45

Leu Gly Leu Ser Tyr Leu Gln Gly Gly Gly Ala Gly Ser Ala Ser Gly  
50 55 60

Gly Ala Ser Gly Gly Ser Ser Gly Gly Ala Ala Ser Gly Ala Gly Pro  
65 70 75 80

Gly Thr Gln Gln Gly Ser Pro Gly Trp Ser Gln Ala Gly Ala Asp Gly  
85 90 95

Ala Ala Tyr Thr Pro Pro Pro Val Ser Pro Arg Phe Ser Phe Pro Gly  
100 105 110

Thr Thr Gly Ser Leu Ala Ala Ala Ala Ala Ala Ala Ala Arg Glu  
115 120 125

Ala Ala Ala Tyr Ser Ser Gly Gly Gly Ala Ala Gly Ala Gly Leu Ala  
130 135 140

Gly Arg Glu Gln Tyr Gly Arg Ala Gly Phe Ala Gly Ser Tyr Ser Ser  
145 150 155 160

Pro Tyr Pro Ala Tyr Met Ala Asp Val Gly Ala Ser Trp Ala Ala Ala  
165 170 175

Ala Ala Ala Ser Ala Gly Pro Phe Asp Ser Pro Val Leu His Ser Leu  
180 185 190

Pro Gly Arg Ala Asn Pro Ala Ala Arg His Pro Asn Leu Val Asp Met  
195 200 205

Phe Asp Asp Phe Ser Glu Gly Arg Glu Cys Val Asn Cys Gly Ala Met  
210 215 220

Ser Thr Pro Leu Trp Arg Arg Asp Gly Thr Gly His Tyr Leu Cys Asn  
225 230 235 240

Ala Cys Gly Leu Tyr His Lys Met Asn Gly Ile Asn Arg Pro Leu Ile  
245 250 255

Lys Pro Gln Arg Arg Leu Ser Ala Ser Arg Arg Val Gly Leu Ser Cys  
260 265 270

Ala Asn Cys Gln Thr Thr Thr Thr Thr Leu Trp Arg Arg Asn Ala Glu  
275 280 285

Gly Glu Pro Val Cys Asn Ala Cys Gly Leu Tyr Met Lys Leu His Gly  
290 295 300

Val Pro Arg Pro Leu Ala Met Arg Lys Glu Gly Ile Gln Thr Arg Lys  
305 310 315 320

Arg Lys Pro Lys Asn Leu Asn Lys Ser Lys Thr Pro Ala Ala Pro Ser  
325 330 335

Gly Ser Glu Ser Leu Pro Pro Ala Ser Gly Ala Ser Ser Asn Ser Ser  
340 345 350

Asn Ala Thr Thr Ser Ser Ser Glu Glu Met Arg Pro Ile Lys Thr Glu

355

360

365

Pro Gly Leu Ser Ser His Tyr Gly His Ser Ser Ser Val Ser Gln Thr  
 370 375 380

Phe Ser Val Ser Ala Met Ser Gly His Gly Pro Ser Ile His Pro Val  
 385 390 395 400

Leu Ser Ala Leu Lys Leu Ser Pro Gln Gly Tyr Ala Ser Pro Val Ser  
 405 410 415

Gln Ser Pro Gln Thr Ser Ser Lys Gln Asp Ser Trp Asn Ser Leu Val  
 420 425 430

Leu Ala Asp Ser His Gly Asp Ile Ile Thr Ala  
 435 440

<210> 52  
 <211> 1332  
 <212> DNA  
 <213> Homo sapiens

<400> 52  
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 acaccgcggg tgccctcctc cgtgctgggc ctgtcctacc tccagggcgg aggcgcgggc 180  
 tctgcgtccg gaggcgcctc gggcggcagc tccggtgggg ccgctctgg tgcggggccc 240  
 gggacccagc agggcagccc gggatggagc caggcgggag ccgacggagc cgcttacacc 300  
 ccgccgccgg tgtcgccgcg cttctccttc ccggggacca ccgggtccct ggcggccgcc 360  
 gccgccgctg ccgcggcccc ggaagctgcg gcctacagca gtggcgggcg agcggcgggt 420  
 gcgggcctgg cgggccgcga gcagtacggg cgcgccggct tcgcgggctc ctactccagc 480  
 ccctacccgg cttacatggc cgacgtgggc gctcctggg ccgcagccgc cgccgcctcc 540  
 gccggccccct tcgacagccc ggtcctgcac agcctgcccc gccgggcca cccggccgcc 600  
 cgacacccca atctcgtaga tatgtttgac gacttctcag aaggcagaga gtgtgtcaac 660

|                                                                     |      |
|---------------------------------------------------------------------|------|
| tgtggggcta tgtccacccc gctctggagg cgagatggga cgggtcacta tctgtgcaac   | 720  |
| gcctgcggcc tctaccacaa gatgaacggc atcaaccggc cgctcatcaa gcctcagcgc   | 780  |
| cggctgtccg cctcccgcg agtgggcctc tcctgtgcca actgccagac caccaccacc    | 840  |
| acgctgtggc gccgcaatgc ggagggcgag cctgtgtgca atgcctgcgg cctctacatg   | 900  |
| aagctccacg ggggtccccag gcctcttgca atgcggaaaag aggggatcca aaccagaaaa | 960  |
| cggaagccca agaacctgaa taaatctaag acaccagcag ctcccttcagg cagtgagagc  | 1020 |
| cttcctcccg ccagcgggtgc ttccagcaac tccagcaacg ccaccaccag cagcagcgag  | 1080 |
| gagatgcgtc ccatcaagac ggagcctggc ctgtcatctc actacgggca cagcagctcc   | 1140 |
| gtgtcccaga cgttctcagt cagtgcgatg tctggccatg ggccctccat ccaccctgtc   | 1200 |
| ctctcggccc tgaagctctc cccacaaggc tatgcgtctc ccgtcagcca gtctccacag   | 1260 |
| accagctcca agcaggactc ttggaacagc ctggctcttg ccgacagtca cggggacata   | 1320 |
| atcactgcgt aa                                                       | 1332 |

<210> 53  
 <211> 268  
 <212> PRT  
 <213> Homo sapiens

<400> 53

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gln | Pro | Leu | Cys | Pro | Pro | Leu | Ser | Glu | Ser | Trp | Met | Leu | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ala | Trp | Gly | Pro | Thr | Arg | Arg | Pro | Pro | Pro | Ser | Asp | Lys | Asp | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Arg | Ser | Leu | Val | Ser | Ser | Pro | Asp | Ser | Trp | Gly | Ser | Thr | Pro | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ser | Pro | Val | Ala | Ser | Pro | Ala | Arg | Pro | Gly | Thr | Leu | Arg | Asp | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ala | Pro | Ser | Val | Gly | Arg | Arg | Gly | Ala | Arg | Ser | Ser | Arg | Leu | Gly |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |
| Ser | Gly | Gln | Arg | Gln | Ser | Ala | Ser | Glu | Arg | Glu | Lys | Leu | Arg | Met | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Leu | Ala | Arg | Ala | Leu | His | Glu | Leu | Arg | Arg | Phe | Leu | Pro | Pro | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Ala | Pro | Ala | Gly | Gln | Ser | Leu | Thr | Lys | Ile | Glu | Thr | Leu | Arg | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Ile | Arg | Tyr | Ile | Gly | His | Leu | Ser | Ala | Val | Leu | Gly | Leu | Ser | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Ser | Leu | Gln | Arg | Arg | Cys | Arg | Gln | Arg | Gly | Asp | Ala | Gly | Ser | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg | Gly | Cys | Pro | Leu | Cys | Pro | Asp | Asp | Cys | Pro | Ala | Gln | Met | Gln | Thr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Thr | Gln | Ala | Glu | Gly | Gln | Gly | Gln | Gly | Arg | Gly | Leu | Gly | Leu | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Ala | Val | Arg | Ala | Gly | Ala | Ser | Trp | Gly | Ser | Pro | Pro | Ala | Cys | Pro |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Ala | Arg | Ala | Ala | Pro | Glu | Pro | Arg | Asp | Pro | Pro | Ala | Leu | Phe | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Glu | Ala | Ala | Cys | Pro | Glu | Gly | Gln | Ala | Met | Glu | Pro | Ser | Pro | Pro | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Pro | Leu | Leu | Pro | Gly | Asp | Val | Leu | Ala | Leu | Leu | Glu | Thr | Trp | Met | Pro |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Ser | Pro | Leu | Glu | Trp | Leu | Pro | Glu | Glu | Pro | Lys |     |     |     |     |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     |     |     |

<210> 54  
<211> 807  
<212> DNA  
<213> Homo sapiens

<400> 54  
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gactcatggg gcagcacccc agccgacagc cccgtggcga gccccgcgcg gccaggcacc 180  
ctccgggacc cccgcgcccc ctccgtaggt aggcgcggcg cgcgcagcag ccgcctgggc 240  
agcgggcaga ggagagcgc cagtgcggcg gagaaactgc gcatgcgcac gctggccccg 300  
gccctgcacg agctgcgcgc ctttctaccg ccgtccgtgg cggccgcggg ccagagcctg 360  
accaagatcg agacgctgcg cctggctatc cgctatatcg gccacctgtc ggccgtgcta 420  
ggcctcagcg aggagagtct ccagcgccgg tgccggcagc gcggtgacgc ggggtcccct 480  
cggggctgcc cgctgtgccc cgacgactgc cccgcgcaga tgcagacacg gacgcaggct 540  
gaggggcagg ggagggggcg cgggctgggc ctggatatccg ccgtccgcgc cggggcgctc 600  
tggggatccc cgcctgcctg ccccgagacc cgagctgcac ccgagccgcg cgacccgcct 660  
gcgctgttcg ccgaggcggc gtgccctgaa gggcaggcga tggagccaag cccaccgtcc 720  
ccgctccttc cgggcgacgt gctggctctg ttggagacct ggatgcccct ctcgcctctg 780  
gagtggtctg ctgaggagcc caagtga 807

