

eolf-seq1
SEQUENCE LISTING

<110> ROQUETTE FRERES

<120> PRODUCTION OF XYLITOL FROM GLUCOSE BY A RECOMBINANT STRAIN

<130> B1828EP

<160> 43

<170> PatentIn version 3.5

<210> 1

<211> 1385

<212> DNA

<213> Artificial sequence

<220>

<223> Sequence encoding NAD-specific D-arabitol 4-oxidoreductase
flanked by restriction site

<220>

<221> misc_feature

<222> (1)..(8)

<223> AscI recognition site

<220>

<221> CDS

<222> (12)..(1379)

<220>

<221> misc_feature

<222> (1380)..(1385)

<223> SphI recognition site

<400> 1

ggcgcgccaa	a	atg	aac	gag	cag	ttc	acc	tgg	ttg	cac	atc	ggt	ttg	ggt	50	
		Met	Asn	Glu	Gln	Phe	Thr	Trp	Leu	His	Ile	Gly	Leu	Gly		
		1				5						10				
tct	ttc	cac	aga	gct	cac	cag	gct	tgg	tac	ttg	cac	aga	ttg	cag	gtt	98
Ser	Phe	His	Arg	Ala	His	Gln	Ala	Trp	Tyr	Leu	His	Arg	Leu	Gln	Val	
	15					20				25						
atg	ggt	gac	aag	aga	tgg	tct	atc	gct	gct	ggt	aac	atc	aga	aac	gac	146
Met	Gly	Asp	Lys	Arg	Trp	Ser	Ile	Ala	Ala	Gly	Asn	Ile	Arg	Asn	Asp	
30					35					40					45	

eolf-seql

gct gag cac gtt gtt cag gct ttg tct gct cag aag ggt aga tac gtt Ala Glu His Val Val Gln Ala Leu Ser Ala Gln Lys Gly Arg Tyr Val 50 55 60	194
ttg gag acc gtt tct cca gag ggt gtt tct gag tac gag gag atc acc Leu Glu Thr Val Ser Pro Glu Gly Val Ser Glu Tyr Glu Glu Ile Thr 65 70 75	242
tct atc cag aag ttg atc cca tgg cag gct gac ttg cag cca ttg atc Ser Ile Gln Lys Leu Ile Pro Trp Gln Ala Asp Leu Gln Pro Leu Ile 80 85 90	290
gct gag ggt gct gac cca aag acc aag gtt atc gct ttc acc gtt acc Ala Glu Gly Ala Asp Pro Lys Thr Lys Val Ile Ala Phe Thr Val Thr 95 100 105	338
gag ggt ggt tac tac ttg aac acc tct cac aag ttg gag gtt aac aac Glu Gly Gly Tyr Tyr Leu Asn Thr Ser His Lys Leu Glu Val Asn Asn 110 115 120 125	386
cca gac ttg gct gct gac ttg aag ggt ggt tgt aag acc atc tac ggt Pro Asp Leu Ala Ala Asp Leu Lys Gly Gly Cys Lys Thr Ile Tyr Gly 130 135 140	434
gtt atc acc aga atc ttg gag gct aga atg gct aac aac gct ggt cca Val Ile Thr Arg Ile Leu Glu Ala Arg Met Ala Asn Asn Ala Gly Pro 145 150 155	482
ttg acc ttg ttg aac tgt gac aac gtt aga cac aac ggt gag aga ttc Leu Thr Leu Leu Asn Cys Asp Asn Val Arg His Asn Gly Glu Arg Phe 160 165 170	530
cac gac ggt ttg gtt gag ttc ttg cag ttg acc ggt aag cag gac gtt His Asp Gly Leu Val Glu Phe Leu Gln Leu Thr Gly Lys Gln Asp Val 175 180 185	578
atc gac tgg ttg tct acc aac acc acc tgt cca aac acc atg gtt gac Ile Asp Trp Leu Ser Thr Asn Thr Thr Cys Pro Asn Thr Met Val Asp 190 195 200 205	626
aga atc acc cca aga cca gct gct gag ttg cca gct aga atc aag gct Arg Ile Thr Pro Arg Pro Ala Ala Glu Leu Pro Ala Arg Ile Lys Ala 210 215 220	674
cag acc ggt atc gct gac aag gct cca gtt atg ggt gag acc ttc atc Gln Thr Gly Ile Ala Asp Lys Ala Pro Val Met Gly Glu Thr Phe Ile 225 230 235	722

eolf-seql

cag tgg gtt gtt gag gac aac ttc aga gac gtt aga cca gct ttg gag Gln Trp Val Val Glu Asp Asn Phe Arg Asp Val Arg Pro Ala Leu Glu 240 245 250	770
aag gtt ggt gtt gag ttg gtt gct tct gtt atc cca tac gag gag gct Lys Val Gly Val Glu Leu Val Ala Ser Val Ile Pro Tyr Glu Glu Ala 255 260 265	818
aag atc aga atc ttg aac tct tct cac tct tgt atc gct tgg gct ggt Lys Ile Arg Ile Leu Asn Ser Ser His Ser Cys Ile Ala Trp Ala Gly 270 275 280 285	866
acc ttg atc ggt cag aag tac atc cac gag tct acc atg acc gac ttc Thr Leu Ile Gly Gln Lys Tyr Ile His Glu Ser Thr Met Thr Asp Phe 290 295 300	914
atc tac cag atc gct gac aga tac gtt acc gag gac gtt atc cca tgt Ile Tyr Gln Ile Ala Asp Arg Tyr Val Thr Glu Asp Val Ile Pro Cys 305 310 315	962
ttg ggt gac aac ggt atc gac ttg cca acc tac aga gac gtt gtt ttg Leu Gly Asp Asn Gly Ile Asp Leu Pro Thr Tyr Arg Asp Val Val Leu 320 325 330	1010
aag aga ttc acc aac cca cac atc cag gac acc aac cag aga gtt gct Lys Arg Phe Thr Asn Pro His Ile Gln Asp Thr Asn Gln Arg Val Ala 335 340 345	1058
gct gac ggt ttc tct aag atc cca gct atg atc gct cca acc ttg aga Ala Asp Gly Phe Ser Lys Ile Pro Ala Met Ile Ala Pro Thr Leu Arg 350 355 360 365	1106
gag tgt tac cag aga ggt gtt aga cca aac gct acc gct atg ttg cca Glu Cys Tyr Gln Arg Gly Val Arg Pro Asn Ala Thr Ala Met Leu Pro 370 375 380	1154
gct ttg ttc tac gtt ttc atg gag cag tgg cac cac ggt aag ttg cca Ala Leu Phe Tyr Val Phe Met Glu Gln Trp His His Gly Lys Leu Pro 385 390 395	1202
tac gag tac cag gac ggt atc ttg gac gct cca gct gtt cac gct atg Tyr Glu Tyr Gln Asp Gly Ile Leu Asp Ala Pro Ala Val His Ala Met 400 405 410	1250
ttg cag tct gct gac cca gtt gct gtt tac gct tct gac aag gct ttg Leu Gln Ser Ala Asp Pro Val Ala Val Tyr Ala Ser Asp Lys Ala Leu 415 420 425	1298

