

SEQUENCE LISTING

<110> Tenaya Therapeutics Inc.
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Lombardi, Laura

<120> CARDIAC CELL REPROGRAMMING WITH ASCL1 OR MYF6

<130> TENA-007/02WO 334682-2062

<150> US 62/852,746

<151> 2019-05-24

<150> US 62/788,479

<151> 2019-01-04

<150> US 62/725,168

<151> 2018-08-30

<160> 84

<170> PatentIn version 3.5

<210> 1

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<212> PRT

<213> Homo sapiens

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Ile Ser Pro Asn Tyr Ser Asn Asp Leu Asn Ser Met Ala Gly Ser Pro
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Leu Ala Asn Gln Gly Ile Ile Pro Pro Leu Lys Arg Pro Ala Glu Phe
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His Glu Gln Arg Lys His Leu Asp Ser Asp Lys Ala Lys Asn Ser Leu
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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
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
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Gln Gln Gln Gln Gln Gln His Arg Phe Ser Tyr Leu Gly Met His Gln
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Ala Gln Leu Lys Glu Pro Asn Glu Gln Met Val Arg Asn Pro Asn Ser
325 330 335

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

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Ile Arg Gly Leu Pro Val Ser Gly Thr Lys Thr Ala Leu Met Asp Arg
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Leu Arg Pro Phe Gln Asp Cys Ser Gly Asn Pro Val Pro Asn Phe Gly
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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
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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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Gly Gly Asn Pro Cys Pro Lys Ser Pro Cys Val Gln Gln Lys Met Ala
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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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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
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Asp Leu Phe Asn Ala His Glu Ile Leu Pro Gly Pro Leu Ser Pro Met
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Gln Thr Gln Phe Ser Pro Ser Ser Val Asp Ser Asn Gly Leu Gln Leu
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Pro Pro Asn Ser Thr Pro Gly Phe Ser Ala Leu Thr Thr Ser Ser Pro
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35 40 45

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
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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
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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
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Pro Met Asn Leu Gly Met Asn Asn Arg Lys Pro Asp Leu Arg Val Leu
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Ile Pro Pro Gly Ser Lys Asn Thr Met Pro Ser Val Asn Gln Arg Ile
260 265 270

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Ala Thr Pro Thr Leu Pro Gly Gln Gly Met Gly Gly Tyr Pro Ser Ala
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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
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Val Thr Gly Trp Gln Gln Gln His Leu His Asn Met Pro Pro Ser Ala
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Leu Ser Gln Leu Gly Ala Cys Thr Ser Thr His Leu Ser Gln Ser Ser
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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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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
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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
325 330 335

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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Trp Pro Ser Met Pro Ser Tyr Ser Ser Cys Thr Val Thr Thr Val Gln
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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
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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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ctaccctacc agcacttctc cgctcacttc acctcggggc ccctggtccc tcggctggct	1320
ggcatggcca accatggctc cccacagctg ggagagggaa tgttccagca ccagacctcc	1380
gtggcccacc agcctgtggt caggcagtgt gggcctcaga ctggcctgca gtcccctggc	1440
acccttcagc cccctgagtt cctctactct catggcgtgc caaggactct atcccctcat	1500
cagtaccact ctgtgcacgg agttggcatg gtgccagagt ggagcgacaa tagctaa	1557

<210> 9
 <211> 20
 <212> PRT
 <213> Unknown

<220>

<223> nuclear localization sequence

<400> 9

Lys Arg Lys Glu 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> Artificial Sequence

<220>

<223> MYOCD 5-413

<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 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> Artificial Sequence

<220>
 <223> MYOCD 764-986

<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> Artificial Sequence

<220>

<223> MYOCD 5-438

<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 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> Artificial Sequence

<220>
<223> MYOCD 1-559

<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

<210> 14
<211> 636
<212> PRT
<213> Artificial Sequence

<220>
<223> MYOCD 1-413; 764-986 (Mydelta1)

<400> 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

<210> 15

<211> 661

<212> PRT

<213> Artificial Sequence

<220>

<223> MYOCD 1-438; 764-986 (Mydelta2)

