

SEQUENCE LISTING

<110> Van der Geize, Robert
 5 <120> METHOD FOR THE PRODUCTION OF MODIFIED STEROID DEGRADING
 MICROORGANISMS AND THEIR USE
 <130> 2007.023
 10 <160> 13
 <170> PatentIn version 3.4
 15 SEQ ID NO: 1
 <210> 1
 <211> 4300
 <212> DNA
 20 <213> Rhodococcus erythropolis
 <400> 1
 gggccggagg ccctacgctc cgtaaccgg cgtcggaaac tccgccttct ccaacagcgt 60
 25 tgccacgacg ggcccgatct ccttcgggtc ccaacggtca cccttgctct cgctcgggccc 120
 gtgacgccag ccctccgcca cggtgatctt tccgccctcg acctcgaaca cccgccccgt 180
 30 gacgtccttg gactcggcgc taccgagcca gacgaccagc ggcgagatgt tctcgggccc 240
 catggcatcg aagccctctt cgggagctgc catcgactcg gccatcgccc caccgcgccc 300
 gacgggtcatg cgcgtgcgcg cagcaggcgc gatcgcgttg aactgacgc cgtaatctct 360
 35 gagctcggct gcggcctgga tggatcatct gcgcataacc gccttcgccg cagcgtagtt 420
 accctggccg atcgaacctt gcagtcctgc acccgaactg gtgttgatga tgcgtgcgtc 480
 gacgggtcttg cctgccttg cctcagcgcg ccagtaggca gcagcgtgac gcagcggcgc 540
 40 gaagtgcccc ttgagggtgca cgcgaatcac cgcgtcccac tcgccttcgc tcatgccgac 600
 cagcatgcgg tcccgcagga agcccgcgtt gttcacgagt acgtccaggc caccgaaggc 660
 45 gtcgatcgcg gtcttgatca gattctcggc gcccgccag tcggcgacgt cgtctccgtt 720
 gaccactgct tggccaccgg cggcgatgat ctccgcgaca acctgctcgg ccggactctc 780
 accggtctcg gaaccgtcgg caccgcacc gatgtcgttg acgacgacct tggcgccctc 840
 50 ggcagcaaac gccaaaggcat gcgcacgtcc gatccgcgca ccagccccgg tgatgatgac 900
 tacgcgtccg tcgaccaatc cactcatatt tgtctcctaa tgcactctgc tcgggcttgt 960
 55 cggctccgct tgtgtgctaa cttaccaagc aatcgcttg tttggtacac agacgtaagg 1020
 aatcccgata tgggcatcag cacctcctcc gacggaaccg gcatcaccac ggtcaccatc 1080
 60 gactacgcgc cggatcaatgc aatcccgctc aagggatggt tcgagcttgc cgacgccatc 1140
 ctcgacgcgg gcaaggatct caacactcac gtggtgatcc tgcgagccga gggacgcgga 1200
 ttcaacgcgg gcgtcgacat caaggagatg caggcgaccg agggattcga cgcactggtc 1260
 65 gccgccaacc gcggttgccg cgcggccttc gcagccgtct acgactgcgc tgtacccgctc 1320

