

SEQ ID NOs final
SEQUENCE LISTING

<110> Danmarks tekniske universitet

<120> STATIN RESISTANCE AND EXPORT

<130> 53429PC01

<160> 20

<170> BiSSAP 1.3

<210> 1

<211> 1662

<212> DNA

<213> Fungi

<220>

<223> mlcE coding sequence, from the compactin biosynthetic gene cluster

<400> 1

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aagcaaccag ttttgattgg agtgatgatg ggtcttagtc agattgccat tgtctgtgga	540
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gcactagaat ggggagggtc gacctacacc tggcgaagtt ccgtcatcat cggcctgttc	840
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gttgccatga ttcctggctc agtggctggg aaacgacaag tgtgggtgctc ttgtttatatt	960
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caagtcatta tggctatggg ttctggcttc gcaattggaa agacaggata ctatttgcct	1140
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gtgggagcta cggcgtgcac gtttgtgttt gcctttggaa tgggatggcg gaagattgca	1620
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<210> 2

<211> 1662

<212> DNA

<213> Fungi

<220>

<223> mlcE coding sequence, synthetic codon optimized version

<400> 2

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aatgacacac tggaagctac cgaatcaaaa tcccagcaca taaccggcct taaacttggg	120
ttggtagtag catctgttac cttcgttgct ttccttatgt tactagatat gtccatcatt	180
gtaacagcta ttcctcacat tacatcagaa ttccattcat tgaatgatgt tggctggtac	240
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ttgctggggg taaagtacac ctttttcgcc tttttgtgta tcttcgaatt aggatctgtc	360
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ctgccaattg gtgccgttgc cgcttttcta ctattggtga ttacaattcc agacagaata	660
tcattctactg actctgagct ttctaccgac aagccaatgg ctaacatcaa atccaccctt	720
agaaagttag atttggttgg ttttgtcggt tttgctgcct tcgctacaat gattagtttg	780
gccttagagt ggggtgggtc cacttacact tggagatcat ctgtaatcat cggcttggtt	840
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gtcgcaatga ttccaggttc tgtggcagga aaaagacagg tgtggtgctc ttgcttggtt	960
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gccaacttag tctttgggtc tggattgagg actggcttat ctaagtacgc cccaacagtt	1440
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gtgggagcta cagcttgac ttttgtattt gcatttggaa tggggtggag aaagatagct	1620
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<210> 3

<211> 2337

<212> DNA

<213> Fungi

<220>

<223> mlcE-mRFP coding sequence, synthetic codon optimized version of
mlcE with mRFP fusion

<400> 3

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SEQ ID NOs final

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gtaacagcta ttcctcacat tacatcagaa ttccattcat tgaatgatgt tggctggtac	240
ggtagtgctt atcttttagc taattgtgcc ctgcaaccat tagctggcaa attgtatact	300
ttgctgggggt taaagtacac ctttttcgcc tttttgtgta tcttcgaatt aggatctgtc	360
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gccttagagt ggggtgggtc cacttacact tggagatcat ctgtaatcat cggcttggtt	840
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aatcttcctg gggttgttaa ggcatattca ttagcagtcg atcatacatt ctatctagca	1560
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gagcggatgt accccgagga cggcgccctg aagggcgaga tcaagatgag gctgaagctg	2160
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cagctgcccc gcgcctacaa gaccgacatc aagctggaca tcacctcca caacgaggac	2280
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<210> 4

<211> 1629

<212> DNA

<213> Fungi

<220>

<223> lovI/H coding sequence

<400> 4

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<210> 5

<211> 1632

<212> DNA

<213> Fungi

<220>

<223> mokI coding sequence

<400> 5

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agccatgtca	ccggcctaaa	gctaggactg	gtagtaacct	cggtgaccct	ggtggtgttt	120
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 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> /note="Primer (combined DNA/RNA)"
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<210> 7
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer (combined DNA/RNA)

