

PHARMAZELL

1

SEQUENCE LISTING

<110> PHARMAZELL GmbH

<120> 12alpha-HSDH

<130> M/48429-PCT

<160> 22

<170> PatentIn version 3.3

<210> 1

<211> 813

<212> DNA

<213> Clostridium sp.

<220>

<221> CDS

<222> (1)..(813)

<400> 1

atg	gat	ttt	att	gat	ttt	aag	gag	atg	ggc	aga	atg	ggg	atc	ttt	gac	48
Met	Asp	Phe	Ile	Asp	Phe	Lys	Glu	Met	Gly	Arg	Met	Gly	Ile	Phe	Asp	
1				5					10					15		

gga	aag	gtc	gca	atc	att	act	ggc	ggg	ggc	aag	gcc	aaa	tcg	atc	ggc	96
Gly	Lys	Val	Ala	Ile	Ile	Thr	Gly	Gly	Gly	Lys	Ala	Lys	Ser	Ile	Gly	
			20					25					30			

tac	ggc	att	gcc	gtg	gcc	tat	gct	aag	gag	ggg	gcc	aac	ctg	gtc	ctg	144
Tyr	Gly	Ile	Ala	Val	Ala	Tyr	Ala	Lys	Glu	Gly	Ala	Asn	Leu	Val	Leu	
		35					40					45				

acc	ggc	aga	aac	gag	cag	aaa	ctg	ctg	gac	gcc	aag	gag	gag	ctg	gag	192
Thr	Gly	Arg	Asn	Glu	Gln	Lys	Leu	Leu	Asp	Ala	Lys	Glu	Glu	Leu	Glu	
	50					55					60					

cgc	ctc	tac	ggc	atc	aag	gtg	ttg	ccg	ctg	gcg	gtg	gac	gtc	acc	ccc	240
Arg	Leu	Tyr	Gly	Ile	Lys	Val	Leu	Pro	Leu	Ala	Val	Asp	Val	Thr	Pro	
65					70					75					80	

agc	gat	gag	tcg	gag	gac	cgg	gtc	aag	gaa	gcc	gtg	cag	aag	gtc	atc	288
Ser	Asp	Glu	Ser	Glu	Asp	Arg	Val	Lys	Glu	Ala	Val	Gln	Lys	Val	Ile	
				85					90					95		

gcc	gaa	ttc	ggc	cgc	atc	gac	gtg	ctg	atc	aac	aac	gcc	cag	gcg	tcg	336
Ala	Glu	Phe	Gly	Arg	Ile	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gln	Ala	Ser	
			100					105					110			

gcc	tcg	ggc	atc	ccc	ctg	tcc	atg	cag	acc	aaa	gac	cac	ttt	gac	ctg	384
Ala	Ser	Gly	Ile	Pro	Leu	Ser	Met	Gln	Thr	Lys	Asp	His	Phe	Asp	Leu	
		115					120					125				

ggc	atc	tac	tcc	ggg	ctc	tac	gcc	acc	ttc	tac	tac	atg	agg	gag	tgc	432
Gly	Ile	Tyr	Ser	Gly	Leu	Tyr	Ala	Thr	Phe	Tyr	Tyr	Met	Arg	Glu	Cys	
	130					135					140					

tat	ccc	tac	ctg	aag	gag	acc	cag	ggc	tcg	gtc	atc	aac	ttc	gcc	tcc	480
Tyr	Pro	Tyr	Leu	Lys	Glu	Thr	Gln	Gly	Ser	Val	Ile	Asn	Phe	Ala	Ser	
145					150					155					160	

