SEQUENCE LISTING

<110> Collier, Steven James
<111> Teo, Ee Ling
<112> Wilson, Robert John
<113> Xu Junye

<120> Improved Lov-D Acyltransferase Mediated Acylation

<130> 376247-044US (105192) {CX2-032}

<141> 2010-09-24

<160> 20

<210> 1
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon optimized Aspergillus terreus lovD

<400> 1
atgggttcta tcattgatgc ggctgcggcc gcggacccgg tggttctgat ggaaacggct 60
ttccgtaaag cggttaaaag ccgccagatt ccgggtgctg ttattatggc gcgtgattgt 120
agtggtaacc tgaactacac tcgctgtttc ggcgcacgca ctgtgcgtcg cgacgagtgc 180
aatcaattac caccgctgca ggtggataca ccatgtcgtc tggcaagcgc tactaaatta 240
ctgaccacga ttatggcact gcagtgcatg gaacgcggcc tggtagactt ggatgaaact 300
gttgaccgcc tgctgccgga cctgagcgcg atgccggtgc tggaaggctt tgatgatgcc 360
ggcaacgccc gtctgcgcga acgccgtggt aaaattacgt tacgccatct gctgacacac 420
accagcggtc tgtcgtacgt cttcctgcat ccgctgctgc gcgagtatat ggcccagggt 480
catttgcaga gcgctgagaa gtttggcatt cagtctcgtc tggcgccgcc agctgttaat 540
gatccaggcg cggaatggat ttatggcgct aatctggact gggcaggcaa attagtggaa 600
cgcgcaacgg gcttggacct ggaacagtac ttgcaggaga acatttgcgc gccgctgggc 660
atcactgata tgacgttcaa actgcagcag cgtccggata tgctggcacg tcgtgccgac 720
cagacccacc gcaactccgc ggatggtcgt ctgcgctatg atgactctgt gtattttcgc 780
gcggacggtg aagagtgttt cgggggccag ggcgtgttca gcggtccagg cagttacatg 840
aaggttctgc actctctgct gaaacgtgac ggcctgttgc tgcagccaca aaccgtggat 900
ctgatgttcc agccggcgct ggaaccgcgc ttggaagaac aaatgaacca gcatatggac 960
gcgtcgccgc acatcaacta tggcggtcca atgcctatgg tcctgcgtcg cagcttcggc 1020
ctgggtggta tcattgcact ggaggatctg gatggtgaga actggcgtcg taaaggctcg 1080
ctgacgtttg gtggcggtcc aaacattgtt tggcagattg acccgaaagc gggtctgtgt 1140
actttagcct ttttccagct ggaaccgtgg aacgacccgg tgtgtcgtga cctgactcgc 1200
acctttgagc acgcgatcta tgcacagtat caacagggct aa 1242

<210> 2
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> Codon optimized Aspergillus terreus lovD

<400> 2
Met Gly Ser Ile Ile Asp Ala Ala Ala Ala Ala Asp Pro Val Val Leu
1 5 10 15
Met Glu Thr Ala Phe Arg Lys Ala Val Lys Ser Arg Gln Ile Pro Gly
20 25 30
Ala Val Ile Met Ala Arg Asp Cys Ser Gly Asn Leu Asn Tyr Thr Arg
35 40 45
Cys Phe Gly Ala Arg Thr Val Arg Arg Asp Glu Cys Asn Gln Leu Pro
50 55 60
Pro Leu Gln Val Asp Thr Pro Cys Arg Leu Ala Ser Ala Thr Lys Leu
65 70 75 80
Leu Thr Thr Ile Met Ala Leu Gln Cys Met Glu Arg Gly Leu Val Asp
85 90 95

```
Leu Asp Glu Thr Val Asp Arg Leu Leu Pro Asp Leu Ser Ala Met Pro
            100                 105                 110
Val Leu Glu Gly Phe Asp Asp Ala Gly Asn Ala Arg Leu Arg Glu Arg
        115                 120                 125
Arg Gly Lys Ile Thr Leu Arg His Leu Leu Thr His Thr Ser Gly Leu
    130                 135                 140
Ser Tyr Val Phe Leu His Pro Leu Leu Arg Glu Tyr Met Ala Gln Gly
145                 150                 155                 160
His Leu Gln Ser Ala Glu Lys Phe Gly Ile Gln Ser Arg Leu Ala Pro
                165                 170                 175
Pro Ala Val Asn Asp Pro Gly Ala Glu Trp Ile Tyr Gly Ala Asn Leu
            180                 185                 190
Asp Trp Ala Gly Lys Leu Val Glu Arg Ala Thr Gly Leu Asp Leu Glu
        195                 200                 205
Gln Tyr Leu Gln Glu Asn Ile Cys Ala Pro Leu Gly Ile Thr Asp Met
    210                 215                 220
Thr Phe Lys Leu Gln Gln Arg Pro Asp Met Leu Ala Arg Arg Ala Asp
225                 230                 235                 240
Gln Thr His Arg Asn Ser Ala Asp Gly Arg Leu Arg Tyr Asp Asp Ser
                245                 250                 255
Val Tyr Phe Arg Ala Asp Gly Glu Glu Cys Phe Gly Gly Gln Gly Val
            260                 265                 270
Phe Ser Gly Pro Gly Ser Tyr Met Lys Val Leu His Ser Leu Leu Lys
        275                 280                 285
Arg Asp Gly Leu Leu Leu Gln Pro Gln Thr Val Asp Leu Met Phe Gln
    290                 295                 300
Pro Ala Leu Glu Pro Arg Leu Glu Glu Gln Met Asn Gln His Met Asp
305                 310                 315                 320
Ala Ser Pro His Ile Asn Tyr Gly Gly Pro Met Pro Met Val Leu Arg
                325                 330                 335
Arg Ser Phe Gly Leu Gly Gly Ile Ile Ala Leu Glu Asp Leu Asp Gly
            340                 345                 350
Glu Asn Trp Arg Arg Lys Gly Ser Leu Thr Phe Gly Gly Gly Pro Asn
        355                 360                 365
Ile Val Trp Gln Ile Asp Pro Lys Ala Gly Leu Cys Thr Leu Ala Phe
    370                 375                 380
Phe Gln Leu Glu Pro Trp Asn Asp Pro Val Cys Arg Asp Leu Thr Arg
385                 390                 395                 400
Thr Phe Glu His Ala Ile Tyr Ala Gln Tyr Gln Gln Gly
                405                 410
```

<210> 3
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of lovD

<400> 3

```
atgggttcta tcattgatgc ggctgcggcc gcggacccgg tggttctgat ggaaacggct 60
ttccgtaaag cggttaaaag ccgccagatt ccgggtgctg ttattatggc gcgtgattgt 120
agtggtaacc tgaactacac tcgctgtttc ggcgcacgca ctgtgcgtcg cgacgagtgc 180
aatcaattac caccgctgca ggtggataca ccatgtcgtc tggcaagcgc tactaaatta 240
ctgaccacga ttatggcact gcagtgcatg gaacgcggcc tggtagactt ggatgaaact 300
gttgaccgcc tgctgccgga cctgagcgcg atgccggtgc tggaaggctt tgatgatgcc 360
ggcaacgccc gtctgcgcga acgccgtggt aaaattacgt tacgccatct gctgacacac 420
accagcggtc tgtcgtacgt cttcctgcat ccgctgctgc gcgagtatat ggcccagggt 480
catttgcaga gcgctgagaa gtttggcatt cagtctcgtc tggcgccgcc agctgttaat 540
gatccaggcg cggaatggat ttatggcgct aatctggact gggcaggcaa attagtggaa 600
cgcgcaacgg gcttggacct ggaacagtac ttgcaggaga acatttgcgc gccgctgggc 660
atcactgata tgacgttcaa actgcagcag cgtccggata tgctggcacg tcgtgccgac 720
cagacccacc gcaactccgc ggatggtcgt ctgcgctatg atgactctgt gtattttcgc 780
gcggacggtg aagagtgttt cgggggccag ggcgtgttca gcggtccagg cagttacatg 840
aaggttctgc actctctgct gaaacgtgac ggcctgttgc tgcagccaca aaccgtggat 900
ctgatgttcc agccggcgct ggaaccgcgc ttggaagaac aaatgaacca gcatatggac 960
gcgtcgccgc acatcaacta tggcggtcca atgcctatgg tcctgcgtcg cagcttcggc 1020
```

ctgggtggta tcattgcact ggaggatctg gatggtgaga actggcgtcg taaaggctcg 1080
atgacgtttg gtggcggtcc aaacattgtt tggcagattg acccgaaagc gggtctgtgt 1140
actttagcct ttttccagct ggaaccgtgg aacgacccgg tgtgtcgtga cctgactcgc 1200
acctttgagc acgcgatcta tgcacagtat caacagggct aa 1242