<400> 7
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<210> 8
 <211> 33
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<220>
 <223> Primer (combined DNA/RNA)

<400> 8
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<210> 9
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 <212> DNA
 <213> Artificial Sequence

<220>
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<210> 10

<211> 30
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<223> Primer (combined DNA/RNA)

<400> 10
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<210> 11
<211> 30
<212> DNA
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<220>
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<400> 11
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<210> 12
<211> 28
<212> DNA
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<220>
<223> Primer (combined DNA/RNA)

<400> 12
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<210> 13
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<220>
<223> Primer (combined DNA/RNA)

<400> 13
agcgatacgu aaaaatggcc tcctccgag 29

<210> 14
<211> 21
<212> DNA
<213> Artificial Sequence

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<220>

<223> Primer

<400> 14

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21

<210> 15

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 15

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59

<210> 16

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 16

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60

ta

62

<210> 17

<211> 557

<212> PRT

<213> Fungi

<220>

<223> MlcE

<400> 17

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			20					25					30		
Ser	Lys	Ser	Gln	His	Ile	Thr	Gly	Leu	Lys	Leu	Gly	Leu	Val	Val	Ala
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Phe	Ala	Phe	Leu	Cys	Ile	Phe	Glu	Leu	Gly	Ser	Val	Leu	Cys	Gly	Ala	115	120	125
Ala	Arg	Ser	Ser	Thr	Met	Leu	Ile	Val	Gly	Arg	Ala	Val	Ala	Gly	Met	130	135	140
Gly	Gly	Ser	Gly	Leu	Val	Asn	Gly	Ala	Leu	Thr	Ile	Leu	Ser	Thr	Ala	145	150	155
Ala	Pro	Lys	His	Lys	Gln	Pro	Val	Leu	Ile	Gly	Val	Met	Met	Gly	Leu	165	170	175
Ser	Gln	Ile	Ala	Ile	Val	Cys	Gly	Pro	Leu	Leu	Gly	Gly	Ala	Phe	Thr	180	185	190
Gln	His	Ala	Thr	Trp	Arg	Trp	Cys	Phe	Tyr	Ile	Asn	Leu	Pro	Ile	Gly	195	200	205
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Ser	Ser	Thr	Asp	Ser	Glu	Leu	Ser	Thr	Asp	Lys	Pro	Met	Ala	Asn	Ile	225	230	235
Lys	Ser	Thr	Leu	Arg	Lys	Leu	Asp	Leu	Val	Gly	Phe	Val	Val	Phe	Ala	245	250	255
Ala	Phe	Ala	Thr	Met	Ile	Ser	Leu	Ala	Leu	Glu	Trp	Gly	Gly	Ser	Thr	260	265	270
Tyr	Thr	Trp	Arg	Ser	Ser	Val	Ile	Ile	Gly	Leu	Phe	Cys	Gly	Gly	Gly	275	280	285
Phe	Ala	Leu	Ile	Ala	Phe	Val	Leu	Trp	Glu	Arg	His	Val	Gly	Asp	Ala	290	295	300
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Ser	Cys	Leu	Phe	Met	Gly	Phe	Phe	Ser	Gly	Ser	Leu	Leu	Val	Phe	Ser	325	330	335
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Ala	Met	Val	Ser	Gly	Phe	Ala	Ile	Gly	Lys	Thr	Gly	Tyr	Tyr	Leu	Pro	370	375	380
Trp	Ala	Leu	Gly	Ser	Ala	Val	Leu	Val	Ala	Ile	Gly	Ala	Gly	Leu	Val	385	390	395
Ser	Thr	Phe	Gln	Pro	His	Thr	Ser	Thr	Val	Lys	Trp	Val	Met	Tyr	Gln	405	410	415
Phe	Ile	Ala	Gly	Phe	Gly	Arg	Gly	Cys	Gly	Met	Gln	Thr	Pro	Ile	Ile	420	425	430
Ala	Ile	Gln	Ser	Thr	Leu	Ser	Pro	Glu	Gln	Gly	Ala	Leu	Gly	Ile	Ser	435	440	445
Leu	Ala	Val	Phe	Gly	Gln	Thr	Phe	Gly	Gly	Ser	Leu	Phe	Leu	Asp	Phe	450	455	460
Ala	Asn	Leu	Val	Phe	Gly	Ser	Gly	Leu	Arg	Thr	Gly	Leu	Ser	Lys	Tyr	465	470	475
Ala	Pro	Thr	Val	Asp	Thr	Gln	Ala	Val	Thr	Ala	Ala	Gly	Ala	Thr	Gly	485	490	495