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ggc gcc ggc ctc ttc ggc aac gtg ggt cag tgc tcc tac gcc gcc gcc 528
 Gly Ala Gly Leu Phe Gly Asn Val Gly Gln Cys Ser Tyr Ala Ala Ala
 165 170 175
 aaa gag ggc atc cgc ggc ctc tcc cgc gtc gcg gcc acc gag tgg ggc 576
 Lys Glu Gly Ile Arg Gly Leu Ser Arg Val Ala Ala Thr Glu Trp Gly
 180 185 190
 aag gac aac atc aac gtc aac gtg gtc tgc ccc ctg gcc atg acc gcc 624
 Lys Asp Asn Ile Asn Val Asn Val Val Cys Pro Leu Ala Met Thr Ala
 195 200 205
 cag ctg gag aac ttc aag ctc tcc tac cct gag gcc tac gag aaa aac 672
 Gln Leu Glu Asn Phe Lys Leu Ser Tyr Pro Glu Ala Tyr Glu Lys Asn
 210 215 220
 ctc aga ggg gtg ccc atg ggc cgc ttc ggt gac ccc gag ctg gac atc 720
 Leu Arg Gly Val Pro Met Gly Arg Phe Gly Asp Pro Glu Leu Asp Ile
 225 230 235 240
 ggc cgg gtc tgc gtg cag ctc ggc tcg ccc gac ttc aag tac atg tcc 768
 Gly Arg Val Cys Val Gln Leu Gly Ser Pro Asp Phe Lys Tyr Met Ser
 245 250 255
 ggc gag acc ctc acc ctg gaa ggc ggc atg ggt cag cgc ccc tag 813
 Gly Glu Thr Leu Thr Leu Glu Gly Gly Met Gly Gln Arg Pro
 260 265 270

<210> 2
 <211> 270
 <212> PRT
 <213> Clostridium sp.

<400> 2

Met Asp Phe Ile Asp Phe Lys Glu Met Gly Arg Met Gly Ile Phe Asp
1 5 10 15

Gly Lys Val Ala Ile Ile Thr Gly Gly Lys Ala Lys Ser Ile Gly
20 25 30

Tyr Gly Ile Ala Val Ala Tyr Ala Lys Glu Gly Ala Asn Leu Val Leu
35 40 45

Thr Gly Arg Asn Glu Gln Lys Leu Leu Asp Ala Lys Glu Glu Leu Glu
50 55 60

Arg Leu Tyr Gly Ile Lys Val Leu Pro Leu Ala Val Asp Val Thr Pro
65 70 75 80

Ser Asp Glu Ser Glu Asp Arg Val Lys Glu Ala Val Gln Lys Val Ile
85 90 95

Ala Glu Phe Gly Arg Ile Asp Val Leu Ile Asn Asn Ala Gln Ala Ser
100 105 110

Ala Ser Gly Ile Pro Leu Ser Met Gln Thr Lys Asp His Phe Asp Leu
115 120 125

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Gly Ile Tyr Ser Gly Leu Tyr Ala Thr Phe Tyr Tyr Met Arg Glu Cys
 130 135 140

Tyr Pro Tyr Leu Lys Glu Thr Gln Gly Ser Val Ile Asn Phe Ala Ser
 145 150 155 160

Gly Ala Gly Leu Phe Gly Asn Val Gly Gln Cys Ser Tyr Ala Ala Ala
 165 170 175

Lys Glu Gly Ile Arg Gly Leu Ser Arg Val Ala Ala Thr Glu Trp Gly
 180 185 190

Lys Asp Asn Ile Asn Val Asn Val Val Cys Pro Leu Ala Met Thr Ala
 195 200 205

Gln Leu Glu Asn Phe Lys Leu Ser Tyr Pro Glu Ala Tyr Glu Lys Asn
 210 215 220

Leu Arg Gly Val Pro Met Gly Arg Phe Gly Asp Pro Glu Leu Asp Ile
 225 230 235 240

Gly Arg Val Cys Val Gln Leu Gly Ser Pro Asp Phe Lys Tyr Met Ser
 245 250 255

Gly Glu Thr Leu Thr Leu Glu Gly Gly Met Gly Gln Arg Pro
 260 265 270

<210> 3
 <211> 774
 <212> DNA
 <213> Artificial

<220>
 <223> Künstliche Kurzsequenz

<220>
 <221> CDS
 <222> (1)..(774)

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 1 5 10 15

tcg atc ggc tac ggc att gcc gtg gcc tat gct aag gag ggg gcc aac 96
 Ser Ile Gly Tyr Gly Ile Ala Val Ala Tyr Ala Lys Glu Gly Ala Asn
 20 25 30

ctg gtc ctg acc ggc aga aac gag cag aaa ctg ctg gac gcc aag gag 144
 Leu Val Leu Thr Gly Arg Asn Glu Gln Lys Leu Leu Asp Ala Lys Glu
 35 40 45

gag ctg gag cgc ctc tac ggc atc aag gtg ttg ccg ctg gcg gtg gac 192
 Glu Leu Glu Arg Leu Tyr Gly Ile Lys Val Leu Pro Leu Ala Val Asp