<400> 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

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

<220>
 <223> MYOCD 1-559; 764-986 (Mydelta3)

<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 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> Unknown

<220>

<223> Mef2c interaction domain (5-120)

<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> Unknown

<220>

<223> SRF domain (210-320)

<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> Unknown

<220>
 <223> SAP domain (360-413)

<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
 50

<210> 20
 <211> 41
 <212> PRT
 <213> Unknown

<220>
 <223> LZ domain (510-550)

<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

<400> 21
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<400> 25

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<400> 29

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<223> MYF6-2A-Mydelta3

<400> 42
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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 ctttcagcta cagacccaaa caagaaaatc ttgagggtgc ggatttcctg 540
cgcacctgca gctcccagtg gccaagtgtt tccgatcatt ccagggggct cgtgataacg 600
gctaaggaag gaggagcaag tattgattcg tcagcctcga gtagccttcg atgcctttct 660
tccatcgtgg acagtatttc ctcggaggaa cgcaaactcc cctgcgtgga ggaagtgggtg 720
gagaaggcca cgaacttctc tctgttaaag caagcaggag acgtggaaga aaaccccgtt 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 aacaggtgca acagtgccga cttggttaat 1020
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ccagacgcta aagcctcaga tacccttcg acaggttctc tggggacaaa ccaggatctt 1380
gcttctggct cagaaaatga cagaaatgac tcagcctcac agcccagcca ccagtcagat 1440

gcggggaagc aggggcttgg cccccccagc acccccatag ccgtgcatgc tgctgtaaag	1500
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gtgaagaagc ttaaatatca ccagtacatt cccccagacc agaaggcaga gaagtcccct	1620
ccacctatgg actcagccta cgctcggctg ctccagcaac agcagctggt cctgcagctc	1680
caaatcctca gccagcagca gcagcagcag caacaccgat tcagctacct agggatgcac	1740
caagctcagc ttaaggaacc aaatgaacag atggtcagaa atccaaactc ttcttcaacg	1800
ccactgagca ataccccctt gtctcctgtc aaaaacagtt tttctggaca aactgggtgc	1860
tcttctttca aaccaggccc actcccacct aacctggatg atctgaaggt ctctgaatta	1920
agacaacagc ttcgaattcg gggcttgcct gtgtcaggca ccaaacggc tctcatggac	1980
cggcttcgac cttccagga ctgctctggc aaccagtgct cgaactttgg ggatataacg	2040
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agtgccctgt ccaacggctt ctaccacttt ggcagcacca gctccagccc cccgatctcc	2160
ccagcctcct ctgacctgtc agtcgctggg tccctgccgg acaccttcaa tgatgcctcc	2220
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tttgatccct atgccaccga cagtgatgag catcttgaag tcttattaaa ttcccagagc	2760
cccctaggaa agatgagtga tgtcaccctt ctaaaaattg ggagcgaaga gcctcacttt	2820
gatgggataa tggatggatt ctctgggaag gctgcagaag acctcttcaa tgcacatgag	2880
atcttgccag gccccctctc tccaatgcag acacagtttt caccctcttc tgtggacagc	2940
aatgggctgc agttaagctt cactgaatct ccctgggaaa ccatggagtg gctggacctc	3000
actccgcca attccacacc aggctttagc gccctcacca ccagcagccc cagcatcttc	3060

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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
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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

atgagtggct ccttcgatcg caagctcagc agcatcctca cgcacatctc cagctccctt 60

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ggctactaca gcgctcccca gcacgattac tactcgggcc agccctatgg ccagacgggtg 180