SEQ ID NOs final

Phe Arg Asp Val Val Ser Lys Asn Asn Leu Pro Gly Val Val Lys Ala
500 505 510
Tyr Ser Leu Ala Val Asp His Thr Phe Tyr Leu Ala Val Gly Ala Thr
515 520 525
Ala Cys Thr Phe Val Phe Ala Phe Gly Met Gly Trp Arg Lys Ile Ala
530 535 540
Thr Lys Asn Asp Thr Arg Ala Val Pro Glu Thr Asp Ala
545 550 555

<210> 18

<211> 542

<212> PRT

<213> Fungi

<220>

<223> LovI/H

<400> 18

Met Thr Ser His His Gly Glu Thr Glu Lys Pro Gln Ser Asn Thr Ala
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Gln Met Gln Ile Asn His Val Thr Gly Leu Arg Leu Gly Leu Val Val
20 25 30
Val Ser Val Thr Leu Val Ala Phe Leu Met Leu Leu Asp Met Ser Ile
35 40 45
Ile Val Thr Ala Ile Pro His Ile Thr Ala Gln Phe His Ser Leu Gly
50 55 60
Asp Val Gly Trp Tyr Gly Ser Ala Tyr Leu Leu Ser Ser Cys Ala Leu
65 70 75 80
Gln Pro Leu Ala Gly Lys Leu Tyr Thr Leu Leu Thr Leu Lys Tyr Thr
85 90 95
Phe Leu Ala Phe Leu Gly Leu Phe Glu Ile Gly Ser Val Leu Cys Gly
100 105 110
Thr Ala Arg Ser Ser Thr Met Leu Ile Val Gly Arg Ala Val Ala Gly
115 120 125
Met Gly Gly Ser Gly Leu Thr Asn Gly Ala Ile Thr Ile Leu Ser Ala
130 135 140
Ala Ala Pro Lys Gln Gln Gln Pro Leu Leu Ile Gly Ile Met Met Gly
145 150 155 160
Leu Ser Gln Ile Ala Ile Val Cys Gly Pro Leu Leu Gly Gly Ala Phe
165 170 175
Thr Gln His Ala Ser Trp Arg Trp Cys Phe Tyr Ile Asn Leu Pro Ile
180 185 190
Gly Ala Phe Ala Thr Phe Leu Leu Leu Val Ile Gln Ile Pro Asn Arg
195 200 205
Leu Pro Ser Thr Ser Asp Ser Thr Thr Asp Gly Thr Asn Pro Lys Arg
210 215 220
Arg Gly Ala Arg Asp Val Leu Thr Gln Leu Asp Phe Leu Gly Phe Val
225 230 235 240
Leu Phe Ala Gly Phe Ala Ile Met Ile Ser Leu Ala Leu Glu Trp Gly
245 250 255
Gly Ser Asp Tyr Ala Trp Asn Ser Ser Val Ile Ile Gly Leu Phe Cys
260 265 270