<210> 4
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of lovD

<400> 4

Met	Gly	Ser	Ile	Ile	Asp	Ala	Ala	Ala	Ala	Ala	Asp	Pro	Val	Val	Leu
1				5				10						15	
Met	Glu	Thr	Ala	Phe	Arg	Lys	Ala	Val	Lys	Ser	Arg	Gln	Ile	Pro	Gly
			20					25					30		
Ala	Val	Ile	Met	Ala	Arg	Asp	Cys	Ser	Gly	Asn	Leu	Asn	Tyr	Thr	Arg
		35					40					45			
Cys	Phe	Gly	Ala	Arg	Thr	Val	Arg	Arg	Asp	Glu	Cys	Asn	Gln	Leu	Pro
	50					55					60				
Pro	Leu	Gln	Val	Asp	Thr	Pro	Cys	Arg	Leu	Ala	Ser	Ala	Thr	Lys	Leu
65					70					75					80
Leu	Thr	Thr	Ile	Met	Ala	Leu	Gln	Cys	Met	Glu	Arg	Gly	Leu	Val	Asp
				85					90					95	
Leu	Asp	Glu	Thr	Val	Asp	Arg	Leu	Leu	Pro	Asp	Leu	Ser	Ala	Met	Pro
			100					105					110		
Val	Leu	Glu	Gly	Phe	Asp	Asp	Ala	Gly	Asn	Ala	Arg	Leu	Arg	Glu	Arg
		115					120					125			
Arg	Gly	Lys	Ile	Thr	Leu	Arg	His	Leu	Leu	Thr	His	Thr	Ser	Gly	Leu
	130					135					140				
Ser	Tyr	Val	Phe	Leu	His	Pro	Leu	Leu	Arg	Glu	Tyr	Met	Ala	Gln	Gly
145					150					155					160
His	Leu	Gln	Ser	Ala	Glu	Lys	Phe	Gly	Ile	Gln	Ser	Arg	Leu	Ala	Pro
				165					170					175	
Pro	Ala	Val	Asn	Asp	Pro	Gly	Ala	Glu	Trp	Ile	Tyr	Gly	Ala	Asn	Leu
			180					185					190		
Asp	Trp	Ala	Gly	Lys	Leu	Val	Glu	Arg	Ala	Thr	Gly	Leu	Asp	Leu	Glu
		195					200					205			
Gln	Tyr	Leu	Gln	Glu	Asn	Ile	Cys	Ala	Pro	Leu	Gly	Ile	Thr	Asp	Met
	210					215					220				
Thr	Phe	Lys	Leu	Gln	Gln	Arg	Pro	Asp	Met	Leu	Ala	Arg	Arg	Ala	Asp
225					230					235					240
Gln	Thr	His	Arg	Asn	Ser	Ala	Asp	Gly	Arg	Leu	Arg	Tyr	Asp	Asp	Ser
				245					250					255	
Val	Tyr	Phe	Arg	Ala	Asp	Gly	Glu	Glu	Cys	Phe	Gly	Gly	Gln	Gly	Val
			260					265					270		
Phe	Ser	Gly	Pro	Gly	Ser	Tyr	Met	Lys	Val	Leu	His	Ser	Leu	Leu	Lys
		275					280					285			
Arg	Asp	Gly	Leu	Leu	Leu	Gln	Pro	Gln	Thr	Val	Asp	Leu	Met	Phe	Gln
	290					295					300				
Pro	Ala	Leu	Glu	Pro	Arg	Leu	Glu	Glu	Gln	Met	Asn	Gln	His	Met	Asp
305					310					315					320
Ala	Ser	Pro	His	Ile	Asn	Tyr	Gly	Gly	Pro	Met	Pro	Met	Val	Leu	Arg
				325					330					335	
Arg	Ser	Phe	Gly	Leu	Gly	Gly	Ile	Ile	Ala	Leu	Glu	Asp	Leu	Asp	Gly
			340					345					350		
Glu	Asn	Trp	Arg	Arg	Lys	Gly	Ser	Met	Thr	Phe	Gly	Gly	Gly	Pro	Asn
		355					360					365			
Ile	Val	Trp	Gln	Ile	Asp	Pro	Lys	Ala	Gly	Leu	Cys	Thr	Leu	Ala	Phe
	370					375					380				
Phe	Gln	Leu	Glu	Pro	Trp	Asn	Asp	Pro	Val	Cys	Arg	Asp	Leu	Thr	Arg
385					390					395					400
Thr	Phe	Glu	His	Ala	Ile	Tyr	Ala	Gln	Tyr	Gln	Gln	Gly			
				405					410						

<210> 5
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of lovD

<400> 5
atgggttcta tcattgatgc ggctgcggcc gcggacccgg tggttctgat ggaaacggct 60
ttccgtaaag cggttaaaag ccgccagatt ccgggtgctg ttattatggc gcgtgattgt 120
agtggtaacc tgaactacac tcgctgtttc ggcgcacgca ctgtgcgtcg cgacgagtgc 180
aatcaattac caccgctgca ggtggataca ccatgtcgtc tggcaagcgc tactaaatta 240
ctgaccacga ttatggcact gcagtgcatg gaacgcggcc tggtagactt ggatgaaact 300
gttgaccgcc tgctgccgga cctgagcgcg atgccggtgc tggaaggctt tgatgatgcc 360
ggcaacccgc gtctgcgcga acgccgtggt aaaattacgt tacgccatct gctgacacac 420
accagcggtc tgtcgtacgt cttcctgcat ccgctgctgc gcgagtatat ggcccagggt 480
catttgcaga gcgctgagaa gtttggcatt cagtctcgtt ttgcgccgcc attagttaat 540
gatccaggcg cggaatggat ttatggcgct tctctggact gggcaggcaa attagtggaa 600
cgcgcaacgg gcttggacct ggaacagtac ttgcaggaga acatttgcgc gccgctgggc 660
atcactgata tgacgttcaa actgcagcag cgtccggata tgctggcacg tcgtgccgac 720
cagacccacc gcaactccag cgatggtcgt ctgcgctatg atgactctgt gtattttcgc 780
gcggacggtg aagagtgttt cgggggccag ggcgtgttca gcggtccagg cagttacatg 840
aaggttctgc actctctgct gaaacgtgac ggcctgttgc tgcagccaca aaccgtggat 900
ctgatgttcc agccggcgct ggaaccgcgc ttggaagaac aaatgaacca gcatatggac 960
gcgtcgccgc acatcaacta tggcggtcca atgcctatgg tcctgcgtcg cagcttcggc 1020
ctgggtggta tcattgcact ggaggatctg gatggtgaga actggcgtcg taaaggctcg 1080
atgacgtttg gtggcggtcc aaacattgtt tggcagattg acccgaaagc gggtctgtgt 1140
actttagcct ttttccagct ggaaccgtgg aacgacccgg tgtgtcgtga cctgactcgc 1200
acctttgagc acgcgatcta tgcacagtat caacagggct aa 1242