	gtcgtggccg	tcaacggatt	ctgtgtcggc	ggtggcatcg	gactggtcgg	caacgcggac	1380
	gtgatcgctg	cttccgacga	cgcgatcttc	tccctccccg	aggtcgaccg	cggcgacttc	1440
5	ggcgctgcca	cacacctctc	acggctggtg	ccgcagcaca	tgatgcgcac	gctctactac	1500
	accgcacaga	gcgtcgacgc	ccacacactc	aaacagttcg	gcagcgtcta	cgacgtggtc	1560
10	ccgcgcgaga	agctcgacga	gtgcgctcgc	gagatcgccg	caaagatcgc	cgcgaaggac	1620
	acccgcatca	tccggtgctc	caaggaagcc	atcaacggca	tcgacccggt	cgacgtcaag	1680
	ggcagctacc	gcctcgagca	gggctacacc	ttcgaactca	acctcctcgg	tgtgtccgac	1740
15	gaacaccgcg	acgaattcgt	cgccaccggc	aagccgcgcg	agaacgcaac	ccagaaggaa	1800
	ggctgagaca	aacatggcta	gcaagcgtga	caagacgaag	tcgctcgacg	aggtagtcgg	1860
20	cgagctccgc	agcggaatga	cgatcggctt	gggcggctgg	ggatctcgcc	gcaagccgat	1920
	ggccttcgtg	cgtgcgattc	tgcgttcgga	catcaaggac	ctgaccgtgg	tcacttacgg	1980
	cggaccggat	ctcgggctgc	tgtgctcggc	cggcaaggtc	aagaaggcgt	actacggttt	2040
25	cgtgtccctg	gactccgctc	cgttctacga	tccgtggttt	gccaaaggac	gcaccgccgg	2100
	tgagatcgaa	gtccgcgaga	tggacgaggg	aatgggtcaag	tgccggcctcg	aagccgctgc	2160
30	cgctcgcctc	cctttcctcc	cgatccgcgc	gggcctgggt	tcggacgttc	gcaacttctg	2220
	gggcgacgaa	ctcaagaccg	tcacctcccc	gtaccagag	gccgacggcc	gttccgagac	2280
	cttgatcgcg	atgcctgcac	tcaacctcga	tgcgtcggtc	gttcacctca	atctcgggtga	2340
35	caagcacggc	aatgccgcgt	acaacggtgt	cgacccgtac	ttcgacgacc	tgtactgcat	2400
	ggccgccgaa	aagcgttacg	tctccgtcga	acgcattgtc	gagaccgagg	aactggtcaa	2460
40	atccgttcca	ctgcagaatc	ttctgtctaa	ccgcgatgat	gtcgacgccg	tcgtcgaggc	2520
	cccgaacggt	gcccaacttc	cgttggccgg	cgaagctac	ggccgcgacg	agaagttcca	2580
	gcgtcactac	gccgaggccg	ccaagacccc	cgagtcgtgg	cagacgttcg	tcgacacctt	2640
45	cctctccggc	agcgaagagg	actaccaagc	cgcagtaaag	aagtttgccg	attcatcaaa	2700
	ggcaggggag	caggcaaaat	gagcgaatcc	accgtcacc	gcgcagagta	cgttgttctc	2760
50	gcgtgcgctg	aaatcttctc	cgggtgcaggc	gaaatcatgg	ccagcccgat	gtcgacgtcg	2820
	tccaccatcg	gcgctcgctt	ggctcggctc	accaccgaac	ccgacctgct	gatcaccgat	2880
	ggtgaagccc	tcattctcga	ggacacccc	gcagtcggaa	cgaagggccc	catcgaagga	2940
55	tggatgcctt	tccgcaagg	gttcgacgtc	gtcgcttcgg	gccgtcgcca	cgtagtcatg	3000
	ggcgccaatc	agctcgatcg	ccacggcaac	cagaacctct	ccgccttcgg	cccgttcag	3060
60	cagccgacgc	gtcagatgtt	cgggtgtcgc	ggcgccccgg	gcaacaccat	caaccacgcg	3120
	acgagctact	tcgtcccca	gcactccaag	cgagtgttcg	tcgacaagg	cgacgtgggtg	3180
	tgcggtgtcg	gctacgacca	gatcgatccc	gagaacccgg	catacaagta	cctgaacatc	3240
65	ccccgcgttg	tcaccaacct	cgggtgtcttc	gacttcggtg	gaccgggaaa	caccttcgcg	3300
	gcgctgagcc	tccatcccgg	cgtcaccgcc	gaagaggtag	ccgagaacac	ctcgttcgag	3360

```

      gtagccggac tcgccgaggc cggtatcacc cgtgacccca ccgccgaaga gttccacctc 3420
5    attcgcgaga ccctcgatcc gcgcaacctt cgggaccgtg aggtctcggc atgaccacctc 3480
      ctctgaagac agcactgacc gaactggctg gtgtcgagta cccgatcgtg cagacgggca 3540
      tgggctgggt ttccggggcca gcgctgacgt cggcgacggc caacgcgggc ggtctcggca 3600
10   tcctggcttc ggccacgatg acctacgacg agctcgagca cgcgatcaag aagacgaagc 3660
      agctcacgga caagccgttc ggtgtcaaca tgcgtgccga cgccaccgac gcgccgcagc 3720
      gcgcggacct gctgatccgt gagggcgctc aggtcgcgtc gtttgccttg gttcccaaga 3780
15   aggaactgat cgccaagctc aaggaccacg gcatcgtcgt cgtaccgtcg atcgggtgccg 3840
      cgaagcatgc ggtcaagggt gcatcttggg gcgcggacgc cgtcatcgtc cagggcgggc 3900
20   aagggtgggtg tcacaccggc ggtgtggcaa cgacattgct tcttccctcg gttctcgacg 3960
      cggtcgatat tccggtcatc gccggtggcg gattcttcga cggccgcggg ctggccgcag 4020
      cgttggcgta cggcgctgcc ggtgtcgcca tggggacgcg tttcttgctc accagtgact 4080
25   cttcggtgcc ggactccgtc aagcaggaat acctcaagcg aggactgacg gatacgacgg 4140
      tctcgcgcaa ggtcgacggc atgcctcatc gtgtgtctaa caccgacctg gtcaacagcc 4200
30   tcgaagggttc cagctatgca accggtttga tcgctgctgc caagaacgcc accaagttca 4260
      aggcaatgac aggtatgaag tggtcgacgc tcgccaagga 4300

