SEQUENCE LISTING

<110> DANISCO US INC.
THE GOODYEAR TIRE & RUBBER COMPANY
Andrew C. ELIOT
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<120> UTILIZATION OF PHOSPHOKETOLASE IN THE PRODUCTION OF MEVALONATE, ISOPRENOID PRECURSORS, AND ISOPRENE

<130> 643842004040

<140> PCT/US2012/059136
<141> 2012-10-05

<150> US 61/545,083
<151> 2011-10-07

<160> 51

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 2412
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

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ttaaaggcag aagatgttaa gcctaagcca attggtcact ggggtactat tgttcctcaa 180
aacttcattt acgcacactt gaaccgtgta attaagaagt atgaccttga tatgttctac 240
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cacttctcat tcccaggcgg tactgcatca cacgctgcac ctgaaacacc aggttcaatc 420
cacgaaggtg gggaacttgg ttactcactt tcacacggtg ttggtgctat cttagataac 480
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gaagctgacc gtgatggtga attcaagggt tacaagcctc acatggaagt tcacgaagaa 780
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gatctttact ggcgtcacca atacccagca ttgaactttg ttgatacttc tactgtattc 1620

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gaattgaaga ttcgttacat caacatcatc gaaattatgc gtttgatgaa cactgacaag 2040
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cgtgtattaa acgaacttga ccggttccac ttagctaagg acgctatcca aagtgttcct 2280
ggttacgaac aaaagagtgc tgcatttgtt gccaagatgg acaacatgat caacaagcac 2340
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<210> 2
<211> 803
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

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

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    290                 295                 300
Lys Thr Asp Leu Asp Gly Asn Pro Ile Glu Asn Ser Phe Arg Ala His
305                 310                 315                 320
Gln Ile Pro Val Pro Val Ser Gln Asp Asp Met Glu His Lys Asp Ile
                325                 330                 335
Leu Val Asp Trp Leu Lys Ser Tyr Lys Pro Glu Glu Leu Phe Asp Glu
            340                 345                 350
Asp Gly His Pro Val Ala Leu Val Glu Glu Asn Thr Pro Glu Gly Asn
        355                 360                 365
Arg Arg Met Ala Met Asn Pro Ile Thr Asn Gly Gly Ile Asp Pro Lys
    370                 375                 380
Pro Leu Val Leu Pro Asn Tyr Arg Asp Phe Ala Ile Asp Val Gln Asn
385                 390                 395                 400
Pro Gly Ser Val Val Lys Gln Asp Met Leu Glu Trp Gly Lys Tyr Leu
                405                 410                 415
Asn Lys Met Ala Glu Leu Asn Pro Thr Asn Phe Arg Gly Phe Gly Pro
            420                 425                 430
Asp Glu Ser Lys Ser Asn Arg Leu Tyr Ala Phe Leu Asp Gly Gln Lys