SEQ ID NOs final

Ala Ala Gly Val Ser Leu Val Leu Phe Gly Cys Trp Glu Arg His Val
275 280 285
Gly Gly Ala Val Ala Met Ile Pro Ile Ser Val Ala Ser Arg Arg Gln
290 295 300
Val Trp Cys Ser Cys Phe Phe Leu Gly Phe Phe Ser Gly Ala Leu Leu
305 310 315 320
Ile Phe Ser Tyr Tyr Leu Pro Ile Tyr Phe Gln Ala Val Lys Asn Val
325 330 335
Ser Pro Thr Met Ser Gly Val Tyr Met Leu Pro Gly Ile Gly Gly Gln
340 345 350
Ile Val Met Ala Ile Val Thr Gly Ala Ile Ile Gly Lys Thr Gly Tyr
355 360 365
Tyr Val Pro Trp Ala Leu Ala Ser Gly Ile Leu Val Ser Ile Ser Ala
370 375 380
Gly Leu Val Ser Thr Phe Gln Pro Glu Thr Ser Ile Ala Ala Trp Val
385 390 395 400
Met Tyr Gln Phe Leu Gly Gly Val Gly Arg Gly Cys Gly Met Gln Thr
405 410 415
Pro Val Val Ala Ile Gln Asn Ala Leu Pro Pro Gln Thr Ser Pro Ile
420 425 430
Gly Ile Ser Leu Ala Met Phe Gly Gln Thr Phe Gly Gly Ser Leu Phe
435 440 445
Leu Thr Leu Thr Glu Leu Val Phe Ser Asn Gly Leu Asp Ser Gly Leu
450 455 460
Arg Gln Tyr Ala Pro Thr Leu Asn Ala Gln Glu Val Thr Ala Ala Gly
465 470 475 480
Ala Thr Gly Phe Arg Gln Val Val Pro Ala Pro Leu Ile Ser Arg Val
485 490 495
Leu Leu Ala Tyr Ser Lys Gly Val Asp His Ala Phe Tyr Val Ala Val
500 505 510
Gly Ala Ser Gly Ala Thr Phe Ile Phe Ala Trp Gly Met Gly Arg Leu
515 520 525
Ala Trp Arg Gly Trp Arg Met Gln Glu Lys Gly Arg Ser Glu
530 535 540

<210> 19

<211> 543

<212> PRT

<213> Fungi

<220>

<223> MokI

<400> 19

Met Ala Ser His Gln Ser Glu Lys Glu Lys Pro Gln Ser Cys Thr Thr
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Glu Val Gln Val Ser His Val Thr Gly Leu Lys Leu Gly Leu Val Val
20 25 30
Thr Ser Val Thr Leu Val Val Phe Leu Met Leu Leu Asp Met Ser Ile
35 40 45
Ile Val Thr Ala Ile Pro His Ile Thr Ala Gln Phe His Ser Leu Gly
50 55 60

