

## SEQUENCE LISTING

<110> Wacker Chemie AG

5 <120> Mikroorganismenstamm und Verfahren zur fermentativen Herstellung von  
C4-Verbindungen aus C5-Zuckern

<130> poxB

10 <160> 7

<170> PatentIn version 3.5

<210> 1

15 <211> 1719

<212> DNA

<213> Raoultella terrigena

20 <220>

<221> CDS

<222> (1)..(1719)

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ggc gtg aag cgc atc tgg ggc gtc acc ggc gat tca ctc aac gga ttg 96  
30 Gly Val Lys Arg Ile Trp Gly Val Thr Gly Asp Ser Leu Asn Gly Leu  
20 25 30

agc gac agc ctg aac cgc atg ggc acc att gca tgg atg ccg acg cgc 144  
Ser Asp Ser Leu Asn Arg Met Gly Thr Ile Ala Trp Met Pro Thr Arg  
35 35 40 45

cat gaa gaa gtt gcc gcg ttt gcc gcc ggc gcc gaa gcc cag ctt acc 192  
His Glu Glu Val Ala Ala Phe Ala Ala Gly Ala Glu Ala Gln Leu Thr

	50	55	60	
	ggc gag ctg gcg gtc tgc gcg ggc tcc tgc ggc ccg ggc aat ctt cat			240
	Gly Glu Leu Ala Val Cys Ala Gly Ser Cys Gly Pro Gly Asn Leu His			
5	65	70	75	80
	ctg atc aac ggc ctt ttt gac tgt cac cgc aac cac gtt ccg gtg ctg			288
	Leu Ile Asn Gly Leu Phe Asp Cys His Arg Asn His Val Pro Val Leu			
	85	90	95	
10	gcc atc gcc gcc cac att ccc tcc agc gaa atc ggc agc ggc tat ttt			336
	Ala Ile Ala Ala His Ile Pro Ser Ser Glu Ile Gly Ser Gly Tyr Phe			
	100	105	110	
15	cag gaa acc cat ccg cag gag ctg ttc cgc gaa tgc agc cac tat tgt			384
	Gln Glu Thr His Pro Gln Glu Leu Phe Arg Glu Cys Ser His Tyr Cys			
	115	120	125	
	gag ctg gtc tcc acc ccg gaa cag atc ccg cag gtg ctg gcc atc gcc			432
20	Glu Leu Val Ser Thr Pro Glu Gln Ile Pro Gln Val Leu Ala Ile Ala			
	130	135	140	
	atg cgc aaa gcg gtc ctc aac cgc ggc gtt tcg gtg gtg gtg ctg ccg			480
	Met Arg Lys Ala Val Leu Asn Arg Gly Val Ser Val Val Val Leu Pro			
25	145	150	155	160
	gga gac gtg gcg ctg aag gcc gcc ccg gaa ggc gcc agc agc cac tgg			528
	Gly Asp Val Ala Leu Lys Ala Ala Pro Glu Gly Ala Ser Ser His Trp			
	165	170	175	
30	tac tcc gcc ccg ctg ccg gag gtg acg ccg ccg gcg gaa gaa ata gct			576
	Tyr Ser Ala Pro Leu Pro Glu Val Thr Pro Pro Ala Glu Glu Ile Ala			
	180	185	190	
35	cgt ctg gcg cag ctg ctg cgc tac tcc agc aac att gcc ctg atg tgc			624
	Arg Leu Ala Gln Leu Leu Arg Tyr Ser Ser Asn Ile Ala Leu Met Cys			
	195	200	205	

	ggc agc ggc tgt gcc gga gcc cat gaa gag ctg gtc gca ttc gcc gcc	672
	Gly Ser Gly Cys Ala Gly Ala His Glu Glu Leu Val Ala Phe Ala Ala	
	210 215 220	
5	aag ctc aag gcg ccc atc gtc cat gcc ctg cgc ggc aag gag cac gtt	720
	Lys Leu Lys Ala Pro Ile Val His Ala Leu Arg Gly Lys Glu His Val	
	225 230 235 240	
	gag tac gac aac cct tat gat gtc gga atg acc ggg ctg atc ggc ttc	768
10	Glu Tyr Asp Asn Pro Tyr Asp Val Gly Met Thr Gly Leu Ile Gly Phe	
	245 250 255	
	tcg tcc ggc ttc cac acc atg atg aac gcc gac acc ctg gtg ctt ctc	816
	Ser Ser Gly Phe His Thr Met Met Asn Ala Asp Thr Leu Val Leu Leu	
15	260 265 270	
	ggc acc cag ttc ccc tac cgg ccc ttc tat ccc agc agc gcg aaa atc	864
	Gly Thr Gln Phe Pro Tyr Arg Pro Phe Tyr Pro Ser Ser Ala Lys Ile	
	275 280 285	
20	att cag att gat atc aat ccc ggc agc atc ggc gcg cac agc aaa gtc	912
	Ile Gln Ile Asp Ile Asn Pro Gly Ser Ile Gly Ala His Ser Lys Val	
	290 295 300	
25	gat atg gcg ctg atc ggc gat atc aaa tcg acc cta aaa gcg ctg ctg	960
	Asp Met Ala Leu Ile Gly Asp Ile Lys Ser Thr Leu Lys Ala Leu Leu	
	305 310 315 320	
	ccg cat ctg gaa gag aag acg gat cgc cgc ttc ctc gac aaa gcc ctt	1008
30	Pro His Leu Glu Glu Lys Thr Asp Arg Arg Phe Leu Asp Lys Ala Leu	
	325 330 335	
	gag cac tac cgc gag gcg cgt aag ggg ctc gac gat ctg gcc aag ccg	1056
	Glu His Tyr Arg Glu Ala Arg Lys Gly Leu Asp Asp Leu Ala Lys Pro	
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	agc gat aag gcc att cac ccc cag tac ctg gcg cag cag ata agc cgc	1104
	Ser Asp Lys Ala Ile His Pro Gln Tyr Leu Ala Gln Gln Ile Ser Arg	