<210> 55  
<211> 242  
<212> PRT  
<213> Homo sapiens

<400> 55

Met Met Met Asp Leu Phe Glu Thr Gly Ser Tyr Phe Phe Tyr Leu Asp  
1 5 10 15

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

Leu Tyr Pro Gly Ser Asp Gly Thr Leu Ser Pro Cys Gln Asp Gln Met  
35 40 45

Pro Pro Glu Ala Gly Ser Asp Ser Ser Gly Glu Glu His Val Leu Ala  
50 55 60

Pro Pro Gly Leu Gln Pro Pro His Cys Pro Gly Gln Cys Leu Ile Trp  
65 70 75 80

Ala Cys Lys Thr Cys Lys Arg Lys Ser Ala Pro Thr Asp Arg Arg Lys  
85 90 95

Ala Ala Thr Leu Arg Glu Arg Arg Arg Leu Lys Lys Ile Asn Glu Ala  
100 105 110

Phe Glu Ala Leu Lys Arg Arg Thr Val Ala Asn Pro Asn Gln Arg Leu  
115 120 125

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

Gln Asp Leu Leu His Arg Leu Asp Gln Gln Glu Lys Met Gln Glu Leu  
145 150 155 160

Gly Val Asp Pro Phe Ser Tyr Arg Pro Lys Gln Glu Asn Leu Glu Gly  
165 170 175

Ala Asp Phe Leu Arg Thr Cys Ser Ser Gln Trp Pro Ser Val Ser Asp  
180 185 190

His Ser Arg Gly Leu Val Ile Thr Ala Lys Glu Gly Gly Ala Ser Ile  
195 200 205

Asp Ser Ser Ala Ser Ser Ser Leu Arg Cys Leu Ser Ser Ile Val Asp  
210 215 220

Ser Ile Ser Ser Glu Glu Arg Lys Leu Pro Cys Val Glu Glu Val Val

225

230

235

240

Glu Lys

&lt;210&gt; 56

&lt;211&gt; 729

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 56

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actctgcagc cattagaagt ggcagaaggc tctcctttgt atccaggaggag tgatggtacc 120

ttgtccccct gccaggacca aatgcccccg gaagcggggga gcgacagcag cggagaggaa 180

catgtcctgg cgccccggg cctgcagcct ccacactgcc ccggccagtg tctgatctgg 240

gcttgcaaga cctgcaagag aaaatctgcc ccactgacc ggcgaaaagc cgccaccctg 300

cgcgaaaagga ggaggctaaa gaaaatcaac gaggccttcg aggactgaa gcggcgaaact 360

gtggccaacc ccaaccagag gctgccaag gtggagattc tgcggagcgc catcagctat 420

attgagcggc tgcaggacct gctgcaccgg ctggatcagc aggagaagat gcaggagctg 480

ggggtggacc ccttcagcta cagacccaaa caagaaaatc ttgagggtgc ggatttcctg 540

cgcacctgca gctcccagtg gccaaagtgt tccgatcatt ccaggggggct cgtgataacg 600

gctaaggaag gaggagcaag tattgattcg tcagcctcga gtagccttcg atgcctttct 660

tccatcgtgg acagtatttc ctcggaggaa cgcaaactcc cctgcgtgga ggaagtgggtg 720

gagaagtaa 729

&lt;210&gt; 57

&lt;211&gt; 1241

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in Lab - synthesized MYOCD-2A-ASCL1 construct

&lt;400&gt; 57

Met Thr Leu Leu Gly Ser Glu His Ser Leu Leu Ile Arg Ser Lys Phe  
1 5 10 15

Arg Ser Val Leu Gln Leu Arg Leu Gln Gln Arg Arg Thr Gln Glu Gln  
20 25 30

Leu Ala Asn Gln Gly Ile Ile Pro Pro Leu Lys Arg Pro Ala Glu Phe  
35 40 45

His Glu Gln Arg Lys His Leu Asp Ser Asp Lys Ala Lys Asn Ser Leu  
50 55 60

Lys Arg Lys Ala Arg Asn Arg Cys Asn Ser Ala Asp Leu Val Asn Met  
65 70 75 80

His Ile Leu Gln Ala Ser Thr Ala Glu Arg Ser Ile Pro Thr Ala Gln  
85 90 95

Met Lys Leu Lys Arg Ala Arg Leu Ala Asp Asp Leu Asn Glu Lys Ile  
100 105 110

Ala Leu Arg Pro Gly Pro Leu Glu Leu Val Glu Lys Asn Ile Leu Pro  
115 120 125

Val Asp Ser Ala Val Lys Glu Ala Ile Lys Gly Asn Gln Val Ser Phe  
130 135 140

Ser Lys Ser Thr Asp Ala Phe Ala Phe Glu Glu Asp Ser Ser Ser Asp  
145 150 155 160

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

Gly Ser Pro Pro Asp Ala Lys Ala Ser Asp Thr Pro Ser Thr Gly Ser  
180 185 190

Leu Gly Thr Asn Gln Asp Leu Ala Ser Gly Ser Glu Asn Asp Arg Asn  
195 200 205

Asp Ser Ala Ser Gln Pro Ser His Gln Ser Asp Ala Gly Lys Gln Gly  
210 215 220

Leu Gly Pro Pro Ser Thr Pro Ile Ala Val His Ala Ala Val Lys Ser  
225 230 235 240

Lys Ser Leu Gly Asp Ser Lys Asn Arg His Lys Lys Pro Lys Asp Pro  
245 250 255

Lys Pro Lys Val Lys Lys Leu Lys Tyr His Gln Tyr Ile Pro Pro Asp  
260 265 270

Gln Lys Ala Glu Lys Ser Pro Pro Pro Met Asp Ser Ala Tyr Ala Arg  
275 280 285

Leu Leu Gln Gln Gln Gln Leu Phe Leu Gln Leu Gln Ile Leu Ser Gln  
290 295 300

Gln Gln Gln Gln Gln Gln His Arg Phe Ser Tyr Leu Gly Met His Gln  
305 310 315 320

Ala Gln Leu Lys Glu Pro Asn Glu Gln Met Val Arg Asn Pro Asn Ser  
325 330 335

Ser Ser Thr Pro Leu Ser Asn Thr Pro Leu Ser Pro Val Lys Asn Ser  
340 345 350

Phe Ser Gly Gln Thr Gly Val Ser Ser Phe Lys Pro Gly Pro Leu Pro  
355 360 365

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

Ile Arg Gly Leu Pro Val Ser Gly Thr Lys Thr Ala Leu Met Asp Arg  
385 390 395 400

Leu Arg Pro Phe Gln Asp Cys Ser Gly Asn Pro Val Pro Asn Phe Gly  
405 410 415

Asp Ile Thr Thr Val Thr Phe Pro Val Thr Pro Asn Thr Leu Pro Asn  
420 425 430

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

Phe Gly Ser Thr Ser Ser Ser Pro Pro Ile Ser Pro Ala Ser Ser Asp  
450 455 460

Leu Ser Val Ala Gly Ser Leu Pro Asp Thr Phe Asn Asp Ala Ser Pro  
465 470 475 480

Ser Phe Gly Leu His Pro Ser Pro Val His Val Cys Thr Glu Glu Ser  
485 490 495

Leu Met Ser Ser Leu Asn Gly Gly Ser Val Pro Ser Glu Leu Asp Gly  
500 505 510

Leu Asp Ser Glu Lys Asp Lys Met Leu Val Glu Lys Gln Lys Val Ile  
515 520 525

Asn Glu Leu Thr Trp Lys Leu Gln Gln Glu Gln Arg Gln Val Glu Glu  
530 535 540

Leu Arg Met Gln Leu Gln Lys Gln Lys Arg Asn Asn Cys Ser Glu Lys  
545 550 555 560

Lys Pro Leu Pro Phe Leu Ala Ala Ser Ile Lys Gln Glu Glu Ala Val  
565 570 575

Ser Ser Cys Pro Phe Ala Ser Gln Val Pro Val Lys Arg Gln Ser Ser  
580 585 590

Ser Ser Glu Cys His Pro Pro Ala Cys Glu Ala Ala Gln Leu Gln Pro  
595 600 605

Leu Gly Asn Ala His Cys Val Glu Ser Ser Asp Gln Thr Asn Val Leu  
610 615 620

Ser Ser Thr Phe Leu Ser Pro Gln Cys Ser Pro Gln His Ser Pro Leu  
625 630 635 640

Gly Ala Val Lys Ser Pro Gln His Ile Ser Leu Pro Pro Ser Pro Asn  
645 650 655

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

Arg Val Ser Ser Pro Ile Ser Ser Gln Val Cys Thr Ala Gln Asn Ser  
675 680 685

Gly Ala His Asp Gly His Pro Pro Ser Phe Ser Pro His Ser Ser Ser  
690 695 700

Leu His Pro Pro Phe Ser Gly Ala Gln Ala Asp Ser Ser His Gly Ala  
705 710 715 720

Gly Gly Asn Pro Cys Pro Lys Ser Pro Cys Val Gln Gln Lys Met Ala  
725 730 735

Gly Leu His Ser Ser Asp Lys Val Gly Pro Lys Phe Ser Ile Pro Ser  
740 745 750

Pro Thr Phe Ser Lys Ser Ser Ser Ala Ile Ser Glu Val Thr Gln Pro  
755 760 765

Pro Ser Tyr Glu Asp Ala Val Lys Gln Gln Met Thr Arg Ser Gln Gln  
770 775 780

Met Asp Glu Leu Leu Asp Val Leu Ile Glu Ser Gly Glu Met Pro Ala  
785 790 795 800

Asp Ala Arg Glu Asp His Ser Cys Leu Gln Lys Val Pro Lys Ile Pro  
805 810 815

Arg Ser Ser Arg Ser Pro Thr Ala Val Leu Thr Lys Pro Ser Ala Ser  
820 825 830

Phe Glu Gln Ala Ser Ser Gly Ser Gln Ile Pro Phe Asp Pro Tyr Ala  
835 840 845

Thr Asp Ser Asp Glu His Leu Glu Val Leu Leu Asn Ser Gln Ser Pro  
850 855 860

Leu Gly Lys Met Ser Asp Val Thr Leu Leu Lys Ile Gly Ser Glu Glu  
865 870 875 880

Pro His Phe Asp Gly Ile Met Asp Gly Phe Ser Gly Lys Ala Ala Glu  
885 890 895

Asp Leu Phe Asn Ala His Glu Ile Leu Pro Gly Pro Leu Ser Pro Met  
900 905 910

Gln Thr Gln Phe Ser Pro Ser Ser Val Asp Ser Asn Gly Leu Gln Leu  
915 920 925

Ser Phe Thr Glu Ser Pro Trp Glu Thr Met Glu Trp Leu Asp Leu Thr  
930 935 940

Pro Pro Asn Ser Thr Pro Gly Phe Ser Ala Leu Thr Thr Ser Ser Pro  
945 950 955 960