<210> 6
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of lovD

<400> 6
Met Gly Ser Ile Ile Asp Ala Ala Ala Ala Ala Asp Pro Val Val Leu
1 5 10 15
Met Glu Thr Ala Phe Arg Lys Ala Val Lys Ser Arg Gln Ile Pro Gly
20 25 30
Ala Val Ile Met Ala Arg Asp Cys Ser Gly Asn Leu Asn Tyr Thr Arg
35 40 45
Cys Phe Gly Ala Arg Thr Val Arg Arg Asp Glu Cys Asn Gln Leu Pro
50 55 60
Pro Leu Gln Val Asp Thr Pro Cys Arg Leu Ala Ser Ala Thr Lys Leu
65 70 75 80
Leu Thr Thr Ile Met Ala Leu Gln Cys Met Glu Arg Gly Leu Val Asp
85 90 95
Leu Asp Glu Thr Val Asp Arg Leu Leu Pro Asp Leu Ser Ala Met Pro
100 105 110
Val Leu Glu Gly Phe Asp Asp Ala Gly Asn Pro Arg Leu Arg Glu Arg
115 120 125
Arg Gly Lys Ile Thr Leu Arg His Leu Leu Thr His Thr Ser Gly Leu
130 135 140
Ser Tyr Val Phe Leu His Pro Leu Leu Arg Glu Tyr Met Ala Gln Gly
145 150 155 160
His Leu Gln Ser Ala Glu Lys Phe Gly Ile Gln Ser Arg Phe Ala Pro
165 170 175
Pro Leu Val Asn Asp Pro Gly Ala Glu Trp Ile Tyr Gly Ala Ser Leu
180 185 190
Asp Trp Ala Gly Lys Leu Val Glu Arg Ala Thr Gly Leu Asp Leu Glu
195 200 205

```
Gln Tyr Leu Gln Glu Asn Ile Cys Ala Pro Leu Gly Ile Thr Asp Met
    210                 215                 220
Thr Phe Lys Leu Gln Gln Arg Pro Asp Met Leu Ala Arg Arg Ala Asp
225                 230                 235                 240
Gln Thr His Arg Asn Ser Ser Asp Gly Arg Leu Arg Tyr Asp Asp Ser
                245                 250                 255
Val Tyr Phe Arg Ala Asp Gly Glu Glu Cys Phe Gly Gly Gln Gly Val
            260                 265                 270
Phe Ser Gly Pro Gly Ser Tyr Met Lys Val Leu His Ser Leu Leu Lys
        275                 280                 285
Arg Asp Gly Leu Leu Leu Gln Pro Gln Thr Val Asp Leu Met Phe Gln
    290                 295                 300
Pro Ala Leu Glu Pro Arg Leu Glu Glu Gln Met Asn Gln His Met Asp
305                 310                 315                 320
Ala Ser Pro His Ile Asn Tyr Gly Gly Pro Met Pro Met Val Leu Arg
                325                 330                 335
Arg Ser Phe Gly Leu Gly Gly Ile Ile Ala Leu Glu Asp Leu Asp Gly
            340                 345                 350
Glu Asn Trp Arg Arg Lys Gly Ser Met Thr Phe Gly Gly Gly Pro Asn
        355                 360                 365
Ile Val Trp Gln Ile Asp Pro Lys Ala Gly Leu Cys Thr Leu Ala Phe
    370                 375                 380
Phe Gln Leu Glu Pro Trp Asn Asp Pro Val Cys Arg Asp Leu Thr Arg
385                 390                 395                 400
Thr Phe Glu His Ala Ile Tyr Ala Gln Tyr Gln Gln Gly
                405                 410
```

<210> 7
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of lovD

<400> 7
```
atgggttcta tcattgatgc ggctgcggcc gcggacccgg tggttctgat ggaaacggct 60
ttccgtaaag cggttaaaag ccgccagatt ccgggtgctg ttattatggc gcgtgattgt 120
agtggtaacc tgaactacac tcgctgtttc ggcgcacgca ctgtgcgtcg cgacgagtgc 180
aatcaattac caccgctgca ggtggataca ccatgtcgtc tggcaagcgc tactaaatta 240
ctgaccacga ttatggcact gcagtgcatg gaacgcggcc tggtagactt ggatgaaact 300
gttgaccgcc tgctgccgga cctgagcgcg atgccggtgc tggaaggctt tgatgatgcc 360
ggcaacccgc gtctgcgcga acgccgtggt aaaattacgt tacgccatct gctgacacac 420
accagcggtc tgtcgtacgt cttcctgcat ccgctgctgc gcgagtatat ggcccagggt 480
catttgcaga gcgctgagaa gtttggcatt cagtctcgtt ttgcgccgcc attagttaat 540
gatccaggcg cggaatggat ttatggcgct tctctggact gggcaggcaa attagtggaa 600
cgcgcaacgg gcttggacct ggaacagtac ttgcaggaga acatttgcgc gccgctgggc 660
atcactgata tgacgttcaa actgcagcag cgtccggata tgctggcacg tcgtgccgac 720
cagacccacc gcaactccag cgatggtcgt ctgcgctatg atgactctgt gtattttcgc 780
gcggacggtg aagagtgttt cgggggccag ggcgtgttca gcagtccagg cagttacatg 840
aaggttctgc actctctgct gaaacgtgac ggcctgttgc tgcagccaca aaccgtggat 900
ctgatgttcc agccggcgct ggaaccgcgc ttggaagaac aaatgaacca gcatatggac 960
gcgtcgccgc acatcaacta tggcggtcca atgcctatgg tcctgcgtcg cagcttcggc 1020
ctgggtggta tcattgcact ggaggatctg gatggtgaga actggcgtcg taaaggctcg 1080
atgacgtttg gtggcggtcc aaacattgtt tggcagattg acccgaaagc gggtctgtgt 1140
actttagcct ttttccagct ggaaccgtgg aacgacccgg tgtgtcgtga cctgactcgc 1200
acctttgagc acgcgatcta tgcacagtat caacagggct aa                    1242
```

<210> 8
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of lovD

<400> 8
Met Gly Ser Ile Ile Asp Ala Ala Ala Ala Ala Asp Pro Val Val Leu
1 5 10 15
Met Glu Thr Ala Phe Arg Lys Ala Val Lys Ser Arg Gln Ile Pro Gly
20 25 30
Ala Val Ile Met Ala Arg Asp Cys Ser Gly Asn Leu Asn Tyr Thr Arg
35 40 45
Cys Phe Gly Ala Arg Thr Val Arg Arg Asp Glu Cys Asn Gln Leu Pro
50 55 60
Pro Leu Gln Val Asp Thr Pro Cys Arg Leu Ala Ser Ala Thr Lys Leu
65 70 75 80
Leu Thr Thr Ile Met Ala Leu Gln Cys Met Glu Arg Gly Leu Val Asp
85 90 95
Leu Asp Glu Thr Val Asp Arg Leu Leu Pro Asp Leu Ser Ala Met Pro
100 105 110
Val Leu Glu Gly Phe Asp Asp Ala Gly Asn Pro Arg Leu Arg Glu Arg
115 120 125
Arg Gly Lys Ile Thr Leu Arg His Leu Leu Thr His Thr Ser Gly Leu
130 135 140
Ser Tyr Val Phe Leu His Pro Leu Leu Arg Glu Tyr Met Ala Gln Gly
145 150 155 160
His Leu Gln Ser Ala Glu Lys Phe Gly Ile Gln Ser Arg Phe Ala Pro
165 170 175
Pro Leu Val Asn Asp Pro Gly Ala Glu Trp Ile Tyr Gly Ala Ser Leu
180 185 190
Asp Trp Ala Gly Lys Leu Val Glu Arg Ala Thr Gly Leu Asp Leu Glu
195 200 205
Gln Tyr Leu Gln Glu Asn Ile Cys Ala Pro Leu Gly Ile Thr Asp Met
210 215 220
Thr Phe Lys Leu Gln Gln Arg Pro Asp Met Leu Ala Arg Arg Ala Asp
225 230 235 240
Gln Thr His Arg Asn Ser Ser Asp Gly Arg Leu Arg Tyr Asp Asp Ser
245 250 255
Val Tyr Phe Arg Ala Asp Gly Glu Glu Cys Phe Gly Gly Gln Gly Val
260 265 270
Phe Ser Ser Pro Gly Ser Tyr Met Lys Val Leu His Ser Leu Leu Lys
275 280 285
Arg Asp Gly Leu Leu Leu Gln Pro Gln Thr Val Asp Leu Met Phe Gln
290 295 300
Pro Ala Leu Glu Pro Arg Leu Glu Glu Gln Met Asn Gln His Met Asp
305 310 315 320
Ala Ser Pro His Ile Asn Tyr Gly Gly Pro Met Pro Met Val Leu Arg
325 330 335
Arg Ser Phe Gly Leu Gly Gly Ile Ile Ala Leu Glu Asp Leu Asp Gly
340 345 350
Glu Asn Trp Arg Arg Lys Gly Ser Met Thr Phe Gly Gly Gly Pro Asn
355 360 365
Ile Val Trp Gln Ile Asp Pro Lys Ala Gly Leu Cys Thr Leu Ala Phe
370 375 380
Phe Gln Leu Glu Pro Trp Asn Asp Pro Val Cys Arg Asp Leu Thr Arg
385 390 395 400
Thr Phe Glu His Ala Ile Tyr Ala Gln Tyr Gln Gln Gly
405 410