SEQ ID NOs final

Asp	Val	Gly	Trp	Tyr	Gly	Ser	Ala	Tyr	Leu	Leu	Ser	Ser	Cys	Ala	Leu	65	70	75	80
Gln	Pro	Leu	Ala	Gly	Lys	Leu	Tyr	Thr	Leu	Leu	Thr	Leu	Lys	Tyr	Thr		85	90	95
Phe	Leu	Ala	Phe	Leu	Gly	Val	Phe	Glu	Val	Gly	Ser	Ala	Leu	Cys	Gly		100	105	110
Ala	Ala	Arg	Cys	Ser	Thr	Met	Leu	Ile	Val	Gly	Arg	Ala	Val	Ala	Gly		115	120	125
Met	Gly	Gly	Ser	Gly	Leu	Thr	Asn	Gly	Ala	Ile	Thr	Ile	Leu	Ala	Ser		130	135	140
Ala	Ala	Pro	Lys	Gln	Gln	Gln	Pro	Leu	Leu	Ile	Gly	Ile	Met	Met	Gly	145	150	155	160
Leu	Ser	Gln	Ile	Ala	Ile	Val	Cys	Gly	Pro	Leu	Leu	Gly	Gly	Ala	Phe		165	170	175
Thr	Gln	His	Ala	Ser	Trp	Arg	Trp	Cys	Phe	Tyr	Ile	Asn	Leu	Pro	Val		180	185	190
Gly	Ala	Leu	Ala	Ala	Ile	Leu	Leu	Leu	Ala	Ile	His	Ile	Pro	Lys	Ser		195	200	205
Val	Pro	Thr	Ser	Asp	Cys	Thr	Met	Pro	Ala	Pro	Arg	Ala	Val	Gly	Val		210	215	220
Arg	Val	Ile	Leu	Ser	Gln	Leu	Asp	Leu	Leu	Gly	Phe	Val	Leu	Phe	Ala	225	230	235	240
Ala	Phe	Ala	Val	Met	Ile	Ser	Leu	Ala	Leu	Glu	Trp	Gly	Gly	Ser	Asp		245	250	255
Tyr	Met	Trp	Asp	Ser	Ser	Val	Ile	Ile	Gly	Leu	Phe	Cys	Gly	Ala	Gly		260	265	270
Ile	Ser	Leu	Val	Val	Phe	Gly	Phe	Trp	Glu	Arg	Tyr	Val	Gly	Asn	Ser		275	280	285
Met	Ala	Met	Ile	Pro	Phe	Ser	Val	Ala	Ser	Arg	Arg	Gln	Val	Trp	Cys	290	295	300	
Ser	Cys	Leu	Phe	Leu	Gly	Phe	Phe	Ser	Gly	Ala	Leu	Leu	Thr	Phe	Ser	305	310	315	320
Tyr	Tyr	Leu	Pro	Ile	Tyr	Phe	Gln	Ala	Val	Lys	Asp	Val	Ser	Pro	Thr		325	330	335
Met	Ser	Gly	Val	Tyr	Met	Leu	Pro	Gly	Ile	Gly	Gly	Gln	Ile	Val	Met		340	345	350
Ala	Ile	Val	Ser	Gly	Ala	Ile	Ile	Gly	Lys	Thr	Gly	Tyr	Tyr	Ile	Pro		355	360	365
Trp	Ala	Leu	Ala	Ser	Gly	Ile	Ile	Val	Ser	Ile	Ser	Ala	Gly	Leu	Val	370	375	380	
Ser	Thr	Phe	Gln	Pro	His	Thr	Ser	Ile	Ala	Ala	Trp	Val	Met	Tyr	Gln	385	390	395	400
Phe	Met	Gly	Gly	Phe	Gly	Arg	Gly	Cys	Gly	Met	Gln	Thr	Pro	Ile	Ile		405	410	415
Ala	Ile	Gln	His	Ala	Leu	Pro	Pro	Gln	Met	Ser	Ala	Leu	Gly	Ile	Ser		420	425	430
Leu	Ala	Met	Phe	Gly	Gln	Thr	Phe	Gly	Gly	Ser	Leu	Phe	Leu	Thr	Leu		435	440	445
Ala	Lys	Leu	Val	Phe	Ser	Ala	Gly	Leu	Asp	Ala	Gly	Leu	Arg	Glu	Tyr	450	455	460	
Ala	Pro	Ala	Val	Ser	Ala	Glu	Ala	Val	Thr	Ala	Ala	Gly	Ala	Thr	Gly	465	470	475	480

SEQ ID NOs final

Phe Arg Asp Val Val Pro Ala Asn Leu Leu Ser Gln Val Leu Leu Ala
485 490 495
Tyr Cys Lys Gly Ile Asp His Thr Phe Tyr Leu Ala Val Gly Ala Ser
500 505 510
Gly Ala Thr Phe Leu Phe Ala Trp Gly Met Gly Gln Val Gly Leu Ile
515 520 525
Trp Trp Gly Glu Glu Arg Thr Gly Phe Gly Arg Asp Glu Arg Val
530 535 540