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50	55	60	
gtc acc ccc agc gat gag tgc gag gac cgg gtc aag gaa gcc gtg cag Val Thr Pro Ser Asp Glu Ser Glu Asp Arg Val Lys Glu Ala Val Gln 65 70 75 80			240
aag gtc atc gcc gaa ttc ggc cgc atc gac gtg ctg atc aac aac gcc Lys Val Ile Ala Glu Phe Gly Arg Ile Asp Val Leu Ile Asn Asn Ala 85 90 95			288
cag gcg tgc gcc tgc ggc atc ccc ctg tcc atg cag acc aaa gac cac Gln Ala Ser Ala Ser Gly Ile Pro Leu Ser Met Gln Thr Lys Asp His 100 105 110			336
ttt gac ctg ggc atc tac tcc ggg ctc tac gcc acc ttc tac tac atg Phe Asp Leu Gly Ile Tyr Ser Gly Leu Tyr Ala Thr Phe Tyr Tyr Met 115 120 125			384
agg gag tgc tat ccc tac ctg aag gag acc cag ggc tgc gtc atc aac Arg Glu Cys Tyr Pro Tyr Leu Lys Glu Thr Gln Gly Ser Val Ile Asn 130 135 140			432
ttc gcc tcc ggc gcc ggc ctc ttc ggc aac gtg ggt cag tgc tcc tac Phe Ala Ser Gly Ala Gly Leu Phe Gly Asn Val Gly Gln Cys Ser Tyr 145 150 155 160			480
gcc gcc gcc aaa gag ggc atc cgc ggc ctc tcc cgc gtc gcg gcc acc Ala Ala Ala Lys Glu Gly Ile Arg Gly Leu Ser Arg Val Ala Ala Thr 165 170 175			528
gag tgg ggc aag gac aac atc aac gtc aac gtg gtc tgc ccc ctg gcc Glu Trp Gly Lys Asp Asn Ile Asn Val Asn Val Val Cys Pro Leu Ala 180 185 190			576
atg acc gcc cag ctg gag aac ttc aag ctc tcc tac cct gag gcc tac Met Thr Ala Gln Leu Glu Asn Phe Lys Leu Ser Tyr Pro Glu Ala Tyr 195 200 205			624
gag aaa aac ctc aga ggg gtg ccc atg ggc cgc ttc ggt gac ccc gag Glu Lys Asn Leu Arg Gly Val Pro Met Gly Arg Phe Gly Asp Pro Glu 210 215 220			672
ctg gac atc ggc cgc gtc tgc gtg cag ctc ggc tgc ccc gac ttc aag Leu Asp Ile Gly Arg Val Cys Val Gln Leu Gly Ser Pro Asp Phe Lys 225 230 235 240			720
tac atg tcc ggc gag acc ctc acc ctg gaa ggc ggc atg ggt cag cgc Tyr Met Ser Gly Glu Thr Leu Thr Leu Glu Gly Gly Met Gly Gln Arg 245 250 255			768
ccc tag Pro			774

<210> 4
 <211> 257
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 4

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

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<210> 5
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Teilsequenz

<400> 5

Leu Ile Asn Asn
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<210> 6
<211> 41
<212> PRT
<213> Artificial

<220>
<223> N-terminale Teilsequenz Langversion

<400> 6

Met Asp Phe Ile Asp Phe Lys Glu Met Gly Arg Met Gly Ile Phe Asp
1 5 10 15

Gly Lys Val Ala Ile Ile Thr Gly Gly Gly Lys Ala Lys Ser Ile Gly
20 25 30

Tyr Gly Ile Ala Val Ala Tyr Ala Lys
35 40

<210> 7
<211> 14
<212> PRT
<213> Artificial

<220>
<223> N-terminale Teilsequenz Langversion

<400> 7

Met Asp Phe Ile Asp Phe Lys Glu Met Gly Arg Met Gly Ile
1 5 10

<210> 8
<211> 15
<212> PRT
<213> Artificial

<220>
<223> N-terminale Teilsequenz Kurzversion

<400> 8

Ile Thr Gly Gly Gly Lys Ala Lys Ser Ile Gly Tyr Gly Ile Ala
1 5 10 15

<210> 9

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<211> 5
<212> PRT
<213> Artificial