<210> 9
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of lovD

<400> 9
atgggttcta tcattgatgc ggctgcggcc gcggacccgg tggttctgat ggaaacggct 60
ttccgtaaag cggttaaaag ccgccagatt ccgggtgctg ttattatggc gcgtgattgt 120
agtggtaacc tgaactacac tcgctgtttc ggcgcacgca ctgtgcgtcg cgacgagtgc 180
aatcaattac caccgctgca ggtggataca ccatgtcgtc tggcaagcgc tactaaatta 240

ctgaccacga ttatggcact gcagtgcatg gaacgcggcc tggtagactt ggatgaaact 300
gttgaccgcc tgctgccgga cctgagcgcg atgccggtgc tggaaggctt tgatgatgcc 360
ggcaacccgc gtctgcgcga acgccgtggt aaaattacgt tacgccatct gctgacacac 420
accagcggtc tgtcgtacgt cttcctgcat ccgctgctgc gcgagtatgt tgcccagggt 480
catttgcaga gcgctgagaa gtttggcatt cagaatcgtt ttgcgccgcc attagttaat 540
gatccaggcg cggaatggat ttatggcgct tctctggact gggcaggcaa attagtggaa 600
cgcgcaacgg gcttggacct ggaacagtac ttgcaggaga acatttgcgc gccgctgggc 660
atcactgata tgacgttcaa actgcagcag cgtccggata tgctggcacg tcgtgccgac 720
cagacccacc gcaactccag cgatggtcgt ctgcgctatg atgactctgt gtattttcgc 780
gcggacggtg aagagtgttt cgggggccag ggcgtgttca gcagtccagg cagttacatg 840
aaggttctgc actctctgct gaaacgtgac ggcctgttgc tgcagccaca aaccgtggat 900
ctgatgttcc agccggcgct ggaaccgcgc ttggaagaac aaatgaacca gcatatggac 960
gcgtcgccgc acatcaacta tggcggtcca atgcctatgg tcctgcgtcg cagcttcggc 1020
ctgggtggta tcattgcact ggaggatctg gatggtgaga actggcgtcg taaaggctcg 1080
atgacgtttg gtggcggtcc aaacattgtt tggcagattg acccgaaagc gggtctgtgt 1140
actttagcct ttttccagct ggaaccgtgg aacgacccgg tgtgtcgtga cctgactcgc 1200
acctttgagc acgcgatcta tgcacagtat caacagggct aa 1242

<210> 10
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of lovD

<400> 10

Met	Gly	Ser	Ile	Ile	Asp	Ala	Ala	Ala	Ala	Ala	Asp	Pro	Val	Val	Leu
1				5					10					15	
Met	Glu	Thr	Ala	Phe	Arg	Lys	Ala	Val	Lys	Ser	Arg	Gln	Ile	Pro	Gly
			20					25					30		
Ala	Val	Ile	Met	Ala	Arg	Asp	Cys	Ser	Gly	Asn	Leu	Asn	Tyr	Thr	Arg
		35					40					45			
Cys	Phe	Gly	Ala	Arg	Thr	Val	Arg	Arg	Asp	Glu	Cys	Asn	Gln	Leu	Pro
	50					55					60				
Pro	Leu	Gln	Val	Asp	Thr	Pro	Cys	Arg	Leu	Ala	Ser	Ala	Thr	Lys	Leu
65					70					75					80
Leu	Thr	Thr	Ile	Met	Ala	Leu	Gln	Cys	Met	Glu	Arg	Gly	Leu	Val	Asp
				85					90					95	
Leu	Asp	Glu	Thr	Val	Asp	Arg	Leu	Leu	Pro	Asp	Leu	Ser	Ala	Met	Pro
			100					105					110		
Val	Leu	Glu	Gly	Phe	Asp	Asp	Ala	Gly	Asn	Pro	Arg	Leu	Arg	Glu	Arg
		115					120					125			
Arg	Gly	Lys	Ile	Thr	Leu	Arg	His	Leu	Leu	Thr	His	Thr	Ser	Gly	Leu
	130					135					140				
Ser	Tyr	Val	Phe	Leu	His	Pro	Leu	Leu	Arg	Glu	Tyr	Val	Ala	Gln	Gly
145					150					155					160
His	Leu	Gln	Ser	Ala	Glu	Lys	Phe	Gly	Ile	Gln	Asn	Arg	Phe	Ala	Pro
				165					170					175	
Pro	Leu	Val	Asn	Asp	Pro	Gly	Ala	Glu	Trp	Ile	Tyr	Gly	Ala	Ser	Leu
			180					185					190		
Asp	Trp	Ala	Gly	Lys	Leu	Val	Glu	Arg	Ala	Thr	Gly	Leu	Asp	Leu	Glu
		195					200					205			
Gln	Tyr	Leu	Gln	Glu	Asn	Ile	Cys	Ala	Pro	Leu	Gly	Ile	Thr	Asp	Met
	210					215					220				
Thr	Phe	Lys	Leu	Gln	Gln	Arg	Pro	Asp	Met	Leu	Ala	Arg	Arg	Ala	Asp
225					230					235					240
Gln	Thr	His	Arg	Asn	Ser	Ser	Asp	Gly	Arg	Leu	Arg	Tyr	Asp	Asp	Ser
				245					250					255	
Val	Tyr	Phe	Arg	Ala	Asp	Gly	Glu	Glu	Cys	Phe	Gly	Gly	Gln	Gly	Val
			260					265					270		
Phe	Ser	Ser	Pro	Gly	Ser	Tyr	Met	Lys	Val	Leu	His	Ser	Leu	Leu	Lys
		275					280					285			
Arg	Asp	Gly	Leu	Leu	Leu	Gln	Pro	Gln	Thr	Val	Asp	Leu	Met	Phe	Gln
	290					295					300				
Pro	Ala	Leu	Glu	Pro	Arg	Leu	Glu	Glu	Gln	Met	Asn	Gln	His	Met	Asp
305					310					315					320