eolf-seql

ttc ggt gac ttg acc gag aga gag gac ttc gct gct ttg ttg aga gag 1346
Phe Gly Asp Leu Thr Glu Arg Glu Asp Phe Ala Ala Leu Leu Arg Glu
430 435 440 445

aag atc gct gac gtt tac gct ttg atc aac taa gcatgc 1385
Lys Ile Ala Asp Val Tyr Ala Leu Ile Asn
450 455

<210>	2
<211>	455
<212>	PRT
<213>	Artificial sequence

<220>
<223> Synthetic Construct

<400> 2

Met Asn Glu Gln Phe Thr Trp Leu His Ile Gly Leu Gly Ser Phe His
1 5 10 15

Arg Ala His Gln Ala Trp Tyr Leu His Arg Leu Gln Val Met Gly Asp
20 25 30

Lys Arg Trp Ser Ile Ala Ala Gly Asn Ile Arg Asn Asp Ala Glu His
35 40 45

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

Val	Ser	Pro	Glu	Gly	Val	Ser	Glu	Tyr	Glu	Glu	Ile	Thr	Ser	Ile	Gln
65					70					75					80

Lys Leu Ile Pro Trp Gln Ala Asp Leu Gln Pro Leu Ile Ala Glu Gly
85 90 95

Ala Asp Pro Lys Thr Lys Val Ile Ala Phe Thr Val Thr Glu Gly Gly
100 105 110

eolf-seql

Tyr Tyr Leu Asn Thr Ser His Lys Leu Glu Val Asn Asn Pro Asp Leu
 115 120 125

Ala Ala Asp Leu Lys Gly Gly Cys Lys Thr Ile Tyr Gly Val Ile Thr
 130 135 140

Arg Ile Leu Glu Ala Arg Met Ala Asn Asn Ala Gly Pro Leu Thr Leu
 145 150 155 160

Leu Asn Cys Asp Asn Val Arg His Asn Gly Glu Arg Phe His Asp Gly
 165 170 175

Leu Val Glu Phe Leu Gln Leu Thr Gly Lys Gln Asp Val Ile Asp Trp
 180 185 190

Leu Ser Thr Asn Thr Thr Cys Pro Asn Thr Met Val Asp Arg Ile Thr
 195 200 205

Pro Arg Pro Ala Ala Glu Leu Pro Ala Arg Ile Lys Ala Gln Thr Gly
 210 215 220

Ile Ala Asp Lys Ala Pro Val Met Gly Glu Thr Phe Ile Gln Trp Val
 225 230 235 240

Val Glu Asp Asn Phe Arg Asp Val Arg Pro Ala Leu Glu Lys Val Gly
 245 250 255

Val Glu Leu Val Ala Ser Val Ile Pro Tyr Glu Glu Ala Lys Ile Arg
 260 265 270

Ile Leu Asn Ser Ser His Ser Cys Ile Ala Trp Ala Gly Thr Leu Ile
 275 280 285

Gly Gln Lys Tyr Ile His Glu Ser Thr Met Thr Asp Phe Ile Tyr Gln
 290 295 300

eolf-seq1

Ile Ala Asp Arg Tyr Val Thr Glu Asp Val Ile Pro Cys Leu Gly Asp
305 310 315 320

Asn Gly Ile Asp Leu Pro Thr Tyr Arg Asp Val Val Leu Lys Arg Phe
325 330 335

Thr Asn Pro His Ile Gln Asp Thr Asn Gln Arg Val Ala Ala Asp Gly
340 345 350

Phe Ser Lys Ile Pro Ala Met Ile Ala Pro Thr Leu Arg Glu Cys Tyr
355 360 365

Gln Arg Gly Val Arg Pro Asn Ala Thr Ala Met Leu Pro Ala Leu Phe
370 375 380

Tyr Val Phe Met Glu Gln Trp His His Gly Lys Leu Pro Tyr Glu Tyr
385 390 395 400

Gln Asp Gly Ile Leu Asp Ala Pro Ala Val His Ala Met Leu Gln Ser
405 410 415

Ala Asp Pro Val Ala Val Tyr Ala Ser Asp Lys Ala Leu Phe Gly Asp
420 425 430

Leu Thr Glu Arg Glu Asp Phe Ala Ala Leu Leu Arg Glu Lys Ile Ala
435 440 445

Asp Val Tyr Ala Leu Ile Asn
450 455

<210> 3

<211> 1368

<212> DNA

<213> artificial sequence

<220>

<223> NAD+ specific D-arabitol 4-oxidoreductase encoding sequence

eolf-seql

<400> 3

atgaacgagc agttcacctg gttgcacatc ggtttgggtt ctttccacag agctcaccag	60
gcttggtact tgcacagatt gcaggttatg ggtgacaaga gatggcttat cgctgctggt	120
aacatcagaa acgacgctga gcacgttggt caggctttgt ctgctcagaa gggtagatac	180
gttttggaga ccgtttctcc agagggtgtt tctgagtacg aggagatcac ctctatccag	240
aagttgatcc catggcaggc tgacttgtag ccattgatcg ctgagggtgc tgacccaaag	300
accaaggtta tcgctttcac cgttaccgag ggtgggttact acttgaacac ctctcacaag	360
ttggaggtta acaaccaga cttggctgct gacttgaagg gtggttgtaa gaccatctac	420
ggtgttatca ccagaatctt ggaggctaga atggctaaca acgctgggcc attgaccttg	480
ttgaactgtg acaacgtag acacaacggt gagagattcc acgacgggtt gggtgagttc	540
ttgcagttga ccggtgaagca ggacgttatc gactgggtgt ctaccaacac cacctgtcca	600
aacaccatgg ttgacagaat caccccaaga ccagctgctg agttgccagc tagaatcaag	660
gctcagaccg gtatcgctga caaggctcca gttatgggtg agaccttcat ccagtgggtt	720
gttgaggaca acttcagaga cgttagacca gctttggaga aggttggtgt tgagttgggt	780