Ser Ile Phe Asn Ile Asp Phe Leu Asp Val Thr Asp Leu Asn Leu Asn  
965 970 975

Ser Ser Met Asp Leu His Leu Gln Gln Trp Ala Thr Asn Phe Ser Leu  
980 985 990

Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Ser  
995 1000 1005

Ser Ala Lys Met Glu Ser Gly Gly Ala Gly Gln Gln Pro Gln Pro  
1010 1015 1020

Gln Pro Gln Gln Pro Phe Leu Pro Pro Ala Ala Cys Phe Phe Ala  
1025 1030 1035

Thr Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Gln  
1040 1045 1050

Ser Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala  
1055 1060 1065

Pro Gln Leu Arg Pro Ala Ala Asp Gly Gln Pro Ser Gly Gly Gly  
1070 1075 1080

His Lys Ser Ala Pro Lys Gln Val Lys Arg Gln Arg Ser Ser Ser  
1085 1090 1095

Pro Glu Leu Met Arg Cys Lys Arg Arg Leu Asn Phe Ser Gly Phe  
1100 1105 1110

Gly Tyr Ser Leu Pro Gln Gln Gln Pro Ala Ala Val Ala Arg Arg  
1115 1120 1125

Asn Glu Arg Glu Arg Asn Arg Val Lys Leu Val Asn Leu Gly Phe  
1130 1135 1140

Ala Thr Leu Arg Glu His Val Pro Asn Gly Ala Ala Asn Lys Lys  
1145 1150 1155

Met Ser Lys Val Glu Thr Leu Arg Ser Ala Val Glu Tyr Ile Arg  
1160 1165 1170

Ala Leu Gln Gln Leu Leu Asp Glu His Asp Ala Val Ser Ala Ala  
1175 1180 1185

Phe Gln Ala Gly Val Leu Ser Pro Thr Ile Ser Pro Asn Tyr Ser  
1190 1195 1200

Asn Asp Leu Asn Ser Met Ala Gly Ser Pro Val Ser Ser Tyr Ser  
1205 1210 1215

Ser Asp Glu Gly Ser Tyr Asp Pro Leu Ser Pro Glu Glu Gln Glu  
1220 1225 1230

Leu Leu Asp Phe Thr Asn Trp Phe  
1235 1240

<210> 58

<211> 1247

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - synthesized MYOCD-2A-MYF6 construct

<400> 58

Met Thr Leu Leu Gly Ser Glu His Ser Leu Leu Ile Arg Ser Lys Phe  
1 5 10 15

Arg Ser Val Leu Gln Leu Arg Leu Gln Gln Arg Arg Thr Gln Glu Gln  
20 25 30

Leu Ala Asn Gln Gly Ile Ile Pro Pro Leu Lys Arg Pro Ala Glu Phe  
35 40 45

His Glu Gln Arg Lys His Leu Asp Ser Asp Lys Ala Lys Asn Ser Leu  
50 55 60

Lys Arg Lys Ala Arg Asn Arg Cys Asn Ser Ala Asp Leu Val Asn Met  
65 70 75 80

His Ile Leu Gln Ala Ser Thr Ala Glu Arg Ser Ile Pro Thr Ala Gln  
85 90 95

Met Lys Leu Lys Arg Ala Arg Leu Ala Asp Asp Leu Asn Glu Lys Ile  
100 105 110

Ala Leu Arg Pro Gly Pro Leu Glu Leu Val Glu Lys Asn Ile Leu Pro  
115 120 125

Val Asp Ser Ala Val Lys Glu Ala Ile Lys Gly Asn Gln Val Ser Phe  
130 135 140

Ser Lys Ser Thr Asp Ala Phe Ala Phe Glu Glu Asp Ser Ser Ser Asp  
145 150 155 160

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

Gly Ser Pro Pro Asp Ala Lys Ala Ser Asp Thr Pro Ser Thr Gly Ser  
180 185 190

Leu Gly Thr Asn Gln Asp Leu Ala Ser Gly Ser Glu Asn Asp Arg Asn  
195 200 205

Asp Ser Ala Ser Gln Pro Ser His Gln Ser Asp Ala Gly Lys Gln Gly  
210 215 220

Leu Gly Pro Pro Ser Thr Pro Ile Ala Val His Ala Ala Val Lys Ser  
225 230 235 240

Lys Ser Leu Gly Asp Ser Lys Asn Arg His Lys Lys Pro Lys Asp Pro  
245 250 255

Lys Pro Lys Val Lys Lys Leu Lys Tyr His Gln Tyr Ile Pro Pro Asp  
260 265 270

Gln Lys Ala Glu Lys Ser Pro Pro Pro Met Asp Ser Ala Tyr Ala Arg  
275 280 285

Leu Leu Gln Gln Gln Gln Leu Phe Leu Gln Leu Gln Ile Leu Ser Gln  
290 295 300

Gln Gln Gln Gln Gln Gln His Arg Phe Ser Tyr Leu Gly Met His Gln  
305 310 315 320

Ala Gln Leu Lys Glu Pro Asn Glu Gln Met Val Arg Asn Pro Asn Ser  
325 330 335

Ser Ser Thr Pro Leu Ser Asn Thr Pro Leu Ser Pro Val Lys Asn Ser  
340 345 350

Phe Ser Gly Gln Thr Gly Val Ser Ser Phe Lys Pro Gly Pro Leu Pro  
355 360 365

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

Ile Arg Gly Leu Pro Val Ser Gly Thr Lys Thr Ala Leu Met Asp Arg  
385 390 395 400

Leu Arg Pro Phe Gln Asp Cys Ser Gly Asn Pro Val Pro Asn Phe Gly  
405 410 415

Asp Ile Thr Thr Val Thr Phe Pro Val Thr Pro Asn Thr Leu Pro Asn  
420 425 430

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

Phe Gly Ser Thr Ser Ser Ser Pro Pro Ile Ser Pro Ala Ser Ser Asp  
450 455 460

Leu Ser Val Ala Gly Ser Leu Pro Asp Thr Phe Asn Asp Ala Ser Pro  
465 470 475 480

Ser Phe Gly Leu His Pro Ser Pro Val His Val Cys Thr Glu Glu Ser  
485 490 495

Leu Met Ser Ser Leu Asn Gly Gly Ser Val Pro Ser Glu Leu Asp Gly  
500 505 510

Leu Asp Ser Glu Lys Asp Lys Met Leu Val Glu Lys Gln Lys Val Ile  
515 520 525

Asn Glu Leu Thr Trp Lys Leu Gln Gln Glu Gln Arg Gln Val Glu Glu  
530 535 540

Leu Arg Met Gln Leu Gln Lys Gln Lys Arg Asn Asn Cys Ser Glu Lys  
545 550 555 560

Lys Pro Leu Pro Phe Leu Ala Ala Ser Ile Lys Gln Glu Glu Ala Val  
565 570 575

Ser Ser Cys Pro Phe Ala Ser Gln Val Pro Val Lys Arg Gln Ser Ser  
580 585 590

Ser Ser Glu Cys His Pro Pro Ala Cys Glu Ala Ala Gln Leu Gln Pro  
595 600 605

Leu Gly Asn Ala His Cys Val Glu Ser Ser Asp Gln Thr Asn Val Leu  
610 615 620

Ser Ser Thr Phe Leu Ser Pro Gln Cys Ser Pro Gln His Ser Pro Leu  
625 630 635 640

Gly Ala Val Lys Ser Pro Gln His Ile Ser Leu Pro Pro Ser Pro Asn  
645 650 655

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

Arg Val Ser Ser Pro Ile Ser Ser Gln Val Cys Thr Ala Gln Asn Ser  
675 680 685

Gly Ala His Asp Gly His Pro Pro Ser Phe Ser Pro His Ser Ser Ser  
690 695 700

Leu His Pro Pro Phe Ser Gly Ala Gln Ala Asp Ser Ser His Gly Ala  
705 710 715 720

Gly Gly Asn Pro Cys Pro Lys Ser Pro Cys Val Gln Gln Lys Met Ala  
725 730 735

Gly Leu His Ser Ser Asp Lys Val Gly Pro Lys Phe Ser Ile Pro Ser  
740 745 750

Pro Thr Phe Ser Lys Ser Ser Ser Ala Ile Ser Glu Val Thr Gln Pro  
755 760 765

Pro Ser Tyr Glu Asp Ala Val Lys Gln Gln Met Thr Arg Ser Gln Gln  
770 775 780

Met Asp Glu Leu Leu Asp Val Leu Ile Glu Ser Gly Glu Met Pro Ala  
785 790 795 800

Asp Ala Arg Glu Asp His Ser Cys Leu Gln Lys Val Pro Lys Ile Pro  
805 810 815

Arg Ser Ser Arg Ser Pro Thr Ala Val Leu Thr Lys Pro Ser Ala Ser  
820 825 830

Phe Glu Gln Ala Ser Ser Gly Ser Gln Ile Pro Phe Asp Pro Tyr Ala  
835 840 845

Thr Asp Ser Asp Glu His Leu Glu Val Leu Leu Asn Ser Gln Ser Pro  
850 855 860

Leu Gly Lys Met Ser Asp Val Thr Leu Leu Lys Ile Gly Ser Glu Glu  
865 870 875 880

Pro His Phe Asp Gly Ile Met Asp Gly Phe Ser Gly Lys Ala Ala Glu  
885 890 895

Asp Leu Phe Asn Ala His Glu Ile Leu Pro Gly Pro Leu Ser Pro Met  
900 905 910

Gln Thr Gln Phe Ser Pro Ser Ser Val Asp Ser Asn Gly Leu Gln Leu  
915 920 925

Ser Phe Thr Glu Ser Pro Trp Glu Thr Met Glu Trp Leu Asp Leu Thr  
930 935 940

Pro Pro Asn Ser Thr Pro Gly Phe Ser Ala Leu Thr Thr Ser Ser Pro  
945 950 955 960