```

35 SEQ ID NO:2

```

      <210> 2
      <211> 909
      <212> DNA
40   <213> Rhodococcus erythropolis

```

```

      <220>
      <221> CDS
45   <222> (1)..(906)
      <223> ipdA

```

```

      <400> 2
50   atg gct agc aag cgt gac aag acg aag tcg ctc gac gag gta gtc ggc 48
      Met Ala Ser Lys Arg Asp Lys Thr Lys Ser Leu Asp Glu Val Val Gly
      1 5 10 15

      gag ctc cgc agc gga atg acg atc ggc ttg ggc ggc tgg gga tct cgc 96
55   Glu Leu Arg Ser Gly Met Thr Ile Gly Leu Gly Gly Trp Gly Ser Arg
      20 25 30

      cgc aag ccg atg gcc ttc gtg cgt gcg att ctg cgt tcg gac atc aag 144
      Arg Lys Pro Met Ala Phe Val Arg Ala Ile Leu Arg Ser Asp Ile Lys
      35 40 45

60   gac ctg acc gtg gtc act tac ggc gga ccg gat ctc ggg ctg ctg tgc 192
      Asp Leu Thr Val Val Thr Tyr Gly Gly Pro Asp Leu Gly Leu Leu Cys
      50 55 60

65   tcg gcc ggc aag gtc aag aag gcg tac tac ggt ttc gtg tcc ctg gac 240
      Ser Ala Gly Lys Val Lys Lys Ala Tyr Tyr Gly Phe Val Ser Leu Asp
      65 70 75 80