        435                 440                 445
Arg Gln Trp Met Glu Ser Val His Glu Pro Asn Asp Glu Asp Val Ala
    450                 455                 460
Pro Gln Gly Arg Met Ile Asp Ser Gln Leu Ser Glu His Gln Ala Glu
465                 470                 475                 480
Gly Phe Leu Glu Gly Tyr Thr Leu Thr Gly Arg His Gly Phe Phe Ala
                485                 490                 495
Thr Tyr Glu Ala Phe Gly Arg Val Val Asp Ser Met Leu Thr Gln His
            500                 505                 510
Met Lys Trp Leu Arg Lys Ala Lys Asp Leu Tyr Trp Arg His Gln Tyr
        515                 520                 525
Pro Ala Leu Asn Phe Val Asp Thr Ser Thr Val Phe Gln Gln Asp His
    530                 535                 540
Asn Gly Tyr Thr His Gln Asp Pro Gly Leu Leu Thr His Leu Phe Glu
545                 550                 555                 560
Lys Glu Arg Pro Asp Leu Val Lys Glu Tyr Leu Pro Ala Asp Thr Asn
                565                 570                 575
Ser Leu Met Ala Val Ser Asn Lys Ala Phe Arg Asn Gln Glu Cys Ile
            580                 585                 590
Asn Leu Phe Val Thr Ser Lys His Pro Arg Ala Gln Trp Phe Ser Ile
        595                 600                 605
Asp Glu Ala Thr Gln Leu Ala Asp Asn Gly Leu Gly Tyr Ile Asp Trp
    610                 615                 620
Ala Ser Thr Asp Gln Gly Thr Glu Pro Asp Val Val Phe Ala Ser Ser
625                 630                 635                 640
Gly Thr Glu Pro Thr Glu Glu Ala Leu Ala Ala Ile Asp Ile Leu His
                645                 650                 655
Asp Asn Phe Pro Glu Leu Lys Ile Arg Tyr Ile Asn Ile Ile Glu Ile
            660                 665                 670
Met Arg Leu Met Asn Thr Asp Lys Asn Pro Glu Gly Leu Thr Asp Ala
        675                 680                 685
Glu Phe Asn Ser Tyr Phe Thr Thr Asp Lys Pro Val Ile Phe Ala Trp
    690                 695                 700
His Gly Phe Arg Asp Met Ile Gln Ala Leu Phe Phe Asp Arg Ala Asn
705                 710                 715                 720
Arg Asn Val His Ile His Ser Tyr Glu Glu Asn Gly Asp Ile Thr Thr
                725                 730                 735
Pro Phe Asp Met Arg Val Leu Asn Glu Leu Asp Arg Phe His Leu Ala
            740                 745                 750
Lys Asp Ala Ile Gln Ser Val Pro Gly Tyr Glu Gln Lys Ser Ala Ala
        755                 760                 765
Phe Val Ala Lys Met Asp Asn Met Ile Asn Lys His Asn His Tyr Ile
    770                 775                 780
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Arg Ser Glu Gly Lys Asp Leu Pro Glu Val Thr Asn Trp Thr Trp Lys
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Gly Leu Lys