Ala Ser Pro His Ile Asn Tyr Gly Gly Pro Met Pro Met Val Leu Arg
325 330 335
Arg Ser Phe Gly Leu Gly Gly Ile Ile Ala Leu Glu Asp Leu Asp Gly
340 345 350
Glu Asn Trp Arg Arg Lys Gly Ser Met Thr Phe Gly Gly Gly Pro Asn
355 360 365
Ile Val Trp Gln Ile Asp Pro Lys Ala Gly Leu Cys Thr Leu Ala Phe
370 375 380
Phe Gln Leu Glu Pro Trp Asn Asp Pro Val Cys Arg Asp Leu Thr Arg
385 390 395 400
Thr Phe Glu His Ala Ile Tyr Ala Gln Tyr Gln Gln Gly
405 410

<210> 11
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of lovD

<400> 11
atgggttcta tcattgatgc ggctgtggcc gcggacccgg tggttctgat ggaaacggct 60
ttccgtaaag cggttgaaag ccgccagatt ccgggtgctg ttattatggc gcgtgattgt 120
agtggtaacc tgaactacac tcgctgtttc ggcgcacgca ctgtgcgtcg cgacgagtgc 180
aatcaattac caccgctgca ggtggataca ccatgtcgtc tggcaagcgc tactaaatta 240
ctgaccacga ttatggcact gcagtgcatg gaacgcggcc tggtagactt ggatgaaact 300
gttgaccgcc tgctgccgga cctgagcgcg atgccggtgc tggaaggctt tgatgatgcc 360
ggcaacccgc gtctgcgcga acgccgtggt aaaattacgt tacgccatct gctgacacac 420
accagcggtc tgtcgtacgt cttcctgcat ccgctgctgc gcgagtatgt tgcccagggt 480
catttgcaga gcgctgagaa gtttggcatt cagaatcgtt ttgcgccgcc attagttaat 540
gatccaggcg cggaatggat ttatggcgct tctatcgact gggcaggcaa attagtggaa 600
cgcgcaacgg gcttggacct ggaacagtac ttgcaggaga acatttgcgc gccgctgggc 660
atcactgata tgacgttcaa actgcagcag cgtccggata tgctggcacg tcgtgccgac 720
cagacccacc gcaactccag cgatggtaaa ctgcgctatg atgactctgt gtattttcgc 780
gcggacggtg aagagtgttt cgggggccag ggcgtgttca gcagtccagg cagttacatg 840
aaggttctgc actctctgct gaaacgtgac ggcctgttgc tgcagccaga aaccgtggat 900
ctgatgttcc agccggcgct ggaaccgcgc ttggaagaac aaatgaacca gcatatggac 960
gcgtcgccgc acatcaacta tggcggtcca atgcctatgg tcctgcgtcg cagcttcggc 1020
ctgggtggta tcattgcact ggaggatctg gatggtgaga actggcgtcg taaaggctcg 1080
atgacgtttg gtggcggtcc aaacattgtt tggcagattg acccgaaagc gggtctgtgt 1140
actttagtct ttttccagct ggaaccgtgg aacgacccgg tgtgtcgtga cctgactcgc 1200
acctttgagc acgcgatcta tgcacagtat caacagggct aa 1242

<210> 12
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of lovD

<400> 12
Met Gly Ser Ile Ile Asp Ala Ala Val Ala Ala Asp Pro Val Val Leu
1 5 10 15
Met Glu Thr Ala Phe Arg Lys Ala Val Glu Ser Arg Gln Ile Pro Gly
20 25 30
Ala Val Ile Met Ala Arg Asp Cys Ser Gly Asn Leu Asn Tyr Thr Arg
35 40 45
Cys Phe Gly Ala Arg Thr Val Arg Arg Asp Glu Cys Asn Gln Leu Pro
50 55 60
Pro Leu Gln Val Asp Thr Pro Cys Arg Leu Ala Ser Ala Thr Lys Leu
65 70 75 80
Leu Thr Thr Ile Met Ala Leu Gln Cys Met Glu Arg Gly Leu Val Asp
85 90 95
Leu Asp Glu Thr Val Asp Arg Leu Leu Pro Asp Leu Ser Ala Met Pro

```
            100                 105                 110
Val Leu Glu Gly Phe Asp Asp Ala Gly Asn Pro Arg Leu Arg Glu Arg
        115                 120                 125
Arg Gly Lys Ile Thr Leu Arg His Leu Leu Thr His Thr Ser Gly Leu
    130                 135                 140
Ser Tyr Val Phe Leu His Pro Leu Leu Arg Glu Tyr Val Ala Gln Gly
145                 150                 155                 160
His Leu Gln Ser Ala Glu Lys Phe Gly Ile Gln Asn Arg Phe Ala Pro
                165                 170                 175
Pro Leu Val Asn Asp Pro Gly Ala Glu Trp Ile Tyr Gly Ala Ser Ile
            180                 185                 190
Asp Trp Ala Gly Lys Leu Val Glu Arg Ala Thr Gly Leu Asp Leu Glu
        195                 200                 205
Gln Tyr Leu Gln Glu Asn Ile Cys Ala Pro Leu Gly Ile Thr Asp Met
    210                 215                 220
Thr Phe Lys Leu Gln Gln Arg Pro Asp Met Leu Ala Arg Arg Ala Asp
225                 230                 235                 240
Gln Thr His Arg Asn Ser Ser Asp Gly Lys Leu Arg Tyr Asp Asp Ser
                245                 250                 255
Val Tyr Phe Arg Ala Asp Gly Glu Glu Cys Phe Gly Gly Gln Gly Val
            260                 265                 270
Phe Ser Ser Pro Gly Ser Tyr Met Lys Val Leu His Ser Leu Leu Lys
        275                 280                 285
Arg Asp Gly Leu Leu Leu Gln Pro Glu Thr Val Asp Leu Met Phe Gln
    290                 295                 300
Pro Ala Leu Glu Pro Arg Leu Glu Glu Gln Met Asn Gln His Met Asp
305                 310                 315                 320
Ala Ser Pro His Ile Asn Tyr Gly Gly Pro Met Pro Met Val Leu Arg
                325                 330                 335
Arg Ser Phe Gly Leu Gly Gly Ile Ile Ala Leu Glu Asp Leu Asp Gly
            340                 345                 350
Glu Asn Trp Arg Arg Lys Gly Ser Met Thr Phe Gly Gly Gly Pro Asn
        355                 360                 365
Ile Val Trp Gln Ile Asp Pro Lys Ala Gly Leu Cys Thr Leu Val Phe
    370                 375                 380
Phe Gln Leu Glu Pro Trp Asn Asp Pro Val Cys Arg Asp Leu Thr Arg
385                 390                 395                 400
Thr Phe Glu His Ala Ile Tyr Ala Gln Tyr Gln Gln Gly
                405                 410
```

<210> 13
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of lovD

<400> 13

```
atgggttcta tcattgatgc ggctgtggcc gcggacccgg tggttctgat ggaaacggct 60
ttccgtaaag cggttgaaag ccgccagatt ccgggtgctg ttattatggc gcgtgattgt 120
agtggtcgtc tgaactacac tcgctgtttc ggcgcacgca ctgtgcgtcg cgacgagtgc 180
aatcaattac caccgctgca ggtggataca ccatgtcgtc tggcaagcgc tactaaatta 240
ctgaccacga ttatggcact gcagtgcatg gaacgcggcc tggtagactt ggatgaaact 300
gttgaccgcc tgctgccgga cctgagcgcg atgccggtgc tggaaggctt tgatgatgcc 360
ggcaacccgc gtctgcgcga acgccgtggt aaaattacgt tacgccatct gctgacacac 420
accagcggtc tgtcgtacgt cttcctgcat ccgctgctgc gcgagtatgt tgcccagggt 480
catttgcagg gcgctgagaa gtttggcatt cagaatcgtt ttgcgccgcc attagttaat 540
gatccaggcg cggaatggat ttatggcgct ggcatcgact gggcaggcaa attagtggaa 600
cgcgcaacgg gcttggacct ggaacagtac ttgcaggaga acatttgcgc gccgctgggc 660
atcactgata tgacgttcaa actgcagcag cgtccggata tgctggcacg tcgtgccgac 720
atgacccacc gcaactccag cgatggtaaa ctgcgctatg atgactctgt gtattttcgc 780
gcggacggtg aagagtgttt cgggggccag ggcgtgttca gcagtccagg cagttacatg 840
aaggttctgc actctctgct gaaacgtgac ggcctgttgc tgcagccaga aaccgtggat 900
ctgatgttcc agccggcgct ggaaccgcgc ttggaagaac aaatgaacca gcatatggac 960
gcgtcgccgc acatcaacta tggcggtcca atgcctatgg tcctgcgtcg cagcttcggc 1020
ctgggtggta tcattgcact ggaggatctg gatggtgaga actggcgtcg taaaggctcg 1080
```

atgacgtttg gtggcggtcc aaacattatt tggcagattg acccgaaagc gggtctgtgt 1140
actttagtct ttttccagct ggaaccgtgg aacgacccgg tgtgtcgtga cctgactcgc 1200
acctttgaga aagcgatcta tgcacagtat caacagggct aa 1242