Ser Ile Phe Asn Ile Asp Phe Leu Asp Val Thr Asp Leu Asn Leu Asn  
965 970 975

Ser Ser Met Asp Leu His Leu Gln Gln Trp Ala Thr Asn Phe Ser Leu  
980 985 990

Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Met Met  
995 1000 1005

Asp Leu Phe Glu Thr Gly Ser Tyr Phe Phe Tyr Leu Asp Gly Glu  
1010 1015 1020

Asn Val Thr Leu Gln Pro Leu Glu Val Ala Glu Gly Ser Pro Leu  
1025 1030 1035

Tyr Pro Gly Ser Asp Gly Thr Leu Ser Pro Cys Gln Asp Gln Met  
1040 1045 1050

Pro Pro Glu Ala Gly Ser Asp Ser Ser Gly Glu Glu His Val Leu  
1055 1060 1065

Ala Pro Pro Gly Leu Gln Pro Pro His Cys Pro Gly Gln Cys Leu  
1070 1075 1080

Ile Trp Ala Cys Lys Thr Cys Lys Arg Lys Ser Ala Pro Thr Asp  
1085 1090 1095

Arg Arg Lys Ala Ala Thr Leu Arg Glu Arg Arg Arg Leu Lys Lys  
1100 1105 1110

Ile Asn Glu Ala Phe Glu Ala Leu Lys Arg Arg Thr Val Ala Asn  
1115 1120 1125

Pro Asn Gln Arg Leu Pro Lys Val Glu Ile Leu Arg Ser Ala Ile  
1130 1135 1140

Ser Tyr Ile Glu Arg Leu Gln Asp Leu Leu His Arg Leu Asp Gln  
1145 1150 1155

Gln Glu Lys Met Gln Glu Leu Gly Val Asp Pro Phe Ser Tyr Arg  
1160 1165 1170

Pro Lys Gln Glu Asn Leu Glu Gly Ala Asp Phe Leu Arg Thr Cys  
1175 1180 1185

Ser Ser Gln Trp Pro Ser Val Ser Asp His Ser Arg Gly Leu Val  
1190 1195 1200

Ile Thr Ala Lys Glu Gly Gly Ala Ser Ile Asp Ser Ser Ala Ser  
1205 1210 1215

Ser Ser Leu Arg Cys Leu Ser Ser Ile Val Asp Ser Ile Ser Ser  
1220 1225 1230

Glu Glu Arg Lys Leu Pro Cys Val Glu Glu Val Val Glu Lys  
1235 1240 1245

<210> 59

<211> 1037

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - synthesized MyDelta3-2A-ASCL1 construct

<400> 59

Met Thr Leu Leu Gly Ser Glu His Ser Leu Leu Ile Arg Ser Lys Phe  
1 5 10 15

Arg Ser Val Leu Gln Leu Arg Leu Gln Gln Arg Arg Thr Gln Glu Gln  
20 25 30

Leu Ala Asn Gln Gly Ile Ile Pro Pro Leu Lys Arg Pro Ala Glu Phe  
35 40 45

His Glu Gln Arg Lys His Leu Asp Ser Asp Lys Ala Lys Asn Ser Leu  
50 55 60

Lys Arg Lys Ala Arg Asn Arg Cys Asn Ser Ala Asp Leu Val Asn Met  
65 70 75 80

His Ile Leu Gln Ala Ser Thr Ala Glu Arg Ser Ile Pro Thr Ala Gln  
85 90 95

Met Lys Leu Lys Arg Ala Arg Leu Ala Asp Asp Leu Asn Glu Lys Ile  
100 105 110

Ala Leu Arg Pro Gly Pro Leu Glu Leu Val Glu Lys Asn Ile Leu Pro  
115 120 125

Val Asp Ser Ala Val Lys Glu Ala Ile Lys Gly Asn Gln Val Ser Phe  
130 135 140

Ser Lys Ser Thr Asp Ala Phe Ala Phe Glu Glu Asp Ser Ser Ser Asp  
145 150 155 160

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

Gly Ser Pro Pro Asp Ala Lys Ala Ser Asp Thr Pro Ser Thr Gly Ser  
180 185 190

Leu Gly Thr Asn Gln Asp Leu Ala Ser Gly Ser Glu Asn Asp Arg Asn  
195 200 205

Asp Ser Ala Ser Gln Pro Ser His Gln Ser Asp Ala Gly Lys Gln Gly  
210 215 220

Leu Gly Pro Pro Ser Thr Pro Ile Ala Val His Ala Ala Val Lys Ser  
225 230 235 240

Lys Ser Leu Gly Asp Ser Lys Asn Arg His Lys Lys Pro Lys Asp Pro  
245 250 255

Lys Pro Lys Val Lys Lys Leu Lys Tyr His Gln Tyr Ile Pro Pro Asp  
260 265 270

Gln Lys Ala Glu Lys Ser Pro Pro Pro Met Asp Ser Ala Tyr Ala Arg  
275 280 285

Leu Leu Gln Gln Gln Gln Leu Phe Leu Gln Leu Gln Ile Leu Ser Gln  
290 295 300

Gln Gln Gln Gln Gln Gln His Arg Phe Ser Tyr Leu Gly Met His Gln  
305 310 315 320

Ala Gln Leu Lys Glu Pro Asn Glu Gln Met Val Arg Asn Pro Asn Ser  
325 330 335

Ser Ser Thr Pro Leu Ser Asn Thr Pro Leu Ser Pro Val Lys Asn Ser  
340 345 350

Phe Ser Gly Gln Thr Gly Val Ser Ser Phe Lys Pro Gly Pro Leu Pro  
355 360 365

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

Ile Arg Gly Leu Pro Val Ser Gly Thr Lys Thr Ala Leu Met Asp Arg  
385 390 395 400

Leu Arg Pro Phe Gln Asp Cys Ser Gly Asn Pro Val Pro Asn Phe Gly  
405 410 415

Asp Ile Thr Thr Val Thr Phe Pro Val Thr Pro Asn Thr Leu Pro Asn  
420 425 430

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

Phe Gly Ser Thr Ser Ser Ser Pro Pro Ile Ser Pro Ala Ser Ser Asp  
450 455 460

Leu Ser Val Ala Gly Ser Leu Pro Asp Thr Phe Asn Asp Ala Ser Pro  
465 470 475 480

Ser Phe Gly Leu His Pro Ser Pro Val His Val Cys Thr Glu Glu Ser  
485 490 495

Leu Met Ser Ser Leu Asn Gly Gly Ser Val Pro Ser Glu Leu Asp Gly  
500 505 510

Leu Asp Ser Glu Lys Asp Lys Met Leu Val Glu Lys Gln Lys Val Ile  
515 520 525

Asn Glu Leu Thr Trp Lys Leu Gln Gln Glu Gln Arg Gln Val Glu Glu  
530 535 540

Leu Arg Met Gln Leu Gln Lys Gln Lys Arg Asn Asn Cys Ser Glu Glu  
545 550 555 560

Val Thr Gln Pro Pro Ser Tyr Glu Asp Ala Val Lys Gln Gln Met Thr  
565 570 575

Arg Ser Gln Gln Met Asp Glu Leu Leu Asp Val Leu Ile Glu Ser Gly  
580 585 590

Glu Met Pro Ala Asp Ala Arg Glu Asp His Ser Cys Leu Gln Lys Val  
595 600 605

Pro Lys Ile Pro Arg Ser Ser Arg Ser Pro Thr Ala Val Leu Thr Lys  
610 615 620

Pro Ser Ala Ser Phe Glu Gln Ala Ser Ser Gly Ser Gln Ile Pro Phe  
625 630 635 640

Asp Pro Tyr Ala Thr Asp Ser Asp Glu His Leu Glu Val Leu Leu Asn  
645 650 655

Ser Gln Ser Pro Leu Gly Lys Met Ser Asp Val Thr Leu Leu Lys Ile  
660 665 670

Gly Ser Glu Glu Pro His Phe Asp Gly Ile Met Asp Gly Phe Ser Gly  
675 680 685

Lys Ala Ala Glu Asp Leu Phe Asn Ala His Glu Ile Leu Pro Gly Pro  
690 695 700

Leu Ser Pro Met Gln Thr Gln Phe Ser Pro Ser Ser Val Asp Ser Asn  
705 710 715 720

Gly Leu Gln Leu Ser Phe Thr Glu Ser Pro Trp Glu Thr Met Glu Trp  
725 730 735

Leu Asp Leu Thr Pro Pro Asn Ser Thr Pro Gly Phe Ser Ala Leu Thr  
740 745 750

Thr Ser Ser Pro Ser Ile Phe Asn Ile Asp Phe Leu Asp Val Thr Asp  
755 760 765

Leu Asn Leu Asn Ser Ser Met Asp Leu His Leu Gln Gln Trp Ala Thr  
770 775 780

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly  
785 790 795 800

Pro Met Glu Ser Ser Ala Lys Met Glu Ser Gly Gly Ala Gly Gln Gln  
805 810 815

Pro Gln Pro Gln Pro Gln Gln Pro Phe Leu Pro Pro Ala Ala Cys Phe  
820 825 830

Phe Ala Thr Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala  
835 840 845

Gln Ser Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala  
850 855 860

Pro Gln Leu Arg Pro Ala Ala Asp Gly Gln Pro Ser Gly Gly Gly His  
865 870 875 880

Lys Ser Ala Pro Lys Gln Val Lys Arg Gln Arg Ser Ser Ser Pro Glu  
885 890 895

Leu Met Arg Cys Lys Arg Arg Leu Asn Phe Ser Gly Phe Gly Tyr Ser  
900 905 910

Leu Pro Gln Gln Gln Pro Ala Ala Val Ala Arg Arg Asn Glu Arg Glu  
915 920 925

Arg Asn Arg Val Lys Leu Val Asn Leu Gly Phe Ala Thr Leu Arg Glu  
930 935 940

His Val Pro Asn Gly Ala Ala Asn Lys Lys Met Ser Lys Val Glu Thr  
945 950 955 960

Leu Arg Ser Ala Val Glu Tyr Ile Arg Ala Leu Gln Gln Leu Leu Asp  
965 970 975

Glu His Asp Ala Val Ser Ala Ala Phe Gln Ala Gly Val Leu Ser Pro  
980 985 990

Thr Ile Ser Pro Asn Tyr Ser Asn Asp Leu Asn Ser Met Ala Gly Ser  
995 1000 1005

Pro Val Ser Ser Tyr Ser Ser Asp Glu Gly Ser Tyr Asp Pro Leu  
1010 1015 1020

Ser Pro Glu Glu Gln Glu Leu Leu Asp Phe Thr Asn Trp Phe  
1025 1030 1035

<210> 60  
<211> 1043  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in Lab - synthesized MyDelta13-2A-MYF6 onstruct

<400> 60

Met Thr Leu Leu Gly Ser Glu His Ser Leu Leu Ile Arg Ser Lys Phe  
1 5 10 15

Arg Ser Val Leu Gln Leu Arg Leu Gln Gln Arg Arg Thr Gln Glu Gln  
20 25 30

Leu Ala Asn Gln Gly Ile Ile Pro Pro Leu Lys Arg Pro Ala Glu Phe  
35 40 45

His Glu Gln Arg Lys His Leu Asp Ser Asp Lys Ala Lys Asn Ser Leu  
50 55 60

Lys Arg Lys Ala Arg Asn Arg Cys Asn Ser Ala Asp Leu Val Asn Met  
65 70 75 80

His Ile Leu Gln Ala Ser Thr Ala Glu Arg Ser Ile Pro Thr Ala Gln  
85 90 95

Met Lys Leu Lys Arg Ala Arg Leu Ala Asp Asp Leu Asn Glu Lys Ile  
100 105 110

Ala Leu Arg Pro Gly Pro Leu Glu Leu Val Glu Lys Asn Ile Leu Pro  
115 120 125

Val Asp Ser Ala Val Lys Glu Ala Ile Lys Gly Asn Gln Val Ser Phe  
130 135 140

Ser Lys Ser Thr Asp Ala Phe Ala Phe Glu Glu Asp Ser Ser Ser Asp  
145 150 155 160