<210> 3
<211> 2478
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

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tatctgcgtt ccaacccgct gatgaaggag cccttcaccc gcgaagatgt gaagcatcgt 180
ctggtgggcc actggggcac taccccctggc ctgaacttcc tcatcggcca catcaaccgt 240
ttcattgctg accacggcca gaacaccgtg atcatcatgg gcccgggcca cggtggcccg 300
gccggtacct cccagtccta cctggacggc acctacaccg agaccttccc gaagatcacc 360
aaggacgaag ctggtctgca gaagttcttc cgtcagttct cttacccggg cggtattccg 420
tcccacttcg ctccggagac cccgggctcc atccacgagg gtggtgagct gggttacgct 480
ctgtcccacg cttacggcgc catcatggac aacccgagcc tgttcgtccc ggccatcgtc 540
ggcgacggcg aggctgagac cggcccgctg gctaccggtt ggcagtccaa caagctcgtg 600
aacccgcgca ccgacggtat cgtgctgccg atcctgcacc tcaacggcta caagatcgcc 660
aacccgacca tcctgtcccg catctccgac gaagagctcc acgagttctt ccacggcatg 720
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cgccgcttcg ccgagctgtg ggagaccatc tgggacgaga tctgcgacat caaggccacc 840
gctcagaccg acaacgtgca ccgtccgttc tacccgatgc tgatcttccg caccccgaag 900
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caggtgccgc tggcctccgc ccgcgacacc gaggcccact tcgaggtcct caagaactgg 1020
ctcgagtcct acaagccgga agagctgttc gacgccaacg gcgccgtcaa ggacgacgtc 1080
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gagttcggcc acggctgggg ccagctcgag gccacccgct ccctgggcgc ctacacccgc 1260
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aaccgtctgc aggcttccta cgaagtcacc aacaagcagt gggatgccgg ctacatctcc 1380
gacgaggtcg acgagcacat gcgcgtctcc ggccaggtcg tcgagcagct gtccgagcac 1440
cagatggaag gcttcctcga ggcctacctg ctgaccggcc gtcacggcat ctggagctcc 1500
tacgagtcct tcgtccacgt gatcgactcc atgctgaacc agcacgccaa gtggcttgag 1560
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<210> 4
<211> 825
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 4
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            20   25   30
Asn Tyr Leu Ser Ile Gly Gln Ile Tyr Leu Arg Ser Asn Pro Leu Met
        35   40   45
Lys Glu Pro Phe Thr Arg Glu Asp Val Lys His Arg Leu Val Gly His
    50   55   60
Trp Gly Thr Thr Pro Gly Leu Asn Phe Leu Ile Gly His Ile Asn Arg
65   70   75   80
Phe Ile Ala Asp His Gly Gln Asn Thr Val Ile Ile Met Gly Pro Gly
                85   90   95
His Gly Gly Pro Ala Gly Thr Ser Gln Ser Tyr Leu Asp Gly Thr Tyr
            100   105   110
Thr Glu Thr Phe Pro Lys Ile Thr Lys Asp Glu Ala Gly Leu Gln Lys
        115   120   125
Phe Phe Arg Gln Phe Ser Tyr Pro Gly Gly Ile Pro Ser His Phe Ala
    130   135   140
Pro Glu Thr Pro Gly Ser Ile His Glu Gly Gly Glu Leu Gly Tyr Ala
145   150   155   160
Leu Ser His Ala Tyr Gly Ala Ile Met Asp Asn Pro Ser Leu Phe Val
                165   170   175
Pro Ala Ile Val Gly Asp Gly Glu Ala Glu Thr Gly Pro Leu Ala Thr
            180   185   190
Gly Trp Gln Ser Asn Lys Leu Val Asn Pro Arg Thr Asp Gly Ile Val
        195   200   205
Leu Pro Ile Leu His Leu Asn Gly Tyr Lys Ile Ala Asn Pro Thr Ile
    210   215   220
Leu Ser Arg Ile Ser Asp Glu Glu Leu His Glu Phe Phe His Gly Met
225   230   235   240
Gly Tyr Glu Pro Tyr Glu Phe Val Ala Gly Phe Asp Asp Glu Asp His
                245   250   255
Met Ser Ile His Arg Arg Phe Ala Glu Leu Trp Glu Thr Ile Trp Asp
            260   265   270
Glu Ile Cys Asp Ile Lys Ala Thr Ala Gln Thr Asp Asn Val His Arg
        275   280   285
Pro Phe Tyr Pro Met Leu Ile Phe Arg Thr Pro Lys Gly Trp Thr Cys
    290   295   300
Pro Lys Tyr Ile Asp Gly Lys Lys Thr Glu Gly Ser Trp Arg Ser His
305   310   315   320
Gln Val Pro Leu Ala Ser Ala Arg Asp Thr Glu Ala His Phe Glu Val
                325   330   335
Leu Lys Asn Trp Leu Glu Ser Tyr Lys Pro Glu Glu Leu Phe Asp Ala
            340   345   350
Asn Gly Ala Val Lys Asp Asp Val Leu Ala Phe Met Pro Lys Gly Glu
        355   360   365
Leu Arg Ile Gly Ala Asn Pro Asn Ala Asn Gly Gly Val Ile Arg Asp
    370   375   380
Asp Leu Lys Leu Pro Asn Leu Glu Asp Tyr Glu Val Lys Glu Val Ala
385   390   395   400
Glu Phe Gly His Gly Trp Gly Gln Leu Glu Ala Thr Arg Ser Leu Gly
                405   410   415
Ala Tyr Thr Arg Asp Ile Ile Lys Asn Asn Pro Arg Asp Phe Arg Ile
            420   425   430
Phe Gly Pro Asp Glu Thr Ala Ser Asn Arg Leu Gln Ala Ser Tyr Glu