```

5	tcc Ser	gct Ala	ccg Pro	ttc Phe	tac Tyr 85	gat Asp	ccg Pro	tgg Trp	ttt Phe	gcc Ala 90	aag Lys	gca Ala	cgc Arg	acc Thr	gcc Ala 95	ggt Gly	288
	gag Glu	atc Ile	gaa Glu	gtc Val 100	cgc Arg	gag Glu	atg Met	gac Asp	gag Glu 105	gga Gly	atg Met	gtc Val	aag Lys	tgc Cys 110	ggc Gly	ctc Leu	336
10	gaa Glu	gcc Ala	gct Ala 115	gcc Ala	gct Ala	cgc Arg	ctc Leu	cct Pro 120	ttc Phe	ctc Leu	ccg Pro	atc Ile	cgc Arg 125	gcg Ala	ggc Gly	ctg Leu	384
15	ggt Gly	tcg Ser 130	gac Asp	gtt Val	cgc Arg	aac Asn	ttc Phe 135	tgg Trp	ggc Gly	gac Asp	gaa Glu	ctc Leu 140	aag Lys	acc Thr	gtc Val	acc Thr	432
20	tcc Ser 145	ccg Pro	tac Tyr	cca Pro	gag Glu	gcc Ala 150	gac Asp	ggc Gly	cgt Arg	tcc Ser	gag Glu 155	acc Thr	ttg Leu	atc Ile	gcg Ala	atg Met 160	480
25	cct Pro	gca Ala	ctc Leu	aac Asn	ctc Leu 165	gat Asp	gcg Ala	tcg Ser	ttc Phe	gtt Val 170	cac His	ctc Leu	aat Asn	ctc Leu	ggt Gly 175	gac Asp	528
	aag Lys	cac His	ggc Gly	aat Asn 180	gcc Ala	gcg Ala	tac Tyr	aac Asn	ggt Gly 185	gtc Val	gac Asp	ccg Pro	tac Tyr	ttc Phe 190	gac Asp	gac Asp	576
30	ctg Leu	tac Tyr	tgc Cys 195	atg Met	gcc Ala	gcc Ala	gaa Glu	aag Lys 200	cgt Arg	tac Tyr	gtc Val	tcc Ser	gtc Val 205	gaa Glu	cgc Arg	att Ile	624
35	gtc Val	gag Glu 210	acc Thr	gag Glu	gaa Glu	ctg Leu	gtc Val 215	aaa Lys	tcc Ser	gtt Val	cca Pro	ctg Leu 220	cag Gln	aat Asn	ctt Leu	ctg Leu	672
40	ctc Leu 225	aac Asn	cgc Arg	atg Met	atg Met	gtc Val 230	gac Asp	gcc Ala	gtc Val	gtc Val	gag Glu 235	gcc Ala	ccg Pro	aac Asn	ggt Gly	gcc Ala 240	720
45	cac His	ttc Phe	acg Thr	ttg Leu	gcc Ala 245	ggc Gly	gaa Glu	agc Ser	tac Tyr	ggc Gly 250	cgc Arg	gac Asp	gag Glu	aag Lys	ttc Phe 255	cag Gln	768
	cgt Arg	cac His	tac Tyr	gcc Ala 260	gag Glu	gcc Ala	gcc Ala	aag Lys	acc Thr 265	ccc Pro	gag Glu	tcg Ser	tgg Trp	cag Gln 270	acg Thr	ttc Phe	816
50	gtc Val	gac Asp	acc Thr 275	ttc Phe	ctc Leu	tcc Ser	ggc Gly	agc Ser 280	gaa Glu	gag Glu	gac Asp	tac Tyr	caa Gln 285	gcc Ala	gca Ala	gta Val	864
55	aag Lys	aag Lys 290	ttt Phe	gcc Ala	gat Asp	tca Ser	tca Ser 295	aag Lys	gca Ala	ggg Gly	gag Glu	cag Gln 300	gca Ala	aaa Lys	tga		909

```

60      SEQ ID NO:3
      <210> 3
      <211> 302
      <212> PRT
      <213> Rhodococcus erythropolis
65      <400> 3

```

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

val Asp Thr Phe Leu Ser Gly Ser Glu Glu Asp Tyr Gln Ala Ala val
 275 280 285
 5 Lys Lys Phe Ala Asp Ser Ser Lys Ala Gly Glu Gln Ala Lys
 290 295 300
 10 SEQ ID NO: 4
 <210> 4
 <211> 756
 <212> DNA
 15 <213> Rhodococcus erythropolis
 <220>
 <221> CDS
 20 <222> (1)..(753)
 <223> ipdB
 <400> 4
 25 atg agc gaa tcc acc gtc acc cgc gca gag tac gtt gtt ctc gcg tgc 48
 Met Ser Glu Ser Thr Val Thr Arg Ala Glu Tyr Val Val Leu Ala Cys
 1 5 10 15
 gct gaa atc ttc tcc ggt gca ggc gaa atc atg gcc agc ccg atg tcg 96
 30 Ala Glu Ile Phe Ser Gly Ala Gly Glu Ile Met Ala Ser Pro Met Ser
 20 25 30
 acg tcg tcc acc atc ggc gct cgc ctg gct cgg ctc acc acc gaa ccc 144
 Thr Ser Ser Thr Ile Gly Ala Arg Leu Ala Arg Leu Thr Thr Glu Pro
 35 40 45
 35 gac ctg ctg atc acc gat ggt gaa gcc ctc att ctc gag gac acc ccg 192
 Asp Leu Leu Ile Thr Asp Gly Glu Ala Leu Ile Leu Glu Asp Thr Pro
 50 55 60
 gca gtc gga acg aag ggc ccc atc gaa gga tgg atg cct ttc cgc aag 240
 40 Ala Val Gly Thr Lys Gly Pro Ile Glu Gly Trp Met Pro Phe Arg Lys
 65 70 75 80
 gtg ttc gac gtc gtc gct tcg ggc cgt cgc cac gta gtc atg ggc gcc 288
 45 Val Phe Asp Val Val Ala Ser Gly Arg Arg His Val Val Met Gly Ala
 85 90 95
 aat cag ctc gat cgc cac ggc aac cag aac ctc tcc gcc ttc ggc ccg 336
 50 Asn Gln Leu Asp Arg His Gly Asn Gln Asn Leu Ser Ala Phe Gly Pro
 100 105 110
 ctt cag cag ccg acg cgt cag atg ttc ggt gtg cgc ggc gcc ccg ggc 384
 Leu Gln Gln Pro Thr Arg Gln Met Phe Gly Val Arg Gly Ala Pro Gly
 115 120 125
 55 aac acc atc aac cac gcg acg agc tac ttc gtc ccc aag cac tcc aag 432
 Asn Thr Ile Asn His Ala Thr Ser Tyr Phe Val Pro Lys His Ser Lys
 130 135 140
 cga gtg ttc gtc gac aag gtc gac gtg gtg tgc ggt gtc ggc tac gac 480
 60 Arg Val Phe Val Asp Lys Val Asp Val Val Cys Gly Val Gly Tyr Asp
 145 150 155 160
 cag atc gat ccc gag aac ccg gca tac aag tac ctg aac atc ccc cgc 528
 65 Gln Ile Asp Pro Glu Asn Pro Ala Tyr Lys Tyr Leu Asn Ile Pro Arg
 165 170 175

