

SEQUENCE LISTING

<110> National University of Singapore

<120> Using Synthetic Lixiviant Biology For The Recovery of Precious
and Toxic Metals from Anthropogenic Sources

<130> SP100913W0

<150> SG10201903117U

<151> 2019-04-08

<150> SG10201904705X

<151> 2019-05-24

<160> 53

<170> PatentIn version 3.5

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<212> DNA

<213> Artificial Sequence

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<223> Forward primer merA

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24

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gatatacata tgcaccacca tcaccatcat

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cggatcagct gtttccgnnk ctgacaatgg tcgaag 36

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cttcgaccat tgtcagmnc ggaaacagct gatccg 36

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 <223> n is a, c, g, or t

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 atcgcttttcg agggttccat tggcctgggtc aacatgctgc aggccaaacg cctgctgcgc 180

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aaggcgttca tcgaggaagg cggtgaggtc tatgcctgcc gtttcgccct gcaggccctg	360
tacgggcaga ccgagaaagc gctgatcgaa ggcatccgcg ccatcaaccc gctggacgtg	420
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tcggtcggcc actacagccg gccggaactg ctcagcctgc tgatcgaccg cacgcctacc	1440
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catgtcagcc tctga	1515

<210> 12
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<223> SC-nit

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

Lys	Val	Leu	Asp	Ala	Ile	Ala	Asn	Ala	Ala	Lys	Lys	Gly	Val	Glu	Leu
		35					40					45			

Ile	Val	Phe	Pro	Glu	Thr	Phe	Val	Pro	Tyr	Tyr	Pro	Tyr	Phe	Ser	Phe
	50						55				60				

Val	Glu	Pro	Pro	Val	Leu	Met	Gly	Lys	Ser	His	Leu	Lys	Leu	Tyr	Gln
65					70					75					80

Glu	Ala	Val	Thr	Val	Pro	Gly	Lys	Val	Thr	Gln	Ala	Ile	Ala	Gln	Ala
				85					90					95	

Ala	Lys	Thr	His	Gly	Met	Val	Val	Val	Leu	Gly	Val	Asn	Glu	Arg	Glu
			100					105					110		

Glu	Gly	Ser	Leu	Tyr	Asn	Thr	Gln	Leu	Ile	Phe	Asp	Ala	Asp	Gly	Ala
		115					120					125			

Leu	Val	Leu	Lys	Arg	Arg	Lys	Ile	Thr	Pro	Thr	Tyr	His	Glu	Arg	Met
	130					135					140				

Val	Trp	Gly	Gln	Gly	Asp	Gly	Ala	Gly	Leu	Arg	Thr	Val	Asp	Thr	Thr
145					150					155					160

Val	Gly	Arg	Leu	Gly	Ala	Leu	Ala	Cys	Trp	Glu	His	Tyr	Asn	Pro	Leu
				165					170					175	

Ala Arg Tyr Ala Leu Met Ala Gln His Glu Gln Ile His Cys Gly Gln
180 185 190

Phe Pro Gly Ser Met Val Gly Gln Ile Phe Ala Asp Gln Met Glu Val
195 200 205

Thr Met Arg His His Ala Leu Glu Ser Gly Cys Phe Val Ile Asn Ala
210 215 220

Thr Gly Trp Leu Thr Ala Glu Gln Lys Leu Gln Ile Thr Thr Asp Glu
225 230 235 240

Lys Met His Gln Ala Leu Ser Gly Gly Cys Tyr Thr Ala Ile Ile Ser
245 250 255

Pro Glu Gly Lys His Leu Cys Glu Pro Ile Ala Glu Gly Glu Gly Leu
260 265 270

Ala Ile Ala Asp Leu Asp Phe Ser Leu Ile Ala Lys Arg Lys Arg Met
275 280 285

Met Asp Ser Val Gly His Tyr Ala Arg Pro Asp Leu Leu Gln Leu Thr
290 295 300

Leu Asn Asn Gln Pro Trp Ser Ala Leu Glu Ala Asn Pro Val Thr Pro
305 310 315 320

Asn Ala Ile Pro Ala Val Ser Asp Pro Glu Leu Thr Glu Thr Ile Glu
325 330 335

Ala Leu Pro Asn Asn Pro Ile Phe Ser His
340 345

<210> 13

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> BP-cynD

<400> 13

Met Thr Ser Ile Tyr Pro Lys Phe Arg Ala Ala Ala Val Gln Ala Ala
1 5 10 15

Pro Ile Tyr Leu Asn Leu Glu Ala Ser Val Glu Lys Ser Cys Glu Leu
20 25 30

Ile Asp Glu Ala Ala Ser Asn Gly Ala Lys Leu Val Ala Phe Pro Glu
35 40 45

Ala Phe Leu Pro Gly Tyr Pro Trp Phe Ala Phe Ile Gly His Pro Glu
50 55 60

Tyr Thr Arg Lys Phe Tyr His Glu Leu Tyr Lys Asn Ala Val Glu Ile
65 70 75 80

Pro Ser Leu Ala Ile Arg Lys Ile Ser Glu Ala Ala Lys Arg Asn Gly
85 90 95

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

Leu Ala Gln Leu Trp Phe Asn Pro Asn Gly Asp Leu Ile Gly Lys His
115 120 125

Arg Lys Met Arg Ala Ser Val Ala Glu Arg Leu Ile Trp Gly Asp Gly
130 135 140

Ser Gly Ser Met Met Pro Val Phe Gln Thr Glu Ile Gly Asn Leu Gly
145 150 155 160

Gly Leu Met Cys Trp Glu His Gln Val Pro Leu Asp Leu Met Ala Met
165 170 175

Asn Ala Gln Asn Glu Gln Val His Val Ala Ser Trp Pro Gly Tyr Phe

180

185

190

Asp Asp Glu Ile Ser Ser Arg Tyr Tyr Ala Ile Ala Thr Gln Thr Phe
 195 200 205

Val Leu Met Thr Ser Ser Ile Tyr Thr Glu Glu Met Lys Glu Met Ile
 210 215 220

Cys Leu Thr Gln Glu Gln Arg Asp Tyr Phe Glu Thr Phe Lys Ser Gly
 225 230 235 240

His Thr Cys Ile Tyr Gly Pro Asp Gly Glu Pro Ile Ser Glu Met Val
 245 250 255

Pro Ala Glu Thr Glu Gly Ile Ala Tyr Ala Glu Ile Asp Val Glu Arg
 260 265 270

Val Ile Asp Tyr Lys Tyr Tyr Ile Asp Pro Ala Gly His Tyr Ser Asn
 275 280 285

Gln Ser Leu Ser Met Asn Phe Asn Gln Gln Pro Thr Pro Val Val Lys
 290 295 300

His Leu Asn His Gln Lys Asn Glu Val Phe Thr Tyr Glu Asp Ile Gln
 305 310 315 320

Tyr Gln His Gly Ile Leu Gly Glu Lys Val
 325 330

<210> 14
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 <212> PRT
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 <223> PS-synD

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Met Ala His Tyr Pro Lys Phe Lys Ala Ala Ala Val Gln Ala Ala Pro

1	5	10	15
Val Tyr Leu Asn Leu Asp Ala Thr Val Glu Lys Ser Val Lys Leu Ile	20	25	30
Glu Glu Ala Ala Ser Asn Gly Ala Lys Leu Val Ala Phe Pro Glu Ala	35	40	45
Phe Ile Pro Gly Tyr Pro Trp Phe Ala Phe Leu Gly His Pro Glu Tyr	50	55	60
Thr Arg Arg Phe Tyr His Thr Leu Tyr Leu Asn Ala Val Glu Ile Pro	65	70	75
Ser Glu Ala Val Gln Lys Ile Ser Ala Ala Ala Arg Lys Asn Lys Ile	85	90	95
Tyr Val Cys Ile Ser Cys Ser Glu Lys Asp Gly Gly Ser Leu Tyr Leu	100	105	110
Ala Gln Leu Trp Phe Asn Pro Glu Gly Asp Leu Ile Gly Lys His Arg	115	120	125
Lys Met Arg Val Ser Val Ala Glu Arg Leu Cys Trp Gly Asp Gly Asn	130	135	140
Gly Ser Met Met Pro Val Phe Glu Thr Glu Ile Gly Asn Leu Gly Gly	145	150	155
Leu Met Cys Trp Glu His Asn Val Pro Leu Asp Ile Ala Ala Met Asn	165	170	175
Ser Gln Asn Glu Gln Val His Val Ala Ala Trp Pro Gly Phe Phe Asp	180	185	190
Asp Glu Thr Ala Ser Ser His Tyr Ala Ile Cys Asn Gln Ala Phe Val	195	200	205

Leu Met Thr Ser Ser Ile Tyr Ser Glu Glu Met Lys Asp Met Leu Cys
210 215 220

Glu Thr Gln Glu Glu Arg Asp Tyr Phe Asn Thr Phe Lys Ser Gly His
225 230 235 240

Thr Arg Ile Tyr Gly Pro Asp Gly Glu Pro Ile Ser Asp Leu Val Pro
245 250 255

Ala Glu Thr Glu Gly Ile Ala Tyr Ala Glu Ile Asp Ile Glu Lys Ile
260 265 270

Ile Asp Phe Lys Tyr Tyr Ile Asp Pro Val Gly His Tyr Ser Asn Gln
275 280 285

Ser Leu Ser Met Asn Phe Asn Gln Ser Pro Asn Pro Val Val Arg Lys
290 295 300

Ile Gly Glu Arg Asp Ser Thr Val Phe Thr Tyr Asp Asp Leu Asn Leu
305 310 315 320

Ser Val Ser Asp Glu Glu Pro Val Val Arg Ser Leu Arg Lys
325 330

<210> 15
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<212> PRT
<213> Artificial Sequence

<220>
<223> NitB

<400> 15

Met Pro Ser Val Asp Ile Ala His Tyr Lys Asp Gly Asp Phe Leu Val
1 5 10 15

Asn Tyr Glu Glu Lys Val Phe Glu Asp Val Lys Ala Glu Pro Gly Glu
20 25 30

Lys Ala Leu Ile Thr Phe His Thr Ile Ala Phe Glu Gly Ser Ile Gly
35 40 45

Leu Val Asn Met Leu Gln Ala Lys Arg Leu Leu Arg Lys Gly Phe Glu
50 55 60

Thr Lys Val Leu Leu Tyr Gly Pro Gly Val Gln Leu Gly Val Gln Arg
65 70 75 80

Gly Phe Pro Thr Leu Gly Asn Glu Ala Phe Pro Gly His Leu Ala Val
85 90 95

Asn Asn Gln Ile Lys Ala Phe Ile Glu Glu Gly Gly Glu Val Tyr Ala
100 105 110

Cys Arg Phe Ala Leu Gln Ala Leu Tyr Gly Gln Thr Glu Lys Ala Leu
115 120 125

Ile Glu Gly Ile Arg Ala Ile Asn Pro Leu Asp Val Met Asp Leu Arg
130 135 140

Leu Leu Met Arg Arg Glu Gly Ala Leu Ile Ile Asp Thr Trp Thr Ala
145 150 155 160

<210> 16
<211> 326
<212> PRT
<213> Artificial Sequence

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<223> NitC

<400> 16

Met Ala Ile Val Arg Ala Ala Ala Val Gln Leu Ser Pro Val Leu Tyr
1 5 10 15

Ser Arg Glu Gly Thr Val Glu Lys Ile Val Gln Thr Ile Leu Arg Leu
20 25 30

Gly Arg Glu Gly Val Gln Phe Ala Val Phe Pro Glu Thr Val Val Pro
35 40 45

Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Pro Pro Phe Met Met Gly Lys
50 55 60

