SEQUENCE LISTING

<110> The Secretary of State for Defence
White, Peter J
Willey, Tara L
Price, Rachel L
Murphy, Melanie J
Squirrell, David

<120> Novel Enzyme

<130> DERA/IPD/P1247/WOD

<140>
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<150> GB 9925161.3
<151> 1999-10-26

<150> GB 0016744.5
<151> 2000-07-10

<160> 13

<170> PatentIn Ver. 2.1

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

<220>
<221> CDS
<222> (3)..(1661)

<220>
<223> Description of Artificial Sequence: cDNA sequence
of the synthetic luciferase gene

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   Ile Gln Met Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro
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ttc tat cct ctg gag gat ggc acc gct ggc gag caa ctg cat aag gct    95
Phe Tyr Pro Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala
     15                  20                  25

atg aag cgt tac gcc ctg gtt cct ggt aca att gct ttt aca gat gca   143
Met Lys Arg Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala
 30                  35                  40                  45

cat atc gag gtg aac atc acg tac gcg gaa tac ttc gaa atg tcc gtt   191
His Ile Glu Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val
                 50                  55                  60

cgc ctg gca gaa gct atg aaa cgc tat ggt ctg aat aca aat cac cgt   239
Arg Leu Ala Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg
             65                  70                  75
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```
atc gtc gta tgc agt gaa aac tct ctt caa ttc ttt atg ccg gtg ctg   287
Ile Val Val Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu
         80                  85                  90

ggc gcg ctt ttt atc ggt gtt gca gtt gcg ccg gcg aac gac att tat   335
Gly Ala Leu Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr
     95                 100                 105

aat gaa cgt gaa ctg ctt aac agt atg aac att tcg cag cct acc gta   383
Asn Glu Arg Glu Leu Leu Asn Ser Met Asn Ile Ser Gln Pro Thr Val
110                 115                 120                 125

gtc ttt gtt tcc aaa aag ggc ctg caa aaa att ctc aac gtg caa aaa   431
Val Phe Val Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys
                130                 135                 140

aaa ctg cca att atc cag aaa att att atc atg gat tct aaa acg gat   479
Lys Leu Pro Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp
            145                 150                 155

tac cag ggc ttt cag tcg atg tac acg ttc gtc aca tct cat ctg cct   527
Tyr Gln Gly Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro
        160                 165                 170

ccg ggt ttt aat gaa tac gat ttt gta cca gag tcc ttt gat cgt gac   575
Pro Gly Phe Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp
    175                 180                 185

aaa aca att gca ctg atc atg aat tcc tct ggc tct act ggt ctg cct   623
Lys Thr Ile Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro
190                 195                 200                 205

aag ggt gtg gcc ctt ccg cat cgt tgt gcc tgc gtc cgt ttc tcg cat   671
Lys Gly Val Ala Leu Pro His Arg Cys Ala Cys Val Arg Phe Ser His
                210                 215                 220

gcc cgc gat cct att ttt ggt aac caa atc att ccg gat act gcg att   719
Ala Arg Asp Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile
            225                 230                 235

ctg agt gtt gtt cca ttc cac cat ggt ttt ggc atg ttt act aca ctc   767
Leu Ser Val Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu
        240                 245                 250

ggc tat ctg atc tgt ggc ttt cgt gtc gtc ctc atg tat cgc ttt gaa   815
Gly Tyr Leu Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu
    255                 260                 265

gaa gag ctg ttt ctg cgc tcc ctg cag gat tac aaa att caa agt gcg   863
Glu Glu Leu Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala
270                 275                 280                 285

ctt ctg gtg cca acc ctg ttt tca ttc ttc gcc aaa agc act ctg att   911
Leu Leu Val Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile
                290                 295                 300

gac aaa tac gat ctg tct aat ctt cac gaa att gct agc ggc ggt gca   959
Asp Lys Tyr Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala
            305                 310                 315

cct ctt tcg aaa gaa gtc gga gaa gcg gtt gca aaa cgc ttc cat ctt  1007
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Pro Leu Ser Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu
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cca ggc atc cgt caa ggc tat ggt ctc act gag act act agt gct att   1055
Pro Gly Ile Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile
    335                 340                 345

ctg att aca ccg aag ggc gat ttc aaa ccg ggc gcg gtc ggt aaa gtg   1103
Leu Ile Thr Pro Lys Gly Asp Phe Lys Pro Gly Ala Val Gly Lys Val
350                 355                 360                 365

gta cca ttt ttt gaa gcg aag gtt gtg gat ctg gat acc ggc aaa acg   1151
Val Pro Phe Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr
                370                 375                 380

ctg ggc gtt aat cag cgt ggc gaa ctg tgt gtc cgc ggt cct atg att   1199
Leu Gly Val Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile
            385                 390                 395

atg tcc ggt tat gta aac aat ccg gaa gcg acc aac gcc ctt att gac   1247
Met Ser Gly Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp
        400                 405                 410

aag gat ggc tgg ctg cat tct ggc gac atc gct tac tgg gac gaa gac   1295
Lys Asp Gly Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp
    415                 420                 425

gaa cac ttc ttc atc gtt gac cgc ctg aag tct ctc att aaa tac aaa   1343
Glu His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys
430                 435                 440                 445

ggc tat cag gtg gcc cca gct gaa ctg gaa tcg atc ctc ctg caa cac   1391
Gly Tyr Gln Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His
                450                 455                 460

cca aac atc ttc gac gcg ggc gtg gca ggt ctt ccg gac gat gac gcc   1439
Pro Asn Ile Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala
            465                 470                 475

ggt gaa ctt ccg gcc gcc gtt gtt gtt ctc gag cac ggt aag acg atg   1487
Gly Glu Leu Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met
        480                 485                 490