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

Gly Ser Pro Pro Asp Ala Lys Ala Ser Asp Thr Pro Ser Thr Gly Ser  
180 185 190

Leu Gly Thr Asn Gln Asp Leu Ala Ser Gly Ser Glu Asn Asp Arg Asn  
195 200 205

Asp Ser Ala Ser Gln Pro Ser His Gln Ser Asp Ala Gly Lys Gln Gly  
210 215 220

Leu Gly Pro Pro Ser Thr Pro Ile Ala Val His Ala Ala Val Lys Ser  
225 230 235 240

Lys Ser Leu Gly Asp Ser Lys Asn Arg His Lys Lys Pro Lys Asp Pro  
245 250 255

Lys Pro Lys Val Lys Lys Leu Lys Tyr His Gln Tyr Ile Pro Pro Asp  
260 265 270

Gln Lys Ala Glu Lys Ser Pro Pro Pro Met Asp Ser Ala Tyr Ala Arg  
275 280 285

Leu Leu Gln Gln Gln Gln Leu Phe Leu Gln Leu Gln Ile Leu Ser Gln  
290 295 300

Gln Gln Gln Gln Gln Gln His Arg Phe Ser Tyr Leu Gly Met His Gln  
305 310 315 320

Ala Gln Leu Lys Glu Pro Asn Glu Gln Met Val Arg Asn Pro Asn Ser  
325 330 335

Ser Ser Thr Pro Leu Ser Asn Thr Pro Leu Ser Pro Val Lys Asn Ser  
340 345 350

Phe Ser Gly Gln Thr Gly Val Ser Ser Phe Lys Pro Gly Pro Leu Pro  
355 360 365

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

Ile Arg Gly Leu Pro Val Ser Gly Thr Lys Thr Ala Leu Met Asp Arg  
385 390 395 400

Leu Arg Pro Phe Gln Asp Cys Ser Gly Asn Pro Val Pro Asn Phe Gly  
405 410 415

Asp Ile Thr Thr Val Thr Phe Pro Val Thr Pro Asn Thr Leu Pro Asn  
420 425 430

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

Phe Gly Ser Thr Ser Ser Ser Pro Pro Ile Ser Pro Ala Ser Ser Asp  
450 455 460

Leu Ser Val Ala Gly Ser Leu Pro Asp Thr Phe Asn Asp Ala Ser Pro  
465 470 475 480

Ser Phe Gly Leu His Pro Ser Pro Val His Val Cys Thr Glu Glu Ser  
485 490 495

Leu Met Ser Ser Leu Asn Gly Gly Ser Val Pro Ser Glu Leu Asp Gly  
500 505 510

Leu Asp Ser Glu Lys Asp Lys Met Leu Val Glu Lys Gln Lys Val Ile  
515 520 525

Asn Glu Leu Thr Trp Lys Leu Gln Gln Glu Gln Arg Gln Val Glu Glu  
530 535 540

Leu Arg Met Gln Leu Gln Lys Gln Lys Arg Asn Asn Cys Ser Glu Glu  
545 550 555 560

Val Thr Gln Pro Pro Ser Tyr Glu Asp Ala Val Lys Gln Gln Met Thr  
565 570 575

Arg Ser Gln Gln Met Asp Glu Leu Leu Asp Val Leu Ile Glu Ser Gly  
580 585 590

Glu Met Pro Ala Asp Ala Arg Glu Asp His Ser Cys Leu Gln Lys Val  
595 600 605

Pro Lys Ile Pro Arg Ser Ser Arg Ser Pro Thr Ala Val Leu Thr Lys  
610 615 620

Pro Ser Ala Ser Phe Glu Gln Ala Ser Ser Gly Ser Gln Ile Pro Phe  
625 630 635 640

Asp Pro Tyr Ala Thr Asp Ser Asp Glu His Leu Glu Val Leu Leu Asn  
645 650 655

Ser Gln Ser Pro Leu Gly Lys Met Ser Asp Val Thr Leu Leu Lys Ile  
660 665 670

Gly Ser Glu Glu Pro His Phe Asp Gly Ile Met Asp Gly Phe Ser Gly  
675 680 685

Lys Ala Ala Glu Asp Leu Phe Asn Ala His Glu Ile Leu Pro Gly Pro  
690 695 700

Leu Ser Pro Met Gln Thr Gln Phe Ser Pro Ser Ser Val Asp Ser Asn  
705 710 715 720

Gly Leu Gln Leu Ser Phe Thr Glu Ser Pro Trp Glu Thr Met Glu Trp  
725 730 735

Leu Asp Leu Thr Pro Pro Asn Ser Thr Pro Gly Phe Ser Ala Leu Thr  
740 745 750

Thr Ser Ser Pro Ser Ile Phe Asn Ile Asp Phe Leu Asp Val Thr Asp  
755 760 765

Leu Asn Leu Asn Ser Ser Met Asp Leu His Leu Gln Gln Trp Ala Thr  
770 775 780

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly  
785 790 795 800

Pro Met Met Met Asp Leu Phe Glu Thr Gly Ser Tyr Phe Phe Tyr Leu  
805 810 815

Asp Gly Glu Asn Val Thr Leu Gln Pro Leu Glu Val Ala Glu Gly Ser  
820 825 830

Pro Leu Tyr Pro Gly Ser Asp Gly Thr Leu Ser Pro Cys Gln Asp Gln  
835 840 845

Met Pro Pro Glu Ala Gly Ser Asp Ser Ser Gly Glu Glu His Val Leu  
850 855 860

Ala Pro Pro Gly Leu Gln Pro Pro His Cys Pro Gly Gln Cys Leu Ile  
865 870 875 880

Trp Ala Cys Lys Thr Cys Lys Arg Lys Ser Ala Pro Thr Asp Arg Arg  
885 890 895

Lys Ala Ala Thr Leu Arg Glu Arg Arg Arg Leu Lys Lys Ile Asn Glu  
900 905 910

Ala Phe Glu Ala Leu Lys Arg Arg Thr Val Ala Asn Pro Asn Gln Arg  
915 920 925

Leu Pro Lys Val Glu Ile Leu Arg Ser Ala Ile Ser Tyr Ile Glu Arg  
930 935 940

Leu Gln Asp Leu Leu His Arg Leu Asp Gln Gln Glu Lys Met Gln Glu  
945 950 955 960

Leu Gly Val Asp Pro Phe Ser Tyr Arg Pro Lys Gln Glu Asn Leu Glu  
965 970 975

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

Asp His Ser Arg Gly Leu Val Ile Thr Ala Lys Glu Gly Gly Ala Ser  
995 1000 1005

Ile Asp Ser Ser Ala Ser Ser Ser Leu Arg Cys Leu Ser Ser Ile  
1010 1015 1020

Val Asp Ser Ile Ser Ser Glu Glu Arg Lys Leu Pro Cys Val Glu  
1025 1030 1035

Glu Val Val Glu Lys  
1040

<210> 61  
<211> 1241  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in Lab - synthesized ASCL1-2A-MYOCD construct

<400> 61

Met Glu Ser Ser Ala Lys Met Glu Ser Gly Gly Ala Gly Gln Gln Pro  
1 5 10 15

Gln Pro Gln Pro Gln Gln Pro Phe Leu Pro Pro Ala Ala Cys Phe Phe  
20 25 30

Ala Thr Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Gln  
35 40 45

Ser Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala Pro  
50 55 60

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

Ser Ala Pro Lys Gln Val Lys Arg Gln Arg Ser Ser Ser Pro Glu Leu  
85 90 95

Met Arg Cys Lys Arg Arg Leu Asn Phe Ser Gly Phe Gly Tyr Ser Leu  
100 105 110

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

Asn Arg Val Lys Leu Val Asn Leu Gly Phe Ala Thr Leu Arg Glu His  
130 135 140

Val Pro Asn Gly Ala Ala Asn Lys Lys Met Ser Lys Val Glu Thr Leu  
145 150 155 160

Arg Ser Ala Val Glu Tyr Ile Arg Ala Leu Gln Gln Leu Leu Asp Glu  
165 170 175

His Asp Ala Val Ser Ala Ala Phe Gln Ala Gly Val Leu Ser Pro Thr  
180 185 190

Ile Ser Pro Asn Tyr Ser Asn Asp Leu Asn Ser Met Ala Gly Ser Pro  
195 200 205

Val Ser Ser Tyr Ser Ser Asp Glu Gly Ser Tyr Asp Pro Leu Ser Pro  
210 215 220

Glu Glu Gln Glu Leu Leu Asp Phe Thr Asn Trp Phe Ala Thr Asn Phe  
225 230 235 240

Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met  
245 250 255

Thr Leu Leu Gly Ser Glu His Ser Leu Leu Ile Arg Ser Lys Phe Arg  
260 265 270

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

Ala Asn Gln Gly Ile Ile Pro Pro Leu Lys Arg Pro Ala Glu Phe His  
290 295 300

Glu Gln Arg Lys His Leu Asp Ser Asp Lys Ala Lys Asn Ser Leu Lys  
305 310 315 320

Arg Lys Ala Arg Asn Arg Cys Asn Ser Ala Asp Leu Val Asn Met His  
325 330 335

Ile Leu Gln Ala Ser Thr Ala Glu Arg Ser Ile Pro Thr Ala Gln Met  
340 345 350

Lys Leu Lys Arg Ala Arg Leu Ala Asp Asp Leu Asn Glu Lys Ile Ala  
355 360 365

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

Asp Ser Ala Val Lys Glu Ala Ile Lys Gly Asn Gln Val Ser Phe Ser  
385 390 395 400

Lys Ser Thr Asp Ala Phe Ala Phe Glu Glu Asp Ser Ser Ser Asp Gly  
405 410 415

Leu Ser Pro Asp Gln Thr Arg Ser Glu Asp Pro Gln Asn Ser Ala Gly  
420 425 430

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

Gly Thr Asn Gln Asp Leu Ala Ser Gly Ser Glu Asn Asp Arg Asn Asp  
450 455 460

Ser Ala Ser Gln Pro Ser His Gln Ser Asp Ala Gly Lys Gln Gly Leu  
465 470 475 480