aaccctaca cctaccacca ccaattcaat ctcaatgggc ttgcaggcac gggcgcttac 240

tcgcccagt cggaatatac ctacggagcc tcctaccggc aatacggggc gtatcgggag 300

cagccgctgc cagcccagga ccagtgctg gtgaaggagg agccggaagc agaggtgcgc 360

atggtgaatg ggaagcccaa gaaggtccga aagccgcgta cgatctactc cagctaccag 420

ctggccgccc tgcagcgccg cttccagaag gccagtagc tggcgctgcc cgagcgcgcc 480

gagctggccg cgcagctggg cctcacgcag acacaggtga aaatctggtt ccagaaccgc 540

cgttccaagt tcaagaaact ctacaagaac ggggaggtgc cgctggagca cagtcccaat 600
 aacagtgatt ccatggcctg caactcacca ccatcacccg ccctctggga cacctcttcc 660
 cactccactc cggcccctgc ccgcagtcag ctgccccgc cgctcccata cagtgcctcc 720
 cccagctacc tggacgaccc caccaactcc tggtatcacg cacagaacct gagtggaccc 780
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 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

<210> 46
<211> 882
<212> DNA
<213> Homo sapiens

<400> 46
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ttcatggagt tcgggcagca gcagcagcag cagcagcaac agcagcagca gcagcagcag 120
caacagcaac agccgccgcc gccgccgccg ccgccgccgc agccgcactc gcagcagagc 180

tccccggcca tggcaggcgc gcactaccct ctgcactgcc tgcactcggc ggcggcggcg	240
gcagcgggccc gctcgcacca ccaccaccac caccagcacc accaccacgg ctcgccctac	300
gcgtcggggcg gaggggaactc ctacaaccac cgctcgtcgc ccgcctaccc ctacatgagc	360
cactcgcagc acagccctta cctccagtcc taccacaaca gcagcgcagc cgcccagacg	420
cgagggggacg acacagatca acaaaaaact acagtgattg aaaacgggga aatcaggttc	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
tcggcgggccc tgtcgccacg ctcgccagcg ctgcctccag tctgggacgt ttctgcctcg	780
gccaagggtg tcagtatgcc cccaacagc tacatgcctg gctatttctca ctggtactcc	840
tctccacacc aggacacgat gcagagacca cagatgatgt ga	882

<210> 47
 <211> 458
 <212> PRT
 <213> Homo sapiens

<400> 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 ccctggtggc 180
 tcttcagacg ccagtgggag ctacagttca accatgaatg gccatcagaa cggacttgac 240

tcgccacctc tctacccttc tgctcctatc ctgggaggtg gtgggcctgt caggaaactg	300
tatgatgact gctccagcac cattgttgaa gatccccaga ccaagtgtga atacatgctc	360
aactcgatgc ccaagagact gtgttttagtg tgtggtgaca tcgcttctgg gtaccactat	420
ggggtagcat catgtgaagc ctgcaaggca ttcttcaaga ggacaattca aggcaatata	480
gaatacagct gccctgccac gaatgaatgt gaaatcacia agcgcagacg taaatcctgc	540
caggcttgcc gcttcatgaa gtgttttaaaa gtgggcatgc tgaaagaagg ggtgcgtctt	600
gacagagtac gtggaggctg gcagaagtac aagcgcagga tagatgcgga gaacagccca	660
tacctgaacc ctgagctggt tcagccagcc aaaaagccat ataacaagat tgtctcacat	720
ttgttggtgg ctgaaccgga gaagatctat gccatgcctg accctactgt ccccgacagt	780
gacatcaaag ccctcactac actgtgtgac ttggccgacc gagagttggt ggttatcatt	840
ggatgggcca agcatattcc aggcttctcc acgctgtccc tggcggacca gatgagcctt	900
ctgcagagtg cttggatgga aattttgatc cttggtgtcg tataccggtc tctttcgttt	960
gaggatgaac ttgtctatgc agacgattat ataatggacg aagaccagtc caaattagca	1020
ggccttcttg atctaaataa tgctatcctg cagctggtaa agaaatacaa gagcatgaag	1080
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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