<220>
<223> N-terminale Teilsequenz Kurzversion

<400> 9

Ile Phe Asp Gly Lys
1 5

<210> 10
<211> 6
<212> PRT
<213> Artificial

<220>
<223> N-terminale Teilsequenz Kurzversion

<400> 10

Gly Ile Phe Asp Gly Lys
1 5

<210> 11
<211> 6
<212> PRT
<213> Artificial

<220>
<223> Teilsequenz 2

<400> 11

Arg Met Gly Ile Phe Asp
1 5

<210> 12
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Teilsequenzmotiv

<400> 12

Val Leu Thr Gly Arg Asn Glu
1 5

<210> 13
<211> 8
<212> PRT
<213> Artificial

<220>
<223> C-terminale Teilsequenz

<400> 13

Phe Gly Asp Pro Glu Leu Asp Ile

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1

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<210> 14
<211> 37
<212> DNA
<213> Artificial

<220>
<223> PCR Primer forward lang

<400> 14
ggattccat atggatttta ttgattttaa ggagatg

37

<210> 15
<211> 33
<212> DNA
<213> Artificial

<220>
<223> PCR Primer Forward kurz

<400> 15
ggattccat atgatctttg acggaaaggc cgc

33

<210> 16
<211> 24
<212> DNA
<213> Artificial

<220>
<223> PCR Primer Revers

<400> 16
cgggatccct aggggcgctg accc

24

<210> 17
<211> 25
<212> DNA
<213> Artificial

<220>
<223> PCR Primer

<400> 17
ctggtcctga ccgacagaaa cgagc

25

<210> 18
<211> 25
<212> DNA
<213> Artificial

<220>
<223> PCR Primer

<400> 18
gctcgtttct gtcggtcagg accag

25

<210> 19
<211> 28
<212> DNA

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<213> Artificial
 <220>
 <223> PCR Primer
 <400> 19
 gtcctgaccg acttaaacga gcagaaac 28
 <210> 20
 <211> 28
 <212> DNA
 <213> Artificial
 <220>
 <223> PCR Primer
 <400> 20
 gtttctgctc gtttaagtcg gtcaggac 28
 <210> 21
 <211> 777
 <212> DNA
 <213> Artificial
 <220>
 <223> Mutant Q97H
 <220>
 <221> CDS
 <222> (1)..(777)
 <400> 21
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 1 5 10 15
 aaa tcg atc ggc tac ggc att gcc gtg gcc tat gct aag gag ggg gcc 96
 Lys Ser Ile Gly Tyr Gly Ile Ala Val Ala Tyr Ala Lys Glu Gly Ala
 20 25 30
 aac ctg gtc ctg acc ggc aga aac gag cag aaa ctg ctg gac gcc aag 144
 Asn Leu Val Leu Thr Gly Arg Asn Glu Gln Lys Leu Leu Asp Ala Lys
 35 40 45
 gag gag ctg gag cgc ctc tac ggc atc aag gtg ttg ccg ctg gcg gtg 192
 Glu Glu Leu Glu Arg Leu Tyr Gly Ile Lys Val Leu Pro Leu Ala Val
 50 55 60
 gac gtc acc ccc agc gat gag tcg gag gac cgg gtc aag gaa gcc gtg 240
 Asp Val Thr Pro Ser Asp Glu Ser Glu Asp Arg Val Lys Glu Ala Val
 65 70 75 80
 cag aag gtc atc gcc gaa ttc ggc cgc atc gac gtg ctg atc aac aac 288
 Gln Lys Val Ile Ala Glu Phe Gly Arg Ile Asp Val Leu Ile Asn Asn
 85 90 95
 gcc cat gcg tcg gcc tcg ggc atc ccc ctg tcc atg cag acc aaa gac 336
 Ala His Ala Ser Ala Ser Gly Ile Pro Leu Ser Met Gln Thr Lys Asp
 100 105 110
 cac ttt gac ctg ggc atc tac tcc ggg ctc tac gcc acc ttc tac tac 384
 His Phe Asp Leu Gly Ile Tyr Ser Gly Leu Tyr Ala Thr Phe Tyr Tyr
 115 120 125