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        435                 440                 445
Val Thr Asn Lys Gln Trp Asp Ala Gly Tyr Ile Ser Asp Glu Val Asp
    450                 455                 460
Glu His Met Arg Val Ser Gly Gln Val Val Glu Gln Leu Ser Glu His
465                 470                 475                 480
Gln Met Glu Gly Phe Leu Glu Ala Tyr Leu Leu Thr Gly Arg His Gly
                485                 490                 495
Ile Trp Ser Ser Tyr Glu Ser Phe Val His Val Ile Asp Ser Met Leu
            500                 505                 510
Asn Gln His Ala Lys Trp Leu Glu Ala Thr Val Arg Glu Ile Pro Trp
        515                 520                 525
Arg Lys Pro Ile Ala Ser Met Asn Leu Leu Val Ser Ser His Val Trp
    530                 535                 540
Arg Gln Asp His Asn Gly Phe Ser His Gln Asp Pro Gly Val Thr Ser
545                 550                 555                 560
Val Leu Leu Asn Lys Cys Phe His Asn Asp His Val Ile Gly Ile Tyr
                565                 570                 575
Phe Ala Thr Asp Ala Asn Met Leu Leu Ala Ile Ala Glu Lys Cys Tyr
            580                 585                 590
Lys Ser Thr Asn Lys Ile Asn Ala Ile Ile Ala Gly Lys Gln Pro Ala
        595                 600                 605
Ala Thr Trp Leu Thr Leu Asp Glu Ala Arg Ala Glu Leu Glu Lys Gly
    610                 615                 620
Ala Ala Ala Trp Asp Trp Ala Ser Thr Ala Lys Thr Asn Asp Glu Ala
625                 630                 635                 640
Glu Ile Val Leu Ala Ala Ala Gly Asp Val Pro Thr Gln Glu Ile Met
                645                 650                 655
Ala Ala Ser Asp Lys Leu Lys Glu Leu Gly Ile Lys Phe Lys Val Val
            660                 665                 670
Asn Val Val Asp Leu Leu Ser Leu Gln Ser Ala Lys Glu Asn Asp Glu
        675                 680                 685
Ala Leu Ser Asn Glu Glu Phe Ala Asp Ile Phe Thr Ala Asp Lys Pro
    690                 695                 700
Val Leu Phe Ala Tyr His Ser Tyr Ala His Asp Val Arg Gly Leu Ile
705                 710                 715                 720
Tyr Asp Arg Pro Asn His Asp Asn Phe Asn Val His Gly Tyr Glu Glu
                725                 730                 735
Glu Gly Ser Thr Thr Thr Pro Tyr Asp Met Val Arg Val Asn Arg Ile
            740                 745                 750
Asp Arg Tyr Glu Leu Thr Ala Glu Ala Leu Arg Met Ile Asp Ala Asp
        755                 760                 765
Lys Tyr Ala Asp Lys Ile Asp Glu Leu Glu Lys Phe Arg Asp Glu Ala
    770                 775                 780
Phe Gln Phe Ala Val Asp Lys Gly Tyr Asp His Pro Asp Tyr Thr Asp
785                 790                 795                 800
Trp Val Tyr Ser Gly Val Asn Thr Gly Lys Lys Gly Ala Val Thr Ala
                805                 810                 815
Thr Ala Ala Thr Ala Gly Asp Asn Glu
            820                 825
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<210> 5
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 5
Met Thr Asp Val Arg Phe Arg Ile Ile Gly Thr Gly Ala Tyr Val Pro