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

<400> 49

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

<210> 50
 <211> 1443
 <212> DNA
 <213> Homo sapiens

<400> 50
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 cctccagacg aggtggacgt cttcttcaat cacctcgact cgcagggcaa cccctactat 180
 gccaaccccg ctacgcgcg ggcgcgcgtc tcctacagcc ccgcgcacgc ccgcctgacc 240
 ggaggccaga tgtgccgcc acacttggtg cacagcccgg gtttgccctg gctggacggg 300
 ggcaaagcag ccctctctgc cgctgcggcc caccaccaca acccctggac cgtgagcccc 360
 ttctccaaga cgccactgca cccctcagct gctggaggcc ctggaggccc actctctgtg 420
 taccagggg ctgggggtgg gagcggggga ggcagcggga gctcagtggc ctccctcacc 480
 cctacagcag cccactctgg ctccacctt ttgggttcc caccacgcc acccaaagaa 540
 gtgtctcctg accctagcac cacgggggct gcgtctccag cctcatcttc cgcggggggg 600
 agtcagccc gaggagagga caaggacggc gtcaagtacc aggtgtcact gacggagagc 660
 atgaagatgg aaagtggcag tcccctgcgc ccaggcctag ctactatggg caccagcct 720
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 agcagcggac tcttccacc cggaggcttc ctggggggac cggcctccag cttcaccct 840
 aagcagcgca gcaaggctcg ttcctgttca gaaggccggg agtgtgtcaa ctgtggggcc 900
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 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 caagaaagg gcggagtgtc tcgaggagct gtcaaagtgc 1260
 atgcaggaga agtcatcccc cttcagtgc gctgccctgg ctggacacat ggcacctgtg 1320

ggccacctcc cgcccttcag ccactccgga cacatcctgc ccactccgac gcccatccac 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
 atgtatcaga gcttggccat ggccgccaac cacgggccgc ccccggtgc ctacgaggcg 60
 ggcgggcccc ggccttcat gcacggcgcg ggcgccgct cctcgccagt ctacgtgccc 120
 acaccgcggg tgccctcctc cgtgctgggc ctgtcctacc tccagggcgg aggcgcgggc 180
 tctgcgtccg gaggcgctc gggcggcagc tccggtgggg ccgctcttgg tgcggggccc 240
 gggacccagc agggcagccc gggatggagc caggcgggag ccgacggagc cgcttacacc 300
 ccgccgccgg tgtcgccgcg cttctccttc ccggggacca ccgggtccct ggcggccgcc 360
 gccgccgctg ccgcggcccc ggaagctgcg gcctacagca gtggcggcgg agcggcgggt 420
 gcgggcctgg cgggcccga gcagtacggg cgcgccggct tcgcgggctc ctactccagc 480
 ccctacccgg cttacatggc cgacgtgggc gcgtcctggg ccgcagccgc cgccgcctcc 540
 gccggcccct tcgacagccc ggtcctgcac agcctgccc gccgggcaa cccggccgcc 600
 cgacacccca atctcgtaga tatgtttgac gacttctcag aaggcagaga gtgtgtcaac 660
 tgtggggcta tgtccacccc gctctggagg cgagatggga cgggtcacta tctgtgcaac 720
 gcctgcggcc tctaccacaa gatgaacggc atcaaccggc cgctcatcaa gcctcagcgc 780
 cggctgtccg cctcccgccg agtgggcctc tcctgtgcca actgccagac caccaccacc 840
 acgctgtggc gccgcaatgc ggagggcgag cctgtgtgca atgcctgcgg cctctacatg 900

aagctccacg ggggtccccag gcctcttgca atgcggaaag aggggatcca aaccagaaaa	960
cggaagccca agaacctgaa taaatctaag acaccagcag ctccttcagg 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 cgcacagtca 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
 atggcccagc ccctgtgccc gccgctctcc gagtctctgga tgctctctgc ggcctggggc 60
 ccaactcggc ggccgccgcc ctccgacaag gactgcggcc gctccctcgt ctcgccccca 120
 gactcatggg gcagcacccc agccgacagc cccgtggcga gccccgcgcg gccaggcacc 180
 ctccgggacc cccgcgcccc ctccgtaggt aggcgcggcg cgcgcagcag ccgcctgggc 240
 agcgggcaga ggcagagcgc cagtgcgcgg gagaaactgc gcatgcgcac gctggcccg 300

