

SEQUENCE LISTING

<110> Deinove

<120> LACCASES AND USES THEREOF

<130> B1085PC00

<160> 9

<170> PatentIn version 3.3

<210> 1

<211> 1446

<212> DNA

<213> Deinococcus sp.

<220>

<221> misc_feature

<223> Laccase 1 derived from Deinococcus cellulolyticus DRH46

<400> 1

atgaaacaga ggctcactgc agcagccctg ctgactgcc ttgtgtccag ttgtgccatg 60

aaaaacccgg atgtcatttc gtatcaggac cctgagccac tggcaggcca gcgcagtggc 120

aaagetgccg aattcacct caccgcgcag aaaagccgtc tggaccttgc aggccagtgc 180

gtggaggccc tgacctaaa cggcacgttc cgggtctc tgctgacct gaaagccgga 240

gaggacgtgc ggatcacct caaaaacaac ctctccgagc ccaccaacct gcacctgcac 300

ggactcccc tetctcaga ggtggatgat cctttgtgg tggccctcc cgggggatct 360

cacacctacg cttccaggt gcctgaagag gtgcatggca cttctggta tcacaccac 420

accacgggg cttctgcagc acaactgtt tcaggcctgg caggaccact gttggtggag 480

gcagcaaagc cgaacaacc cattgagcac atggagacc acacggtggt ctcaaggac 540

ctgccaggtg cgcagcacgc agacgacgt gtctgatga acggacgtga aaacacctg 600

ctggtcaatg gcctgtctc tcccatttg aagaccgaaa acagctgggt gcagctccgc 660

ctgatcaatg cctccaatgc cgttacctg cgctgaaac tggatgatgg cctcttcag 720

gtggtggccc gtgacggcat cgacctcca ggcattggaac gggcacagga actgctgctg 780
 acccccggcg agcgggcaga tgtgtggtc tccttcagg accaccagaa cctcaaactg 840
 cagaacctgc cttacgaccg tggcgtgcac agcatgggga gccattcggg ccacacggag 900
 agcaagacag ctgtggtcct gacctgcag gggccacaga aacctggagc cagcgttccc 960
 cgcgttgaat ctgcacctc accctttta caactgcagg gcaatgaaa agtgcggaaa 1020
 gtgacctgc aggaacctc gcagcccgat aagttctca tcaacggacg cagcttcgac 1080
 atgaaccggg tggattcca tgtctcagg ggcagcaccg aaatctggga attgcagaac 1140
 accaccgaaa tggaccacce ttccacctc cacaccttc caatgcagct gattcgcac 1200
 ggtggcaagg aggtccctc ggtctggaag gacaccgta acatcccgaa aaacagcacc 1260
 gtcactgtgg ccgtgcactt caaaggctc acgggcaaga ccgtttcca ctgcacac 1320
 gccgagcatg aagaagccg gatgatgggt ctcttcagg tgcacctc tgggacaga 1380
 ctcccgccct ctctggagcc cattgaacc acagtgggtc caggagaaga cgcacaacac 1440
 gggcac 1446

<210> 2
 <211> 482
 <212> PRT
 <213> Deinococcus sp.

<220>
 <221> MISC_FEATURE
 <223> Laccase 1 derived from Deinococcus cellulolyticus DRH46