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Glu Arg Ile Val Ser Asn Asp Glu Val Gly Ala Pro Ala Gly Val Asp
            20                  25                  30
Asp Asp Trp Ile Thr Arg Lys Thr Gly Ile Arg Gln Arg Arg Trp Ala
        35                  40                  45
Ala Asp Asp Gln Ala Thr Ser Asp Leu Ala Thr Ala Ala Gly Arg Ala
    50                  55                  60
Ala Leu Lys Ala Ala Gly Ile Thr Pro Glu Gln Leu Thr Val Ile Ala
65                  70                  75                  80
Val Ala Thr Ser Thr Pro Asp Arg Pro Gln Pro Pro Thr Ala Ala Tyr
                85                  90                  95
Val Gln His His Leu Gly Ala Thr Gly Thr Ala Ala Phe Asp Val Asn
            100                 105                 110
Ala Val Cys Ser Gly Thr Val Phe Ala Leu Ser Ser Val Ala Gly Thr
        115                 120                 125
Leu Val Tyr Arg Gly Gly Tyr Ala Leu Val Ile Gly Ala Asp Leu Tyr
    130                 135                 140
Ser Arg Ile Leu Asn Pro Ala Asp Arg Lys Thr Val Val Leu Phe Gly
145                 150                 155                 160
Asp Gly Ala Gly Ala Met Val Leu Gly Pro Thr Ser Thr Gly Thr Gly
                165                 170                 175
Pro Ile Val Arg Arg Val Ala Leu His Thr Phe Gly Gly Leu Thr Asp
            180                 185                 190
Leu Ile Arg Val Pro Ala Gly Gly Ser Arg Gln Pro Leu Asp Thr Asp
        195                 200                 205
Gly Leu Asp Ala Gly Leu Gln Tyr Phe Ala Met Asp Gly Arg Glu Val
    210                 215                 220
Arg Arg Phe Val Thr Glu His Leu Pro Gln Leu Ile Lys Gly Phe Leu
225                 230                 235                 240
His Glu Ala Gly Val Asp Ala Ala Asp Ile Ser His Phe Val Pro His
                245                 250                 255
Gln Ala Asn Gly Val Met Leu Asp Glu Val Phe Gly Glu Leu His Leu
            260                 265                 270
Pro Arg Ala Thr Met His Arg Thr Val Glu Thr Tyr Gly Asn Thr Gly
        275                 280                 285
Ala Ala Ser Ile Pro Ile Thr Met Asp Ala Ala Val Arg Ala Gly Ser
    290                 295                 300
Phe Arg Pro Gly Glu Leu Val Leu Leu Ala Gly Phe Gly Gly Gly Met
305                 310                 315                 320
Ala Ala Ser Phe Ala Leu Ile Glu Trp
                325
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<210> 6
<211> 2439
<212> DNA
<213> Artificial Sequence

<220>
<223> L.grayi mvaE

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aagaacgacc aggtcaaaga ccatgtagaa caagtcattt ttggcaacgt tttacaggca 180
gggaacggcc agaatcccgc ccgtcagatc gcccttaatt ctggcctgtc cgcagagata 240
ccggcttcga ctattaacca ggtgtgtggt tctggcctga aagcaataag catggcgcgc 300
caacagatcc tactcggaga agcggaagta atagtagcag gaggtatcga atccatgacg 360
aatgcgccga gtattacata ttataataaa gaagaagaca ccctctcaaa gcctgttcct 420
acgatgacct tcgatggtct gaccgacgcg tttagcggaa agattatggg tttaacagcc 480
gaaaatgttg ccgaacagta cggcgtatca cgtgaggccc aggacgcctt tgcgtatgga 540

tcgcagatga aagcagcaaa ggcccaagaa cagggcattt tcgcagctga aatactgcct 600
cttgaaatag gggacgaagt tattactcag gacgaggggg ttcgtcaaga gaccaccctc 660
gaaaaattaa gtctgcttcg gaccattttt aaagaagatg gtactgttac agcgggcaac 720
gcctcaacga tcaatgatgg cgcctcagcc gtgatcattg catcaaagga gtttgctgag 780
acaaaccaga ttccctacct tgcgatcgta catgatatta cagagatagg cattgatcca 840
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gcaatattaa tagaagtgcc tcaggaagat cagccggtta aaaaatttta tcaattggcc 1200
cgtgaggacc gtctggctag acttcaggag caagccgtga tcagcccagc tacaaaacat 1260
gtactggcag aaatgacact tcctgaagat attgccgaca atctgatcga aaatcaaata 1320
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attgtactta tgaacgtcaa agaacccgca actatcgagc atacgatcac ggcagagaaa 1560
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<210> 7
<211> 2442
<212> DNA
<213> Artificial Sequence