gcttctgtta tcccatacga ggaggctaag atcagaatct tgaactcttc tcaactttgt	840
atcgcttggg ctggtacctt gatcggtcag aagtacatcc acgagtctac catgaccgac	900
ttcatctacc agatcgctga cagatacgtt accgaggacg ttatcccatg tttgggtgac	960
aacggtatcg acttgccaac ctacagagac gttgttttga agagattcac caaccacac	1020
atccaggaca ccaaccagag agttgctgct gacggtttct ctaagatccc agctatgatc	1080
gctccaacct tgagagagtg ttaccagaga ggtgttagac caaacgctac cgctatgttg	1140
ccagctttgt tctacgtttt catggagcag tggcaccacg gtaagttgcc atacgagtac	1200
caggacggtg tcttgacgc tccagctgtt cacgctatgt tgcagtctgc tgaccagtt	1260
gctgtttacg cttctgacaa ggctttgttc ggtgacttga ccgagagaga ggacttcgct	1320
gctttgttga gagagaagat cgctgacgtt tacgctttga tcaactaa	1368

eolf-seq1

<210> 4
 <211> 1107
 <212> DNA
 <213> artificial sequence

 <220>
 <223> Sequence encoding NADPH-specific xylitol dehydrogenase flanked by restriction sites

 <220>
 <221> misc_feature
 <222> (1)..(6)
 <223> HindIII recognition site

 <220>
 <221> CDS
 <222> (10)..(1101)

 <220>
 <221> misc_feature
 <222> (1102)..(1107)
 <223> SacII recognition site

 <400> 4
 aagcttaaa atg act gct aac cct tcc ttg gtg ttg aac aag atc gac gac 51
 Met Thr Ala Asn Pro Ser Leu Val Leu Asn Lys Ile Asp Asp
 1 5 10

 att tcg ttc gaa act tac gat gcc cca gaa atc tct gaa cct acc gat 99
 Ile Ser Phe Glu Thr Tyr Asp Ala Pro Glu Ile Ser Glu Pro Thr Asp
 15 20 25 30

 gtc ctc gtc cag gtc aag aaa acc ggt atc tgt ggt tcc gac atc cac 147
 Val Leu Val Gln Val Lys Lys Thr Gly Ile Cys Gly Ser Asp Ile His
 35 40 45

 ttc tac gcc cat ggt aga atc ggt aac ttc gtt ttg acc aag cca atg 195
 Phe Tyr Ala His Gly Arg Ile Gly Asn Phe Val Leu Thr Lys Pro Met
 50 55 60

 gtc ttg ggt cac gaa tcc gcc ggt act gtt gtc cag gtt ggt aag ggt 243
 Val Leu Gly His Glu Ser Ala Gly Thr Val Val Gln Val Gly Lys Gly
 65 70 75

 gtc acc tct ctt aag gtt ggt gac aac gtc gct atc gaa cca ggt att 291
 Val Thr Ser Leu Lys Val Gly Asp Asn Val Ala Ile Glu Pro Gly Ile
 80 85 90

eolf-seql

cca tcc aga ttc tcc gac gaa tac aag agc ggt cac tac aac ttg tgt	339
Pro Ser Arg Phe Ser Asp Glu Tyr Lys Ser Gly His Tyr Asn Leu Cys	
95 100 105 110	
cct cac atg gcc ttc gcc gct act cct aac tcc aag gaa ggc gaa cca	387
Pro His Met Ala Phe Ala Ala Thr Pro Asn Ser Lys Glu Gly Glu Pro	
115 120 125	
aac cca cca ggt acc tta tgt aag tac ttc aag tcg cca gaa gac ttc	435
Asn Pro Pro Gly Thr Leu Cys Lys Tyr Phe Lys Ser Pro Glu Asp Phe	
130 135 140	
ttg gtc aag ttg cca gac cac gtc agc ttg gaa ctc ggt gct ctt gtt	483
Leu Val Lys Leu Pro Asp His Val Ser Leu Glu Leu Gly Ala Leu Val	
145 150 155	
gag cca ttg tct gtt ggt gtc cac gcc tcc aag ttg ggt tcc gtt gct	531
Glu Pro Leu Ser Val Gly Val His Ala Ser Lys Leu Gly Ser Val Ala	
160 165 170	
ttc ggc gac tac gtt gcc gtc ttt ggt gct ggt cct gtt ggt ctt ttg	579
Phe Gly Asp Tyr Val Ala Val Phe Gly Ala Gly Pro Val Gly Leu Leu	
175 180 185 190	
gct gct gct gtc gcc aag acc ttc ggt gct aag ggt gtc atc gtc gtt	627
Ala Ala Ala Val Ala Lys Thr Phe Gly Ala Lys Gly Val Ile Val Val	
195 200 205	
gct aga tca gac aga aag ttg aag atg gcc aag gac att ggt gct gct	675
Ala Arg Ser Asp Arg Lys Leu Lys Met Ala Lys Asp Ile Gly Ala Ala	
210 215 220	
act cac acc ttc aac tcc aag acc ggt ggt tct gaa gaa ttg atc aag	723
Thr His Thr Phe Asn Ser Lys Thr Gly Gly Ser Glu Glu Leu Ile Lys	
225 230 235	
gct ttc ggt ggt aac gtg cca aac gtc gtt ttg gaa tgt act ggt gct	771
Ala Phe Gly Gly Asn Val Pro Asn Val Val Leu Glu Cys Thr Gly Ala	
240 245 250	
gaa cct tgt atc aag ttg ggt gtt gac gcc att gcc cca ggt ggt cgt	819
Glu Pro Cys Ile Lys Leu Gly Val Asp Ala Ile Ala Pro Gly Gly Arg	
255 260 265 270	
ttc gtt caa gtt ggt aac gct gct ggt cca gtc agc ttc cca atc acc	867
Phe Val Gln Val Gly Asn Ala Ala Gly Pro Val Ser Phe Pro Ile Thr	
275 280 285	