Glu His Leu Arg Leu Leu Glu Glu Ser Val Gln Val Pro Ser Ala Ala
65 70 75 80

Thr Ala Ala Ile Ala Glu Ala Cys Arg Glu Ala Arg Met Val Val Ser
85 90 95

Leu Gly Ile Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Ala Gln Leu
100 105 110

Leu Phe Asp Ala Asp Gly Ser Leu Ile Gln His Arg Arg Lys Ile Thr
115 120 125

Pro Thr Tyr His Glu Arg Met Val Trp Gly Gln Gly Asp Gly Ser Gly
130 135 140

Leu Arg Ala Val Ala Ser Gln Val Gly Arg Ile Gly Ser Leu Ala Cys
145 150 155 160

Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala Asp Gly
165 170 175

Glu Gln Ile His Ala Ala Met Phe Pro Gly Ser Leu Val Gly Glu Ile
180 185 190

Phe Ala Glu Gln Ile Glu Val Ser Ile Arg His His Ala Leu Glu Ser
195 200 205

Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Glu Pro Glu Gln Gln
210 215 220

Gln Arg Ile Met Val Asp Thr Gly Cys Gly Leu Gly Pro Ile Ser Gly

225 230 235 240

Pro Leu Arg Ser Gly Glu Gly Glu Val Ile Ala Asp Leu Asp Leu Thr
260 265 270

Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Thr Ala His
290 295 300

Val Glu His Val Ser Leu
325

<220>
<223> dCas9

Met Asp Lys Lys Tyr Ser Ile Gly Leu Ala Ile Gly Thr Asn Ser Val
1 5 10 15

Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn Leu Ile
35 40 45

50

55

60

Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys
 65 70 75 80

Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
 85 90 95

Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
 100 105 110

His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
 115 120 125

His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
 130 135 140

Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
 145 150 155 160

Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro
 165 170 175

Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr
 180 185 190

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

Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
 210 215 220

Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
 225 230 235 240

Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
 245 250 255

Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
260 265 270

Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
275 280 285

Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
290 295 300

Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser
305 310 315 320

Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
325 330 335

Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
340 345 350

Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
355 360 365

Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
370 375 380

Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
385 390 395 400

Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu
405 410 415

Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe
420 425 430

Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile
435 440 445

Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp

450

455

460

Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu
 465 470 475 480

Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr
 485 490 495

Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser
 500 505 510

Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys
 515 520 525

Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
 530 535 540

Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
 545 550 555 560

Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
 565 570 575

Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
 580 585 590

Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
 595 600 605

Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
 610 615 620

Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
 625 630 635 640

His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
 645 650 655

Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
660 665 670

Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
675 680 685

Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
690 695 700

Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
705 710 715 720

His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
725 730 735

Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
740 745 750

Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
755 760 765

Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
770 775 780

Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
785 790 795 800

Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
805 810 815

Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
820 825 830

Leu Ser Asp Tyr Asp Val Asp Ala Ile Val Pro Gln Ser Phe Leu Lys
835 840 845

Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg

850

855

860

Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
 865 870 875 880

Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
 885 890 895

Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
 900 905 910

Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
 915 920 925

Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
 930 935 940

Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
 945 950 955 960

Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
 965 970 975

Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
 980 985 990

Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe
 995 1000 1005

Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile Ala
 1010 1015 1020

Lys Ser Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe
 1025 1030 1035

Tyr Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala
 1040 1045 1050

Asn Gly Glu Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu
1055 1060 1065

Thr Gly Glu Ile Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val
1070 1075 1080

Arg Lys Val Leu Ser Met Pro Gln Val Asn Ile Val Lys Lys Thr
1085 1090 1095

Glu Val Gln Thr Gly Gly Phe Ser Lys Glu Ser Ile Leu Pro Lys
1100 1105 1110

Arg Asn Ser Asp Lys Leu Ile Ala Arg Lys Lys Asp Trp Asp Pro
1115 1120 1125

Lys Lys Tyr Gly Gly Phe Asp Ser Pro Thr Val Ala Tyr Ser Val
1130 1135 1140

Leu Val Val Ala Lys Val Glu Lys Gly Lys Ser Lys Lys Leu Lys
1145 1150 1155

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

Phe Glu Lys Asn Pro Ile Asp Phe Leu Glu Ala Lys Gly Tyr Lys
1175 1180 1185

Glu Val Lys Lys Asp Leu Ile Ile Lys Leu Pro Lys Tyr Ser Leu
1190 1195 1200

Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu Ala Ser Ala Gly
1205 1210 1215

Glu Leu Gln Lys Gly Asn Glu Leu Ala Leu Pro Ser Lys Tyr Val
1220 1225 1230

Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu Lys Leu Lys Gly Ser

1235		1240		1245
Pro Glu Asp Asn Glu Gln Lys	Gln Leu Phe Val Glu	Gln His Lys		
1250	1255	1260		
His Tyr Leu Asp Glu Ile Ile	Glu Gln Ile Ser Glu	Phe Ser Lys		
1265	1270	1275		
Arg Val Ile Leu Ala Asp Ala	Asn Leu Asp Lys Val	Leu Ser Ala		
1280	1285	1290		
Tyr Asn Lys His Arg Asp Lys	Pro Ile Arg Glu Gln	Ala Glu Asn		
1295	1300	1305		
Ile Ile His Leu Phe Thr Leu	Thr Asn Leu Gly Ala	Pro Ala Ala		
1310	1315	1320		
Phe Lys Tyr Phe Asp Thr Thr	Ile Asp Arg Lys Arg	Tyr Thr Ser		
1325	1330	1335		
Thr Lys Glu Val Leu Asp Ala	Thr Leu Ile His Gln	Ser Ile Thr		
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Gly Leu Tyr Glu Thr Arg Ile	Asp Leu Ser Gln Leu	Gly Gly Asp		
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<220>
 <223> vioA promoter targeted

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 cgtccgccgt tgccgcgcgg

<210> 19
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 <212> DNA

<213> Artificial Sequence

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<223> vioB promoter targeted

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cgtcgccgcc cggttccggg 20

<210> 20

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<212> DNA

<213> Artificial Sequence

<220>

<223> vioC promoter targeted

<400> 20

agagcaatca tagtcggagg 20

<210> 21

<211> 1190

<212> DNA

<213> Artificial Sequence

<220>

<223> ParaBAD

<400> 21

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aacattgcga ccgacgggtgg cgataggcat ccgggtgggtg ctcaaaagca gcttcgcctg 180

gctgatacgt tggctcctgc gccagcttaa gacgctaadc cctaactgct ggcggaaaag 240

atgtgacaga cgcgacggcg acaagcaaac atgctgtgcg acgctggcga tatcaaaatt 300

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<210> 22
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<220>
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<213> Artificial Sequence

<220>
<223> Gols

<400> 24

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

Phe Ile Arg Arg Ala Arg Asp Leu Gly Phe Ser Val Ala Glu Ile Ser
50 55 60

Asp Leu Leu Asn Leu Trp Asn Asn Gln Ser Arg Gln Ser Ala Asp Val
65 70 75 80

Lys Arg Leu Ala Gln Thr His Ile Asp Glu Leu Asp Arg Arg Ile Gln
85 90 95

Asn Met Gln His Met Ala Gln Thr Leu Lys Ala Leu Ile His Cys Cys
100 105 110

Ala Gly Asp Ala Leu Pro Asp Cys Pro Ile Leu His Thr Leu Gly Gln
115 120 125

Pro Asp Asp Ser Glu Pro Glu Ala Arg Thr Gly Ala Val Leu Arg Arg
130 135 140

Pro Arg Arg His Gly Leu Ala Lys Arg Leu
145 150

<210> 25
<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> PgolTS

<400> 25
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<210> 26
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> PgolB

<400> 26
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cacaaaagga gttcact 77

<210> 27
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> GolS-mt1 A38I

<400> 27

Met Asn Ile Gly Lys Ala Ala Lys Ala Ser Lys Val Ser Ala Lys Met
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20 25 30

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

Phe Ile Arg Arg Ala Arg Asp Leu Gly Phe Ser Val Ala Glu Ile Ser
50 55 60

Asp Leu Leu Asn Leu Trp Asn Asn Gln Ser Arg Gln Ser Ala Asp Val
65 70 75 80

Lys Arg Leu Ala Gln Thr His Ile Asp Glu Leu Asp Arg Arg Ile Gln
85 90 95

Asn Met Gln His Met Ala Gln Thr Leu Lys Ala Leu Ile His Cys Cys
100 105 110

Ala Gly Asp Ala Leu Pro Asp Cys Pro Ile Leu His Thr Leu Gly Gln
115 120 125

Pro Asp Asp Ser Glu Pro Glu Ala Arg Thr Gly Ala Val Leu Arg Arg
130 135 140

Pro Arg Arg His Gly Leu Ala Lys Arg Leu
145 150

<210> 28
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> GolS-mt2 A38Q N97D

<400> 28

Met Asn Ile Gly Lys Ala Ala Lys Ala Ser Lys Val Ser Ala Lys Met
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Ile Arg Tyr Tyr Glu Gln Ile Gly Leu Ile Pro Ala Ala Ser Arg Thr
20 25 30

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

Phe Ile Arg Arg Ala Arg Asp Leu Gly Phe Ser Val Ala Glu Ile Ser
50 55 60

Asp Leu Leu Asn Leu Trp Asn Asn Gln Ser Arg Gln Ser Ala Asp Val
65 70 75 80

Lys Arg Leu Ala Gln Thr His Ile Asp Glu Leu Asp Arg Arg Ile Gln
85 90 95

Asp Met Gln His Met Ala Gln Thr Leu Lys Ala Leu Ile His Cys Cys
100 105 110

Ala Gly Asp Ala Leu Pro Asp Cys Pro Ile Leu His Thr Leu Gly Gln
115 120 125

Pro Asp Asp Ser Glu Pro Glu Ala Arg Thr Gly Ala Val Leu Arg Arg
130 135 140

Pro Arg Arg His Gly Leu Ala Lys Arg Leu
145 150

<210> 29
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> GolS-mt3-A38K V60L

<400> 29

Met Asn Ile Gly Lys Ala Ala Lys Ala Ser Lys Val Ser Ala Lys Met
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Ile Arg Tyr Tyr Glu Gln Ile Gly Leu Ile Pro Ala Ala Ser Arg Thr
20 25 30