Gly Pro Pro Ser Thr Pro Ile Ala Val His Ala Ala Val Lys Ser Lys  
485 490 495

Ser Leu Gly Asp Ser Lys Asn Arg His Lys Lys Pro Lys Asp Pro Lys  
500 505 510

Pro Lys Val Lys Lys Leu Lys Tyr His Gln Tyr Ile Pro Pro Asp Gln  
515 520 525

Lys Ala Glu Lys Ser Pro Pro Pro Met Asp Ser Ala Tyr Ala Arg Leu  
530 535 540

Leu Gln Gln Gln Gln Leu Phe Leu Gln Leu Gln Ile Leu Ser Gln Gln  
545 550 555 560

Gln Gln Gln Gln Gln His Arg Phe Ser Tyr Leu Gly Met His Gln Ala  
565 570 575

Gln Leu Lys Glu Pro Asn Glu Gln Met Val Arg Asn Pro Asn Ser Ser  
580 585 590

Ser Thr Pro Leu Ser Asn Thr Pro Leu Ser Pro Val Lys Asn Ser Phe  
595 600 605

Ser Gly Gln Thr Gly Val Ser Ser Phe Lys Pro Gly Pro Leu Pro Pro  
610 615 620

Asn Leu Asp Asp Leu Lys Val Ser Glu Leu Arg Gln Gln Leu Arg Ile  
625 630 635 640

Arg Gly Leu Pro Val Ser Gly Thr Lys Thr Ala Leu Met Asp Arg Leu  
645 650 655

Arg Pro Phe Gln Asp Cys Ser Gly Asn Pro Val Pro Asn Phe Gly Asp  
660 665 670

Ile Thr Thr Val Thr Phe Pro Val Thr Pro Asn Thr Leu Pro Asn Tyr  
675 680 685

Gln Ser Ser Ser Ser Thr Ser Ala Leu Ser Asn Gly Phe Tyr His Phe  
690 695 700

Gly Ser Thr Ser Ser Ser Pro Pro Ile Ser Pro Ala Ser Ser Asp Leu  
705 710 715 720

Ser Val Ala Gly Ser Leu Pro Asp Thr Phe Asn Asp Ala Ser Pro Ser  
725 730 735

Phe Gly Leu His Pro Ser Pro Val His Val Cys Thr Glu Glu Ser Leu  
740 745 750

Met Ser Ser Leu Asn Gly Gly Ser Val Pro Ser Glu Leu Asp Gly Leu  
755 760 765

Asp Ser Glu Lys Asp Lys Met Leu Val Glu Lys Gln Lys Val Ile Asn  
770 775 780

Glu Leu Thr Trp Lys Leu Gln Gln Glu Gln Arg Gln Val Glu Glu Leu  
785 790 795 800

Arg Met Gln Leu Gln Lys Gln Lys Arg Asn Asn Cys Ser Glu Lys Lys  
805 810 815

Pro Leu Pro Phe Leu Ala Ala Ser Ile Lys Gln Glu Glu Ala Val Ser  
820 825 830

Ser Cys Pro Phe Ala Ser Gln Val Pro Val Lys Arg Gln Ser Ser Ser  
835 840 845

Ser Glu Cys His Pro Pro Ala Cys Glu Ala Ala Gln Leu Gln Pro Leu  
850 855 860

Gly Asn Ala His Cys Val Glu Ser Ser Asp Gln Thr Asn Val Leu Ser  
865 870 875 880

Ser Thr Phe Leu Ser Pro Gln Cys Ser Pro Gln His Ser Pro Leu Gly  
885 890 895

Ala Val Lys Ser Pro Gln His Ile Ser Leu Pro Pro Ser Pro Asn Asn  
900 905 910

Pro His Phe Leu Pro Ser Ser Ser Gly Ala Gln Gly Glu Gly His Arg  
915 920 925

Val Ser Ser Pro Ile Ser Ser Gln Val Cys Thr Ala Gln Asn Ser Gly  
930 935 940

Ala His Asp Gly His Pro Pro Ser Phe Ser Pro His Ser Ser Ser Leu  
945 950 955 960

His Pro Pro Phe Ser Gly Ala Gln Ala Asp Ser Ser His Gly Ala Gly  
965 970 975

Gly Asn Pro Cys Pro Lys Ser Pro Cys Val Gln Gln Lys Met Ala Gly  
980 985 990

Leu His Ser Ser Asp Lys Val Gly Pro Lys Phe Ser Ile Pro Ser Pro  
995 1000 1005

Thr Phe Ser Lys Ser Ser Ser Ala Ile Ser Glu Val Thr Gln Pro  
1010 1015 1020

Pro Ser Tyr Glu Asp Ala Val Lys Gln Gln Met Thr Arg Ser Gln  
1025 1030 1035

Gln Met Asp Glu Leu Leu Asp Val Leu Ile Glu Ser Gly Glu Met  
1040 1045 1050

Pro Ala Asp Ala Arg Glu Asp His Ser Cys Leu Gln Lys Val Pro  
1055 1060 1065

Lys Ile Pro Arg Ser Ser Arg Ser Pro Thr Ala Val Leu Thr Lys  
1070 1075 1080

Pro Ser Ala Ser Phe Glu Gln Ala Ser Ser Gly Ser Gln Ile Pro  
1085 1090 1095

Phe Asp Pro Tyr Ala Thr Asp Ser Asp Glu His Leu Glu Val Leu  
1100 1105 1110

Leu Asn Ser Gln Ser Pro Leu Gly Lys Met Ser Asp Val Thr Leu  
1115 1120 1125

Leu Lys Ile Gly Ser Glu Glu Pro His Phe Asp Gly Ile Met Asp  
1130 1135 1140

Gly Phe Ser Gly Lys Ala Ala Glu Asp Leu Phe Asn Ala His Glu  
1145 1150 1155

Ile Leu Pro Gly Pro Leu Ser Pro Met Gln Thr Gln Phe Ser Pro  
1160 1165 1170

Ser Ser Val Asp Ser Asn Gly Leu Gln Leu Ser Phe Thr Glu Ser  
1175 1180 1185

Pro Trp Glu Thr Met Glu Trp Leu Asp Leu Thr Pro Pro Asn Ser  
1190 1195 1200

Thr Pro Gly Phe Ser Ala Leu Thr Thr Ser Ser Pro Ser Ile Phe  
1205 1210 1215

Asn Ile Asp Phe Leu Asp Val Thr Asp Leu Asn Leu Asn Ser Ser  
1220 1225 1230

Met Asp Leu His Leu Gln Gln Trp  
1235 1240

<210> 62  
<211> 1247  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in Lab - synthesized MYF6-2A-MY OCD construct

<400> 62

Met Met Met Asp Leu Phe Glu Thr Gly Ser Tyr Phe Phe Tyr Leu Asp  
1 5 10 15

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

Leu Tyr Pro Gly Ser Asp Gly Thr Leu Ser Pro Cys Gln Asp Gln Met  
35 40 45

Pro Pro Glu Ala Gly Ser Asp Ser Ser Gly Glu Glu His Val Leu Ala  
50 55 60

Pro Pro Gly Leu Gln Pro Pro His Cys Pro Gly Gln Cys Leu Ile Trp  
65 70 75 80

Ala Cys Lys Thr Cys Lys Arg Lys Ser Ala Pro Thr Asp Arg Arg Lys  
85 90 95

Ala Ala Thr Leu Arg Glu Arg Arg Arg Leu Lys Lys Ile Asn Glu Ala  
100 105 110

Phe Glu Ala Leu Lys Arg Arg Thr Val Ala Asn Pro Asn Gln Arg Leu  
115 120 125

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

Gln Asp Leu Leu His Arg Leu Asp Gln Gln Glu Lys Met Gln Glu Leu  
145 150 155 160

Gly Val Asp Pro Phe Ser Tyr Arg Pro Lys Gln Glu Asn Leu Glu Gly  
165 170 175

Ala Asp Phe Leu Arg Thr Cys Ser Ser Gln Trp Pro Ser Val Ser Asp  
180 185 190

His Ser Arg Gly Leu Val Ile Thr Ala Lys Glu Gly Gly Ala Ser Ile  
195 200 205

Asp Ser Ser Ala Ser Ser Ser Leu Arg Cys Leu Ser Ser Ile Val Asp  
210 215 220

Ser Ile Ser Ser Glu Glu Arg Lys Leu Pro Cys Val Glu Glu Val Val  
225 230 235 240

Glu Lys Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu  
245 250 255

Glu Asn Pro Gly Pro Met Thr Leu Leu Gly Ser Glu His Ser Leu Leu  
260 265 270

Ile Arg Ser Lys Phe Arg Ser Val Leu Gln Leu Arg Leu Gln Gln Arg  
275 280 285

Arg Thr Gln Glu Gln Leu Ala Asn Gln Gly Ile Ile Pro Pro Leu Lys  
290 295 300

Arg Pro Ala Glu Phe His Glu Gln Arg Lys His Leu Asp Ser Asp Lys  
305 310 315 320

Ala Lys Asn Ser Leu Lys Arg Lys Ala Arg Asn Arg Cys Asn Ser Ala  
325 330 335

Asp Leu Val Asn Met His Ile Leu Gln Ala Ser Thr Ala Glu Arg Ser  
340 345 350

Ile Pro Thr Ala Gln Met Lys Leu Lys Arg Ala Arg Leu Ala Asp Asp  
355 360 365

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

Lys Asn Ile Leu Pro Val Asp Ser Ala Val Lys Glu Ala Ile Lys Gly  
385 390 395 400

Asn Gln Val Ser Phe Ser Lys Ser Thr Asp Ala Phe Ala Phe Glu Glu  
405 410 415

Asp Ser Ser Ser Asp Gly Leu Ser Pro Asp Gln Thr Arg Ser Glu Asp  
420 425 430

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

Pro Ser Thr Gly Ser Leu Gly Thr Asn Gln Asp Leu Ala Ser Gly Ser  
450 455 460

Glu Asn Asp Arg Asn Asp Ser Ala Ser Gln Pro Ser His Gln Ser Asp  
465 470 475 480