<400> 2

Met Lys Gln Arg Leu Thr Ala Ala Ala Leu Leu Thr Ala Leu Leu Ser
 1 5 10 15

Ser Cys Ala Met Lys Asn Pro Asp Val Ile Ser Tyr Gln Asp Pro Glu
 20 25 30

Pro Leu Ala Gly Gln Arg Ser Gly Lys Ala Ala Glu Phe Thr Leu Thr
35 40 45

Ala Gln Lys Ser Arg Leu Asp Leu Ala Gly Gln Ser Val Glu Ala Leu
50 55 60

Thr Tyr Asn Gly Thr Phe Pro Gly Pro Leu Leu Thr Leu Lys Ala Gly
65 70 75 80

Glu Asp Val Arg Ile Thr Leu Lys Asn Asn Leu Ser Glu Pro Thr Asn
85 90 95

Leu His Leu His Gly Leu Pro Leu Ser Pro Glu Val Asp Asp Pro Phe
100 105 110

Val Val Val Pro Pro Gly Gly Ser His Thr Tyr Ala Phe Gln Val Pro
115 120 125

Glu Glu Val His Gly Thr Phe Trp Tyr His Thr His Thr His Gly Ala
130 135 140

Ser Ala Ala Gln Leu Phe Ser Gly Leu Ala Gly Pro Leu Leu Val Glu
145 150 155 160

Ala Ala Lys Pro Asn Asn Pro Ile Glu His Met Glu Thr His Thr Val
165 170 175

Val Phe Lys Asp Leu Pro Gly Ala Gln His Ala Asp Asp Gly Val Leu
180 185 190

Met Asn Gly Arg Glu Asn Thr Leu Leu Val Asn Gly Leu Val Ser Pro
195 200 205

Thr Leu Lys Thr Glu Asn Ser Trp Val Gln Leu Arg Leu Ile Asn Ala
210 215 220

Ser Asn Ala Arg Tyr Leu Arg Leu Lys Leu Asp Asp Gly Leu Leu Gln
225 230 235 240

Val Val Ala Arg Asp Gly Ile Asp Leu Pro Gly Met Glu Arg Ala Gln
245 250 255

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

Gln Asp His Gln Asn Leu Lys Leu Gln Asn Leu Pro Tyr Asp Arg Gly
275 280 285

Val His Ser Met Gly Ser His Ser Gly His Thr Glu Ser Lys Thr Ala
290 295 300

Val Val Leu Thr Leu Gln Gly Pro Gln Lys Pro Gly Ala Ser Val Pro
305 310 315 320

Arg Val Glu Thr Ala Pro Pro Pro Phe Leu Gln Leu Gln Gly Asn Glu
325 330 335

Lys Val Arg Lys Val Ile Leu Gln Glu Thr Met Gln Pro Val Lys Phe
340 345 350

Phe Ile Asn Gly Arg Ser Phe Asp Met Asn Arg Val Asp Phe His Val
355 360 365

Ser Glu Gly Ser Thr Glu Ile Trp Glu Leu Gln Asn Thr Thr Glu Met
370 375 380

Asp His Pro Phe His Leu His Thr Phe Pro Met Gln Leu Ile Arg Ile
385 390 395 400

Gly Gly Lys Glu Val Pro Pro Val Trp Lys Asp Thr Val Asn Ile Pro
405 410 415

Lys Asn Ser Thr Val Thr Val Ala Val His Phe Lys Gly Phe Thr Gly
420 425 430

Lys Thr Val Phe His Cys His Ile Ala Glu His Glu Glu Ala Gly Met
435 440 445

Met Gly Leu Leu Gln Val His Pro Ser Gly Thr Ala Leu Pro Ala Ser
450 455 460

Leu Glu Pro Ile Glu Pro Thr Val Gly Pro Gly Glu Asp Ala Gln His
465 470 475 480

Gly His

<210> 3

<211> 1476

<212> DNA

<213> Deinococcus sp.

<220>

<221> misc_feature

<223> Laccase 2 derived from Deinococcus cellulolyticus DRH46

<400> 3

atgattcgaa cctcaette cctcaccctg ctgaccgtgg cgctcacegc atgcgtcca 60

aaaggaagtc ccatgaccga gtaccacaac cctgctgaag tgcaagcaag ccgcacagaa 120

aaaggcagca ccttcaccct caccgccgca gaaaccagca tcacctgga cggcaaagag 180

gtgaaagcac agctettcaa ccagagtttt cccggacccc agctcaccct gcaggccgga 240

gaacaggtga acctcaccct caaaaacgac ctccgtgaac ccaccaacct gcacctgcac 300

ggctgacc tcccggcagg ggtggacgat ccccttctgc aggtccagcc cggagaaagc 360
 cacacctaca gcttcaactgt tccgcaaggc ctgcacggca ccttctggta ccacaccac 420
 acccatgggc acctcggaac acaactcttc cagggcctcg caggaccctt gatcgtegag 480
 gacccacct ttgacagcca catccagggg atggagacc acaccgtggt gctcaaagac 540
 ctccctgttg aagtacagga cagtgcggc acccgcatga acggccggga aggcaaactg 600
 ctggtcaacg gcctctctc cccaccctg aagaccgaaa gcagctgggt gaggtccgc 660
 ctgateaacg ctcaaacgc ccgctatgac ctgctgaaac tctctgggtc agctttctc 720
 cagtcacg ccaaggacgg gatcgacctg cccaaaaccg agcaggtgaa agaactctc 780
 ctacccccg ggcagcgggc cgatgtgtg atttccgtgc aagaccagca ggacctcgg 840
 ctggaaaacc accttacga ccgggggggtg catgagatgg acggggggca tcagggtcac 900
 acaccagca caccagaggt gctctcacc ctgcaggga agaaaggag cgtctcagcc 960
 agcgtgccac aacctgccct gcagccccgt ccatctga agtgactgg caacgaagcc 1020
 attcgcaagg tgggtctgca agaaacctg cagcctgtga aattctcat caacggacgc 1080
 acgtttgaca tgaaccgggt ggatttccat gtctctgaag gcaccacca aatctgggag 1140
 gtggagaacc agaccgaaat ggaccacccc ttccactgc acacctccc ggtgcaggtc 1200
 ctctcgggtg acggccagga agtgcctcgg gtgtggaagg acaccgtgaa cgtccctgcg 1260
 aaagcaaaag tgcaggtggc cgtgaaattt gagggcttca ccggcaagac ggtcttcac 1320
 tgccacattg ccgagcacga agaagagggc atgatggcg tcttcaggt gcatccagca 1380
 ggtgagcgc tccctgcgtc tctcacacc accttcccc ctgcagctgc ttggaggac 1440
 atgcctgaca tgcccggcat ggaccacagt ggccac 1476