Asp Ser Gly Tyr Arg Lys Tyr Thr Gln Ala Asp Val Asn Gln Leu His
35 40 45

Phe Ile Arg Arg Ala Arg Asp Leu Gly Phe Ser Leu Ala Glu Ile Ser
50 55 60

Asp Leu Leu Asn Leu Trp Asn Asn Gln Ser Arg Gln Ser Ala Asp Val
65 70 75 80

Lys Arg Leu Ala Gln Thr His Ile Asp Glu Leu Asp Arg Arg Ile Gln
85 90 95

Asn Met Gln His Met Ala Gln Thr Leu Lys Ala Leu Ile His Cys Cys
100 105 110

Ala Gly Asp Ala Leu Pro Asp Cys Pro Ile Leu His Thr Leu Gly Gln
115 120 125

Pro Asp Asp Ser Glu Pro Glu Ala Arg Thr Gly Ala Val Leu Arg Arg
130 135 140

Pro Arg Arg His Gly Leu Ala Lys Arg Leu
145 150

<210> 30
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> GolS-mt4-D33P

<400> 30

Met Asn Ile Gly Lys Ala Ala Lys Ala Ser Lys Val Ser Ala Lys Met
1 5 10 15

Ile Arg Tyr Tyr Glu Gln Ile Gly Leu Ile Pro Ala Ala Ser Arg Thr
20 25 30

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

Phe Ile Arg Arg Ala Arg Asp Leu Gly Phe Ser Val Ala Glu Ile Ser
50 55 60

Asp Leu Leu Asn Leu Trp Asn Asn Gln Ser Arg Gln Ser Ala Asp Val
65 70 75 80

Lys Arg Leu Ala Gln Thr His Ile Asp Glu Leu Asp Arg Arg Ile Gln
85 90 95

Asn Met Gln His Met Ala Gln Thr Leu Lys Ala Leu Ile His Cys Cys
100 105 110

Ala Gly Asp Ala Leu Pro Asp Cys Pro Ile Leu His Thr Leu Gly Gln
115 120 125

Pro Asp Asp Ser Glu Pro Glu Ala Arg Thr Gly Ala Val Leu Arg Arg
130 135 140

Pro Arg Arg His Gly Leu Ala Lys Arg Leu
145 150

<210> 31
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> PhlF

<400> 31

Met Ala Arg Thr Pro Ser Arg Ser Ser Ile Gly Ser Leu Arg Ser Pro
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His Thr His Lys Ala Ile Leu Thr Ser Thr Ile Glu Ile Leu Lys Glu
20 25 30

Cys Gly Tyr Ser Gly Leu Ser Ile Glu Ser Val Ala Arg Arg Ala Gly
35 40 45

Ala Ser Lys Pro Thr Ile Tyr Arg Trp Trp Thr Asn Lys Ala Ala Leu
50 55 60

Ile Ala Glu Val Tyr Glu Asn Glu Ser Glu Gln Val Arg Lys Phe Pro
65 70 75 80

Asp Leu Gly Ser Phe Lys Ala Asp Leu Asp Phe Leu Leu Arg Asn Leu
85 90 95

Trp Lys Val Trp Arg Glu Thr Ile Cys Gly Glu Ala Phe Arg Cys Val
100 105 110

Ile Ala Glu Ala Gln Leu Asp Pro Ala Thr Leu Thr Gln Leu Lys Asp
115 120 125

Gln Phe Met Glu Arg Arg Arg Glu Met Pro Lys Lys Leu Val Glu Asn
130 135 140

Ala Ile Ser Asn Gly Glu Leu Pro Lys Asp Thr Asn Arg Glu Leu Leu
145 150 155 160

Leu Asp Met Ile Phe Gly Phe Cys Trp Tyr Arg Leu Leu Thr Glu Gln
165 170 175

Leu Thr Val Glu Gln Asp Ile Glu Glu Phe Thr Phe Leu Leu Ile Asn
180 185 190

Gly Val Cys Pro Gly Thr Gln Arg
195 200

<210> 32

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> phlF operator

<400> 32

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<210> 33

<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

<223> merA nucleic acid sequence

<400> 33

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<210> 34
 <211> 467
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MerA amino acid sequence

<400> 34

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Ile	Glu	Arg	Gly	Thr	Ile	Gly	Gly	Thr	Cys	Val	Asn	Val	Gly	Cys	Val
		35					40					45			

Pro	Ser	Lys	Ile	Met	Ile	Arg	Ala	Ala	His	Ile	Ala	His	Leu	Arg	Arg
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Glu	Ser	Pro	Phe	Asp	Gly	Gly	Ile	Ala	Ala	Thr	Val	Pro	Thr	Ile	Asp
65					70					75				80	

Arg	Ser	Lys	Leu	Leu	Ala	Gln	Gln	Gln	Ala	Arg	Val	Asp	Glu	Leu	Arg
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His	Ala	Lys	Tyr	Glu	Gly	Ile	Leu	Gly	Gly	Asn	Pro	Ala	Ile	Thr	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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145					150					155					160
Ser	Pro	Tyr	Trp	Thr	Ser	Thr	Glu	Ala	Leu	Ala	Ser	Asp	Thr	Ile	Pro
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Glu	Arg	Leu	Ala	Val	Ile	Gly	Ser	Ser	Val	Val	Ala	Leu	Glu	Leu	Ala
			180					185					190		
Gln	Ala	Phe	Ala	Arg	Leu	Gly	Ser	Lys	Val	Thr	Val	Leu	Ala	Arg	Asn
	195						200					205			
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	210					215					220				
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225					230					235					240
Gln	Val	Ala	His	Met	Asp	Gly	Glu	Phe	Val	Leu	Thr	Thr	Thr	His	Gly
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Glu	Leu	Arg	Ala	Asp	Lys	Leu	Leu	Val	Ala	Thr	Gly	Arg	Thr	Pro	Asn
			260					265					270		
Thr	Arg	Ser	Leu	Ala	Leu	Asp	Ala	Ala	Gly	Val	Thr	Val	Asn	Ala	Gln
		275					280					285			
Gly	Ala	Ile	Val	Ile	Asp	Gln	Gly	Met	Arg	Thr	Ser	Asn	Pro	Asn	Ile
	290					295					300				

Tyr Ala Ala Gly Asp Cys Thr Asp Gln Pro Gln Phe Val Tyr Val Ala
305 310 315 320

Ala Ala Ala Gly Thr Arg Ala Ala Ile Asn Met Thr Gly Gly Asp Ala
325 330 335

Ala Leu Asp Leu Thr Ala Met Pro Ala Val Val Phe Thr Asp Pro Gln
340 345 350

Val Ala Thr Val Gly Tyr Ser Glu Ala Glu Ala His His Asp Gly Ile
355 360 365

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

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

Ser His Arg Leu Ile Gly Val Gln Ala Val Ala Pro Glu Ala Gly Glu
405 410 415

Leu Ile Gln Thr Ala Ala Leu Ala Ile Arg Asn Arg Met Thr Val Gln
420 425 430

Glu Leu Ala Asp Gln Leu Phe Pro Tyr Leu Thr Met Val Glu Gly Leu
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Lys Leu Ala Ala Gln Thr Phe Asn Lys Asp Val Lys Gln Leu Ser Cys
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Cys Ala Gly
465

<210> 35

<211> 2976

<212> DNA

<213> Artificial Sequence

<220>

<223> hcnABC

<400> 35

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gcagccgcgg caacatccac ctggccggcg acatcggcgg cctgcgcggc ggccaagcgg	1260
cgatgatcag cggccgcata gccgcgtgt ccatgctgct gcagctgggc aagctggacg	1320
agcaacaggc gctgcgcaa cgccaggcat gcctggacca gatggcgtcc atcctgcgt	1380

tccgcaaggg catagacagc ttcacccgcc gcggccgcgg ccagttggcg ctgccggcgc	1440
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aacagggcgt caacgacctg atcagcctga agatgcgcac ccgggtcagc atgggcgact	1560
gccagggcaa gatgtgcgtc ggctattgca gcgaccgcct gcgagcac accggcaagc	1620
gcgacgtggg ctggatacgc ccgcgcttcc cgctggaccc gctgccgttc tcggccttct	1680
ccgccatcga cgccaacag actgaagaga tttgacatga gcaagcaata cgacatcgtg	1740
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ctgaaaatcg cgctgatcga cagcaagcgt cccggcaacg cgtcgcgcg ctcggccggc	1860
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acctcggcca agcgcaagcg cgaggcggcc ggcgcgcgcg tggcgggtgga cgccagcacg	1980
ccgcacatcc tgccgcagag cttcttcgac ttcgcgctgg cctccaacgc gctgtacccg	2040
gccctgcacc aggaactgat ggaaaaccac ggcatggact tcaagttcga gcgcaccggg	2100
ctcaagtaca tcatttacga tgaagaagac cagctgtacg ccgagcacat cgccgccag	2160
attccgcacc tggccagcga ggtgagctgg ctggaccgcg ccagctgcg cgagagcgag	2220
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ttcaacgtca acgtcaccgg cgtcacccgc cagggcagcc gcgtgaccgg cgtgcgcacc	2400
gccgaggccg gcgatttctc ttgcaatacg ctgatcaacg ccggcggctc ctgggcggcc	2460
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atcgcgcaga aggacaacgg cgagatcctg atcggcagca ccaccgagga caagggtac	2640
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gacgagctgc ctatcctggg gccggaagac ggcgtcgagg ggtatctgaa cgcctgcggc	2820
cacttccgca ccggcatcct cacctcggcc atcaccgggg tgctgctgaa cgggctggtg	2880

cgcggcgagc cgctgccgct ggacatcgcg cccttcctgg ccggccgctt ccctaaccgc	2940
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<210> 36
 <211> 1233
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> serA

<400> 36	
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gcgctggatg atgaacaatt aaaagaatcc atccgcgatg cccacttcat cggcctgcga	180
tcccgtaacc atctgactga agacgtgatc aacgccgcag aaaaactggc cgctattggc	240
tgtttctgta tcggaacaaa ccaggttgat ctggatgcgg cggcaaagcg cgggatcccg	300
gtattttaacg caccgttctc aaatacgcg cttgttgctg agctggatgat tggcgaactg	360
ctgctgctat tgcgcggcgt gccggaagcc aatgctaaag cgcaccgtgg cgtgtggaac	420
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gatattgaaa ataaactgcc gctgggcaac gccactcagg tacagcatct ttctgacctg	600
ctgaatatga gcgatgtggg gagtctgcat gtaccagaga atccgtccac caaaaatatg	660
atgggcgcga aagaaatttc actaatgaag cccggctcgc tgctgattaa tgcttcgcgc	720
ggtactgtgg tggatattcc ggcgctgtgt gatgcgctgg cgagcaaaca tctggcgggg	780
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caggagaata tcggcctgga agttgcgggt aaattgatca agtattctga caatggctca	960
acgctctctg cggatgaactt cccggaagtc tcgctgccac tgcacgggtg gcgtcgtctg	1020
atgcacatcg ccgaagcccg tccgggcgtg ctaactgcgc tgaacaaaat cttcgccgag	1080

cagggcgtca acatcgccgc gcaatatctg caaacttccg cccagatggg ttatgtggtt 1140
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ccgggtacca ttcgcgcccg tctgctgtac taa 1233