Ala Gly Lys Gln Gly Leu Gly Pro Pro Ser Thr Pro Ile Ala Val His  
485 490 495

Ala Ala Val Lys Ser Lys Ser Leu Gly Asp Ser Lys Asn Arg His Lys  
500 505 510

Lys Pro Lys Asp Pro Lys Pro Lys Val Lys Lys Leu Lys Tyr His Gln  
515 520 525

Tyr Ile Pro Pro Asp Gln Lys Ala Glu Lys Ser Pro Pro Pro Met Asp  
530 535 540

Ser Ala Tyr Ala Arg Leu Leu Gln Gln Gln Gln Leu Phe Leu Gln Leu  
545 550 555 560

Gln Ile Leu Ser Gln Gln Gln Gln Gln Gln Gln His Arg Phe Ser Tyr  
565 570 575

Leu Gly Met His Gln Ala Gln Leu Lys Glu Pro Asn Glu Gln Met Val  
580 585 590

Arg Asn Pro Asn Ser Ser Ser Thr Pro Leu Ser Asn Thr Pro Leu Ser  
595 600 605

Pro Val Lys Asn Ser Phe Ser Gly Gln Thr Gly Val Ser Ser Phe Lys  
610 615 620

Pro Gly Pro Leu Pro Pro Asn Leu Asp Asp Leu Lys Val Ser Glu Leu  
625 630 635 640

Arg Gln Gln Leu Arg Ile Arg Gly Leu Pro Val Ser Gly Thr Lys Thr  
645 650 655

Ala Leu Met Asp Arg Leu Arg Pro Phe Gln Asp Cys Ser Gly Asn Pro  
660 665 670

Val Pro Asn Phe Gly Asp Ile Thr Thr Val Thr Phe Pro Val Thr Pro  
675 680 685

Asn Thr Leu Pro Asn Tyr Gln Ser Ser Ser Ser Thr Ser Ala Leu Ser  
690 695 700

Asn Gly Phe Tyr His Phe Gly Ser Thr Ser Ser Ser Pro Pro Ile Ser  
705 710 715 720

Pro Ala Ser Ser Asp Leu Ser Val Ala Gly Ser Leu Pro Asp Thr Phe  
725 730 735

Asn Asp Ala Ser Pro Ser Phe Gly Leu His Pro Ser Pro Val His Val  
740 745 750

Cys Thr Glu Glu Ser Leu Met Ser Ser Leu Asn Gly Gly Ser Val Pro  
755 760 765

Ser Glu Leu Asp Gly Leu Asp Ser Glu Lys Asp Lys Met Leu Val Glu  
770 775 780

Lys Gln Lys Val Ile Asn Glu Leu Thr Trp Lys Leu Gln Gln Glu Gln  
785 790 795 800

Arg Gln Val Glu Glu Leu Arg Met Gln Leu Gln Lys Gln Lys Arg Asn  
805 810 815

Asn Cys Ser Glu Lys Lys Pro Leu Pro Phe Leu Ala Ala Ser Ile Lys  
820 825 830

Gln Glu Glu Ala Val Ser Ser Cys Pro Phe Ala Ser Gln Val Pro Val  
835 840 845

Lys Arg Gln Ser Ser Ser Ser Glu Cys His Pro Pro Ala Cys Glu Ala  
850 855 860

Ala Gln Leu Gln Pro Leu Gly Asn Ala His Cys Val Glu Ser Ser Asp  
865 870 875 880

Gln Thr Asn Val Leu Ser Ser Thr Phe Leu Ser Pro Gln Cys Ser Pro  
885 890 895

Gln His Ser Pro Leu Gly Ala Val Lys Ser Pro Gln His Ile Ser Leu  
900 905 910

Pro Pro Ser Pro Asn Asn Pro His Phe Leu Pro Ser Ser Ser Gly Ala  
915 920 925

Gln Gly Glu Gly His Arg Val Ser Ser Pro Ile Ser Ser Gln Val Cys  
930 935 940

Thr Ala Gln Asn Ser Gly Ala His Asp Gly His Pro Pro Ser Phe Ser  
945 950 955 960

Pro His Ser Ser Ser Leu His Pro Pro Phe Ser Gly Ala Gln Ala Asp  
965 970 975

Ser Ser His Gly Ala Gly Gly Asn Pro Cys Pro Lys Ser Pro Cys Val  
980 985 990

Gln Gln Lys Met Ala Gly Leu His Ser Ser Asp Lys Val Gly Pro Lys  
995 1000 1005

Phe Ser Ile Pro Ser Pro Thr Phe Ser Lys Ser Ser Ser Ala Ile  
1010 1015 1020

Ser Glu Val Thr Gln Pro Pro Ser Tyr Glu Asp Ala Val Lys Gln  
1025 1030 1035

Gln Met Thr Arg Ser Gln Gln Met Asp Glu Leu Leu Asp Val Leu  
1040 1045 1050

Ile Glu Ser Gly Glu Met Pro Ala Asp Ala Arg Glu Asp His Ser  
1055 1060 1065

Cys Leu Gln Lys Val Pro Lys Ile Pro Arg Ser Ser Arg Ser Pro  
1070 1075 1080

Thr Ala Val Leu Thr Lys Pro Ser Ala Ser Phe Glu Gln Ala Ser  
1085 1090 1095

Ser Gly Ser Gln Ile Pro Phe Asp Pro Tyr Ala Thr Asp Ser Asp  
1100 1105 1110



Gln Pro Gln Pro Gln Gln Pro Phe Leu Pro Pro Ala Ala Cys Phe Phe  
20 25 30

Ala Thr Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Gln  
35 40 45

Ser Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala Pro  
50 55 60

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

Ser Ala Pro Lys Gln Val Lys Arg Gln Arg Ser Ser Ser Pro Glu Leu  
85 90 95

Met Arg Cys Lys Arg Arg Leu Asn Phe Ser Gly Phe Gly Tyr Ser Leu  
100 105 110

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

Asn Arg Val Lys Leu Val Asn Leu Gly Phe Ala Thr Leu Arg Glu His  
130 135 140

Val Pro Asn Gly Ala Ala Asn Lys Lys Met Ser Lys Val Glu Thr Leu  
145 150 155 160

Arg Ser Ala Val Glu Tyr Ile Arg Ala Leu Gln Gln Leu Leu Asp Glu  
165 170 175

His Asp Ala Val Ser Ala Ala Phe Gln Ala Gly Val Leu Ser Pro Thr  
180 185 190

Ile Ser Pro Asn Tyr Ser Asn Asp Leu Asn Ser Met Ala Gly Ser Pro  
195 200 205

Val Ser Ser Tyr Ser Ser Asp Glu Gly Ser Tyr Asp Pro Leu Ser Pro  
210 215 220

Glu Glu Gln Glu Leu Leu Asp Phe Thr Asn Trp Phe Ala Thr Asn Phe  
225 230 235 240

Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met  
245 250 255

Thr Leu Leu Gly Ser Glu His Ser Leu Leu Ile Arg Ser Lys Phe Arg  
260 265 270

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

Ala Asn Gln Gly Ile Ile Pro Pro Leu Lys Arg Pro Ala Glu Phe His  
290 295 300

Glu Gln Arg Lys His Leu Asp Ser Asp Lys Ala Lys Asn Ser Leu Lys  
305 310 315 320

Arg Lys Ala Arg Asn Arg Cys Asn Ser Ala Asp Leu Val Asn Met His  
325 330 335

Ile Leu Gln Ala Ser Thr Ala Glu Arg Ser Ile Pro Thr Ala Gln Met  
340 345 350

Lys Leu Lys Arg Ala Arg Leu Ala Asp Asp Leu Asn Glu Lys Ile Ala  
355 360 365

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

Asp Ser Ala Val Lys Glu Ala Ile Lys Gly Asn Gln Val Ser Phe Ser  
385 390 395 400

Lys Ser Thr Asp Ala Phe Ala Phe Glu Glu Asp Ser Ser Ser Asp Gly  
405 410 415

Leu Ser Pro Asp Gln Thr Arg Ser Glu Asp Pro Gln Asn Ser Ala Gly  
420 425 430

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

Gly Thr Asn Gln Asp Leu Ala Ser Gly Ser Glu Asn Asp Arg Asn Asp  
450 455 460

Ser Ala Ser Gln Pro Ser His Gln Ser Asp Ala Gly Lys Gln Gly Leu  
465 470 475 480

Gly Pro Pro Ser Thr Pro Ile Ala Val His Ala Ala Val Lys Ser Lys  
485 490 495

Ser Leu Gly Asp Ser Lys Asn Arg His Lys Lys Pro Lys Asp Pro Lys  
500 505 510

Pro Lys Val Lys Lys Leu Lys Tyr His Gln Tyr Ile Pro Pro Asp Gln  
515 520 525

Lys Ala Glu Lys Ser Pro Pro Pro Met Asp Ser Ala Tyr Ala Arg Leu  
530 535 540

Leu Gln Gln Gln Gln Leu Phe Leu Gln Leu Gln Ile Leu Ser Gln Gln  
545 550 555 560

Gln Gln Gln Gln Gln His Arg Phe Ser Tyr Leu Gly Met His Gln Ala  
565 570 575

Gln Leu Lys Glu Pro Asn Glu Gln Met Val Arg Asn Pro Asn Ser Ser  
580 585 590

Ser Thr Pro Leu Ser Asn Thr Pro Leu Ser Pro Val Lys Asn Ser Phe  
595 600 605

Ser Gly Gln Thr Gly Val Ser Ser Phe Lys Pro Gly Pro Leu Pro Pro  
610 615 620

Asn Leu Asp Asp Leu Lys Val Ser Glu Leu Arg Gln Gln Leu Arg Ile  
625 630 635 640

Arg Gly Leu Pro Val Ser Gly Thr Lys Thr Ala Leu Met Asp Arg Leu  
645 650 655

Arg Pro Phe Gln Asp Cys Ser Gly Asn Pro Val Pro Asn Phe Gly Asp  
660 665 670

Ile Thr Thr Val Thr Phe Pro Val Thr Pro Asn Thr Leu Pro Asn Tyr  
675 680 685

Gln Ser Ser Ser Ser Thr Ser Ala Leu Ser Asn Gly Phe Tyr His Phe  
690 695 700

Gly Ser Thr Ser Ser Ser Pro Pro Ile Ser Pro Ala Ser Ser Asp Leu  
705 710 715 720

Ser Val Ala Gly Ser Leu Pro Asp Thr Phe Asn Asp Ala Ser Pro Ser  
725 730 735

Phe Gly Leu His Pro Ser Pro Val His Val Cys Thr Glu Glu Ser Leu  
740 745 750

Met Ser Ser Leu Asn Gly Gly Ser Val Pro Ser Glu Leu Asp Gly Leu  
755 760 765

Asp Ser Glu Lys Asp Lys Met Leu Val Glu Lys Gln Lys Val Ile Asn  
770 775 780

Glu Leu Thr Trp Lys Leu Gln Gln Glu Gln Arg Gln Val Glu Glu Leu  
785 790 795 800