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	ttc gcc gct gac gat gcc att ttc acc tgc gac gtc ggt acg cca acc			1152
	Phe Ala Ala Asp Asp Ala Ile Phe Thr Cys Asp Val Gly Thr Pro Thr			
5	370	375	380	
	gtc tgg gcc gca cgc tat ctg aag atg aac ggc agg cgc cgg ctg atc			1200
	Val Trp Ala Ala Arg Tyr Leu Lys Met Asn Gly Arg Arg Arg Leu Ile			
	385	390	395	400
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	ggc tcg ttt aac cac ggc tca atg gcc aac gcc atg ccg cag gcg att			1248
	Gly Ser Phe Asn His Gly Ser Met Ala Asn Ala Met Pro Gln Ala Ile			
	405	410	415	
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	ggc gcg aag gca acg gcg ccg gag cgt cag gtg gtg gcg atg tgc ggc			1296
	Gly Ala Lys Ala Thr Ala Pro Glu Arg Gln Val Val Ala Met Cys Gly			
	420	425	430	
	gac ggc ggc ttc agc atg ctg atg ggc gac ttc ctc tcg ctg gcg cag			1344
20	Asp Gly Gly Phe Ser Met Leu Met Gly Asp Phe Leu Ser Leu Ala Gln			
	435	440	445	
	atg aag ctg ccg gta aaa atc gtg atc ttt aac aac agc gtg ctg gga			1392
	Met Lys Leu Pro Val Lys Ile Val Ile Phe Asn Asn Ser Val Leu Gly			
25	450	455	460	
	ttt gtc gca atg gag atg aag gcc ggg ggc tat ctg acc gac ggt acc			1440
	Phe Val Ala Met Glu Met Lys Ala Gly Gly Tyr Leu Thr Asp Gly Thr			
	465	470	475	480
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	gag ctg cac gac acc aat ttc gcc cgc att gct gaa gcc tgc ggc ata			1488
	Glu Leu His Asp Thr Asn Phe Ala Arg Ile Ala Glu Ala Cys Gly Ile			
	485	490	495	
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	aaa ggc att cgc gtc gaa aaa gcc tct gag gtc gac gac gcg ctg caa			1536
	Lys Gly Ile Arg Val Glu Lys Ala Ser Glu Val Asp Asp Ala Leu Gln			
	500	505	510	

acc gcg ttt agc acc gac ggc ccg gtg ctg gtc gat gtg gtg gtt gcc 1584  
 Thr Ala Phe Ser Thr Asp Gly Pro Val Leu Val Asp Val Val Val Ala  
 515 520 525

5 aag gaa gag ctg gcg atc ccg ccg caa atc aag ctg gat cag gcc aag 1632  
 Lys Glu Glu Leu Ala Ile Pro Pro Gln Ile Lys Leu Asp Gln Ala Lys  
 530 535 540

10 ggt ttc agc ctg tat atg ctg cgc gcc atc atc agc gga cgc gga gat 1680  
 Gly Phe Ser Leu Tyr Met Leu Arg Ala Ile Ile Ser Gly Arg Gly Asp  
 545 550 555 560

15 gaa gtt atc gaa ctg gcg aaa acc aac tgg ctc agg taa 1719  
 Glu Val Ile Glu Leu Ala Lys Thr Asn Trp Leu Arg  
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35 Ser Asp Ser Leu Asn Arg Met Gly Thr Ile Ala Trp Met Pro Thr Arg  
 35 40 45

His Glu Glu Val Ala Ala Phe Ala Ala Gly Ala Glu Ala Gln Leu Thr  
 50 55 60

Gly Glu Leu Ala Val Cys Ala Gly Ser Cys Gly Pro Gly Asn Leu His  
65 70 75 80

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Leu Ile Asn Gly Leu Phe Asp Cys His Arg Asn His Val Pro Val Leu  
85 90 95