<210> 37
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCon6

<400> 37
ctgatggcta gctcagtcct agggattatg ctagc 35

<210> 38
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> DM1 P49I

<400> 38

Met Glu Pro Pro Val Gln Val Ala Val Ile Gly Ser Gly Gly Ala Ala
1 5 10 15

Met Ala Ala Ala Leu Lys Ala Val Glu Gln Gly Ala Gln Val Thr Leu
20 25 30

Ile Glu Arg Gly Thr Ile Gly Gly Thr Cys Val Asn Val Gly Cys Val
35 40 45

Ile Ser Lys Ile Met Ile Arg Ala Ala His Ile Ala His Leu Arg Arg
50 55 60

Glu Ser Pro Phe Asp Gly Gly Ile Ala Ala Thr Val Pro Thr Ile Asp
65 70 75 80

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

85

90

95

His Ala Lys Tyr Glu Gly Ile Leu Gly Gly Asn Pro Ala Ile Thr Val
 100 105 110

Val His Gly Glu Ala Arg Phe Lys Asp Asp Gln Ser Leu Thr Val Arg
 115 120 125

Leu Asn Glu Gly Gly Glu Arg Val Val Met Phe Asp Arg Cys Leu Val
 130 135 140

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

Ser Pro Tyr Trp Thr Ser Thr Glu Ala Leu Ala Ser Asp Thr Ile Pro
 165 170 175

Glu Arg Leu Ala Val Ile Gly Ser Ser Val Val Ala Leu Glu Leu Ala
 180 185 190

Gln Ala Phe Ala Arg Leu Gly Ser Lys Val Thr Val Leu Ala Arg Asn
 195 200 205

Thr Leu Phe Phe Arg Glu Asp Pro Ala Ile Gly Glu Ala Val Thr Ala
 210 215 220

Ala Phe Arg Ala Glu Gly Ile Glu Val Leu Glu His Thr Gln Ala Ser
 225 230 235 240

Gln Val Ala His Met Asp Gly Glu Phe Val Leu Thr Thr Thr His Gly
 245 250 255

Glu Leu Arg Ala Asp Lys Leu Leu Val Ala Thr Gly Arg Thr Pro Asn
 260 265 270

Thr Arg Ser Leu Ala Leu Asp Ala Ala Gly Val Thr Val Asn Ala Gln
 275 280 285

Gly Ala Ile Val Ile Asp Gln Gly Met Arg Thr Ser Asn Pro Asn Ile
290 295 300

Tyr Ala Ala Gly Asp Cys Thr Asp Gln Pro Gln Phe Val Tyr Val Ala
305 310 315 320

Ala Ala Ala Gly Thr Arg Ala Ala Ile Asn Met Thr Gly Gly Asp Ala
325 330 335

Ala Leu Asp Leu Thr Ala Met Pro Ala Val Val Phe Thr Asp Pro Gln
340 345 350

Val Ala Thr Val Gly Tyr Ser Glu Ala Glu Ala His His Asp Gly Ile
355 360 365

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

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

Ser His Arg Leu Ile Gly Val Gln Ala Val Ala Pro Glu Ala Gly Glu
405 410 415

Leu Ile Gln Thr Ala Ala Leu Ala Ile Arg Asn Arg Met Thr Val Gln
420 425 430

Glu Leu Ala Asp Gln Leu Phe Pro Tyr Leu Thr Met Val Glu Gly Leu
435 440 445

Lys Leu Ala Ala Gln Thr Phe Asn Lys Asp Val Lys Gln Leu Ser Cys
450 455 460

Cys Ala Gly
465

<210> 39

<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> DM2 I293F

<400> 39

Met Glu Pro Pro Val Gln Val Ala Val Ile Gly Ser Gly Gly Ala Ala
1 5 10 15

Met Ala Ala Ala Leu Lys Ala Val Glu Gln Gly Ala Gln Val Thr Leu
20 25 30

Ile Glu Arg Gly Thr Ile Gly Gly Thr Cys Val Asn Val Gly Cys Val
35 40 45

Pro Ser Lys Ile Met Ile Arg Ala Ala His Ile Ala His Leu Arg Arg
50 55 60

Glu Ser Pro Phe Asp Gly Gly Ile Ala Ala Thr Val Pro Thr Ile Asp
65 70 75 80

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

His Ala Lys Tyr Glu Gly Ile Leu Gly Gly Asn Pro Ala Ile Thr Val
100 105 110

Val His Gly Glu Ala Arg Phe Lys Asp Asp Gln Ser Leu Thr Val Arg
115 120 125

Leu Asn Glu Gly Gly Glu Arg Val Val Met Phe Asp Arg Cys Leu Val
130 135 140

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

Ser Pro Tyr Trp Thr Ser Thr Glu Ala Leu Ala Ser Asp Thr Ile Pro

165

170

175

Glu Arg Leu Ala Val Ile Gly Ser Ser Val Val Ala Leu Glu Leu Ala
 180 185 190

Gln Ala Phe Ala Arg Leu Gly Ser Lys Val Thr Val Leu Ala Arg Asn
 195 200 205

Thr Leu Phe Phe Arg Glu Asp Pro Ala Ile Gly Glu Ala Val Thr Ala
 210 215 220

Ala Phe Arg Ala Glu Gly Ile Glu Val Leu Glu His Thr Gln Ala Ser
 225 230 235 240

Gln Val Ala His Met Asp Gly Glu Phe Val Leu Thr Thr Thr His Gly
 245 250 255

Glu Leu Arg Ala Asp Lys Leu Leu Val Ala Thr Gly Arg Thr Pro Asn
 260 265 270

Thr Arg Ser Leu Ala Leu Asp Ala Ala Gly Val Thr Val Asn Ala Gln
 275 280 285

Gly Ala Ile Val Phe Asp Gln Gly Met Arg Thr Ser Asn Pro Asn Ile
 290 295 300

Tyr Ala Ala Gly Asp Cys Thr Asp Gln Pro Gln Phe Val Tyr Val Ala
 305 310 315 320

Ala Ala Ala Gly Thr Arg Ala Ala Ile Asn Met Thr Gly Gly Asp Ala
 325 330 335

Ala Leu Asp Leu Thr Ala Met Pro Ala Val Val Phe Thr Asp Pro Gln
 340 345 350

Val Ala Thr Val Gly Tyr Ser Glu Ala Glu Ala His His Asp Gly Ile
 355 360 365

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

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

Ser His Arg Leu Ile Gly Val Gln Ala Val Ala Pro Glu Ala Gly Glu
405 410 415

Leu Ile Gln Thr Ala Ala Leu Ala Ile Arg Asn Arg Met Thr Val Gln
420 425 430

Glu Leu Ala Asp Gln Leu Phe Pro Tyr Leu Thr Met Val Glu Gly Leu
435 440 445

Lys Leu Ala Ala Gln Thr Phe Asn Lys Asp Val Lys Gln Leu Ser Cys
450 455 460

Cys Ala Gly
465

<210> 40
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> DM3 T299R

<400> 40

Met Glu Pro Pro Val Gln Val Ala Val Ile Gly Ser Gly Gly Ala Ala
1 5 10 15

Met Ala Ala Ala Leu Lys Ala Val Glu Gln Gly Ala Gln Val Thr Leu
20 25 30

Ile Glu Arg Gly Thr Ile Gly Gly Thr Cys Val Asn Val Gly Cys Val
35 40 45

Pro Ser Lys Ile Met Ile Arg Ala Ala His Ile Ala His Leu Arg Arg
50 55 60

Glu Ser Pro Phe Asp Gly Gly Ile Ala Ala Thr Val Pro Thr Ile Asp
65 70 75 80

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

His Ala Lys Tyr Glu Gly Ile Leu Gly Gly Asn Pro Ala Ile Thr Val
100 105 110

Val His Gly Glu Ala Arg Phe Lys Asp Asp Gln Ser Leu Thr Val Arg
115 120 125

Leu Asn Glu Gly Gly Glu Arg Val Val Met Phe Asp Arg Cys Leu Val
130 135 140

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

Ser Pro Tyr Trp Thr Ser Thr Glu Ala Leu Ala Ser Asp Thr Ile Pro
165 170 175

Glu Arg Leu Ala Val Ile Gly Ser Ser Val Val Ala Leu Glu Leu Ala
180 185 190

Gln Ala Phe Ala Arg Leu Gly Ser Lys Val Thr Val Leu Ala Arg Asn
195 200 205

Thr Leu Phe Phe Arg Glu Asp Pro Ala Ile Gly Glu Ala Val Thr Ala
210 215 220

Ala Phe Arg Ala Glu Gly Ile Glu Val Leu Glu His Thr Gln Ala Ser
225 230 235 240

Gln Val Ala His Met Asp Gly Glu Phe Val Leu Thr Thr Thr His Gly

	245		250		255										
Glu	Leu	Arg	Ala	Asp	Lys	Leu	Leu	Val	Ala	Thr	Gly	Arg	Thr	Pro	Asn
	260							265					270		
Thr	Arg	Ser	Leu	Ala	Leu	Asp	Ala	Ala	Gly	Val	Thr	Val	Asn	Ala	Gln
	275						280					285			
Gly	Ala	Ile	Val	Ile	Asp	Gln	Gly	Met	Arg	Arg	Ser	Asn	Pro	Asn	Ile
	290					295					300				
Tyr	Ala	Ala	Gly	Asp	Cys	Thr	Asp	Gln	Pro	Gln	Phe	Val	Tyr	Val	Ala
305					310					315					320
Ala	Ala	Ala	Gly	Thr	Arg	Ala	Ala	Ile	Asn	Met	Thr	Gly	Gly	Asp	Ala
				325					330					335	
Ala	Leu	Asp	Leu	Thr	Ala	Met	Pro	Ala	Val	Val	Phe	Thr	Asp	Pro	Gln
			340					345					350		
Val	Ala	Thr	Val	Gly	Tyr	Ser	Glu	Ala	Glu	Ala	His	His	Asp	Gly	Ile
	355						360					365			
Glu	Thr	Asp	Ser	Arg	Thr	Leu	Thr	Leu	Asp	Asn	Val	Pro	Arg	Ala	Leu
	370					375					380				
Ala	Asn	Phe	Asp	Thr	Arg	Gly	Phe	Ile	Lys	Leu	Val	Ile	Glu	Glu	Gly
385					390					395					400
Ser	His	Arg	Leu	Ile	Gly	Val	Gln	Ala	Val	Ala	Pro	Glu	Ala	Gly	Glu
			405					410						415	
Leu	Ile	Gln	Thr	Ala	Ala	Leu	Ala	Ile	Arg	Asn	Arg	Met	Thr	Val	Gln
		420						425					430		
Glu	Leu	Ala	Asp	Gln	Leu	Phe	Pro	Tyr	Leu	Thr	Met	Val	Glu	Gly	Leu
	435						440					445			