<210> 4

<211> 492

<212> PRT

<213> *Deinococcus* sp.

<220>

<221> MISC_FEATURE

<223> Laccase 2 derived from *Deinococcus cellulolyticus* DRH46

<400> 4

Met Ile Arg Thr Leu Thr Ser Leu Thr Leu Leu Thr Val Ala Leu Thr
1 5 10 15

Ala Cys Ala Pro Lys Gly Ser Pro Met Thr Glu Tyr His Asn Pro Ala
20 25 30

Glu Val Gln Ala Ser Arg Thr Glu Lys Gly Ser Thr Phe Thr Leu Thr
35 40 45

Ala Ala Glu Thr Ser Ile Thr Leu Asp Gly Lys Glu Val Lys Ala Gln
50 55 60

Leu Phe Asn Gln Ser Phe Pro Gly Pro Gln Leu Thr Leu Gln Ala Gly
65 70 75 80

Glu Gln Val Asn Leu Thr Leu Lys Asn Asp Leu Arg Glu Pro Thr Asn
85 90 95

Leu His Leu His Gly Leu Thr Leu Pro Ala Gly Val Asp Asp Pro Phe
100 105 110

Leu Gln Val Gln Pro Gly Glu Ser His Thr Tyr Ser Phe Thr Val Pro
115 120 125

Gln Gly Leu His Gly Thr Phe Trp Tyr His Thr His Thr His Gly His
130 135 140

Leu Gly Thr Gln Leu Phe Gln Gly Leu Ala Gly Pro Leu Ile Val Glu
145 150 155 160

Asp Pro Thr Phe Asp Ser His Ile Gln Gly Met Glu Thr His Thr Val
165 170 175

Val Leu Lys Asp Leu Pro Val Glu Val Gln Asp Ser Asp Gly Thr Arg
180 185 190

Met Asn Gly Arg Glu Gly Lys Leu Leu Val Asn Gly Leu Ser Ser Pro
195 200 205

Thr Leu Lys Thr Glu Ser Ser Trp Val Arg Leu Arg Leu Ile Asn Ala
210 215 220

Ser Asn Ala Arg Tyr Asp Leu Leu Lys Leu Ser Gly Ser Ala Phe Leu
225 230 235 240

His Val Ile Ala Lys Asp Gly Ile Asp Leu Pro Lys Thr Glu Gln Val
245 250 255

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

Val Gln Asp Gln Gln Asp Leu Arg Leu Glu Asn His Pro Tyr Asp Arg
275 280 285

Gly Val His Glu Met Asp Gly Gly His Gln Gly His Thr Pro Ser Thr
290 295 300

Pro Glu Val Leu Leu Thr Leu Gln Gly Lys Lys Gly Ser Val Ser Ala
305 310 315 320

Ser Val Pro Gln Pro Ala Leu Gln Pro Arg Pro Phe Leu Lys Val Thr
325 330 335

Gly Asn Glu Ala Ile Arg Lys Val Val Leu Gln Glu Thr Met Gln Pro
340 345 350

Val Lys Phe Phe Ile Asn Gly Arg Thr Phe Asp Met Asn Arg Val Asp
355 360 365

Phe His Val Ser Glu Gly Thr Thr Glu Ile Trp Glu Val Glu Asn Gln
370 375 380

Thr Glu Met Asp His Pro Phe His Leu His Thr Phe Pro Val Gln Val
385 390 395 400

Leu Ser Val Asn Gly Gln Glu Val Pro Pro Val Trp Lys Asp Thr Val
405 410 415

Asn Val Pro Ala Lys Ala Lys Val Gln Val Ala Val Lys Phe Glu Gly
420 425 430

Phe Thr Gly Lys Thr Val Phe His Cys His Ile Ala Glu His Glu Glu
435 440 445

Glu Gly Met Met Gly Val Leu Gln Val His Pro Ala Gly Glu Ala Leu
450 455 460

Pro Ala Ser Leu Thr Pro Thr Leu Pro Pro Ala Ala Ala Ser Glu Asp
465 470 475 480

Met Pro Asp Met Pro Gly Met Asp His Ser Gly His
485 490

<210> 5

<211> 814

<212> DNA

<213> Deinococcus sp.