<220>
<223> E. faecium mvaE

<400> 7
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<210> 8
<211> 2448
<212> DNA
<213> Artificial Sequence

<220>
<223> E. gallinarum mvaE

<400> 8
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aaccagaaaa tcaaagagga gatcgcgcag gtcataattg gtaatgtctt gcaggcagga 180
aatggccaga accccgcgcg gcaagttgct cttcaatcag ggttgtccgt tgacattccc 240
gcttctacaa ttaacgaggt ttgtgggtct ggtttgaaag ctatcttgat gggcatggaa 300
caaatccaac tcggcaaagc gcaagtagtg ctggcaggcg gcattgaatc aatgacaaat 360
gcgccaagcc tgtcccacta taacaaggcg gaggatacgt atagtgtccc agtgtcgagc 420
atgacactgg atggtctgac agacgcattt tctagtaaac ctatgggatt aacagcggaa 480
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<210> 9
<211> 2475
<212> DNA
<213> Artificial Sequence

<220>
<223> E. casseliflavus mvaE

<400> 9
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aatcagcaag caaaagaaca catagcgcaa gttattattg gcaacgtcct gcaagccgga 180
agtgggcaga atccaggccg acaagtcagt ttacagtcag gattgtcttc tgatatcccc 240
gctagcacga tcaatgaagt gtgtggctcg ggtatgaaag cgattctgat gggtatggag 300
caaattcagc tgaacaaagc ctctgtggtc ttaacaggcg gaattgaaag catgaccaac 360
gcgccgctgt ttagttatta caacaaggct gaggatcaat attcggcgcc ggttagcaca 420
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caaatgaagg cggccaaagc ccaggcggcg aaaaagtttg atcaggaaat tgtacccctg 600
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gaaataagaa attaa 2475

<210> 10
<211> 1158
<212> DNA
<213> Artificial Sequence

<220>
<223> L.grayi mvaS

<400> 10
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atgactgatc tggcagtagc acgggatgtc gatcccaata agtttctgat tggtattggc 120
caggaccaga tggcagttaa tccgaaaacg caggatattg tgacatttgc cacaaatgct 180
gccaaaaaca tactgtcagc tgaggacctt gataaaattg atatggtcat agtcggcacc 240
gagagtggaa tcgatgaatc caaagcgagt gccgtagtgc ttcacaggtt gctcggtatc 300
cagaagtttg ctcgctcctt tgaaatcaaa gaagcctgtt atgggggtac cgcggcttta 360
cagttcgctg taaaccacat taggaatcat cctgaatcaa aggttcttgt agttgcatca 420
gatatcgcga aatacggcct ggcttctgga ggtgaaccaa cgcaaggtgc aggcgctgtg 480
gctatgctcg tctcaactga ccctaagatc attgctttca acgacgatag cctcgcgctt 540
acacaagata tctatgactt ctggcgacca gttggacatg actatcctat ggtcgacggg 600
cctcttagta cagagaccta catccagtca tttcagaccg tatggcagga atacacaaaa 660
cggtcgcagc atgcactggc agactttgct gcccttagct ttcatatccc gtatactaaa 720
atgggcaaaa aggcgctgct tgcaatcctt gaaggcgaat cagaggaggc tcagaaccgt 780
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cgtgagtaca ggagttga 1158

<210> 11
<211> 1155
<212> DNA
<213> Artificial Sequence

<220>
<223> E. faecium mvaS

<400> 11
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cagatggcag tgaatcgcgc aaacgaggac atcataacac tgggtgcaaa cgctgcgagt 180
aagatcgtga cagagaaaga ccgcgagttg attgatatgg taatcgttgg cacggaatca 240
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gcgcgttatg gtttggccag cggaggagaa gttactcaag gcgtgggggc cgtagccatg 480
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tattataaaa tctga 1155