Lys Leu Ala Ala Gln Thr Phe Asn Lys Asp Val Lys Gln Leu Ser Cys
450 455 460

Cys Ala Gly
465

<210> 41
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> DM4 A323D

<400> 41

Met Glu Pro Pro Val Gln Val Ala Val Ile Gly Ser Gly Gly Ala Ala
1 5 10 15

Met Ala Ala Ala Leu Lys Ala Val Glu Gln Gly Ala Gln Val Thr Leu
20 25 30

Ile Glu Arg Gly Thr Ile Gly Gly Thr Cys Val Asn Val Gly Cys Val
35 40 45

Pro Ser Lys Ile Met Ile Arg Ala Ala His Ile Ala His Leu Arg Arg
50 55 60

Glu Ser Pro Phe Asp Gly Gly Ile Ala Ala Thr Val Pro Thr Ile Asp
65 70 75 80

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

His Ala Lys Tyr Glu Gly Ile Leu Gly Gly Asn Pro Ala Ile Thr Val
100 105 110

Val His Gly Glu Ala Arg Phe Lys Asp Asp Gln Ser Leu Thr Val Arg
115 120 125

Leu Asn Glu Gly Gly Glu Arg Val Val Met Phe Asp Arg Cys Leu Val
130 135 140

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

Ser Pro Tyr Trp Thr Ser Thr Glu Ala Leu Ala Ser Asp Thr Ile Pro
165 170 175

Glu Arg Leu Ala Val Ile Gly Ser Ser Val Val Ala Leu Glu Leu Ala
180 185 190

Gln Ala Phe Ala Arg Leu Gly Ser Lys Val Thr Val Leu Ala Arg Asn
195 200 205

Thr Leu Phe Phe Arg Glu Asp Pro Ala Ile Gly Glu Ala Val Thr Ala
210 215 220

Ala Phe Arg Ala Glu Gly Ile Glu Val Leu Glu His Thr Gln Ala Ser
225 230 235 240

Gln Val Ala His Met Asp Gly Glu Phe Val Leu Thr Thr Thr His Gly
245 250 255

Glu Leu Arg Ala Asp Lys Leu Leu Val Ala Thr Gly Arg Thr Pro Asn
260 265 270

Thr Arg Ser Leu Ala Leu Asp Ala Ala Gly Val Thr Val Asn Ala Gln
275 280 285

Gly Ala Ile Val Ile Asp Gln Gly Met Arg Thr Ser Asn Pro Asn Ile
290 295 300

Tyr Ala Ala Gly Asp Cys Thr Asp Gln Pro Gln Phe Val Tyr Val Ala
305 310 315 320

Ala Ala Asp Gly Thr Arg Ala Ala Ile Asn Met Thr Gly Gly Asp Ala

325

330

335

Ala Leu Asp Leu Thr Ala Met Pro Ala Val Val Phe Thr Asp Pro Gln
 340 345 350

Val Ala Thr Val Gly Tyr Ser Glu Ala Glu Ala His His Asp Gly Ile
 355 360 365

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

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

Ser His Arg Leu Ile Gly Val Gln Ala Val Ala Pro Glu Ala Gly Glu
 405 410 415

Leu Ile Gln Thr Ala Ala Leu Ala Ile Arg Asn Arg Met Thr Val Gln
 420 425 430

Glu Leu Ala Asp Gln Leu Phe Pro Tyr Leu Thr Met Val Glu Gly Leu
 435 440 445

Lys Leu Ala Ala Gln Thr Phe Asn Lys Asp Val Lys Gln Leu Ser Cys
 450 455 460

Cys Ala Gly
 465

<210> 42
 <211> 425
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DM5 A323D (del324 - 365)

<400> 42

Met Glu Pro Pro Val Gln Val Ala Val Ile Gly Ser Gly Gly Ala Ala

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Met	Ala	Ala	Ala
	20		
Leu	Lys	Ala	Val
		25	
Glu	Gln	Gly	Ala
			30
Gln	Val	Thr	Leu
Ile	Glu	Arg	Gly
	35		
Thr	Ile	Gly	Gly
		40	
Thr	Cys	Val	Asn
			45
Val	Gly	Cys	Val
Pro	Ser	Lys	Ile
	50		
Met	Ile	Arg	Ala
		55	
Ala	Ala	His	Ile
			60
Ala	His	Leu	Arg
			Arg
Glu	Ser	Pro	Phe
			Asp
		70	
Gly	Gly	Ile	Ala
			Ala
		75	
Thr	Val	Pro	Thr
			Ile
			Asp
			80
Arg	Ser	Lys	Leu
			85
Leu	Ala	Gln	Gln
			Gln
		90	
Ala	Arg	Val	Asp
			Glu
			95
Leu	Arg		
His	Ala	Lys	Tyr
			100
Glu	Gly	Ile	Leu
			105
Gly	Gly	Asn	Pro
			Ala
			110
Ile	Thr	Val	
Val	His	Gly	Glu
			115
Ala	Arg	Phe	Lys
			120
Asp	Asp	Gln	Ser
			125
Leu	Thr	Val	Arg
Leu	Asn	Glu	Gly
			130
Gly	Glu	Arg	Val
		135	
Val	Met	Phe	Asp
			140
Arg	Cys	Leu	Val
Ala	Thr	Gly	Ala
			Ser
		150	
Pro	Ala	Val	Pro
			Pro
		155	
Ile	Pro	Gly	Leu
			Lys
			Glu
			160
Ser	Pro	Tyr	Trp
			165
Thr	Ser	Thr	Glu
			Ala
		170	
Leu	Ala	Ser	Asp
			Thr
			175
Ile	Pro		
Glu	Arg	Leu	Ala
			180
Val	Ile	Gly	Ser
			Ser
		185	
Val	Val	Ala	Leu
			Glu
			190
Leu	Ala	Arg	Asn
Gln	Ala	Phe	Ala
			195
Arg	Leu	Gly	Ser
			Lys
		200	
Val	Thr	Val	Leu
			Ala
			205