<210> 20

<211> 778

<212> PRT

<213> Fungi

<220>

<223> MlcE-mRFP

<400> 20

Met Ser Glu Pro Leu Pro Pro Lys Glu Gly Glu Pro Arg Pro Gln Lys
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Glu Glu Ser Gln Asn Asp Thr Leu Glu Ala Thr Glu Ser Lys Ser Gln
20 25 30
His Ile Thr Gly Leu Lys Leu Gly Leu Val Val Ala Ser Val Thr Phe
35 40 45
Val Ala Phe Leu Met Leu Leu Asp Met Ser Ile Ile Val Thr Ala Ile
50 55 60
Pro His Ile Thr Ser Glu Phe His Ser Leu Asn Asp Val Gly Trp Tyr
65 70 75 80
Gly Ser Ala Tyr Leu Leu Ala Asn Cys Ala Leu Gln Pro Leu Ala Gly
85 90 95
Lys Leu Tyr Thr Leu Leu Gly Leu Lys Tyr Thr Phe Phe Ala Phe Leu
100 105 110
Cys Ile Phe Glu Leu Gly Ser Val Leu Cys Gly Ala Ala Arg Ser Ser
115 120 125
Thr Met Leu Ile Val Gly Arg Ala Val Ala Gly Met Gly Gly Ser Gly
130 135 140
Leu Val Asn Gly Ala Leu Thr Ile Leu Ser Thr Ala Ala Pro Lys His
145 150 155 160
Lys Gln Pro Val Leu Ile Gly Val Met Met Gly Leu Ser Gln Ile Ala
165 170 175
Ile Val Cys Gly Pro Leu Leu Gly Gly Ala Phe Thr Gln His Ala Thr
180 185 190
Trp Arg Trp Cys Phe Tyr Ile Asn Leu Pro Ile Gly Ala Val Ala Ala
195 200 205
Phe Leu Leu Leu Val Ile Thr Ile Pro Asp Arg Ile Ser Ser Thr Asp
210 215 220
Ser Glu Leu Ser Thr Asp Lys Pro Met Ala Asn Ile Lys Ser Thr Leu
225 230 235 240
Arg Lys Leu Asp Leu Val Gly Phe Val Val Phe Ala Ala Phe Ala Thr
245 250 255
Met Ile Ser Leu Ala Leu Glu Trp Gly Gly Ser Thr Tyr Thr Trp Arg
260 265 270