eolf-seql

gtt ttc gcc atg aag gaa ttg act ttg ttc ggt tct ttc aga tac gga 915
Val Phe Ala Met Lys Glu Leu Thr Leu Phe Gly Ser Phe Arg Tyr Gly
290 295 300

ttc aac gac tac aag act gct gtt gga atc ttt gac act aac tac caa 963
Phe Asn Asp Tyr Lys Thr Ala Val Gly Ile Phe Asp Thr Asn Tyr Gln
305 310 315

aac ggt aga gaa aat gct cca att gac ttt gaa caa ttg atc acc cac 1011
Asn Gly Arg Glu Asn Ala Pro Ile Asp Phe Glu Gln Leu Ile Thr His
320 325 330

aga tac aag ttc aag gac gct att gaa gcc tac gac ttg gtc aga gcc 1059
Arg Tyr Lys Phe Lys Asp Ala Ile Glu Ala Tyr Asp Leu Val Arg Ala
335 340 345 350

ggt aag ggt gct gtc aag tgt ctc att gac ggc cct gag taa ccgcgg 1107
Gly Lys Gly Ala Val Lys Cys Leu Ile Asp Gly Pro Glu
355 360

<210> 5
<211> 363
<212> PRT
<213> artificial sequence

<220>
<223> Synthetic Construct

<400> 5

Met Thr Ala Asn Pro Ser Leu Val Leu Asn Lys Ile Asp Asp Ile Ser
1 5 10 15

Phe Glu Thr Tyr Asp Ala Pro Glu Ile Ser Glu Pro Thr Asp Val Leu
20 25 30

Val Gln Val Lys Lys Thr Gly Ile Cys Gly Ser Asp Ile His Phe Tyr
35 40 45

Ala His Gly Arg Ile Gly Asn Phe Val Leu Thr Lys Pro Met Val Leu
50 55 60

eolf-seql

Gly His Glu Ser Ala Gly Thr Val Val Gln Val Gly Lys Gly Val Thr
65 70 75 80

Ser Leu Lys Val Gly Asp Asn Val Ala Ile Glu Pro Gly Ile Pro Ser
85 90 95

Arg Phe Ser Asp Glu Tyr Lys Ser Gly His Tyr Asn Leu Cys Pro His
100 105 110

Met Ala Phe Ala Ala Thr Pro Asn Ser Lys Glu Gly Glu Pro Asn Pro
115 120 125

Pro Gly Thr Leu Cys Lys Tyr Phe Lys Ser Pro Glu Asp Phe Leu Val
130 135 140

Lys Leu Pro Asp His Val Ser Leu Glu Leu Gly Ala Leu Val Glu Pro
145 150 155 160

Leu Ser Val Gly Val His Ala Ser Lys Leu Gly Ser Val Ala Phe Gly
165 170 175

Asp Tyr Val Ala Val Phe Gly Ala Gly Pro Val Gly Leu Leu Ala Ala
180 185 190

Ala Val Ala Lys Thr Phe Gly Ala Lys Gly Val Ile Val Val Ala Arg
195 200 205

Ser Asp Arg Lys Leu Lys Met Ala Lys Asp Ile Gly Ala Ala Thr His
210 215 220

Thr Phe Asn Ser Lys Thr Gly Gly Ser Glu Glu Leu Ile Lys Ala Phe
225 230 235 240

Gly Gly Asn Val Pro Asn Val Val Leu Glu Cys Thr Gly Ala Glu Pro
245 250 255

eolf-seql

Cys Ile Lys Leu Gly Val Asp Ala Ile Ala Pro Gly Gly Arg Phe Val
260 265 270

Gln Val Gly Asn Ala Ala Gly Pro Val Ser Phe Pro Ile Thr Val Phe
275 280 285

Ala Met Lys Glu Leu Thr Leu Phe Gly Ser Phe Arg Tyr Gly Phe Asn
290 295 300

Asp Tyr Lys Thr Ala Val Gly Ile Phe Asp Thr Asn Tyr Gln Asn Gly
305 310 315 320

Arg Glu Asn Ala Pro Ile Asp Phe Glu Gln Leu Ile Thr His Arg Tyr
325 330 335

Lys Phe Lys Asp Ala Ile Glu Ala Tyr Asp Leu Val Arg Ala Gly Lys
340 345 350

Gly Ala Val Lys Cys Leu Ile Asp Gly Pro Glu
355 360

<210> 6
<211> 1092
<212> DNA
<213> artificial sequence

<220>
<223> sequence encoding NADPH specific xylitol dehydrogenase

<400> 6
atgactgcta acccttcctt ggtgttgaac aagatcgacg acatttcgtt cgaaacttac 60
gatgccccag aaatctctga acctaccgat gtcctcgtcc aggtcaagaa aaccggtatc 120
tgtggttccg acatccactt ctacgcccac ggtagaatcg gtaacttcgt ttgaccaag 180
ccaatggtct tgggtcacga atccgccggt actgttgtcc aggttggtaa ggggtgcacc 240
tctcttaagg ttggtgacaa cgtcgctatc gaaccaggta ttccatccag attctccgac 300
gaatacaaga gcggtcacta caacttgtgt cctcacatgg ccttcgccgc tactcctaac 360