Thr Leu Phe Phe Arg Glu Asp Pro Ala Ile Gly Glu Ala Val Thr Ala
210 215 220

Ala Phe Arg Ala Glu Gly Ile Glu Val Leu Glu His Thr Gln Ala Ser
225 230 235 240

Gln Val Ala His Met Asp Gly Glu Phe Val Leu Thr Thr Thr His Gly
245 250 255

Glu Leu Arg Ala Asp Lys Leu Leu Val Ala Thr Gly Arg Thr Pro Asn
260 265 270

Thr Arg Ser Leu Ala Leu Asp Ala Ala Gly Val Thr Val Asn Ala Gln
275 280 285

Gly Ala Ile Val Ile Asp Gln Gly Met Arg Thr Ser Asn Pro Asn Ile
290 295 300

Tyr Ala Ala Gly Asp Cys Thr Asp Gln Pro Gln Phe Val Tyr Val Ala
305 310 315 320

Ala Ala Asp Asp Gly Ile Glu Thr Asp Ser Arg Thr Leu Thr Leu Asp
325 330 335

Asn Val Pro Arg Ala Leu Ala Asn Phe Asp Thr Arg Gly Phe Ile Lys
340 345 350

Leu Val Ile Glu Glu Gly Ser His Arg Leu Ile Gly Val Gln Ala Val
355 360 365

Ala Pro Glu Ala Gly Glu Leu Ile Gln Thr Ala Ala Leu Ala Ile Arg
370 375 380

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

Thr Met Val Glu Gly Leu Lys Leu Ala Ala Gln Thr Phe Asn Lys Asp

405

410

415

Val Lys Gln Leu Ser Cys Cys Ala Gly
 420 425

<210> 43

<211> 467

<212> PRT

<213> Artificial Sequence

<220>

<223> DM6 L395D

<400> 43

Met Glu Pro Pro Val Gln Val Ala Val Ile Gly Ser Gly Gly Ala Ala
 1 5 10 15

Met Ala Ala Ala Leu Lys Ala Val Glu Gln Gly Ala Gln Val Thr Leu
 20 25 30

Ile Glu Arg Gly Thr Ile Gly Gly Thr Cys Val Asn Val Gly Cys Val
 35 40 45

Pro Ser Lys Ile Met Ile Arg Ala Ala His Ile Ala His Leu Arg Arg
 50 55 60

Glu Ser Pro Phe Asp Gly Gly Ile Ala Ala Thr Val Pro Thr Ile Asp
 65 70 75 80

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

His Ala Lys Tyr Glu Gly Ile Leu Gly Gly Asn Pro Ala Ile Thr Val
 100 105 110

Val His Gly Glu Ala Arg Phe Lys Asp Asp Gln Ser Leu Thr Val Arg
 115 120 125

Leu Asn Glu Gly Gly Glu Arg Val Val Met Phe Asp Arg Cys Leu Val

130

135

140

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

Ser Pro Tyr Trp Thr Ser Thr Glu Ala Leu Ala Ser Asp Thr Ile Pro
 165 170 175

Glu Arg Leu Ala Val Ile Gly Ser Ser Val Val Ala Leu Glu Leu Ala
 180 185 190

Gln Ala Phe Ala Arg Leu Gly Ser Lys Val Thr Val Leu Ala Arg Asn
 195 200 205

Thr Leu Phe Phe Arg Glu Asp Pro Ala Ile Gly Glu Ala Val Thr Ala
 210 215 220

Ala Phe Arg Ala Glu Gly Ile Glu Val Leu Glu His Thr Gln Ala Ser
 225 230 235 240

Gln Val Ala His Met Asp Gly Glu Phe Val Leu Thr Thr Thr His Gly
 245 250 255

Glu Leu Arg Ala Asp Lys Leu Leu Val Ala Thr Gly Arg Thr Pro Asn
 260 265 270

Thr Arg Ser Leu Ala Leu Asp Ala Ala Gly Val Thr Val Asn Ala Gln
 275 280 285

Gly Ala Ile Val Ile Asp Gln Gly Met Arg Thr Ser Asn Pro Asn Ile
 290 295 300

Tyr Ala Ala Gly Asp Cys Thr Asp Gln Pro Gln Phe Val Tyr Val Ala
 305 310 315 320

Ala Ala Ala Gly Thr Arg Ala Ala Ile Asn Met Thr Gly Gly Asp Ala
 325 330 335

Ala Leu Asp Leu Thr Ala Met Pro Ala Val Val Phe Thr Asp Pro Gln
340 345 350

Val Ala Thr Val Gly Tyr Ser Glu Ala Glu Ala His His Asp Gly Ile
355 360 365

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

Ala Asn Phe Asp Thr Arg Gly Phe Ile Lys Asp Val Ile Glu Glu Gly
385 390 395 400

Ser His Arg Leu Ile Gly Val Gln Ala Val Ala Pro Glu Ala Gly Glu
405 410 415

Leu Ile Gln Thr Ala Ala Leu Ala Ile Arg Asn Arg Met Thr Val Gln
420 425 430

Glu Leu Ala Asp Gln Leu Phe Pro Tyr Leu Thr Met Val Glu Gly Leu
435 440 445

Lys Leu Ala Ala Gln Thr Phe Asn Lys Asp Val Lys Gln Leu Ser Cys
450 455 460

Cys Ala Gly
465

<210> 44
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> DM7 G406D

<400> 44

Met Glu Pro Pro Val Gln Val Ala Val Ile Gly Ser Gly Gly Ala Ala
1 5 10 15

Met Ala Ala Ala Leu Lys Ala Val Glu Gln Gly Ala Gln Val Thr Leu
20 25 30

Ile Glu Arg Gly Thr Ile Gly Gly Thr Cys Val Asn Val Gly Cys Val
35 40 45

Pro Ser Lys Ile Met Ile Arg Ala Ala His Ile Ala His Leu Arg Arg
50 55 60

Glu Ser Pro Phe Asp Gly Gly Ile Ala Ala Thr Val Pro Thr Ile Asp
65 70 75 80

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

His Ala Lys Tyr Glu Gly Ile Leu Gly Gly Asn Pro Ala Ile Thr Val
100 105 110

Val His Gly Glu Ala Arg Phe Lys Asp Asp Gln Ser Leu Thr Val Arg
115 120 125

Leu Asn Glu Gly Gly Glu Arg Val Val Met Phe Asp Arg Cys Leu Val
130 135 140

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

Ser Pro Tyr Trp Thr Ser Thr Glu Ala Leu Ala Ser Asp Thr Ile Pro
165 170 175

Glu Arg Leu Ala Val Ile Gly Ser Ser Val Val Ala Leu Glu Leu Ala
180 185 190

Gln Ala Phe Ala Arg Leu Gly Ser Lys Val Thr Val Leu Ala Arg Asn
195 200 205

Thr Leu Phe Phe Arg Glu Asp Pro Ala Ile Gly Glu Ala Val Thr Ala

210

215

220

Ala Phe Arg Ala Glu Gly Ile Glu Val Leu Glu His Thr Gln Ala Ser
 225 230 235 240

Gln Val Ala His Met Asp Gly Glu Phe Val Leu Thr Thr Thr His Gly
 245 250 255

Glu Leu Arg Ala Asp Lys Leu Leu Val Ala Thr Gly Arg Thr Pro Asn
 260 265 270

Thr Arg Ser Leu Ala Leu Asp Ala Ala Gly Val Thr Val Asn Ala Gln
 275 280 285

Gly Ala Ile Val Ile Asp Gln Gly Met Arg Thr Ser Asn Pro Asn Ile
 290 295 300

Tyr Ala Ala Gly Asp Cys Thr Asp Gln Pro Gln Phe Val Tyr Val Ala
 305 310 315 320

Ala Ala Ala Gly Thr Arg Ala Ala Ile Asn Met Thr Gly Gly Asp Ala
 325 330 335

Ala Leu Asp Leu Thr Ala Met Pro Ala Val Val Phe Thr Asp Pro Gln
 340 345 350

Val Ala Thr Val Gly Tyr Ser Glu Ala Glu Ala His His Asp Gly Ile
 355 360 365

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

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

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

Leu Ile Gln Thr Ala Ala Leu Ala Ile Arg Asn Arg Met Thr Val Gln
420 425 430

Glu Leu Ala Asp Gln Leu Phe Pro Tyr Leu Thr Met Val Glu Gly Leu
435 440 445

Lys Leu Ala Ala Gln Thr Phe Asn Lys Asp Val Lys Gln Leu Ser Cys
450 455 460

Cys Ala Gly
465

<210> 45
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> DM8 A411Q

<400> 45

Met Glu Pro Pro Val Gln Val Ala Val Ile Gly Ser Gly Gly Ala Ala
1 5 10 15

Met Ala Ala Ala Leu Lys Ala Val Glu Gln Gly Ala Gln Val Thr Leu
20 25 30

Ile Glu Arg Gly Thr Ile Gly Gly Thr Cys Val Asn Val Gly Cys Val
35 40 45

Pro Ser Lys Ile Met Ile Arg Ala Ala His Ile Ala His Leu Arg Arg
50 55 60

Glu Ser Pro Phe Asp Gly Gly Ile Ala Ala Thr Val Pro Thr Ile Asp
65 70 75 80

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

His Ala Lys Tyr Glu Gly Ile Leu Gly Gly Asn Pro Ala Ile Thr Val
100 105 110

Val His Gly Glu Ala Arg Phe Lys Asp Asp Gln Ser Leu Thr Val Arg
115 120 125

Leu Asn Glu Gly Gly Glu Arg Val Val Met Phe Asp Arg Cys Leu Val
130 135 140

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

Ser Pro Tyr Trp Thr Ser Thr Glu Ala Leu Ala Ser Asp Thr Ile Pro
165 170 175

Glu Arg Leu Ala Val Ile Gly Ser Ser Val Val Ala Leu Glu Leu Ala
180 185 190

Gln Ala Phe Ala Arg Leu Gly Ser Lys Val Thr Val Leu Ala Arg Asn
195 200 205

Thr Leu Phe Phe Arg Glu Asp Pro Ala Ile Gly Glu Ala Val Thr Ala
210 215 220

Ala Phe Arg Ala Glu Gly Ile Glu Val Leu Glu His Thr Gln Ala Ser
225 230 235 240

Gln Val Ala His Met Asp Gly Glu Phe Val Leu Thr Thr Thr His Gly
245 250 255

Glu Leu Arg Ala Asp Lys Leu Leu Val Ala Thr Gly Arg Thr Pro Asn
260 265 270

Thr Arg Ser Leu Ala Leu Asp Ala Ala Gly Val Thr Val Asn Ala Gln
275 280 285

Gly Ala Ile Val Ile Asp Gln Gly Met Arg Thr Ser Asn Pro Asn Ile

290

295

300

Tyr Ala Ala Gly Asp Cys Thr Asp Gln Pro Gln Phe Val Tyr Val Ala
 305 310 315 320

Ala Ala Ala Gly Thr Arg Ala Ala Ile Asn Met Thr Gly Gly Asp Ala
 325 330 335

Ala Leu Asp Leu Thr Ala Met Pro Ala Val Val Phe Thr Asp Pro Gln
 340 345 350

Val Ala Thr Val Gly Tyr Ser Glu Ala Glu Ala His His Asp Gly Ile
 355 360 365

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

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

Ser His Arg Leu Ile Gly Val Gln Ala Val Gln Pro Glu Ala Gly Glu
 405 410 415

Leu Ile Gln Thr Ala Ala Leu Ala Ile Arg Asn Arg Met Thr Val Gln
 420 425 430

Glu Leu Ala Asp Gln Leu Phe Pro Tyr Leu Thr Met Val Glu Gly Leu
 435 440 445

Lys Leu Ala Ala Gln Thr Phe Asn Lys Asp Val Lys Gln Leu Ser Cys
 450 455 460

Cys Ala Gly
 465

<210> 46
 <211> 467
 <212> PRT

<213> Artificial Sequence

<220>

<223> DM9 A411C

<400> 46

Met Glu Pro Pro Val Gln Val Ala Val Ile Gly Ser Gly Gly Ala Ala
1 5 10 15

Met Ala Ala Ala Leu Lys Ala Val Glu Gln Gly Ala Gln Val Thr Leu
20 25 30

Ile Glu Arg Gly Thr Ile Gly Gly Thr Cys Val Asn Val Gly Cys Val
35 40 45

Pro Ser Lys Ile Met Ile Arg Ala Ala His Ile Ala His Leu Arg Arg
50 55 60

Glu Ser Pro Phe Asp Gly Gly Ile Ala Ala Thr Val Pro Thr Ile Asp
65 70 75 80

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

His Ala Lys Tyr Glu Gly Ile Leu Gly Gly Asn Pro Ala Ile Thr Val
100 105 110

Val His Gly Glu Ala Arg Phe Lys Asp Asp Gln Ser Leu Thr Val Arg
115 120 125

Leu Asn Glu Gly Gly Glu Arg Val Val Met Phe Asp Arg Cys Leu Val
130 135 140

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

Ser Pro Tyr Trp Thr Ser Thr Glu Ala Leu Ala Ser Asp Thr Ile Pro
165 170 175

Glu Arg Leu Ala Val Ile Gly Ser Ser Val Val Ala Leu Glu Leu Ala
180 185 190

Gln Ala Phe Ala Arg Leu Gly Ser Lys Val Thr Val Leu Ala Arg Asn
195 200 205

Thr Leu Phe Phe Arg Glu Asp Pro Ala Ile Gly Glu Ala Val Thr Ala
210 215 220

Ala Phe Arg Ala Glu Gly Ile Glu Val Leu Glu His Thr Gln Ala Ser
225 230 235 240

Gln Val Ala His Met Asp Gly Glu Phe Val Leu Thr Thr Thr His Gly
245 250 255

Glu Leu Arg Ala Asp Lys Leu Leu Val Ala Thr Gly Arg Thr Pro Asn
260 265 270

Thr Arg Ser Leu Ala Leu Asp Ala Ala Gly Val Thr Val Asn Ala Gln
275 280 285

Gly Ala Ile Val Ile Asp Gln Gly Met Arg Thr Ser Asn Pro Asn Ile
290 295 300

Tyr Ala Ala Gly Asp Cys Thr Asp Gln Pro Gln Phe Val Tyr Val Ala
305 310 315 320

Ala Ala Ala Gly Thr Arg Ala Ala Ile Asn Met Thr Gly Gly Asp Ala
325 330 335

Ala Leu Asp Leu Thr Ala Met Pro Ala Val Val Phe Thr Asp Pro Gln
340 345 350

Val Ala Thr Val Gly Tyr Ser Glu Ala Glu Ala His His Asp Gly Ile
355 360 365

Glu Thr Asp Ser Arg Thr Leu Thr Leu Asp Asn Val Pro Arg Ala Leu

370

375

380

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

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

Leu Ile Gln Thr Ala Ala Leu Ala Ile Arg Asn Arg Met Thr Val Gln
 420 425 430

Glu Leu Ala Asp Gln Leu Phe Pro Tyr Leu Thr Met Val Glu Gly Leu
 435 440 445

Lys Leu Ala Ala Gln Thr Phe Asn Lys Asp Val Lys Gln Leu Ser Cys
 450 455 460

Cys Ala Gly
 465

<210> 47
 <211> 467
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DM10 A414E