<220>

<221> misc_feature

<223> Laccase 3 derived from *Deinococcus maricopensis* DSM 21211

<400> 5

```
atgacgtcc atactgacct gatgtgctg cgtccccc acctcacgtt cccgcacg 60
ttctcgacgc gggcgggagg cgtctgagt ggcccgtagc cgggctgaa cctcgacgac 120
cgcgaggacg acgcgcacag cgtcgccgag aaccgccgcc gctcaccac gcagctcggg 180
ttacgccccg cacgcgtagc gagectcaca caggteacg gcgcggacgt cgccgtggcg 240
agcgcgcccc gctgcacag cggtagcgc atcgtaccg cccagccgga cctgtgctc 300
gccatcatga cggccgactg ctaccgctg ctcttgagg acgcgaggc cgccgtgatc 360
ggcgccggcg acgccgatg gcgcggcag gtgcccgcga tcggcgccgc caccattgag 420
gccatgaccg gctggggcg ccggccggaa cgcacccg cgccggcgg ccccgccac 480
tgtggcgccg ggtacgccgt cggcgaggac gtgcgcgcgc agttccgcgc cgcgggcctc 540
ggggacgcgc tgagcgggct gcagctggac ctgcgcggg cgaacacaca ggtgctcgtc 600
gacgcggggc tctccgcgc gcacctgtgg gtgtggggc gctgcaccac cgaaccggac 660
ttctactcgt accgacggga tgccggacgc accgggggga tgtgggcct gatcgccgc 720
ggagggcag aacctcacg gtgtgcgcgc gcgccgacc ctaaatggt gggtgcttg 780
gacaccaca cctctgccg ggagggcgc gcgc 814
```

<210> 6

<211> 271

<212> PRT

<213> *Deinococcus* sp.

<220>

<221> MISC_FEATURE

<223> Laccase 3 derived from *Deinococcus maricopensis* DSM 21211

<400> 6

Met Thr Leu His Thr Asp Leu Met Leu Leu Arg Ser Pro His Leu Thr
1 5 10 15

Phe Pro His Ala Phe Ser Thr Arg Ala Gly Gly Val Ser Ser Gly Pro
 20 25 30

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

Ala Glu Asn Arg Arg Arg Leu Thr Thr Gln Leu Gly Phe Thr Pro Ala
 50 55 60

Arg Val Ala Ser Leu Thr Gln Val His Gly Ala Asp Val Ala Val Ala
65 70 75 80

Ser Ala Pro Gly Val His Ser Gly Asp Ala Ile Val Thr Ala Gln Pro
 85 90 95

Asp Leu Leu Leu Ala Ile Met Thr Ala Asp Cys Tyr Pro Leu Leu Leu
 100 105 110

Glu Asp Ala Glu Ala Gly Val Ile Gly Ala Ala His Ala Gly Trp Arg
 115 120 125

Gly Thr Val Ala Arg Ile Gly Ala Arg Thr Ile Glu Ala Met Thr Arg
 130 135 140

Leu Gly Ala Arg Pro Glu Arg Ile Arg Ala Ala Val Gly Pro Gly Ile
145 150 155 160

Cys Gly Ala Arg Tyr Ala Val Gly Glu Asp Val Ala Ala Gln Phe Arg
 165 170 175

Ala Ala Gly Leu Gly Asp Ala Leu Ser Gly Leu Gln Leu Asp Leu Ala
 180 185 190

Arg Ala Asn Thr Gln Val Leu Val Asp Ala Gly Val Ser Ala Ser His
195 200 205

Leu Trp Val Ser Gly Arg Cys Thr Thr Glu Pro Asp Phe Tyr Ser Tyr
210 215 220

Arg Arg Asp Ala Gly Arg Thr Gly Arg Met Trp Ala Leu Ile Gly Arg
225 230 235 240

Gly Gly Ala Glu Pro His Gly Val Arg Arg Ala Pro Asp Pro Lys Met
245 250 255

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

<210> 7
<211> 21
<212> DNA
<213> Artificial

<220>
<223> 6(His) tag

<400> 7
catcatcacc atcaccatta a 21

<210> 8
<211> 23
<212> DNA
<213> Artificial

<220>
<223> primer 16S rDNA

<400> 8
gttaccgga atcactgggc gta 23

<210> 9
<211> 23
<212> DNA
<213> Artificial

<220>
<223> primer 16S rDNA

<400> 9
ggatctctacg cattccaccg cta