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Ala Ile Ala Ala His Ile Pro Ser Ser Glu Ile Gly Ser Gly Tyr Phe  
100 105 110

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Gln Glu Thr His Pro Gln Glu Leu Phe Arg Glu Cys Ser His Tyr Cys  
115 120 125

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Glu Leu Val Ser Thr Pro Glu Gln Ile Pro Gln Val Leu Ala Ile Ala  
130 135 140

25

Met Arg Lys Ala Val Leu Asn Arg Gly Val Ser Val Val Val Leu Pro  
145 150 155 160

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Gly Asp Val Ala Leu Lys Ala Ala Pro Glu Gly Ala Ser Ser His Trp  
165 170 175

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Tyr Ser Ala Pro Leu Pro Glu Val Thr Pro Pro Ala Glu Glu Ile Ala  
180 185 190

Arg Leu Ala Gln Leu Leu Arg Tyr Ser Ser Asn Ile Ala Leu Met Cys  
195 200 205

Gly Ser Gly Cys Ala Gly Ala His Glu Glu Leu Val Ala Phe Ala Ala  
210 215 220

5 Lys Leu Lys Ala Pro Ile Val His Ala Leu Arg Gly Lys Glu His Val  
225 230 235 240

10 Glu Tyr Asp Asn Pro Tyr Asp Val Gly Met Thr Gly Leu Ile Gly Phe  
245 250 255

15 Ser Ser Gly Phe His Thr Met Met Asn Ala Asp Thr Leu Val Leu Leu  
260 265 270

Gly Thr Gln Phe Pro Tyr Arg Pro Phe Tyr Pro Ser Ser Ala Lys Ile  
275 280 285

20 Ile Gln Ile Asp Ile Asn Pro Gly Ser Ile Gly Ala His Ser Lys Val  
290 295 300

25 Asp Met Ala Leu Ile Gly Asp Ile Lys Ser Thr Leu Lys Ala Leu Leu  
305 310 315 320

30 Pro His Leu Glu Glu Lys Thr Asp Arg Arg Phe Leu Asp Lys Ala Leu  
325 330 335

35 Glu His Tyr Arg Glu Ala Arg Lys Gly Leu Asp Asp Leu Ala Lys Pro  
340 345 350

Ser Asp Lys Ala Ile His Pro Gln Tyr Leu Ala Gln Gln Ile Ser Arg  
355 360 365

5 Phe Ala Ala Asp Asp Ala Ile Phe Thr Cys Asp Val Gly Thr Pro Thr  
370 375 380

10 Val Trp Ala Ala Arg Tyr Leu Lys Met Asn Gly Arg Arg Arg Leu Ile  
385 390 395 400

15 Gly Ser Phe Asn His Gly Ser Met Ala Asn Ala Met Pro Gln Ala Ile  
405 410 415

20 Asp Gly Gly Phe Ser Met Leu Met Gly Asp Phe Leu Ser Leu Ala Gln  
435 440 445

25 Met Lys Leu Pro Val Lys Ile Val Ile Phe Asn Asn Ser Val Leu Gly  
450 455 460

30 Phe Val Ala Met Glu Met Lys Ala Gly Gly Tyr Leu Thr Asp Gly Thr  
465 470 475 480

35 Glu Leu His Asp Thr Asn Phe Ala Arg Ile Ala Glu Ala Cys Gly Ile  
485 490 495

50 Lys Gly Ile Arg Val Glu Lys Ala Ser Glu Val Asp Asp Ala Leu Gln  
500 505 510



Thr Ala Phe Ser Thr Asp Gly Pro Val Leu Val Asp Val Val Val Ala  
515 520 525

5 Lys Glu Glu Leu Ala Ile Pro Pro Gln Ile Lys Leu Asp Gln Ala Lys  
530 535 540

Gly Phe Ser Leu Tyr Met Leu Arg Ala Ile Ile Ser Gly Arg Gly Asp  
10 545 550 555 560

Glu Val Ile Glu Leu Ala Lys Thr Asn Trp Leu Arg  
565 570

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&lt;212&gt; DNA

20 &lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; PCR primer

25 &lt;400&gt; 3

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gagctgcttc 70

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&lt;210&gt; 4

&lt;211&gt; 70

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

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&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 4

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gcagttcgaa 70

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&lt;210&gt; 5

&lt;211&gt; 25

&lt;212&gt; DNA

10 &lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; PCR primer

15 &lt;400&gt; 5

atgaaacaga ccgtggccgc atacg 25

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20 &lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

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25 &lt;223&gt; PCR primer

&lt;400&gt; 6

ttacctgagc cagttggttt tcgcc 25

30

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&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

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&lt;220&gt;

&lt;223&gt; PCR primer

Co11221 / P

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<400> 7

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5