	gtt gtc acc aac ctc ggt gtc ttc gac ttc ggt gga ccg gga aac acc	576
	Val Val Thr Asn 180 Leu Gly Val Phe Asp 185 Phe Gly Gly Pro Gly Asn Thr	
5	ttc cgc gcg ctg agc ctc cat ccc ggc gtc acc gcc gaa gag gta gcc	624
	Phe Arg Ala 195 Leu Ser Leu His Pro 200 Gly Val Thr Ala Glu 205 Glu Val Ala	
10	gag aac acc tcg ttc gag gta gcc gga ctc gcc gag gcc ggt atc acc	672
	Glu Asn 210 Thr Ser Phe Gly Val 215 Ala Gly Leu Ala Glu 220 Ala Gly Ile Thr	
15	cgt gac ccc acc gcc gaa gag ctc cac ctc att cgc gag acc ctc gat	720
	Arg Asp Pro Thr Ala Glu 230 Glu Leu His Leu Ile 235 Arg Glu Thr Leu Asp 240	
20	ccg cgc aac ctt cgg gac cgt gag gtc tcg gca tga	756
	Pro Arg Asn Leu Arg 245 Asp Arg Glu Val Ser 250 Ala	
	SEQ ID NO: 5	
25	<210> 5	
	<211> 251	
	<212> PRT	
	<213> Rhodococcus erythropolis	
30	<400> 5	
	Met Ser Glu Ser Thr Val Thr Arg Ala Glu Tyr Val Val Leu Ala Cys	
	1 5 10 15	
35	Ala Glu Ile Phe Ser Gly Ala Gly Glu Ile Met Ala Ser Pro Met Ser	
	20 25 30	
40	Thr Ser Ser Thr Ile Gly Ala Arg Leu Ala Arg Leu Thr Thr Glu Pro	
	35 40 45	
45	Asp Leu Leu Ile Thr Asp Gly Glu Ala Leu Ile Leu Glu Asp Thr Pro	
	50 55 60	
50	Ala Val Gly Thr Lys Gly Pro Ile Glu Gly Trp Met Pro Phe Arg Lys	
	65 70 75 80	
55	Val Phe Asp Val Val Ala Ser Gly Arg Arg His Val Val Met Gly Ala	
	85 90 95	
60	Asn Gln Leu Asp Arg His Gly Asn Gln Asn Leu Ser Ala Phe Gly Pro	
	100 105 110	
65	Leu Gln Gln Pro Thr Arg Gln Met Phe Gly Val Arg Gly Ala Pro Gly	
	115 120 125	
	Asn Thr Ile Asn His Ala Thr Ser Tyr Phe Val Pro Lys His Ser Lys	
	130 135 140	
	Arg Val Phe Val Asp Lys Val Asp Val Val Cys Gly Val Gly Tyr Asp	