eolf-seq1

tccaaggaag gcgaacaaaa cccaccaggt accttatgta agtacttcaa gtcgccagaa	420
gacttcttgg tcaagttgcc agaccacgtc agcttggaac tcggtgctct tgttgagcca	480
ttgtctgttg gtgtccacgc ctccaagttg ggttccgttg ctttcggcga ctacgttgcc	540
gtctttggtg ctggtcctgt tggctttttg gctgctgctg tcgccaagac cttcggtgct	600
aagggtgtca tcgtcgttgc tagatcagac agaaaagttga agatggccaa ggacattggt	660
gctgctactc acaccttcaa ctccaagacc ggtggttctg aagaattgat caaggctttc	720
ggtggtaacg tgccaaacgt cgttttggaa tgtactgggtg ctgaaccttg tatcaagttg	780
ggtgttgacg ccattgcccc aggtggtcgt ttcgttcaag ttggtaacgc tgctgggtcca	840
gtcagcttcc caatcacctg tttcgccatg aaggaattga ctttgttcgg ttctttcaga	900
tacggattca acgactacaa gactgctgtt ggaatctttg acactaacta ccaaaacggt	960
agagaaaaatg ctccaattga ctttgaacaa ttgatcacc acagatacaa gttcaaggac	1020
gctattgaag cctacgactt ggtcagagcc ggtaagggtg ctgtcaagtg ttcattgac	1080
ggccctgagt aa	1092

<210> 7
 <211> 806
 <212> DNA
 <213> artificial sequence

<220>
 <223> sequence encoding NADPH-specific xylitol dehydrogenase flanked by restriction sites

<220>
 <221> misc_feature
 <222> (1)..(8)
 <223> AscI recognition site

<220>
 <221> CDS
 <222> (12)..(800)

<220>

eolf-seql

<221> misc_feature

<222> (801)..(806)

<223> SphI recognition site

<400> 7

ggcgcgccaa a atg tct aag aag ttc aac ggt aag gtt tgt ttg gtt acc	50
Met Ser Lys Lys Phe Asn Gly Lys Val Cys Leu Val Thr	
1 5 10	
ggt gct ggt ggt aac atc ggt ttg gct acc gct ttg aga ttg gct gag	98
Gly Ala Gly Gly Asn Ile Gly Leu Ala Thr Ala Leu Arg Leu Ala Glu	
15 20 25	
gag ggt acc gct atc gct ttg ttg tct aga aac aga gag gct ttg gag	146
Glu Gly Thr Ala Ile Ala Leu Leu Ser Arg Asn Arg Glu Ala Leu Glu	
30 35 40 45	
aag gct gag gct tct gtt aga gag aag ggt gtt gag gct aga tct tac	194
Lys Ala Glu Ala Ser Val Arg Glu Lys Gly Val Glu Ala Arg Ser Tyr	
50 55 60	
gtt tgt gac gtt acc tct gag gag gct gtt atc ggt acc gtt gac tct	242
Val Cys Asp Val Thr Ser Glu Glu Ala Val Ile Gly Thr Val Asp Ser	
65 70 75	
gtt gtt aga gac ttc ggt aag atc gac ttc ttg ttc aac aac gct ggt	290
Val Val Arg Asp Phe Gly Lys Ile Asp Phe Leu Phe Asn Asn Ala Gly	
80 85 90	
tac cag ggt gct ttc gct cca gtt cag gac tac cca tct gac gac ttc	338
Tyr Gln Gly Ala Phe Ala Pro Val Gln Asp Tyr Pro Ser Asp Asp Phe	
95 100 105	
gct aga gtt ttg acc atc aac gtt acc ggt gct ttc cac gtt ttg aag	386
Ala Arg Val Leu Thr Ile Asn Val Thr Gly Ala Phe His Val Leu Lys	
110 115 120 125	
gct gtt tct aga cag atg atc acc cag aac tac ggt aga atc gtt aac	434
Ala Val Ser Arg Gln Met Ile Thr Gln Asn Tyr Gly Arg Ile Val Asn	
130 135 140	
acc gct tct atg gct ggt gtt aag ggt cca cca aac atg gct gct tac	482
Thr Ala Ser Met Ala Gly Val Lys Gly Pro Pro Asn Met Ala Ala Tyr	
145 150 155	
ggt acc tct aag ggt gct atc atc gct ttg acc gag acc gct gct ttg	530
Gly Thr Ser Lys Gly Ala Ile Ile Ala Leu Thr Glu Thr Ala Ala Leu	
160 165 170	

eolf-seql

gac ttg gct cca tac aac atc aga gtt aac gct atc tct cca ggt tac 578
Asp Leu Ala Pro Tyr Asn Ile Arg Val Asn Ala Ile Ser Pro Gly Tyr
175 180 185

atg ggt cca ggt ttc atg tgg gag aga cag gtt gag ttg cag gct aag 626
Met Gly Pro Gly Phe Met Trp Glu Arg Gln Val Glu Leu Gln Ala Lys
190 195 200 205

gtt ggt tct cag tac ttc tct acc gac cca aag gtt gtt gct cag cag 674
Val Gly Ser Gln Tyr Phe Ser Thr Asp Pro Lys Val Val Ala Gln Gln
210 215 220

atg atc ggt tct gtt cca atg aga aga tac ggt gac atc aac gag atc 722
Met Ile Gly Ser Val Pro Met Arg Arg Tyr Gly Asp Ile Asn Glu Ile
225 230 235

cca ggt gtt gtt gct ttc ttg ttg ggt gac gac tct tct ttc atg acc 770
Pro Gly Val Val Ala Phe Leu Leu Gly Asp Asp Ser Ser Phe Met Thr
240 245 250

ggt gtt aac ttg cca atc gct ggt ggt tga gcatgc 806
Gly Val Asn Leu Pro Ile Ala Gly Gly
255 260