<400> 47

Met Glu Pro Pro Val Gln Val Ala Val Ile Gly Ser Gly Gly Ala Ala
 1 5 10 15

Met Ala Ala Ala Leu Lys Ala Val Glu Gln Gly Ala Gln Val Thr Leu
 20 25 30

Ile Glu Arg Gly Thr Ile Gly Gly Thr Cys Val Asn Val Gly Cys Val
 35 40 45

Pro Ser Lys Ile Met Ile Arg Ala Ala His Ile Ala His Leu Arg Arg

50

55

60

Glu Ser Pro Phe Asp Gly Gly Ile Ala Ala Thr Val Pro Thr Ile Asp
65 70 75 80

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

His Ala Lys Tyr Glu Gly Ile Leu Gly Gly Asn Pro Ala Ile Thr Val
100 105 110

Val His Gly Glu Ala Arg Phe Lys Asp Asp Gln Ser Leu Thr Val Arg
115 120 125

Leu Asn Glu Gly Gly Glu Arg Val Val Met Phe Asp Arg Cys Leu Val
130 135 140

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

Ser Pro Tyr Trp Thr Ser Thr Glu Ala Leu Ala Ser Asp Thr Ile Pro
165 170 175

Glu Arg Leu Ala Val Ile Gly Ser Ser Val Val Ala Leu Glu Leu Ala
180 185 190

Gln Ala Phe Ala Arg Leu Gly Ser Lys Val Thr Val Leu Ala Arg Asn
195 200 205

Thr Leu Phe Phe Arg Glu Asp Pro Ala Ile Gly Glu Ala Val Thr Ala
210 215 220

Ala Phe Arg Ala Glu Gly Ile Glu Val Leu Glu His Thr Gln Ala Ser
225 230 235 240

Gln Val Ala His Met Asp Gly Glu Phe Val Leu Thr Thr Thr His Gly
245 250 255

Glu Leu Arg Ala Asp Lys Leu Leu Val Ala Thr Gly Arg Thr Pro Asn
260 265 270

Thr Arg Ser Leu Ala Leu Asp Ala Ala Gly Val Thr Val Asn Ala Gln
275 280 285

Gly Ala Ile Val Ile Asp Gln Gly Met Arg Thr Ser Asn Pro Asn Ile
290 295 300

Tyr Ala Ala Gly Asp Cys Thr Asp Gln Pro Gln Phe Val Tyr Val Ala
305 310 315 320

Ala Ala Ala Gly Thr Arg Ala Ala Ile Asn Met Thr Gly Gly Asp Ala
325 330 335

Ala Leu Asp Leu Thr Ala Met Pro Ala Val Val Phe Thr Asp Pro Gln
340 345 350

Val Ala Thr Val Gly Tyr Ser Glu Ala Glu Ala His His Asp Gly Ile
355 360 365

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

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

Ser His Arg Leu Ile Gly Val Gln Ala Val Ala Pro Glu Glu Gly Glu
405 410 415

Leu Ile Gln Thr Ala Ala Leu Ala Ile Arg Asn Arg Met Thr Val Gln
420 425 430

Glu Leu Ala Asp Gln Leu Phe Pro Tyr Leu Thr Met Val Glu Gly Leu
435 440 445

Lys Leu Ala Ala Gln Thr Phe Asn Lys Asp Val Lys Gln Leu Ser Cys

450

455

460

Cys Ala Gly

465

<210> 48

<211> 467

<212> PRT

<213> Artificial Sequence

<220>

<223> DM11 G415I

<400> 48

Met Glu Pro Pro Val Gln Val Ala Val Ile Gly Ser Gly Gly Ala Ala
 1 5 10 15

Met Ala Ala Ala Leu Lys Ala Val Glu Gln Gly Ala Gln Val Thr Leu
 20 25 30

Ile Glu Arg Gly Thr Ile Gly Gly Thr Cys Val Asn Val Gly Cys Val
 35 40 45

Pro Ser Lys Ile Met Ile Arg Ala Ala His Ile Ala His Leu Arg Arg
 50 55 60

Glu Ser Pro Phe Asp Gly Gly Ile Ala Ala Thr Val Pro Thr Ile Asp
 65 70 75 80

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

His Ala Lys Tyr Glu Gly Ile Leu Gly Gly Asn Pro Ala Ile Thr Val
 100 105 110

Val His Gly Glu Ala Arg Phe Lys Asp Asp Gln Ser Leu Thr Val Arg
 115 120 125

Leu Asn Glu Gly Gly Glu Arg Val Val Met Phe Asp Arg Cys Leu Val

130

135

140

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

Ser Pro Tyr Trp Thr Ser Thr Glu Ala Leu Ala Ser Asp Thr Ile Pro
 165 170 175

Glu Arg Leu Ala Val Ile Gly Ser Ser Val Val Ala Leu Glu Leu Ala
 180 185 190

Gln Ala Phe Ala Arg Leu Gly Ser Lys Val Thr Val Leu Ala Arg Asn
 195 200 205

Thr Leu Phe Phe Arg Glu Asp Pro Ala Ile Gly Glu Ala Val Thr Ala
 210 215 220

Ala Phe Arg Ala Glu Gly Ile Glu Val Leu Glu His Thr Gln Ala Ser
 225 230 235 240

Gln Val Ala His Met Asp Gly Glu Phe Val Leu Thr Thr Thr His Gly
 245 250 255

Glu Leu Arg Ala Asp Lys Leu Leu Val Ala Thr Gly Arg Thr Pro Asn
 260 265 270

Thr Arg Ser Leu Ala Leu Asp Ala Ala Gly Val Thr Val Asn Ala Gln
 275 280 285

Gly Ala Ile Val Ile Asp Gln Gly Met Arg Thr Ser Asn Pro Asn Ile
 290 295 300

Tyr Ala Ala Gly Asp Cys Thr Asp Gln Pro Gln Phe Val Tyr Val Ala
 305 310 315 320

Ala Ala Ala Gly Thr Arg Ala Ala Ile Asn Met Thr Gly Gly Asp Ala
 325 330 335

Ala Leu Asp Leu Thr Ala Met Pro Ala Val Val Phe Thr Asp Pro Gln
340 345 350

Val Ala Thr Val Gly Tyr Ser Glu Ala Glu Ala His His Asp Gly Ile
355 360 365

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

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

Ser His Arg Leu Ile Gly Val Gln Ala Val Ala Pro Glu Ala Ile Glu
405 410 415

Leu Ile Gln Thr Ala Ala Leu Ala Ile Arg Asn Arg Met Thr Val Gln
420 425 430

Glu Leu Ala Asp Gln Leu Phe Pro Tyr Leu Thr Met Val Glu Gly Leu
435 440 445

Lys Leu Ala Ala Gln Thr Phe Asn Lys Asp Val Lys Gln Leu Ser Cys
450 455 460

Cys Ala Gly
465

<210> 49
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> DM12 E416C

<400> 49

Met Glu Pro Pro Val Gln Val Ala Val Ile Gly Ser Gly Gly Ala Ala
1 5 10 15

Met Ala Ala Ala Leu Lys Ala Val Glu Gln Gly Ala Gln Val Thr Leu
20 25 30

Ile Glu Arg Gly Thr Ile Gly Gly Thr Cys Val Asn Val Gly Cys Val
35 40 45

Pro Ser Lys Ile Met Ile Arg Ala Ala His Ile Ala His Leu Arg Arg
50 55 60

Glu Ser Pro Phe Asp Gly Gly Ile Ala Ala Thr Val Pro Thr Ile Asp
65 70 75 80

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

His Ala Lys Tyr Glu Gly Ile Leu Gly Gly Asn Pro Ala Ile Thr Val
100 105 110

Val His Gly Glu Ala Arg Phe Lys Asp Asp Gln Ser Leu Thr Val Arg
115 120 125

Leu Asn Glu Gly Gly Glu Arg Val Val Met Phe Asp Arg Cys Leu Val
130 135 140

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

Ser Pro Tyr Trp Thr Ser Thr Glu Ala Leu Ala Ser Asp Thr Ile Pro
165 170 175

Glu Arg Leu Ala Val Ile Gly Ser Ser Val Val Ala Leu Glu Leu Ala
180 185 190

Gln Ala Phe Ala Arg Leu Gly Ser Lys Val Thr Val Leu Ala Arg Asn
195 200 205

Thr Leu Phe Phe Arg Glu Asp Pro Ala Ile Gly Glu Ala Val Thr Ala

210

215

220

Ala Phe Arg Ala Glu Gly Ile Glu Val Leu Glu His Thr Gln Ala Ser
 225 230 235 240

Gln Val Ala His Met Asp Gly Glu Phe Val Leu Thr Thr Thr His Gly
 245 250 255

Glu Leu Arg Ala Asp Lys Leu Leu Val Ala Thr Gly Arg Thr Pro Asn
 260 265 270

Thr Arg Ser Leu Ala Leu Asp Ala Ala Gly Val Thr Val Asn Ala Gln
 275 280 285

Gly Ala Ile Val Ile Asp Gln Gly Met Arg Thr Ser Asn Pro Asn Ile
 290 295 300

Tyr Ala Ala Gly Asp Cys Thr Asp Gln Pro Gln Phe Val Tyr Val Ala
 305 310 315 320

Ala Ala Ala Gly Thr Arg Ala Ala Ile Asn Met Thr Gly Gly Asp Ala
 325 330 335

Ala Leu Asp Leu Thr Ala Met Pro Ala Val Val Phe Thr Asp Pro Gln
 340 345 350

Val Ala Thr Val Gly Tyr Ser Glu Ala Glu Ala His His Asp Gly Ile
 355 360 365

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

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

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

Leu Ile Gln Thr Ala Ala Leu Ala Ile Arg Asn Arg Met Thr Val Gln
420 425 430

Glu Leu Ala Asp Gln Leu Phe Pro Tyr Leu Thr Met Val Glu Gly Leu
435 440 445

Lys Leu Ala Ala Gln Thr Phe Asn Lys Asp Val Lys Gln Leu Ser Cys
450 455 460

Cys Ala Gly
465

<210> 50
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> DM13 L417I

<400> 50

Met Glu Pro Pro Val Gln Val Ala Val Ile Gly Ser Gly Gly Ala Ala
1 5 10 15

Met Ala Ala Ala Leu Lys Ala Val Glu Gln Gly Ala Gln Val Thr Leu
20 25 30

Ile Glu Arg Gly Thr Ile Gly Gly Thr Cys Val Asn Val Gly Cys Val
35 40 45

Pro Ser Lys Ile Met Ile Arg Ala Ala His Ile Ala His Leu Arg Arg
50 55 60

Glu Ser Pro Phe Asp Gly Gly Ile Ala Ala Thr Val Pro Thr Ile Asp
65 70 75 80

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

His Ala Lys Tyr Glu Gly Ile Leu Gly Gly Asn Pro Ala Ile Thr Val
100 105 110

Val His Gly Glu Ala Arg Phe Lys Asp Asp Gln Ser Leu Thr Val Arg
115 120 125

Leu Asn Glu Gly Gly Glu Arg Val Val Met Phe Asp Arg Cys Leu Val
130 135 140

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

Ser Pro Tyr Trp Thr Ser Thr Glu Ala Leu Ala Ser Asp Thr Ile Pro
165 170 175

Glu Arg Leu Ala Val Ile Gly Ser Ser Val Val Ala Leu Glu Leu Ala
180 185 190

Gln Ala Phe Ala Arg Leu Gly Ser Lys Val Thr Val Leu Ala Arg Asn
195 200 205

Thr Leu Phe Phe Arg Glu Asp Pro Ala Ile Gly Glu Ala Val Thr Ala
210 215 220

Ala Phe Arg Ala Glu Gly Ile Glu Val Leu Glu His Thr Gln Ala Ser
225 230 235 240