atg agg gag tgc tat ccc tac ctg aag gag act cag ggc tcg gtc atc 432
 Met Arg Glu Cys Tyr Pro Tyr Leu Lys Glu Thr Gln Gly Ser Val Ile
 130 135 140

 aac ttc gcc tcc ggc gcc ggc ctc ttc ggc aac gtg ggt cag tgc tcc 480
 Asn Phe Ala Ser Gly Ala Gly Leu Phe Gly Asn Val Gly Gln Cys Ser
 145 150 155 160

 tac gcc gcc gcc aaa gag ggc atc cgc ggc ctc tcc cgc gtc gcg gcc 528
 Tyr Ala Ala Ala Lys Glu Gly Ile Arg Gly Leu Ser Arg Val Ala Ala
 165 170 175

 acc gag tgg ggc aag gac aac atc aac gtc aac gtg gtc tgc ccc ctg 576
 Thr Glu Trp Gly Lys Asp Asn Ile Asn Val Asn Val Val Cys Pro Leu
 180 185 190

 gcc atg acc gcc cag ctg gag aac ttc aag ctc tcc tac cct gag gcc 624
 Ala Met Thr Ala Gln Leu Glu Asn Phe Lys Leu Ser Tyr Pro Glu Ala
 195 200 205

 tac gag aaa aac ctc aga ggg gtg ccc atg ggc cgc ttc ggt gac ccc 672
 Tyr Glu Lys Asn Leu Arg Gly Val Pro Met Gly Arg Phe Gly Asp Pro
 210 215 220

 gag ctg gac atc ggc cgg gtc tgc gtg cag ctc ggc tcg ccc gac ttc 720
 Glu Leu Asp Ile Gly Arg Val Cys Val Gln Leu Gly Ser Pro Asp Phe
 225 230 235 240

 aag tac atg tcc ggc gag acc ctc acc ctg gaa ggc ggc atg ggt cag 768
 Lys Tyr Met Ser Gly Glu Thr Leu Thr Leu Glu Gly Gly Met Gly Gln
 245 250 255

 cgc ccc tag 777
 Arg Pro

<210> 22
 <211> 258
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 22

Met Ile Phe Asp Gly Lys Val Ala Ile Ile Thr Gly Gly Gly Lys Ala
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Lys Ser Ile Gly Tyr Gly Ile Ala Val Ala Tyr Ala Lys Glu Gly Ala
20 25 30

Asn Leu Val Leu Thr Gly Arg Asn Glu Gln Lys Leu Leu Asp Ala Lys
35 40 45

Glu Glu Leu Glu Arg Leu Tyr Gly Ile Lys Val Leu Pro Leu Ala Val
50 55 60

Asp Val Thr Pro Ser Asp Glu Ser Glu Asp Arg Val Lys Glu Ala Val
65 70 75 80

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Gln Lys Val Ile Ala Glu Phe Gly Arg Ile Asp Val Leu Ile Asn Asn
85 90 95

Ala His Ala Ser Ala Ser Gly Ile Pro Leu Ser Met Gln Thr Lys Asp
100 105 110

His Phe Asp Leu Gly Ile Tyr Ser Gly Leu Tyr Ala Thr Phe Tyr Tyr
115 120 125

Met Arg Glu Cys Tyr Pro Tyr Leu Lys Glu Thr Gln Gly Ser Val Ile
130 135 140

Asn Phe Ala Ser Gly Ala Gly Leu Phe Gly Asn Val Gly Gln Cys Ser
145 150 155 160

Tyr Ala Ala Ala Lys Glu Gly Ile Arg Gly Leu Ser Arg Val Ala Ala
165 170 175

Thr Glu Trp Gly Lys Asp Asn Ile Asn Val Asn Val Val Cys Pro Leu
180 185 190

Ala Met Thr Ala Gln Leu Glu Asn Phe Lys Leu Ser Tyr Pro Glu Ala
195 200 205

Tyr Glu Lys Asn Leu Arg Gly Val Pro Met Gly Arg Phe Gly Asp Pro
210 215 220

Glu Leu Asp Ile Gly Arg Val Cys Val Gln Leu Gly Ser Pro Asp Phe
225 230 235 240

Lys Tyr Met Ser Gly Glu Thr Leu Thr Leu Glu Gly Gly Met Gly Gln
245 250 255

Arg Pro