<210> 8
<211> 262
<212> PRT
<213> artificial sequence

<220>
<223> Synthetic Construct

<400> 8

Met Ser Lys Lys Phe Asn Gly Lys Val Cys Leu Val Thr Gly Ala Gly
1 5 10 15

Gly Asn Ile Gly Leu Ala Thr Ala Leu Arg Leu Ala Glu Glu Gly Thr
20 25 30

Ala Ile Ala Leu Leu Ser Arg Asn Arg Glu Ala Leu Glu Lys Ala Glu
35 40 45

eolf-seql

Ala Ser Val Arg Glu Lys Gly Val Glu Ala Arg Ser Tyr Val Cys Asp
50 55 60

Val Thr Ser Glu Glu Ala Val Ile Gly Thr Val Asp Ser Val Val Arg
65 70 75 80

Asp Phe Gly Lys Ile Asp Phe Leu Phe Asn Asn Ala Gly Tyr Gln Gly
85 90 95

Ala Phe Ala Pro Val Gln Asp Tyr Pro Ser Asp Asp Phe Ala Arg Val
100 105 110

Leu Thr Ile Asn Val Thr Gly Ala Phe His Val Leu Lys Ala Val Ser
115 120 125

Arg Gln Met Ile Thr Gln Asn Tyr Gly Arg Ile Val Asn Thr Ala Ser
130 135 140

Met Ala Gly Val Lys Gly Pro Pro Asn Met Ala Ala Tyr Gly Thr Ser
145 150 155 160

Lys Gly Ala Ile Ile Ala Leu Thr Glu Thr Ala Ala Leu Asp Leu Ala
165 170 175

Pro Tyr Asn Ile Arg Val Asn Ala Ile Ser Pro Gly Tyr Met Gly Pro
180 185 190

Gly Phe Met Trp Glu Arg Gln Val Glu Leu Gln Ala Lys Val Gly Ser
195 200 205

Gln Tyr Phe Ser Thr Asp Pro Lys Val Val Ala Gln Gln Met Ile Gly
210 215 220

Ser Val Pro Met Arg Arg Tyr Gly Asp Ile Asn Glu Ile Pro Gly Val
225 230 235 240

eolf-seql

Val	Ala	Phe	Leu	Leu	Gly	Asp	Asp	Ser	Ser	Phe	Met	Thr	Gly	Val	Asn
			245					250						255	

Leu Pro Ile Ala Gly Gly
260

<210> 9
 <211> 789
 <212> DNA
 <213> artificial sequence

<220>
 <223> sequence encoding NADPH specific xylitol dehydrogenase

<400> 9

atgtctaaga agttcaacgg taaggtttgt ttggttaccg gtgctggtgg taacatcggt	60
ttggctaccg ctttgagatt ggctgaggag ggtaccgcta tcgctttgtt gtctagaaac	120
agagaggcctt tggagaaggc tgaggcttct gttagagaga aggggtgttga ggctagatct	180
tacgtttgtg acgttacctc tgaggaggct gttatcggtta ccgttgactc tgttggttaga	240
gacttcggta agatcgactt cttgttcaac aacgctgggt accagggtgc tttcgctcca	300
gttcaggact acccatctga cgacttcgct agagttttga ccatcaacgt taccggtgct	360
ttccacgttt tgaaggctgt ttctagacag atgatcacc agaactacgg tagaatcggt	420
aacaccgctt ctatggctgg tgtaagggt ccaccaaaca tggctgctta cggtagctct	480
aagggtgcta tcatcgcttt gaccgagacc gctgctttgg acttggtcc atacaacatc	540
agagttaacg ctatctctcc aggttacatg ggtccagggt tcatgtggga gagacagggt	600
gagttgcagg ctaagggttg ttctcagtag ttctctaccg acccaaagggt tgttgctcag	660
cagatgatcg gttctgttcc aatgagaaga tacgggtgaca tcaacgagat cccagggtgtt	720
gttgctttct tgttggttga cgactcttct ttcattgacc gtgttaactt gccaatcgct	780
ggtggttga	789

<210> 10
 <211> 873

eolf-seql

<212> DNA

<213> artificial sequence

<220>

<223> sequence encoding tagatose-3-epimerase

<220>

<221> CDS

<222> (1)..(873)

<400> 10

atg aac aaa gtt ggc atg ttc tac acc tac tgg tcg act gag tgg atg	48
Met Asn Lys Val Gly Met Phe Tyr Thr Tyr Trp Ser Thr Glu Trp Met	
1 5 10 15	

gtc gac ttt ccg gcg act gcg aag cgc att gcc ggg ctc ggc ttc gac	96
Val Asp Phe Pro Ala Thr Ala Lys Arg Ile Ala Gly Leu Gly Phe Asp	
20 25 30	

tta atg gaa atc tcg ctc ggc gag ttt cac aat ctt tcc gac gcg aag	144
Leu Met Glu Ile Ser Leu Gly Glu Phe His Asn Leu Ser Asp Ala Lys	
35 40 45	

aag cgt gag cta aaa gcc gtg gct gat gat ctg ggg ctc acg gtg atg	192
Lys Arg Glu Leu Lys Ala Val Ala Asp Asp Leu Gly Leu Thr Val Met	
50 55 60	

tgc tgt atc gga ctg aag tct gag tac gac ttt gcc tcg ccg gac aag	240
Cys Cys Ile Gly Leu Lys Ser Glu Tyr Asp Phe Ala Ser Pro Asp Lys	
65 70 75 80	

agc gtt cgt gat gcc ggc acg gaa tat gtg aag cgc ttg ctc gac gac	288
Ser Val Arg Asp Ala Gly Thr Glu Tyr Val Lys Arg Leu Leu Asp Asp	
85 90 95	

tgt cac ctc ctc ggt gcg ccg gtc ttt gct ggc ctt acg ttc tgc gcg	336
Cys His Leu Leu Gly Ala Pro Val Phe Ala Gly Leu Thr Phe Cys Ala	
100 105 110	

tgg ccc caa tct ccg ccg ctg gac atg aag gat aag cgc cct tac gtc	384
Trp Pro Gln Ser Pro Pro Leu Asp Met Lys Asp Lys Arg Pro Tyr Val	
115 120 125	

gac cgt gca atc gaa agc gtt cgt cgt gtt atc aag gta gct gaa gac	432
Asp Arg Ala Ile Glu Ser Val Arg Arg Val Ile Lys Val Ala Glu Asp	
130 135 140	