gccctgcacg agctgcgccg ctttctaccg ccgtccgtgg cggccgcggg ccagagcctg 360
 accaagatcg agacgctgcg cctggctatc cgctatatcg gccacctgtc ggccgtgcta 420
 ggccctcagcg aggagagtct ccagcgccgg tgccggcagc gcggtgacgc ggggtcccct 480
 cggggctgcc cgctgtgccc cgacgactgc cccgcgcaga tgcagacacg gacgcaggct 540
 gaggggcagg ggcaggggcg cgggctgggc ctggtatccg ccgtccgcgc cggggcgtcc 600
 tggggatccc cgcctgcctg ccccgagacc cgagctgcac ccgagccgcg cgacccgcct 660
 gcgctgttcg ccgaggcggc gtgccctgaa gggcaggcga tggagccaag cccaccgtcc 720
 ccgctccttc cgggcgacgt gctggctctg ttggagacct ggatgccct ctcgcctctg 780
 gagtggctgc 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

<210> 56
<211> 729
<212> DNA
<213> Homo sapiens

<400> 56
atgatgatgg acctttttga aactggctcc tatttcttct acttgatgg ggaaaatgtt 60
actctgcagc cattagaagt ggcagaaggc tctcctttgt atccaggag 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 ctttcagcta cagacccaaa caagaaaatc ttgagggtgc ggatttcctg 540
cgcacctgca gctcccagtg gccaagtgtt tccgatcatt ccagggggct cgtgataacg 600
gctaaggaag gaggagcaag tattgattcg tcagcctcga gtagccttcg atgcctttct 660
tccatcgtgg acagtatttc ctcggaggaa cgcaaactcc cctgcgtgga ggaagtgggtg 720
gagaagtaa 729

<210> 57
<211> 1241
<212> PRT
<213> Artificial Sequence

<220>
<223> MYOCD-2A-ASCL1

<400> 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 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> MYOCD-2A-MYF6

<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> Mydelta3-2A-ASCL1

<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
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> Mydelta3-2A-MYF6

<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 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> ASCL1-2A-MYOC

<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 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> MYF6-2A-MY OCD

<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

Glu His Leu Glu Val Leu Leu Asn Ser Gln Ser Pro Leu Gly Lys
1115 1120 1125

Met Ser Asp Val Thr Leu Leu Lys Ile Gly Ser Glu Glu Pro His
1130 1135 1140

Phe Asp Gly Ile Met Asp Gly Phe Ser Gly Lys Ala Ala Glu Asp
1145 1150 1155

Leu Phe Asn Ala His Glu Ile Leu Pro Gly Pro Leu Ser Pro Met
1160 1165 1170

Gln Thr Gln Phe Ser Pro Ser Ser Val Asp Ser Asn Gly Leu Gln
1175 1180 1185

Leu Ser Phe Thr Glu Ser Pro Trp Glu Thr Met Glu Trp Leu Asp
1190 1195 1200

Leu Thr Pro Pro Asn Ser Thr Pro Gly Phe Ser Ala Leu Thr Thr
1205 1210 1215

Ser Ser Pro Ser Ile Phe Asn Ile Asp Phe Leu Asp Val Thr Asp
1220 1225 1230

Leu Asn Leu Asn Ser Ser Met Asp Leu His Leu Gln Gln Trp
1235 1240 1245

<210> 63
<211> 1037
<212> PRT
<213> Artificial Sequence

<220>
<223> ASCL1-2A-Mydelta3

<400> 63

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 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> MYF6-2A-Mydelta3

<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
1010 1015 1020

Phe Leu Asp Val Thr Asp Leu Asn Leu Asn Ser Ser Met Asp Leu
1025 1030 1035

His Leu Gln Gln Trp
1040

<210> 65
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - AAV capsid insert

<400> 65

Asn Lys Ile Gln Arg Thr Asp
1 5

<210> 66
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - AAV capsid insert