<210> 12
<211> 1155
<212> DNA
<213> Artificial Sequence

<220>
<223> E. gallinarum mvaS

<400> 12
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cagatggctg tgagcaaaaa gacgcacgat atcgtaacat tcgcggctag tgccgcgaag 180
gaaattttag aacctgagga cttgcaagct atagacatgg ttatagttgg taccgaatcg 240
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gctcggtatg gtcttcggtc aggtggagag cccacacaag gcgcaggggc agttgctatg 480
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gatatttatg acttctggag accacttggt cacgcttacc ctatggtaga tggccacctt 600
tccaatcaag tctatattga cagttttaag aaggtctggc aagcacattg cgaacgcaat 660
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<210> 13
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> E. casseliflavus mvaS

<400> 13
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cagatggcag taaacaagaa aacgcaagat atcgtaacgt tcgcgatgca cgccgcgaag 180
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aaactgacta tcgcagagta cgaagccatg tttaatgaaa ccattgatat tgatcaggac 1080
cagtcatttg aggatgactt actgtactcc atcagagaga tcaaaaacac tattcgctac 1140

tataacgagg agaatgaata a 1161

<210> 14
<211> 125
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14
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gacataaata ccactggcgg tgatactgag cacatcagca ggacgcactg accaccatga 120
aggtg 125

<210> 15
<211> 6843
<212> DNA
<213> Artifical Sequence

<220>
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<210> 17
<211> 2496
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 17
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accgcaaccg cagccaccgc aggcgataat gaataa 2496

<210> 18
<211> 2382
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 18
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<210> 19
<211> 2352
<212> DNA
<213> Artifical Sequence

<220>
<223> Synthetic Construct

<400> 19
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cagctcgacc acatcaagcc gcgcctgctt ggccactggg gtacgacccc cggcctcaat 180
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<210> 20
<211> 2385
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 20
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<210> 21
<211> 2367
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 21
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tggaaatgga atcagccgac ccagtaa 2367

<210> 22
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 22
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

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<211> 2400
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

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<210> 25
<211> 2478
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

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<210> 26
<211> 2496
<212> DNA
<213> Artifical Sequence

<220>

<223> Synthetic Construct

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<210> 27
<211> 2382
<212> DNA
<213> Artifical Sequence

<220>
<223> Synthetic Construct

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gttcgtcaga caatggcaga tgcacgtacc cgtcatcatg catggattcg tgaacatggc 2340
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<210> 28
<211> 2391
<212> DNA
<213> Artifical Sequence

<220>
<223> Synthetic Construct

<400> 28
atgcaaagta taataggaaa acataaggat gaaggaaaaa tcacaccgga gtatctaaag 60
aaaattgatg catattggcg tgcagctaat tttatatctg taggtcaatt gtatttgcta 120
gacaatccat tgcttagaga acctttaaaa ccagaacatc taaaaagaaa agttgttggt 180
cactggggta ctattcctgg tcaaaacttt atttatgctc atcttaaccg tgttattaaa 240
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tccaattctt atctagatgg aacctatagt gaagtttatc caaatgttag tcgtgatttg 360
aatggcttaa aaaagctatg taaacaattc tcttttccag gtggaatttc tagccatatg 420
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tcttttggtg ctgtttttga taaccctgat ttgattactg cttgtgttgt tggagacgga 540
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ccttattttg tagaaggtga agatcctgaa acaatgcata aattaatggc agaaacatta 780
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ggagcacatc ttgttcagtt aatgaatgat aaattagtag aacataacca atacattcgt 2340
gaggttggag aagatttgcc agaaataact aattggcagt ggcatgtata a 2391