Gln Val Ala His Met Asp Gly Glu Phe Val Leu Thr Thr Thr His Gly
245 250 255

Glu Leu Arg Ala Asp Lys Leu Leu Val Ala Thr Gly Arg Thr Pro Asn
260 265 270

Thr Arg Ser Leu Ala Leu Asp Ala Ala Gly Val Thr Val Asn Ala Gln
275 280 285

Gly Ala Ile Val Ile Asp Gln Gly Met Arg Thr Ser Asn Pro Asn Ile

290

295

300

Tyr Ala Ala Gly Asp Cys Thr Asp Gln Pro Gln Phe Val Tyr Val Ala
 305 310 315 320

Ala Ala Ala Gly Thr Arg Ala Ala Ile Asn Met Thr Gly Gly Asp Ala
 325 330 335

Ala Leu Asp Leu Thr Ala Met Pro Ala Val Val Phe Thr Asp Pro Gln
 340 345 350

Val Ala Thr Val Gly Tyr Ser Glu Ala Glu Ala His His Asp Gly Ile
 355 360 365

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

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

Ser His Arg Leu Ile Gly Val Gln Ala Val Ala Pro Glu Ala Gly Glu
 405 410 415

Ile Ile Gln Thr Ala Ala Leu Ala Ile Arg Asn Arg Met Thr Val Gln
 420 425 430

Glu Leu Ala Asp Gln Leu Phe Pro Tyr Leu Thr Met Val Glu Gly Leu
 435 440 445

Lys Leu Ala Ala Gln Thr Phe Asn Lys Asp Val Lys Gln Leu Ser Cys
 450 455 460

Cys Ala Gly
 465

<210> 51
 <211> 467
 <212> PRT

<213> Artificial Sequence

<220>

<223> DM14 I418D

<400> 51

Met Glu Pro Pro Val Gln Val Ala Val Ile Gly Ser Gly Gly Ala Ala
1 5 10 15

Met Ala Ala Ala Leu Lys Ala Val Glu Gln Gly Ala Gln Val Thr Leu
20 25 30

Ile Glu Arg Gly Thr Ile Gly Gly Thr Cys Val Asn Val Gly Cys Val
35 40 45

Pro Ser Lys Ile Met Ile Arg Ala Ala His Ile Ala His Leu Arg Arg
50 55 60

Glu Ser Pro Phe Asp Gly Gly Ile Ala Ala Thr Val Pro Thr Ile Asp
65 70 75 80

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

His Ala Lys Tyr Glu Gly Ile Leu Gly Gly Asn Pro Ala Ile Thr Val
100 105 110

Val His Gly Glu Ala Arg Phe Lys Asp Asp Gln Ser Leu Thr Val Arg
115 120 125

Leu Asn Glu Gly Gly Glu Arg Val Val Met Phe Asp Arg Cys Leu Val
130 135 140

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

Ser Pro Tyr Trp Thr Ser Thr Glu Ala Leu Ala Ser Asp Thr Ile Pro
165 170 175

Glu Arg Leu Ala Val Ile Gly Ser Ser Val Val Ala Leu Glu Leu Ala
180 185 190

Gln Ala Phe Ala Arg Leu Gly Ser Lys Val Thr Val Leu Ala Arg Asn
195 200 205

Thr Leu Phe Phe Arg Glu Asp Pro Ala Ile Gly Glu Ala Val Thr Ala
210 215 220

Ala Phe Arg Ala Glu Gly Ile Glu Val Leu Glu His Thr Gln Ala Ser
225 230 235 240

Gln Val Ala His Met Asp Gly Glu Phe Val Leu Thr Thr Thr His Gly
245 250 255

Glu Leu Arg Ala Asp Lys Leu Leu Val Ala Thr Gly Arg Thr Pro Asn
260 265 270

Thr Arg Ser Leu Ala Leu Asp Ala Ala Gly Val Thr Val Asn Ala Gln
275 280 285

Gly Ala Ile Val Ile Asp Gln Gly Met Arg Thr Ser Asn Pro Asn Ile
290 295 300

Tyr Ala Ala Gly Asp Cys Thr Asp Gln Pro Gln Phe Val Tyr Val Ala
305 310 315 320

Ala Ala Ala Gly Thr Arg Ala Ala Ile Asn Met Thr Gly Gly Asp Ala
325 330 335

Ala Leu Asp Leu Thr Ala Met Pro Ala Val Val Phe Thr Asp Pro Gln
340 345 350

Val Ala Thr Val Gly Tyr Ser Glu Ala Glu Ala His His Asp Gly Ile
355 360 365

Glu Thr Asp Ser Arg Thr Leu Thr Leu Asp Asn Val Pro Arg Ala Leu

370

375

380

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

Ser His Arg Leu Ile Gly Val Gln Ala Val Ala Pro Glu Ala Gly Glu
 405 410 415

Leu Asp Gln Thr Ala Ala Leu Ala Ile Arg Asn Arg Met Thr Val Gln
 420 425 430

Glu Leu Ala Asp Gln Leu Phe Pro Tyr Leu Thr Met Val Glu Gly Leu
 435 440 445

Lys Leu Ala Ala Gln Thr Phe Asn Lys Asp Val Lys Gln Leu Ser Cys
 450 455 460

Cys Ala Gly
 465

<210> 52
 <211> 467
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DM15 A422N

<400> 52

Met Glu Pro Pro Val Gln Val Ala Val Ile Gly Ser Gly Gly Ala Ala
 1 5 10 15

Met Ala Ala Ala Leu Lys Ala Val Glu Gln Gly Ala Gln Val Thr Leu
 20 25 30

Ile Glu Arg Gly Thr Ile Gly Gly Thr Cys Val Asn Val Gly Cys Val
 35 40 45

Pro Ser Lys Ile Met Ile Arg Ala Ala His Ile Ala His Leu Arg Arg

50

55

60

Glu Ser Pro Phe Asp Gly Gly Ile Ala Ala Thr Val Pro Thr Ile Asp
65 70 75 80

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

His Ala Lys Tyr Glu Gly Ile Leu Gly Gly Asn Pro Ala Ile Thr Val
100 105 110

Val His Gly Glu Ala Arg Phe Lys Asp Asp Gln Ser Leu Thr Val Arg
115 120 125

Leu Asn Glu Gly Gly Glu Arg Val Val Met Phe Asp Arg Cys Leu Val
130 135 140

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

Ser Pro Tyr Trp Thr Ser Thr Glu Ala Leu Ala Ser Asp Thr Ile Pro
165 170 175

Glu Arg Leu Ala Val Ile Gly Ser Ser Val Val Ala Leu Glu Leu Ala
180 185 190

Gln Ala Phe Ala Arg Leu Gly Ser Lys Val Thr Val Leu Ala Arg Asn
195 200 205

Thr Leu Phe Phe Arg Glu Asp Pro Ala Ile Gly Glu Ala Val Thr Ala
210 215 220

Ala Phe Arg Ala Glu Gly Ile Glu Val Leu Glu His Thr Gln Ala Ser
225 230 235 240

Gln Val Ala His Met Asp Gly Glu Phe Val Leu Thr Thr Thr His Gly
245 250 255

Glu Leu Arg Ala Asp Lys Leu Leu Val Ala Thr Gly Arg Thr Pro Asn
260 265 270

Thr Arg Ser Leu Ala Leu Asp Ala Ala Gly Val Thr Val Asn Ala Gln
275 280 285

Gly Ala Ile Val Ile Asp Gln Gly Met Arg Thr Ser Asn Pro Asn Ile
290 295 300

Tyr Ala Ala Gly Asp Cys Thr Asp Gln Pro Gln Phe Val Tyr Val Ala
305 310 315 320

Ala Ala Ala Gly Thr Arg Ala Ala Ile Asn Met Thr Gly Gly Asp Ala
325 330 335

Ala Leu Asp Leu Thr Ala Met Pro Ala Val Val Phe Thr Asp Pro Gln
340 345 350

Val Ala Thr Val Gly Tyr Ser Glu Ala Glu Ala His His Asp Gly Ile
355 360 365

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

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

Ser His Arg Leu Ile Gly Val Gln Ala Val Ala Pro Glu Ala Gly Glu
405 410 415

Leu Ile Gln Thr Ala Asn Leu Ala Ile Arg Asn Arg Met Thr Val Gln
420 425 430

Glu Leu Ala Asp Gln Leu Phe Pro Tyr Leu Thr Met Val Glu Gly Leu
435 440 445

Lys Leu Ala Ala Gln Thr Phe Asn Lys Asp Val Lys Gln Leu Ser Cys

450

455

460

Cys Ala Gly

465

<210> 53

<211> 467

<212> PRT

<213> Artificial Sequence

<220>

<223> DM16 L448T

<400> 53

Met Glu Pro Pro Val Gln Val Ala Val Ile Gly Ser Gly Gly Ala Ala
1 5 10 15

Met Ala Ala Ala Leu Lys Ala Val Glu Gln Gly Ala Gln Val Thr Leu
20 25 30

Ile Glu Arg Gly Thr Ile Gly Gly Thr Cys Val Asn Val Gly Cys Val
35 40 45

Pro Ser Lys Ile Met Ile Arg Ala Ala His Ile Ala His Leu Arg Arg
50 55 60

Glu Ser Pro Phe Asp Gly Gly Ile Ala Ala Thr Val Pro Thr Ile Asp
65 70 75 80

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

His Ala Lys Tyr Glu Gly Ile Leu Gly Gly Asn Pro Ala Ile Thr Val
100 105 110

Val His Gly Glu Ala Arg Phe Lys Asp Asp Gln Ser Leu Thr Val Arg
115 120 125

Leu Asn Glu Gly Gly Glu Arg Val Val Met Phe Asp Arg Cys Leu Val

130

135

140

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

Ser Pro Tyr Trp Thr Ser Thr Glu Ala Leu Ala Ser Asp Thr Ile Pro
 165 170 175

Glu Arg Leu Ala Val Ile Gly Ser Ser Val Val Ala Leu Glu Leu Ala
 180 185 190

Gln Ala Phe Ala Arg Leu Gly Ser Lys Val Thr Val Leu Ala Arg Asn
 195 200 205

Thr Leu Phe Phe Arg Glu Asp Pro Ala Ile Gly Glu Ala Val Thr Ala
 210 215 220

Ala Phe Arg Ala Glu Gly Ile Glu Val Leu Glu His Thr Gln Ala Ser
 225 230 235 240

Gln Val Ala His Met Asp Gly Glu Phe Val Leu Thr Thr Thr His Gly
 245 250 255

Glu Leu Arg Ala Asp Lys Leu Leu Val Ala Thr Gly Arg Thr Pro Asn
 260 265 270

Thr Arg Ser Leu Ala Leu Asp Ala Ala Gly Val Thr Val Asn Ala Gln
 275 280 285

Gly Ala Ile Val Ile Asp Gln Gly Met Arg Thr Ser Asn Pro Asn Ile
 290 295 300

Tyr Ala Ala Gly Asp Cys Thr Asp Gln Pro Gln Phe Val Tyr Val Ala
 305 310 315 320

Ala Ala Ala Gly Thr Arg Ala Ala Ile Asn Met Thr Gly Gly Asp Ala
 325 330 335

Ala Leu Asp Leu Thr Ala Met Pro Ala Val Val Phe Thr Asp Pro Gln
340 345 350

Val Ala Thr Val Gly Tyr Ser Glu Ala Glu Ala His His Asp Gly Ile
355 360 365

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

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

Ser His Arg Leu Ile Gly Val Gln Ala Val Ala Pro Glu Ala Gly Glu
405 410 415

Leu Ile Gln Thr Ala Ala Leu Ala Ile Arg Asn Arg Met Thr Val Gln
420 425 430

Glu Leu Ala Asp Gln Leu Phe Pro Tyr Leu Thr Met Val Glu Gly Thr
435 440 445

Lys Leu Ala Ala Gln Thr Phe Asn Lys Asp Val Lys Gln Leu Ser Cys
450 455 460

Cys Ala Gly
465