<210> 14
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of lovD

<400> 14

Met	Gly	Ser	Ile	Ile	Asp	Ala	Ala	Val	Ala	Ala	Asp	Pro	Val	Val	Leu
1				5					10					15	
Met	Glu	Thr	Ala	Phe	Arg	Lys	Ala	Val	Glu	Ser	Arg	Gln	Ile	Pro	Gly
			20					25					30		
Ala	Val	Ile	Met	Ala	Arg	Asp	Cys	Ser	Gly	Arg	Leu	Asn	Tyr	Thr	Arg
		35					40					45			
Cys	Phe	Gly	Ala	Arg	Thr	Val	Arg	Arg	Asp	Glu	Cys	Asn	Gln	Leu	Pro
	50					55					60				
Pro	Leu	Gln	Val	Asp	Thr	Pro	Cys	Arg	Leu	Ala	Ser	Ala	Thr	Lys	Leu
65					70					75					80
Leu	Thr	Thr	Ile	Met	Ala	Leu	Gln	Cys	Met	Glu	Arg	Gly	Leu	Val	Asp
				85					90					95	
Leu	Asp	Glu	Thr	Val	Asp	Arg	Leu	Leu	Pro	Asp	Leu	Ser	Ala	Met	Pro
			100					105					110		
Val	Leu	Glu	Gly	Phe	Asp	Asp	Ala	Gly	Asn	Pro	Arg	Leu	Arg	Glu	Arg
		115					120					125			
Arg	Gly	Lys	Ile	Thr	Leu	Arg	His	Leu	Leu	Thr	His	Thr	Ser	Gly	Leu
	130					135					140				
Ser	Tyr	Val	Phe	Leu	His	Pro	Leu	Leu	Arg	Glu	Tyr	Val	Ala	Gln	Gly
145					150					155					160
His	Leu	Gln	Gly	Ala	Glu	Lys	Phe	Gly	Ile	Gln	Asn	Arg	Phe	Ala	Pro
				165					170					175	
Pro	Leu	Val	Asn	Asp	Pro	Gly	Ala	Glu	Trp	Ile	Tyr	Gly	Ala	Gly	Ile
			180					185					190		
Asp	Trp	Ala	Gly	Lys	Leu	Val	Glu	Arg	Ala	Thr	Gly	Leu	Asp	Leu	Glu
		195					200					205			
Gln	Tyr	Leu	Gln	Glu	Asn	Ile	Cys	Ala	Pro	Leu	Gly	Ile	Thr	Asp	Met
	210					215					220				
Thr	Phe	Lys	Leu	Gln	Gln	Arg	Pro	Asp	Met	Leu	Ala	Arg	Arg	Ala	Asp
225					230					235					240
Met	Thr	His	Arg	Asn	Ser	Ser	Asp	Gly	Lys	Leu	Arg	Tyr	Asp	Asp	Ser
				245					250					255	
Val	Tyr	Phe	Arg	Ala	Asp	Gly	Glu	Glu	Cys	Phe	Gly	Gly	Gln	Gly	Val
			260					265					270		
Phe	Ser	Ser	Pro	Gly	Ser	Tyr	Met	Lys	Val	Leu	His	Ser	Leu	Leu	Lys
		275					280					285			
Arg	Asp	Gly	Leu	Leu	Leu	Gln	Pro	Glu	Thr	Val	Asp	Leu	Met	Phe	Gln
	290					295					300				
Pro	Ala	Leu	Glu	Pro	Arg	Leu	Glu	Glu	Gln	Met	Asn	Gln	His	Met	Asp
305					310					315					320
Ala	Ser	Pro	His	Ile	Asn	Tyr	Gly	Gly	Pro	Met	Pro	Met	Val	Leu	Arg
				325					330					335	
Arg	Ser	Phe	Gly	Leu	Gly	Gly	Ile	Ile	Ala	Leu	Glu	Asp	Leu	Asp	Gly
			340					345					350		
Glu	Asn	Trp	Arg	Arg	Lys	Gly	Ser	Met	Thr	Phe	Gly	Gly	Gly	Pro	Asn
		355					360					365			
Ile	Ile	Trp	Gln	Ile	Asp	Pro	Lys	Ala	Gly	Leu	Cys	Thr	Leu	Val	Phe
	370					375					380				
Phe	Gln	Leu	Glu	Pro	Trp	Asn	Asp	Pro	Val	Cys	Arg	Asp	Leu	Thr	Arg
385					390					395					400
Thr	Phe	Glu	Lys	Ala	Ile	Tyr	Ala	Gln	Tyr	Gln	Gln	Gly			
				405					410						

<210> 15
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of lovD

<400> 15
atgggttcta tcattgatgc ggctgtggcc gcggacccgg tggttctgat ggaaacggct 60
ttccgtaaag cggttgaaag ccgccagatt ccgggtgctg ttattatggc gcgtgattgt 120
agcggtcgtc tgaactacac tcgctgtttc ggcgcacgca ctgtgcgtcg cgacgagtgc 180
aatcaattac caccgctgca ggtggataca ccatgtcgtc tggcaagcgc tactaaatta 240
ctgaccacga ttatggcact gcagtgcatg gaacgcggcc tggtagactt ggatgaaact 300
gttgaccgcc tgctgccgga cctgagcgcg atgccggtgc tggaaggctt tgatgatgcc 360
ggcaacccgc gtctgcgcga acgccgtggt aaaattacgt tacgccatct gctgacacac 420
accagcggtc tgtcgtacgt cttcctgcat ccgctgctgc gcgagtatgt tgcccagggt 480
catttgcagg gcgctgagaa gtttggcatt cagaatcgtt ttgcgccgcc attagttaat 540
gatccaggcg cggaatggat ttatggcgct ggcatcgact gggcaggcaa attagtggaa 600
cgcgcaacgg gcttggacct ggaacagtac ttgcaggaga acatttgcgc gccgctgggc 660
atcactgata tgacgttcaa actgcagcag cgcccggata tgctggcacg tcgtgccgac 720
atgacccacc gcaactccag cgatggtaaa ctgcgctatg atgacacggt gtattttcgc 780
gttgacggtg aagagtgttt cgggggccag ggcgtgttca gcagtccagg cagttacatg 840
aaggttctgc actctctgct gaaacgtgac ggcctgttgc tgcagccagg gaccgtggat 900
ctgatgttcc agccggcgct ggaaccgcgc ttggaagaac aaatgaacca gcatatggac 960
gcgtcgccgc acatcaacta tggcggtcca atgcctatgg tcctgcgtcg cagcttcggc 1020
ctgggtggta tcattgcact ggaggatctg gatggtgaga actggcgtcg taaaggctcg 1080
atgacgtttg gtggcggtcc aaacattatt tggcagattg acccgaaagc gggtctgtgt 1140
actttagtct ttttccagct ggaaccgtgg agtgacccgg tgtgtcgtga cctgactcgc 1200
acctttgaga aagcgatcta tgcacagtat caacagggct aa 1242