	eolf-seql																
tac Tyr 145	ggc Gly	att Ile	att Ile	tat Tyr	gca Ala 150	ctg Leu	gaa Glu	gtg Val	gtg Val	aac Asn 155	cga Arg	ttc Phe	gag Glu	cag Gln	tgg Trp 160	480	
ctt Leu	tgc Cys	aat Asn	gac Asp	gcc Ala 165	aag Lys	gaa Glu	gca Ala	att Ile	gcg Ala 170	ttt Phe	gcc Ala	gac Asp	gcg Ala	gtt Val 175	gac Asp	528	
agt Ser	ccg Pro	gcg Ala	tgc Cys 180	aag Lys	gtc Val	cag Gln	ctc Leu	gac Asp 185	aca Thr	ttc Phe	cac His	atg Met	aat Asn 190	atc Ile	gaa Glu	576	
gag Glu	act Thr	tcc Ser 195	ttc Phe	cgc Arg	gat Asp	gca Ala 200	atc Ile	ctt Leu	gcc Ala	tgc Cys	aag Lys 205	ggc Gly	aag Lys	atg Met	ggc Gly	624	
cat His 210	ttc Phe	cat His	ttg Leu	ggc Gly	gaa Glu	gcg Ala 215	aac Asn	cgt Arg	ctg Leu	ccg Pro	ccg Pro 220	ggc Gly	gag Glu	ggc Gly	cgc Arg	672	
ctg Leu 225	ccg Pro	tgg Trp	gat Asp	gaa Glu	ata Ile 230	ttc Phe	ggg Gly	gcg Ala	ctg Leu	aag Lys 235	gaa Glu	atc Ile	gga Gly	tat Tyr	gac Asp 240	720	
ggc Gly	acc Thr	atc Ile	gtt Val 245	atg Met	gaa Glu	ccg Pro	ttc Phe	atg Met 250	cgc Arg	aag Lys	ggc Gly	ggc Gly	tcg Ser	gtc Val 255	agc Ser	768	
cgc Arg	gcg Ala	gtg Val	ggc Gly 260	gta Val	tgg Trp	cgg Arg	gat Asp	atg Met 265	tcg Ser	aac Asn	ggc Gly	gcg Ala	acg Thr 270	gac Asp	gaa Glu	816	
gag Glu	atg Met	gac Asp 275	gag Glu	cgc Arg	gct Ala	cgc Arg	cgc Arg 280	tcg Ser	ttg Leu	cag Gln	ttt Phe	gtt Val 285	cgt Arg	gac Asp	aag Lys	864	
ctg Leu 290	gcc Ala	tga														873	

eolf-seql

<400> 11

Met Asn Lys Val Gly Met Phe Tyr Thr Tyr Trp Ser Thr Glu Trp Met
1 5 10 15

Val Asp Phe Pro Ala Thr Ala Lys Arg Ile Ala Gly Leu Gly Phe Asp
20 25 30

Leu Met Glu Ile Ser Leu Gly Glu Phe His Asn Leu Ser Asp Ala Lys
35 40 45

Lys Arg Glu Leu Lys Ala Val Ala Asp Asp Leu Gly Leu Thr Val Met
50 55 60

Cys Cys Ile Gly Leu Lys Ser Glu Tyr Asp Phe Ala Ser Pro Asp Lys
65 70 75 80

Ser Val Arg Asp Ala Gly Thr Glu Tyr Val Lys Arg Leu Leu Asp Asp
85 90 95

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

Trp Pro Gln Ser Pro Pro Leu Asp Met Lys Asp Lys Arg Pro Tyr Val
115 120 125

Asp Arg Ala Ile Glu Ser Val Arg Arg Val Ile Lys Val Ala Glu Asp
130 135 140

Tyr Gly Ile Ile Tyr Ala Leu Glu Val Val Asn Arg Phe Glu Gln Trp
145 150 155 160

Leu Cys Asn Asp Ala Lys Glu Ala Ile Ala Phe Ala Asp Ala Val Asp
165 170 175

Ser Pro Ala Cys Lys Val Gln Leu Asp Thr Phe His Met Asn Ile Glu

eolf-seql

180

185

190

Glu Thr Ser Phe Arg Asp Ala Ile Leu Ala Cys Lys Gly Lys Met Gly
195 200 205

His Phe His Leu Gly Glu Ala Asn Arg Leu Pro Pro Gly Glu Gly Arg
210 215 220

Leu Pro Trp Asp Glu Ile Phe Gly Ala Leu Lys Glu Ile Gly Tyr Asp
225 230 235 240

Gly Thr Ile Val Met Glu Pro Phe Met Arg Lys Gly Gly Ser Val Ser
245 250 255

Arg Ala Val Gly Val Trp Arg Asp Met Ser Asn Gly Ala Thr Asp Glu
260 265 270

Glu Met Asp Glu Arg Ala Arg Arg Ser Leu Gln Phe Val Arg Asp Lys
275 280 285

Leu Ala
290

<210> 12
<211> 26
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 12
gaactagtgg atccgtagaa atcttg