<210> 29
<211> 2367
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 29
atgaccaccg attatagcag tccggcatat ctgcaaaaag tggataaata ctggcgtgca 60
gcaaattatc tgagcgttgg tcagctgtat ctgaaagatt atccgctgct gcaacagccg 120
ctgaaagcaa gtgatgttaa agttcatccg atttgtcatt ggggcaccat tgcaggtcag 180
aatagcattt atgcacatct gaatcgcgtg atcaacaaat atggcctgaa aatgttttat 240
gtggaaggtc cgggtcatgg tggtcaggtt atggttagca atagctatct ggatggcacc 300
tataccgata tttatccgga aattacccag gatgttgaag gtatgcagaa actgttcaaa 360
cagttcagct ttccgggtgg tgttgcaagc catgcagcac cggaaacacc gggtagcatt 420
catgaaggtg gtgaactggg ttatagcatt agccatggtg ttggtgcaat tctggataat 480
ccggatgaaa ttgcagcagt tgttgttggt gatggtgaaa gcgaaaccgg tccgctggca 540
accagctggc agagcaccaa atttatcaat ccgattaatg atggtgccgt tctgccgatt 600
ctgaatctga atggctttaa aatcagcaac ccgaccattt ttggtcgtac cagtgatgca 660
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gcgatccaga aacatgcccg tgaaaatgat gatgcaaccc tgccggtttg gccgatgatt 840
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atgctggcaa aacataacgc ctatattcgt gatgcaggta cagatctgcc ggaagttaat 2340
gattggcagt ggaaaggtct gaaataa 2367

<210> 30
<211> 32
<212> DNA
<213> Artifical Sequence

<220>
<223> Synthetiic Construct (Primer CMP283)

<400> 30
ctgtattcat gacgagtcct gttattggca cc 32

<210> 31
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct (Primer CMP284)

<400> 31
ctctatgaat tctcactcgt tgtcgccagc g 31

<210> 32
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct (Primer CMP34)

<400> 32
taaggaggaa taaacatggc agtagattac gattccaag 39

<210> 33
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct (Primer CMP 335)

<400> 33
ttctagaaag cttcgttact taagaccctt ccaagtccag 40

<210> 34
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 34
tatttaattt ttaatcatct aatttgacaa tcattcaaca aagttgttac aattaaccct 60
cactaaaggg cgg 73

<210> 35
<211> 147
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 35
tcaacagctg tatccccgtt gagggtgagt tttgcttttg tatcagccat atattccacc 60
agctatttgt tagtgaataa aagtggttga attatttgct caggatgtgg cathgtcaag 120
ggctaatacg actcactata gggctcg 147

<210> 36
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 36
ggcagtatag gctgttcaca aaatc 25

<210> 37
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 37
cttgacccag cgtgcctttc agc 23

<210> 38
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 38
aaaattttca ttctgtgaca gagaaaaagt agccgaagat gacggtttgt cacatggagt 60
tggcaggatg tttgattaca tgggaattag ccatggtcc 99

<210> 39
<211> 100
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 39
gaccagccgc gtaacctggc aaaatcggtt acggttgagt aataaatgga tgccctgcgt 60
aagcggggca tttttcttgg tgtaggctgg agctgcttcg 100

<210> 40
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 40
ggcttaccgt ttacgctttc cagc 24

<210> 41
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 41
ctaatgcaat acgtgtcccg agc 23

<210> 42
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct (Primer CMP283)

<400> 42
ctgtattcat gacgagtcct gttattggca cc 32

<210> 43
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct (Primer CMP284)

<400> 43
ctctatgaat tctcactcgt tgtcgccagc g 31

<210> 44
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct (Primer CMP34)

<400> 44
taaggaggaa taaacatggc agtagattac gattccaag 39

<210> 45
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct (Primer CMP335)

<400> 45
ttctagaaag cttcgttact taagaccctt ccaagtccag 40

<210> 46
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 46
taaggaggaa taaaccatga cattagccag tcctctacaa ac 42

<210> 47
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 47
ttctagaaag cttcgttaat agggccactt ccagtcacg 39

<210> 48
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 48
taaggaggaa taaaccatgt ccgacgtgtt gtccaacgat c 41

<210> 49
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 49
ttctagaaag cttcgtcagg ccgaccagcg ccag 34

<210> 50
<211> 51
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 50
taaggaggaa taaaccatgc aaagtataat aggaaaacat aaggatgaag g 51

<210> 51
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 51
ttctagaaag cttcgttata catgccactg ccaattagtt atttc 45