<400> 66

Asn Lys Thr Thr Asn Lys Asp
1 5

<210> 67

<211> 615

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - CAG promoter

<400> 67

ataacttacg gtaaattggcc cgcctggctg accgcccac gacccccgcc cattgacgtc	60
aataatgacg tatgtttcca tagtaacgcc aatagggact ttccattgac gtcaatgggt	120
ggagtattta cggtaaaactg cccacttggc agtacatcaa gtgtatcata tgccaagtac	180
gccccctatt gacgtcaatg acggtaaatg gcccgctgg cattatgccc agtacatgac	240
cttatgggac tttcctactt ggcagtacat ctactcgagg ccacgttctg cttcactctc	300
cccatctccc cccctcccc accccaatt ttgtatttat ttatTTTTTA attattttgt	360
gcagc gatgg gggcgggggg gggggggggg cgcgcgccag gcggggcggg gcggggcgag	420
gggcggggcg gggcgaggcg gagaggtgcg gcggcagcca atcagagcgg cgcgctccga	480
aagtttcctt ttatggcgag gcggcgggcg cgggcgccct ataaaaagcg aagcgcgcg	540
cgggcggggag cgggatcagc caccgcggtg gcggcctaga gtcgacgagg aactgaaaaa	600
ccagaaagtt aactg	615

<210> 68

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - SCP promoter

<400> 68

gtacttatat aagggggtgg gggcgcgttc gtcctcagtc gcgatcgaac actcgagccg	60
agcagacgtg cctacggacc g	81

<210> 69

<211> 96

<212> DNA
 <213> Human betaherpesvirus 5

 <400> 69
 gtaagtaccg cctatagact ctataggcac acccctttgg ctcttatgca tgctgacaga 60

 ctaacagact gttcctttcc tgggtctttt ctgcag 96

 <210> 70
 <211> 724
 <212> PRT
 <213> Adeno-associated virus 5

 <400> 70

 Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
 1 5 10 15

 Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
 20 25 30

 Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
 35 40 45

 Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
 50 55 60

 Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
 65 70 75 80

 Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
 85 90 95

 Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
 100 105 110

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

 Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
 130 135 140

 Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
 145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
180 185 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
195 200 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
210 215 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225 230 235 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
245 250 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
260 265 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
275 280 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
290 295 300

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

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
325 330 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
340 345 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
355 360 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
370 375 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385 390 395 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
405 410 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
420 425 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
435 440 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
450 455 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465 470 475 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
485 490 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
500 505 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
515 520 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
530 535 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545 550 555 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
565 570 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
580 585 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 71
<211> 2175
<212> DNA
<213> Adeno-associated virus 5

<400> 71
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gcccgtgggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180
ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240
cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc	360
aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc	420
ggaaagcggg tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc	480
aagccttcca cctcgtcaga cgccgaagct ggaccagcg gatcccagca gctgcaaadc	540
ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca	600
ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc	660
gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc	720
agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc	780
aacgcctact ttggatacag cccccctgg gggtactttg actttaaccg cttccacagc	840
cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg	900
tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc	960
accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag	1020
ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc	1080
tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc	1140
gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac	1200
aactttgagt ttacctaca ctttgaggag gtgcccttcc actccagctt cgctcccagt	1260
cagaacctct tcaagctggc caaccgctg gtggaccagt acttgtaccg cttcgtgagc	1320
acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc	1380
tacaaaaact ggttcccggg gcccatgggc cgaaccaggg gctggaacct gggctccggg	1440
gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg	1500
agttaccagg tgccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc	1560
tatgccctgg agaacactat gatcttcaac agccagccgg cgaaccggg caccaccgcc	1620
acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc	1680
gtggcgtaac acgtcggcgg gcagatggcc accaacaacc agagctccac cactgcccc	1740
gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac	1800
gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc	1860
tctccggcca tgggcggatt cggactcaaa caccaccgc ccatgatgct catcaagaac	1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc	1980
cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc	2040
aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac	2100
tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt	2160
acccgacccc tttaa	2175

<210> 72
 <211> 2346
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Made in Lab - MyDeta3 polynucleotide