SEQ ID NOs final

Ser	Ser	Val	Ile	Ile	Gly	Leu	Phe	Cys	Gly	Gly	Gly	Phe	Ala	Leu	Ile	275	280	285
Ala	Phe	Val	Leu	Trp	Glu	Arg	His	Val	Gly	Asp	Ala	Val	Ala	Met	Ile	290	295	300
Pro	Gly	Ser	Val	Ala	Gly	Lys	Arg	Gln	Val	Trp	Cys	Ser	Cys	Leu	Phe	305	310	315
Met	Gly	Phe	Phe	Ser	Gly	Ser	Leu	Leu	Val	Phe	Ser	Tyr	Tyr	Leu	Pro	320	325	330
Ile	Tyr	Phe	Gln	Ala	Val	Lys	Asp	Val	Ser	Pro	Thr	Leu	Ser	Gly	Val	335	340	345
Tyr	Met	Leu	Pro	Gly	Ile	Leu	Gly	Gln	Val	Ile	Met	Ala	Met	Val	Ser	350	355	360
Gly	Phe	Ala	Ile	Gly	Lys	Thr	Gly	Tyr	Tyr	Leu	Pro	Trp	Ala	Leu	Gly	365	370	375
Ser	Ala	Val	Leu	Val	Ala	Ile	Gly	Ala	Gly	Leu	Val	Ser	Thr	Phe	Gln	380	385	390
Pro	His	Thr	Ser	Thr	Val	Lys	Trp	Val	Met	Tyr	Gln	Phe	Ile	Ala	Gly	395	400	405
Phe	Gly	Arg	Gly	Cys	Gly	Met	Gln	Thr	Pro	Ile	Ile	Ala	Ile	Gln	Ser	410	415	420
Thr	Leu	Ser	Pro	Glu	Gln	Gly	Ala	Leu	Gly	Ile	Ser	Leu	Ala	Val	Phe	425	430	435
Gly	Gln	Thr	Phe	Gly	Gly	Ser	Leu	Phe	Leu	Asp	Phe	Ala	Asn	Leu	Val	440	445	450
Phe	Gly	Ser	Gly	Leu	Arg	Thr	Gly	Leu	Ser	Lys	Tyr	Ala	Pro	Thr	Val	455	460	465
Asp	Thr	Gln	Ala	Val	Thr	Ala	Ala	Gly	Ala	Thr	Gly	Phe	Arg	Asp	Val	470	475	480
Val	Ser	Lys	Asn	Asn	Leu	Pro	Gly	Val	Val	Lys	Ala	Tyr	Ser	Leu	Ala	485	490	495
Val	Asp	His	Thr	Phe	Tyr	Leu	Ala	Val	Gly	Ala	Thr	Ala	Cys	Thr	Phe	500	505	510
Val	Phe	Ala	Phe	Gly	Met	Gly	Trp	Arg	Lys	Ile	Ala	Thr	Lys	Asn	Asp	515	520	525
Thr	Arg	Ala	Val	Pro	Glu	Thr	Asp	Ala	Met	Ala	Ser	Ser	Glu	Asp	Val	530	535	540
Ile	Lys	Glu	Phe	Met	Arg	Phe	Lys	Val	Arg	Met	Glu	Gly	Ser	Val	Asn	545	550	555
Gly	His	Glu	Phe	Glu	Ile	Glu	Gly	Glu	Gly	Glu	Gly	Arg	Pro	Tyr	Glu	560	565	570
Gly	Thr	Gln	Thr	Ala	Lys	Leu	Lys	Val	Thr	Lys	Gly	Gly	Pro	Leu	Pro	575	580	585
Phe	Ala	Trp	Asp	Ile	Leu	Ser	Pro	Gln	Phe	Gln	Tyr	Gly	Ser	Lys	Ala	590	595	600
Tyr	Val	Lys	His	Pro	Ala	Asp	Ile	Pro	Asp	Tyr	Leu	Lys	Leu	Ser	Phe	605	610	615
Pro	Glu	Gly	Phe	Lys	Trp	Glu	Arg	Val	Met	Asn	Phe	Glu	Asp	Gly	Gly	620	625	630
Val	Val	Thr	Val	Thr	Gln	Asp	Ser	Ser	Leu	Gln	Asp	Gly	Glu	Phe	Ile	635	640	645
Tyr	Lys	Val	Lys	Leu	Arg	Gly	Thr	Asn	Phe	Pro	Ser	Asp	Gly	Pro	Val	650	655	660
																665	670	675
																680	685	

SEQ ID NOs final															
Met	Gln	Lys	Lys	Thr	Met	Gly	Trp	Glu	Ala	Ser	Thr	Glu	Arg	Met	Tyr
690						695						700			
Pro	Glu	Asp	Gly	Ala	Leu	Lys	Gly	Glu	Ile	Lys	Met	Arg	Leu	Lys	Leu
705					710					715					720
Lys	Asp	Gly	Gly	His	Tyr	Asp	Ala	Glu	Val	Lys	Thr	Thr	Tyr	Met	Ala
				725					730					735	
Lys	Lys	Pro	Val	Gln	Leu	Pro	Gly	Ala	Tyr	Lys	Thr	Asp	Ile	Lys	Leu
			740					745					750		
Asp	Ile	Thr	Ser	His	Asn	Glu	Asp	Tyr	Thr	Ile	Val	Glu	Gln	Tyr	Glu
		755					760					765			
Arg	Ala	Glu	Gly	Arg	His	Ser	Thr	Gly	Ala						
770						775									