acg gaa aaa gag atc gtg gat tac gtc gcc agt caa gta aca acc gcg   1535
Thr Glu Lys Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala
    495                 500                 505

aaa aag ctg cgc ggt ggc gtt gtg ttt gtg gac gaa gta ccg aaa ggt   1583
Lys Lys Leu Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly
510                 515                 520                 525

ctt acc ggc aaa ctc gac gca cgt aaa atc cgc gag atc ctc att aag   1631
Leu Thr Gly Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys
                530                 535                 540

gcc aag aag ggc ggt aag tcc aag ctt taa                          1661
Ala Lys Lys Gly Gly Lys Ser Lys Leu
            545                 550
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<210> 2
<211> 552
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Encoded amino acid sequence of the cDNA sequence of synthetic luciferase gene

<400> 2

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Tyr Pro Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met
15                  20                  25                  30
Lys Arg Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His
                35                  40                  45
Ile Glu Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg
            50                  55                  60
Leu Ala Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile
        65                  70                  75
Val Val Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly
     80                  85                  90
Ala Leu Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn
 95                  100                 105                 110
Glu Arg Glu Leu Leu Asn Ser Met Asn Ile Ser Gln Pro Thr Val Val
                115                 120                 125
Phe Val Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys
            130                 135                 140
Leu Pro Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr
        145                 150                 155
Gln Gly Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro
    160                 165                 170
Gly Phe Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys
175                 180                 185                 190
Thr Ile Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys
                195                 200                 205
Gly Val Ala Leu Pro His Arg Cys Ala Cys Val Arg Phe Ser His Ala
            210                 215                 220
Arg Asp Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu
        225                 230                 235
Ser Val Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly
    240                 245                 250
Tyr Leu Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu
255                 260                 265                 270
Glu Leu Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu
                275                 280                 285
Leu Val Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp
            290                 295                 300
Lys Tyr Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro
        305                 310                 315
Leu Ser Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro
    320                 325                 330
Gly Ile Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu
335                 340                 345                 350
Ile Thr Pro Lys Gly Asp Phe Lys Pro Gly Ala Val Gly Lys Val Val
                355                 360                 365
Pro Phe Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu
            370                 375                 380
Gly Val Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met
        385                 390                 395
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```
Ser Gly Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys
    400                 405                 410
Asp Gly Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu
415                 420                 425                 430
His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly
                435                 440                 445
Tyr Gln Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro
            450                 455                 460
Asn Ile Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly
        465                 470                 475
Glu Leu Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr
    480                 485                 490
Glu Lys Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys
495                 500                 505                 510
Lys Leu Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu
                515                 520                 525
Thr Gly Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala
            530                 535                 540
Lys Lys Gly Gly Lys Ser Lys Leu
        545                 550
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<210> 3
<211> 1661
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: cDNA sequence
of synthetic luciferase gene

<400> 3

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ctttttcgcg gttgttactt gactggcgac gtaatccacg atctcttttt ccgtcatcgt 180
cttaccgtgc tcgagaacaa caacggcggc cggaagttca ccggcgtcat cgtccggaag 240
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tggggccacc tgatagcctt tgtatttaat gagagacttc aggcggtcaa cgatgaagaa 360
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acacagttcg ccacgctgat taacgcccag cgttttgccg gtatccagat ccacaacctt 540
cgcttcaaaa aatggtacca ctttaccgac cgcgcccggt ttgaaatcgc ccttcggtgt 600
aatcagaata gcactagtag tctcagtgag accatagcct tgacggatgc ctggaagatg 660
gaagcgtttt gcaaccgctt ctccgacttc tttcgaaaga ggtgcaccgc cgctagcaat 720
ttcgtgaaga ttagacagat cgtatttgtc aatcagagtg cttttggcga agaatgaaaa 780
cagggttggc accagaagcg cactttgaat tttgtaatcc tgcagggagc gcagaaacag 840
ctcttcttca aagcgataca tgaggacgac acgaaagcca cagatcagat agccgagtgt 900
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gatttggtta ccaaaaatag gatcgcgggc atgcgagaaa cggacgcagg cacaacgatg 1020
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tgttttgtca cgatcaaagg actctggtac aaaatcgtat tcattaaaac ccggaggcag 1140
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gataataatt ttctggataa ttggcagttt tttttgcacg ttgagaattt tttgcaggcc 1260
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gatgttcacc tcgatatgtg catctgtaaa agcaattgta ccaggaacca gggcgtaacg 1560
cttcatagcc ttatgcagtt gctcgccagc ggtgccatcc tccagaggat agaatggcgc 1620
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<210> 4
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 4
cacccgaggg ggattataaa ccgggcgcgg 30

<210> 5
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
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<400> 5
cacccgaggg ggatvycaaa ccgggcgcgg tcgg 34

<210> 6
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
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<400> 6
cacccgaggg ggattdsaaa ccgggcgcgg tcgg 34

<210> 7
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
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<400> 7
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<210> 8
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

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

<220>
<223> Description of Artificial Sequence:
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<400> 9
cgggtgtaat cagaatagca ctagtagtct cagtgagccc 40

<210> 10
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
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<400> 10
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<210> 11
<211> 36
<212> DNA
<213> Artificial Sequence

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<210> 12
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<213> Artificial Sequence

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<222> (24)..(25)
<223> n=a or g or c or t

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<222> (33)..(34)
<223> n=a or g or c or t

<220>

<223> Description of Artificial Sequence:
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ta 62

<210> 13
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<213> Artificial Sequence

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<223> n=a or g or c or t

<220>
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<222> (35)..(36)
<223> n=a or g or c or t

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