	145		150		155		160										
5	Gln	Ile	Asp	Pro	Glu 165	Asn	Pro	Ala	Tyr	Lys 170	Tyr	Leu	Asn	Ile	Pro	Arg 175	
10	Val	Val	Thr	Asn 180	Leu	Gly	Val	Phe	Asp 185	Phe	Gly	Gly	Pro	Gly 190	Asn	Thr	
15	Phe	Arg	Ala 195	Leu	Ser	Leu	His	Pro 200	Gly	Val	Thr	Ala	Glu 205	Glu	Val	Ala	
20	Glu	Asn 210	Thr	Ser	Phe	Glu	Val 215	Ala	Gly	Leu	Ala	Glu 220	Ala	Gly	Ile	Thr	
25	Arg 225	Asp	Pro	Thr	Ala	Glu 230	Glu	Leu	His	Leu	Ile 235	Arg	Glu	Thr	Leu	Asp 240	
30	Pro	Arg	Asn	Leu	Arg 245	Asp	Arg	Glu	Val	Ser 250	Ala						
SEQ ID NO: 6																	
35	<210>	6															
40	<211>	915															
	<212>	DNA															
	<213>	Rhodococcus erythropolis															
45	<220>																
	<221>	CDS															
	<222>	(1)..(912)															
	<223>	ipdF															
50	<400>	6															
	atg	agt	gga	ttg	gtc	gac	gga	cgc	gta	gtc	atc	atc	acc	ggg	gct	ggt	48
	Met	Ser	Gly	Leu	Val	Asp	Gly	Arg	Val	Val	Ile	Ile	Thr	Gly	Ala	Gly	
	1				5					10					15		
55	cgc	ggg	atc	gga	cgt	gcg	cat	gcc	ttg	gcg	ttt	gct	gcc	gag	ggc	gcc	96
	Arg	Gly	Ile	Gly	Arg	Ala	His	Ala	Leu	Ala	Phe	Ala	Ala	Glu	Gly	Ala	
				20					25					30			
60	aag	gtc	gtc	gtc	aac	gac	atc	ggt	gcg	ggt	gcc	gac	ggt	tcc	gag	acc	144
	Lys	Val	Val	Val	Asn	Asp	Ile	Gly	Ala	Gly	Ala	Asp	Gly	Ser	Glu	Thr	
			35					40					45				
65	ggt	gag	agt	ccg	gcc	gag	cag	gtt	gtc	gcg	gag	atc	atc	gcc	gcc	ggt	192
	Gly	Glu	Ser	Pro	Ala	Glu	Gln	Val	Val	Ala	Glu	Ile	Ile	Ala	Ala	Gly	
		50					55					60					
70	ggc	caa	gca	gtg	gtc	aac	gga	gac	gac	gtc	gcc	gac	tgg	gcg	ggc	gcc	240
	Gly	Gln	Ala	Val	Val	Asn	Gly	Asp	Asp	Val	Ala	Asp	Trp	Ala	Gly	Ala	
	65					70					75					80	
75	gag	aat	ctg	atc	aag	acc	gcg	atc	gac	acc	ttc	ggt	ggc	ctg	gac	gta	288
	Glu	Asn	Leu	Ile	Lys	Thr	Ala	Ile	Asp	Thr	Phe	Gly	Gly	Leu	Asp	Val	
					85					90					95		
80	ctc	gtg	aac	aac	gcg	ggc	ttc	ctg	cgg	gac	cgc	atg	ctg	gtc	ggc	atg	336
	Leu	Val	Asn	Asn	Ala	Gly	Phe	Leu	Arg	Asp	Arg	Met	Leu	Val	Gly	Met	