<210> 16
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of lovD

<400> 16
Met Gly Ser Ile Ile Asp Ala Ala Val Ala Ala Asp Pro Val Val Leu
1 5 10 15
Met Glu Thr Ala Phe Arg Lys Ala Val Glu Ser Arg Gln Ile Pro Gly
20 25 30
Ala Val Ile Met Ala Arg Asp Cys Ser Gly Arg Leu Asn Tyr Thr Arg
35 40 45
Cys Phe Gly Ala Arg Thr Val Arg Arg Asp Glu Cys Asn Gln Leu Pro
50 55 60
Pro Leu Gln Val Asp Thr Pro Cys Arg Leu Ala Ser Ala Thr Lys Leu
65 70 75 80
Leu Thr Thr Ile Met Ala Leu Gln Cys Met Glu Arg Gly Leu Val Asp
85 90 95
Leu Asp Glu Thr Val Asp Arg Leu Leu Pro Asp Leu Ser Ala Met Pro
100 105 110
Val Leu Glu Gly Phe Asp Asp Ala Gly Asn Pro Arg Leu Arg Glu Arg
115 120 125
Arg Gly Lys Ile Thr Leu Arg His Leu Leu Thr His Thr Ser Gly Leu
130 135 140
Ser Tyr Val Phe Leu His Pro Leu Leu Arg Glu Tyr Val Ala Gln Gly
145 150 155 160
His Leu Gln Gly Ala Glu Lys Phe Gly Ile Gln Asn Arg Phe Ala Pro
165 170 175
Pro Leu Val Asn Asp Pro Gly Ala Glu Trp Ile Tyr Gly Ala Gly Ile
180 185 190
Asp Trp Ala Gly Lys Leu Val Glu Arg Ala Thr Gly Leu Asp Leu Glu
195 200 205
Gln Tyr Leu Gln Glu Asn Ile Cys Ala Pro Leu Gly Ile Thr Asp Met

```
    210                 215                 220
Thr Phe Lys Leu Gln Gln Arg Pro Asp Met Leu Ala Arg Arg Ala Asp
225                 230                 235                 240
Met Thr His Arg Asn Ser Ser Asp Gly Lys Leu Arg Tyr Asp Asp Thr
                245                 250                 255
Val Tyr Phe Arg Val Asp Gly Glu Glu Cys Phe Gly Gly Gln Gly Val
            260                 265                 270
Phe Ser Ser Pro Gly Ser Tyr Met Lys Val Leu His Ser Leu Leu Lys
        275                 280                 285
Arg Asp Gly Leu Leu Leu Gln Pro Gly Thr Val Asp Leu Met Phe Gln
    290                 295                 300
Pro Ala Leu Glu Pro Arg Leu Glu Glu Gln Met Asn Gln His Met Asp
305                 310                 315                 320
Ala Ser Pro His Ile Asn Tyr Gly Gly Pro Met Pro Met Val Leu Arg
                325                 330                 335
Arg Ser Phe Gly Leu Gly Gly Ile Ile Ala Leu Glu Asp Leu Asp Gly
            340                 345                 350
Glu Asn Trp Arg Arg Lys Gly Ser Met Thr Phe Gly Gly Gly Pro Asn
        355                 360                 365
Ile Ile Trp Gln Ile Asp Pro Lys Ala Gly Leu Cys Thr Leu Val Phe
    370                 375                 380
Phe Gln Leu Glu Pro Trp Ser Asp Pro Val Cys Arg Asp Leu Thr Arg
385                 390                 395                 400
Thr Phe Glu Lys Ala Ile Tyr Ala Gln Tyr Gln Gln Gly
                405                 410
```

<210> 17
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of lovD

<400> 17

```
atgggttcta acattgatgc ggctgtggcc gcggacccgg tggttctgat ggaaacggct 60
ttccgtaaag cggttgaaag ctctcagatt ccgggtgctg ttattatggc gcgtgattgt 120
agcggtcgtc tgaactacac tcgctgtttc ggcgcacgca ctgtgcgtcg cgacgagtgc 180
aatcaattac caccgctgca ggtggataca ccatgtcgtc tggcaagcgc tactaaatta 240
ctgaccacga ttatggcact gcagtgcatg gaacgcggcc tggtagactt ggatgaaact 300
gttgaccgcc tgctgccgga cctgagcgcg atgccggtgc tggaaggctt tgatgatgcc 360
ggcaacccgc gtctgcgcga acgccgtggt aaaattacgt tacgccatct gctgacacac 420
accagcggtc tgtcgtacgt cttcctgcat ccgctgctgc gcgagtatgt tgcccagggt 480
catttgcagg gcgctgagaa gtttggcatt cagaatcgtt ttgcgccgcc attagttaat 540
gatccaggcg cggaatggat ttatggcgct ggcatcgact gggcaggcaa attagtggaa 600
cgcgcaacgg gcttggacct ggaacagtac ttgcaggaga acatttgcgc gccgctgggc 660
atcactgata tgacgttcaa actgcagcag cgcccggata tgctggcacg tcgtgccgac 720
atgacccacc gcaactccag cgatggtaaa ctgcgctatg atgacacggt gtattttcgc 780
catgacggtg aagagtgttt cgggggccag ggcgtgttca gcagtccagg cagttacatg 840
aaggttctgc actctctgct gaaacgtgac ggcctgttgc tgcagccagg gaccgtggat 900
ctgatgttcc agccggcgct ggaaccgcgt ttggaagaac aaatgaacca gcatatggac 960
gcgtcgccgc acatcaacta tggcggtcca atgcctatgg tcctgcgtcg cagcttcggc 1020
ctgggtggta tcattgcact ggaggatctg gatggtgaga actggcgtcg taaaggctcg 1080
atgacgtttg gtggcggtcc aaacattatt tggcagattg acccgaaagc gggtctgtgt 1140
actttagtct ttttccagct ggaaccgtgg agtgacccgg tgtgtcgtga cctgactcgc 1200
acctttgaga aagcgatcta tgcacagtat caacagggct aa                    1242
```

<210> 18
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of lovD

<400> 18

```
Met Gly Ser Asn Ile Asp Ala Ala Val Ala Ala Asp Pro Val Val Leu
1               5                  10                  15
Met Glu Thr Ala Phe Arg Lys Ala Val Glu Ser Ser Gln Ile Pro Gly
            20                  25                  30
Ala Val Ile Met Ala Arg Asp Cys Ser Gly Arg Leu Asn Tyr Thr Arg
        35                  40                  45
Cys Phe Gly Ala Arg Thr Val Arg Arg Asp Glu Cys Asn Gln Leu Pro
    50                  55                  60
Pro Leu Gln Val Asp Thr Pro Cys Arg Leu Ala Ser Ala Thr Lys Leu
65                  70                  75                  80
Leu Thr Thr Ile Met Ala Leu Gln Cys Met Glu Arg Gly Leu Val Asp
                85                  90                  95
Leu Asp Glu Thr Val Asp Arg Leu Leu Pro Asp Leu Ser Ala Met Pro
            100                 105                 110
Val Leu Glu Gly Phe Asp Asp Ala Gly Asn Pro Arg Leu Arg Glu Arg
        115                 120                 125
Arg Gly Lys Ile Thr Leu Arg His Leu Leu Thr His Thr Ser Gly Leu
    130                 135                 140
Ser Tyr Val Phe Leu His Pro Leu Leu Arg Glu Tyr Val Ala Gln Gly
145                 150                 155                 160
His Leu Gln Gly Ala Glu Lys Phe Gly Ile Gln Asn Arg Phe Ala Pro
                165                 170                 175
Pro Leu Val Asn Asp Pro Gly Ala Glu Trp Ile Tyr Gly Ala Gly Ile
            180                 185                 190
Asp Trp Ala Gly Lys Leu Val Glu Arg Ala Thr Gly Leu Asp Leu Glu
        195                 200                 205
Gln Tyr Leu Gln Glu Asn Ile Cys Ala Pro Leu Gly Ile Thr Asp Met
    210                 215                 220
Thr Phe Lys Leu Gln Gln Arg Pro Asp Met Leu Ala Arg Arg Ala Asp
225                 230                 235                 240
Met Thr His Arg Asn Ser Ser Asp Gly Lys Leu Arg Tyr Asp Asp Thr
                245                 250                 255
Val Tyr Phe Arg His Asp Gly Glu Glu Cys Phe Gly Gly Gln Gly Val
            260                 265                 270
Phe Ser Ser Pro Gly Ser Tyr Met Lys Val Leu His Ser Leu Leu Lys
        275                 280                 285
Arg Asp Gly Leu Leu Leu Gln Pro Gly Thr Val Asp Leu Met Phe Gln
    290                 295                 300
Pro Ala Leu Glu Pro Arg Leu Glu Glu Gln Met Asn Gln His Met Asp
305                 310                 315                 320
Ala Ser Pro His Ile Asn Tyr Gly Gly Pro Met Pro Met Val Leu Arg
                325                 330                 335
Arg Ser Phe Gly Leu Gly Gly Ile Ile Ala Leu Glu Asp Leu Asp Gly
            340                 345                 350
Glu Asn Trp Arg Arg Lys Gly Ser Met Thr Phe Gly Gly Gly Pro Asn
        355                 360                 365
Ile Ile Trp Gln Ile Asp Pro Lys Ala Gly Leu Cys Thr Leu Val Phe
    370                 375                 380
Phe Gln Leu Glu Pro Trp Ser Asp Pro Val Cys Arg Asp Leu Thr Arg
385                 390                 395                 400
Thr Phe Glu Lys Ala Ile Tyr Ala Gln Tyr Gln Gln Gly
                405                 410
```