<400> 72	
atgacactcc tggggtctga gcattccttg ctgattagga gcaagttcag atcagtttta	60
cagttaagac ttcaacaaag aaggaccag gaacaactgg ctaaccaagg cataatacca	120
ccactgaaac gtccagctga attccatgag caaagaaaac atttggatag tgacaaggct	180
aaaaattccc tgaagcgcaa agccagaaac aggtgcaaca gtgccgactt ggttaatatg	240
cacatactcc aagcttcac 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 tgcatgctgc tgtaaagtcc	720
aaatccttgg gtgacagtaa gaaccgccac aaaaagccca aggaccccaa gccaaaggtg	780
aagaagctta aatatcacca gtacattccc ccagaccaga aggcagagaa gtccccctcca	840
cctatggact cagcctacgc tcggctgctc cagcaacagc agctgttcct gcagctccaa	900
atcctcagcc agcagcagca gcagcagcaa caccgattca gctacctagg gatgcaccaa	960
gctcagctta aggaaccaa tgaacagatg gtcagaaatc caaactcttc ttcaacgcca	1020

ctgagcaata cccccctgtc tcctgtcaaa aacagttttt ctggacaaac tgggtgtctct	1080
tctttcaaac caggcccact cccacctaac ctggatgata tgaaggtctc tgaattaaga	1140
caacagcttc gaattcgggg cttgcctgtg tcaggcacca aaacggctct catggaccgg	1200
cttcgaccct tccaggactg ctctggcaac ccagtgccga actttgggga tataacgact	1260
gtcacttttc ctgtcacacc caacacgtg cccaattacc agtcttcctc ttctaccagt	1320
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cagtgg	2346

<210> 73
 <211> 97
 <212> DNA
 <213> Simian virus 40

<400> 73	
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agaactgctc ctcaagtggat gttgccttta cttctag 97

<210> 74
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in Lab - PolyA signal sequence

<400> 74
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<210> 75
<211> 589
<212> DNA
<213> Woodchuck hepatitis virus

<400> 75
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<210> 76
<211> 130
<212> DNA
<213> Adeno-associated virus 2

<400> 76
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aggggttcct 130

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<211> 4376
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in Lab - Bicistronic AAV5-MyDeta3A expression cassette

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<210> 78
 <211> 4636
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Made in Lab - Bicistronic AAV5-MyDeta3A expression cassette

<400> 78

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<210> 79
<211> 7447
<212> DNA
<213> Artificial Sequence

<220>

<223> Made in Lab - Bicistronic AAV5-MyDeta3A transfer plasmid

<400> 79

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<213> Artificial Sequence

<220>

<223> Made in Lab - Monocistronic AAV5-MyDeta3A expression cassette

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<212> DNA

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<220>

<223> Made in Lab - Monocistronic AAV5-MyDeta3A expression cassette

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<223> Made in Lab - Monocistronic AAV5-MyDeta3A transfer plasmid

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Leu Ala Asn Gln Gly Ile Ile Pro Pro Leu Lys Arg Pro Ala Glu Phe
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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
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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
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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
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
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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
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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
485 490 495

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
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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 Glu
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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
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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
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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 Gly Ser
770 775 780

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

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

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

Ala Cys Phe Phe Ala Thr Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
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Ala Ala Ala Gln Ser Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
850 855 860

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

Gly Gly His Lys Ser Ala Pro Lys Gln Val Lys Arg Gln Arg Ser Ser
885 890 895

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

Gly Tyr Ser Leu Pro Gln Gln Gln Pro Ala Ala Val Ala Arg Arg Asn
915 920 925

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

Leu Arg Glu His Val Pro Asn Gly Ala Ala Asn Lys Lys Met Ser Lys
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Val Glu Thr Leu Arg Ser Ala Val Glu Tyr Ile Arg Ala Leu Gln Gln
965 970 975

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

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

Ala Gly Ser Pro Val Ser Ser Tyr Ser Ser Asp Glu Gly Ser Tyr
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Asp Pro Leu Ser Pro Glu Glu Gln Glu Leu Leu Asp Phe Thr Asn
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Trp Phe
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<400> 84

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Glu Glu Asn Pro Gly Pro
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