	100				105				110								
5	agc Ser	gaa Glu	ggc Gly 115	gag Glu	tgg Trp	gac Asp	gcg Ala	gtg Val 120	att Ile	cgc Arg	gtg Val	cac His	ctc Leu 125	aag Lys	ggg Gly	cac His	384
	ttc Phe	gcg Ala 130	ccg Pro	ctg Leu	cgt Arg	cac His	gct Ala 135	gct Ala	gcc Ala	tac Tyr	tgg Trp	cgc Arg 140	gct Ala	gag Glu	gcc Ala	aag Lys	432
10	gca Ala 145	ggc Gly	aag Lys	acc Thr	gtc Val	gac Asp 150	gca Ala	cgc Arg	atc Ile	atc Ile	aac Asn 155	acc Thr	agt Ser	tcg Ser	ggt Gly	gca Ala 160	480
15	gga Gly	ctg Leu	caa Gln	ggt Gly	tcg Ser 165	atc Ile	ggc Gly	cag Gln	ggt Gly	aac Asn 170	tac Tyr	gct Ala	gcg Ala	gcg Ala	aag Lys 175	gcc Ala	528
20	ggt Gly	atc Ile	gcc Ala	gag Glu 180	atg Met	acc Thr	atc Ile	cag Gln	gcc Ala 185	gca Ala	gcc Ala	gag Glu	ctc Leu	aag Lys 190	aat Asn	tac Tyr	576
25	ggc Gly	gtc Val	agt Ser 195	gtc Val	aac Asn	gcg Ala	atc Ile	gcg Ala 200	cct Pro	gct Ala	gcg Ala	cgc Arg	acg Thr 205	cgc Arg	atg Met	acc Thr	624
	gtc Val	ggc Gly 210	gcg Ala	ggt Gly	ggg Gly	gcg Ala	atg Met 215	gcc Ala	gag Glu	tcg Ser	atg Met	gca Ala 220	gct Ala	ccc Pro	gaa Glu	gag Glu	672
30	ggc Gly 225	ttc Phe	gat Asp	gcc Ala	atg Met	gcg Ala 230	ccc Pro	gag Glu	aac Asn	atc Ile	tcg Ser 235	ccg Pro	ctg Leu	gtc Val	gtc Val	tgg Trp 240	720
35	ctc Leu	ggt Gly	agc Ser	gcc Ala	gag Glu 245	tcc Ser	aag Lys	gac Asp	gtc Val	acg Thr 250	ggg Gly	cgg Arg	gtg Val	ttc Phe	gag Glu 255	gtc Val	768
40	gag Glu	ggc Gly	gga Gly	aag Lys 260	atc Ile	acc Thr	gtc Val	gcg Ala	gag Glu 265	ggc Gly	tgg Trp	cgt Arg	cac His	ggc Gly 270	ccg Pro	agc Ser	816
45	gag Glu	gac Asp	aag Lys 275	ggt Gly	gac Asp	cgt Arg	tgg Trp	gac Asp 280	ccg Pro	aag Lys	gag Glu	atc Ile	ggg Gly 285	ccc Pro	gtc Val	gtg Val	864
	gca Ala	acg Thr 290	ctg Leu	ttg Leu	gag Glu	aag Lys	gcg Ala 295	gag Glu	att Ile	ccg Pro	acg Thr	ccg Pro 300	gtg Val	tac Tyr	gga Gly	gcg Ala	912
50	tag																915
55	SEQ ID NO: 7																
	<210> 7																
	<211> 304																
	<212> PRT																
60	<213> Rhodococcus erythropolis																
	<400> 7																
65	Met 1	Ser	Gly	Leu	Val 5	Asp	Gly	Arg	Val	Val 10	Ile	Ile	Thr	Gly	Ala 15	Gly	
	Arg	Gly	Ile	Gly	Arg	Ala	His	Ala	Leu	Ala	Phe	Ala	Ala	Glu	Gly	Ala	

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

Ala Thr Leu Leu Glu Lys Ala Glu Ile Pro Thr Pro Val Tyr Gly Ala
 290 295 300

5 SEQ ID NO: 8
 <210> 8
 <211> 28
 <212> DNA
 10 <213> Artificial
 <220>
 <223> P1 (XbaI) Forward primer
 15 <400> 8
 gcgtctagac tgcgagccga gggacgcg 28
 20 SEQ ID NO: 9
 <210> 9
 <211> 30
 <212> DNA
 <213> Artificial
 25 <220>
 <223> P2 (BamHI) reverse primer
 <400> 9
 30 gcgggatccg tccgaacgca gaatcgcacg 30
 SEQ ID NO: 10
 35 <210> 10
 <211> 29
 <212> DNA
 <213> Artificial
 40 <220>
 <223> P3 (BamHI) forward primer
 <400> 10
 45 gcgggatccc tcgccgaggc cggtatcac 29
 SEQ ID NO: 11
 50 <210> 11
 <211> 29
 <212> DNA
 <213> Artificial
 55 <220>
 <223> P4 (SmaI) reverse primer
 <400> 11
 gcgggatccc tcgccgaggc cggtatcac 29
 60 SEQ ID NO: 12
 <210> 12
 <211> 28
 65 <212> DNA
 <213> Artificial

<220>
 <223> IpdF-F forward primer
 <400> 12
 5 atacatatga gtggattggt cgacggac 28

 SEQ ID NO: 13
 10 <210> 13
 <211> 31
 <212> DNA
 <213> Artificial
 15 <220>
 <223> IpdF-R reverse primer
 <400> 13
 20 ataggatccc tacgctccgt acaccggcgt c 31