<210> 19
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of lovD

<400> 19

```
atgggttcta acattgatgc ggctgtggcc gcggacccgg tggttctgat ggaaacggct 60
ttccgtaaag cggttgaaag ctctcagatt ccgggtgctg ttttgatggc gcgtgattgt 120
agcggtcgtc tgaactacac tcgctgtttc ggcgcacgca ctgtgcgtcg cgacgagtgc 180
aatcaattac caccgctgca ggtggataca ccatgtcgtc tggcaagcgc tactaaatta 240
ctgaccacga ttatggcact gcagtgcatg gaacgcggcc tggtacgctt ggatgaaact 300
```

```
gttgaccgcc tgctgccgga cctgtgcgcg atgccggtgc tggaaggctt tgatgatgcc 360
ggcaacccgc gtctgcgcga acgccgtggt aaaattacgt tacgccatct gctgacacac 420
accagcggtc tgtcgtacgt cttcctgcat ccgctgctgc gcgagtatgt tgcccagggt 480
catttgcagg gcgctgagaa gtttggcatt cagaatcgtt ttgcgccgcc attagttaat 540
gatccaggcg cggaatggat ttatggcgct ggcatcgact gggcaggcaa attagtggaa 600
cgcgcaacgg gcttggacct ggaacagtac ttgcaggaga acatttgcgc gccgctgggc 660
atcactgata tgacgttcaa actgcagcag cgcccggata tgctggcacg tcgtgccgac 720
atgacccacc gcaactccag cgatggtaaa ctgcgctatg atgacacggt gtattttcgc 780
catgacggtg aagagtgttt cgggggccag ggcgtgttca gcagtccagg cagttacatg 840
aaggttctgc actctctgct gaaacgtgac ggcctgttgc tgcagccagg gaccgtggat 900
ctgatgttcc agccggcgct ggaaccgcgt ttggaagaac aaatgaacca gcatatggac 960
gcgtcgccgc acatcaacta tggcggtcca atgcctatgg tcatgcgtcg cagcttcggc 1020
ctgggtggta tcattgcact ggaggatctg gatggtgaga actggcgtcg taaaggctcg 1080
atgacgtttg gtggcggtcc aaacattatt tggcagattg acccgaaagc gggtctgtgt 1140
actttagtct ttttccagct ggaaccgtgg agtgacccgg tgtgtcgtga cctgactcgc 1200
acctttgaga aagcgatcta tgcacagtat caacagggct aa                    1242


<210> 20
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of lovD

<400> 20
Met Gly Ser Asn Ile Asp Ala Ala Val Ala Ala Asp Pro Val Val Leu
1               5                  10                  15
Met Glu Thr Ala Phe Arg Lys Ala Val Glu Ser Ser Gln Ile Pro Gly
            20                  25                  30
Ala Val Leu Met Ala Arg Asp Cys Ser Gly Arg Leu Asn Tyr Thr Arg
        35                  40                  45
Cys Phe Gly Ala Arg Thr Val Arg Arg Asp Glu Cys Asn Gln Leu Pro
    50                  55                  60
Pro Leu Gln Val Asp Thr Pro Cys Arg Leu Ala Ser Ala Thr Lys Leu
65                  70                  75                  80
Leu Thr Thr Ile Met Ala Leu Gln Cys Met Glu Arg Gly Leu Val Arg
                85                  90                  95
Leu Asp Glu Thr Val Asp Arg Leu Leu Pro Asp Leu Cys Ala Met Pro
            100                 105                 110
Val Leu Glu Gly Phe Asp Asp Ala Gly Asn Pro Arg Leu Arg Glu Arg
        115                 120                 125
Arg Gly Lys Ile Thr Leu Arg His Leu Leu Thr His Thr Ser Gly Leu
    130                 135                 140
Ser Tyr Val Phe Leu His Pro Leu Leu Arg Glu Tyr Val Ala Gln Gly
145                 150                 155                 160
His Leu Gln Gly Ala Glu Lys Phe Gly Ile Gln Asn Arg Phe Ala Pro
                165                 170                 175
Pro Leu Val Asn Asp Pro Gly Ala Glu Trp Ile Tyr Gly Ala Gly Ile
            180                 185                 190
Asp Trp Ala Gly Lys Leu Val Glu Arg Ala Thr Gly Leu Asp Leu Glu
        195                 200                 205
Gln Tyr Leu Gln Glu Asn Ile Cys Ala Pro Leu Gly Ile Thr Asp Met
    210                 215                 220
Thr Phe Lys Leu Gln Gln Arg Pro Asp Met Leu Ala Arg Arg Ala Asp
225                 230                 235                 240
Met Thr His Arg Asn Ser Ser Asp Gly Lys Leu Arg Tyr Asp Asp Thr
                245                 250                 255
Val Tyr Phe Arg His Asp Gly Glu Glu Cys Phe Gly Gly Gln Gly Val
            260                 265                 270
Phe Ser Ser Pro Gly Ser Tyr Met Lys Val Leu His Ser Leu Leu Lys
        275                 280                 285
Arg Asp Gly Leu Leu Leu Gln Pro Gly Thr Val Asp Leu Met Phe Gln
    290                 295                 300
Pro Ala Leu Glu Pro Arg Leu Glu Glu Gln Met Asn Gln His Met Asp
305                 310                 315                 320
Ala Ser Pro His Ile Asn Tyr Gly Gly Pro Met Pro Met Val Met Arg
```

```
                 325                 330                 335
Arg Ser Phe Gly Leu Gly Gly Ile Ile Ala Leu Glu Asp Leu Asp Gly
            340                 345                 350
Glu Asn Trp Arg Arg Lys Gly Ser Met Thr Phe Gly Gly Gly Pro Asn
        355                 360                 365
Ile Ile Trp Gln Ile Asp Pro Lys Ala Gly Leu Cys Thr Leu Val Phe
    370                 375                 380
Phe Gln Leu Glu Pro Trp Ser Asp Pro Val Cys Arg Asp Leu Thr Arg
385                 390                 395                 400
Thr Phe Glu Lys Ala Ile Tyr Ala Gln Tyr Gln Gln Gly
                405                 410
```