Arg Met Gln Leu Gln Lys Gln Lys Arg Asn Asn Cys Ser Glu Glu Val  
805 810 815

Thr Gln Pro Pro Ser Tyr Glu Asp Ala Val Lys Gln Gln Met Thr Arg  
820 825 830

Ser Gln Gln Met Asp Glu Leu Leu Asp Val Leu Ile Glu Ser Gly Glu  
835 840 845

Met Pro Ala Asp Ala Arg Glu Asp His Ser Cys Leu Gln Lys Val Pro  
850 855 860

Lys Ile Pro Arg Ser Ser Arg Ser Pro Thr Ala Val Leu Thr Lys Pro  
865 870 875 880

Ser Ala Ser Phe Glu Gln Ala Ser Ser Gly Ser Gln Ile Pro Phe Asp  
885 890 895

Pro Tyr Ala Thr Asp Ser Asp Glu His Leu Glu Val Leu Leu Asn Ser  
900 905 910

Gln Ser Pro Leu Gly Lys Met Ser Asp Val Thr Leu Leu Lys Ile Gly  
915 920 925

Ser Glu Glu Pro His Phe Asp Gly Ile Met Asp Gly Phe Ser Gly Lys  
930 935 940

Ala Ala Glu Asp Leu Phe Asn Ala His Glu Ile Leu Pro Gly Pro Leu  
945 950 955 960

Ser Pro Met Gln Thr Gln Phe Ser Pro Ser Ser Val Asp Ser Asn Gly  
965 970 975

Leu Gln Leu Ser Phe Thr Glu Ser Pro Trp Glu Thr Met Glu Trp Leu  
980 985 990

Asp Leu Thr Pro Pro Asn Ser Thr Pro Gly Phe Ser Ala Leu Thr Thr  
995 1000 1005

Ser Ser Pro Ser Ile Phe Asn Ile Asp Phe Leu Asp Val Thr Asp  
1010 1015 1020

Leu Asn Leu Asn Ser Ser Met Asp Leu His Leu Gln Gln Trp  
1025 1030 1035

<210> 64  
<211> 1043  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in Lab - synthesized MYF6-2A-MyDetal3

<400> 64

Met Met Met Asp Leu Phe Glu Thr Gly Ser Tyr Phe Phe Tyr Leu Asp  
1 5 10 15

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

Leu Tyr Pro Gly Ser Asp Gly Thr Leu Ser Pro Cys Gln Asp Gln Met  
35 40 45

Pro Pro Glu Ala Gly Ser Asp Ser Ser Gly Glu Glu His Val Leu Ala  
50 55 60

Pro Pro Gly Leu Gln Pro Pro His Cys Pro Gly Gln Cys Leu Ile Trp  
65 70 75 80

Ala Cys Lys Thr Cys Lys Arg Lys Ser Ala Pro Thr Asp Arg Arg Lys  
85 90 95

Ala Ala Thr Leu Arg Glu Arg Arg Arg Leu Lys Lys Ile Asn Glu Ala  
100 105 110

Phe Glu Ala Leu Lys Arg Arg Thr Val Ala Asn Pro Asn Gln Arg Leu  
115 120 125

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

Gln Asp Leu Leu His Arg Leu Asp Gln Gln Glu Lys Met Gln Glu Leu  
145 150 155 160

Gly Val Asp Pro Phe Ser Tyr Arg Pro Lys Gln Glu Asn Leu Glu Gly  
165 170 175

Ala Asp Phe Leu Arg Thr Cys Ser Ser Gln Trp Pro Ser Val Ser Asp  
180 185 190

His Ser Arg Gly Leu Val Ile Thr Ala Lys Glu Gly Gly Ala Ser Ile  
195 200 205

Asp Ser Ser Ala Ser Ser Ser Leu Arg Cys Leu Ser Ser Ile Val Asp  
210 215 220

Ser Ile Ser Ser Glu Glu Arg Lys Leu Pro Cys Val Glu Glu Val Val  
225 230 235 240

Glu Lys Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu  
245 250 255

Glu Asn Pro Gly Pro Met Thr Leu Leu Gly Ser Glu His Ser Leu Leu  
260 265 270

Ile Arg Ser Lys Phe Arg Ser Val Leu Gln Leu Arg Leu Gln Gln Arg  
275 280 285

Arg Thr Gln Glu Gln Leu Ala Asn Gln Gly Ile Ile Pro Pro Leu Lys  
290 295 300

Arg Pro Ala Glu Phe His Glu Gln Arg Lys His Leu Asp Ser Asp Lys  
305 310 315 320

Ala Lys Asn Ser Leu Lys Arg Lys Ala Arg Asn Arg Cys Asn Ser Ala  
325 330 335

Asp Leu Val Asn Met His Ile Leu Gln Ala Ser Thr Ala Glu Arg Ser  
340 345 350

Ile Pro Thr Ala Gln Met Lys Leu Lys Arg Ala Arg Leu Ala Asp Asp  
355 360 365

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

Lys Asn Ile Leu Pro Val Asp Ser Ala Val Lys Glu Ala Ile Lys Gly  
385 390 395 400

Asn Gln Val Ser Phe Ser Lys Ser Thr Asp Ala Phe Ala Phe Glu Glu  
405 410 415

Asp Ser Ser Ser Asp Gly Leu Ser Pro Asp Gln Thr Arg Ser Glu Asp  
420 425 430

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

Pro Ser Thr Gly Ser Leu Gly Thr Asn Gln Asp Leu Ala Ser Gly Ser  
450 455 460

Glu Asn Asp Arg Asn Asp Ser Ala Ser Gln Pro Ser His Gln Ser Asp  
465 470 475 480

Ala Gly Lys Gln Gly Leu Gly Pro Pro Ser Thr Pro Ile Ala Val His  
485 490 495

Ala Ala Val Lys Ser Lys Ser Leu Gly Asp Ser Lys Asn Arg His Lys  
500 505 510

Lys Pro Lys Asp Pro Lys Pro Lys Val Lys Lys Leu Lys Tyr His Gln  
515 520 525

Tyr Ile Pro Pro Asp Gln Lys Ala Glu Lys Ser Pro Pro Pro Met Asp  
530 535 540

Ser Ala Tyr Ala Arg Leu Leu Gln Gln Gln Gln Leu Phe Leu Gln Leu  
545 550 555 560

Gln Ile Leu Ser Gln Gln Gln Gln Gln Gln His Arg Phe Ser Tyr  
565 570 575

Leu Gly Met His Gln Ala Gln Leu Lys Glu Pro Asn Glu Gln Met Val  
580 585 590

Arg Asn Pro Asn Ser Ser Ser Thr Pro Leu Ser Asn Thr Pro Leu Ser  
595 600 605

Pro Val Lys Asn Ser Phe Ser Gly Gln Thr Gly Val Ser Ser Phe Lys  
610 615 620

Pro Gly Pro Leu Pro Pro Asn Leu Asp Asp Leu Lys Val Ser Glu Leu  
625 630 635 640

Arg Gln Gln Leu Arg Ile Arg Gly Leu Pro Val Ser Gly Thr Lys Thr  
645 650 655

Ala Leu Met Asp Arg Leu Arg Pro Phe Gln Asp Cys Ser Gly Asn Pro  
660 665 670

Val Pro Asn Phe Gly Asp Ile Thr Thr Val Thr Phe Pro Val Thr Pro  
675 680 685

Asn Thr Leu Pro Asn Tyr Gln Ser Ser Ser Ser Thr Ser Ala Leu Ser  
690 695 700

Asn Gly Phe Tyr His Phe Gly Ser Thr Ser Ser Ser Pro Pro Ile Ser  
705 710 715 720

Pro Ala Ser Ser Asp Leu Ser Val Ala Gly Ser Leu Pro Asp Thr Phe  
725 730 735

Asn Asp Ala Ser Pro Ser Phe Gly Leu His Pro Ser Pro Val His Val  
740 745 750

Cys Thr Glu Glu Ser Leu Met Ser Ser Leu Asn Gly Gly Ser Val Pro  
755 760 765

Ser Glu Leu Asp Gly Leu Asp Ser Glu Lys Asp Lys Met Leu Val Glu  
770 775 780

Lys Gln Lys Val Ile Asn Glu Leu Thr Trp Lys Leu Gln Gln Glu Gln  
785 790 795 800

Arg Gln Val Glu Glu Leu Arg Met Gln Leu Gln Lys Gln Lys Arg Asn  
805 810 815

Asn Cys Ser Glu Glu Val Thr Gln Pro Pro Ser Tyr Glu Asp Ala Val  
820 825 830

Lys Gln Gln Met Thr Arg Ser Gln Gln Met Asp Glu Leu Leu Asp Val  
835 840 845

Leu Ile Glu Ser Gly Glu Met Pro Ala Asp Ala Arg Glu Asp His Ser  
850 855 860

Cys Leu Gln Lys Val Pro Lys Ile Pro Arg Ser Ser Arg Ser Pro Thr  
865 870 875 880

Ala Val Leu Thr Lys Pro Ser Ala Ser Phe Glu Gln Ala Ser Ser Gly  
885 890 895

Ser Gln Ile Pro Phe Asp Pro Tyr Ala Thr Asp Ser Asp Glu His Leu  
900 905 910

Glu Val Leu Leu Asn Ser Gln Ser Pro Leu Gly Lys Met Ser Asp Val  
915 920 925

Thr Leu Leu Lys Ile Gly Ser Glu Glu Pro His Phe Asp Gly Ile Met  
 930 935 940

Asp Gly Phe Ser Gly Lys Ala Ala Glu Asp Leu Phe Asn Ala His Glu  
 945 950 955 960

Ile Leu Pro Gly Pro Leu Ser Pro Met Gln Thr Gln Phe Ser Pro Ser  
 965 970 975

Ser Val Asp Ser Asn Gly Leu Gln Leu Ser Phe Thr Glu Ser Pro Trp  
 980 985 990

Glu Thr Met Glu Trp Leu Asp Leu Thr Pro Pro Asn Ser Thr Pro Gly  
 995 1000 1005

Phe Ser Ala Leu Thr Thr Ser Ser Pro Ser Ile Phe Asn Ile Asp  
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Phe Leu Asp Val Thr Asp Leu Asn Leu Asn Ser Ser Met Asp Leu  
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His Leu Gln Gln Trp  
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 ccttcaacca gctgtagcta tgcattga 88

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atccatgcaa aactgactgt ggtagtg 87

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