26

<210> 13
<211> 44
<212> DNA
<213> artificial sequence

eolf-seql

<220>

<223> primer

<400> 13

ctttgttcat tttggcgcgc cttttagttt aataagggtc cgtg

44

<210> 14

<211> 38

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 14

aaactaaaag gcgcgcaaaa atgaacaaag ttggcatg

38

<210> 15

<211> 36

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 15

ttctcttcga gagcatgctc aggccagctt gtcacg

36

<210> 16

<211> 35

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 16

aagctggcct gagcatgctc tcgaagagaa tctag

35

<210> 17

<211> 26

<212> DNA

<213> artificial sequence

eolf-seq1

<220>

<223> primer

<400> 17

gttccgcgga gaatgacacg gccgac

26

<210> 18

<211> 31

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 18

aaggcgcgcc aaaatgactg ctaacccttc c

31

<210> 19

<211> 27

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 19

gagcatgctt actcagggcc gtcaatg

27

<210> 20

<211> 22

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 20

gaagactagt tcacgtgatc tc

22

<210> 21

<211> 30

<212> DNA

<213> artificial sequence

eolf-seq1

<220>

<223> primer

<400> 21

cactggcgcg ccttttgtgt ggtggtgtcc

30

<210> 22

<211> 33

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 22

tagcagcatg cataggtag tgaatgaggt atg

33

<210> 23

<211> 28

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 23

taggtccg cg ggagcttcgt taaagggc

28

<210> 24

<211> 116

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 24

cactggcgcg ccactgcat gcgtcgacaa cccttaatat aacttcgtat aatgtatgct

60

atacgaagtt attaggctta gacacatcgt ggatccaagc tatcaacgag agagtc

116

<210> 25

<211> 105

<212> DNA

eolf-seql

<213> artificial sequence

<220>

<223> primer

<400> 25

agtggctagc agtgccatgg cctaataact tcgtatagca tacattatac gaagttatat 60

taagggttct cgagacgcgt catctagcat ctcatctacc aactc 105

<210> 26

<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 26

cactctgcag cactggcgcg cccactgcat 30

<210> 27

<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 27

cactgatatc agtggctagc agtgccatgg 30

<210> 28

<211> 590

<212> DNA

<213> artificial sequence

<220>

<223> sequence encoding the nat1 gene of Streptomyces noursei

<400> 28

ggcgcgcaa aatgggtacc actttggacg aactgctta cagatacaga acctctgtcc 60

caggtgacgc cgaggccatc gaggctttgg atggttcctt caccaccgac accgtcttca 120

eolf-seq1

gagtcaccgc caccggtgac ggtttcacct tgagagaggt tccagttgac ccacctttga	180
ccaaggtttt cccagacgac gaatctgacg acgaatctga cgacggtgag gacggtgacc	240
cagactccag aactttcgtc gcctacggtg acgacggtga cttggctggt ttcgttgtcg	300
tctcttactc cggttggaac agaagattga ccgtcgagga catcgaggtc gccccagagc	360
acagaggtca cgggtgctggt agagctttga tgggtttggc tactgagttc gccagagaga	420
gaggtgccgg tcacttgtgg ttggaggtca ccaacgtcaa cgctccagct atccacgctt	480
acagaagaat gggtttcacc ttgtgtggtt tggacaccgc cttgtacgac ggtaccgcct	540
ccgacggtga gcaggctttg tacatgtcca tgccatgtcc ataagcatgc	590

<210> 29
 <211> 29
 <212> DNA
 <213> artificial sequence

<220>
 <223> primer

<400> 29	
caagcatgcg ggaatgataa gagactttg	29

<210> 30
 <211> 31
 <212> DNA
 <213> artificial sequence

<220>
 <223> primer

<400> 30	
ggaccgcgga aaggtgagga agtatatgaa c	31

<210> 31
 <211> 38
 <212> DNA
 <213> artificial sequence

<220>
 <223> primer

eolf-seq1

<400> 31
cacttctaga cactatcgat ggatccgtag aaatcttg 38

<210> 32
<211> 29
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 32
cactacgcgt aaaggtgagg aagtatatg 29

<210> 33
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 33
cactctgcag gatccaagct atcaacgaga 30

<210> 34
<211> 28
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 34
cactgcatgc gttgcggaaa aaacagcc 28

<210> 35
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> primer

eolf-seq1

<400> 35
cactccatgg agtaggtata taaaaatata agag 34

<210> 36
<211> 28
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 36
cactgctagc gtcgacaaca gcaactag 28

<210> 37
<211> 19
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 37
caagtcgtgg agattctgc 19

<210> 38
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 38
caaggcgcgc caaaatgtct accaaaacca ttac 34

<210> 39
<211> 28
<212> DNA
<213> artificial sequence

<220>
<223> primer

eolf-seql

<400> 39
ggagcatgcc tactttccct cagccaag 28

<210> 40
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 40
atatcccggg caccgtcatc accgaaacgc 30

<210> 41
<211> 29
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 41
atatcccggg cacgaccacg ctgatgagc 29

<210> 42
<211> 1415
<212> DNA
<213> artificial sequence

<220>
<223> Sequence encoding the NAD⁺-specific D-arabitol 4-oxidoreductase
from R. solanacearum

<220>
<221> CDS
<222> (12)..(1409)

<400> 42
ggcgcgccaa a atg acc aga tct tct ttg gct aga gct cca gtt ttg ttg 50
Met Thr Arg Ser Ser Leu Ala Arg Ala Pro Val Leu Leu
1 5 10

eolf-seql																
cac atc ggt gct ggt tct ttc cac aga gct cac cag gct tgg tac ttg	98															
His Ile Gly Ala Gly Ser Phe His Arg Ala His Gln Ala Trp Tyr Leu																
15 20 25																
cac aga gtt aac gct gct gtt cca cca ggt gag aga tgg acc ttg acc	146															
His Arg Val Asn Ala Ala Val Pro Pro Gly Glu Arg Trp Thr Leu Thr																
30 35 40 45																
ggt ggt aac atc aga gac gac atg cac gct acc ttg gct gct ttg gct	194															
Val Gly Asn Ile Arg Asp Asp Met His Ala Thr Leu Ala Ala Leu Ala																
50 55 60																
gct cag cag ggt gct tac acc ttg gag acc gtt acc cca cag ggt gag	242															
Ala Gln Gln Gly Ala Tyr Thr Leu Glu Thr Val Thr Pro Gln Gly Glu																
65 70 75																
aga gct tac gag acc atc aga tct atc gct aga gtt ttg cct tgg tct	290															
Arg Ala Tyr Glu Thr Ile Arg Ser Ile Ala Arg Val Leu Pro Trp Ser																
80 85 90																
gct gac ttg gct gct ttg atc aac acc ggt gct gac cca gct tgt aga	338															
Ala Asp Leu Ala Ala Leu Ile Asn Thr Gly Ala Asp Pro Ala Cys Arg																
95 100 105																
atc gtt tct ttc acc gtt acc gag ggt ggt tac tac ttg gac gag cac	386															
Ile Val Ser Phe Thr Val Thr Glu Gly Gly Tyr Tyr Leu Asp Glu His																
110 115 120 125																
gac aga ttg gac gtt acc cac cca gac ttg gct gct gac ttg aga ggt	434															
Asp Arg Leu Asp Val Thr His Pro Asp Leu Ala Ala Asp Leu Arg Gly																
130 135 140																
gct aga tct acc ttg tac ggt gct ttg gct gct ttg ttg gct gag aga	482															
Ala Arg Ser Thr Leu Tyr Gly Ala Leu Ala Ala Leu Leu Ala Glu Arg																
145 150 155																
aga cag aga ggt gct ggt cca ttg acc ttg cag tct tgt gac aac ttg	530															
Arg Gln Arg Gly Ala Gly Pro Leu Thr Leu Gln Ser Cys Asp Asn Leu																
160 165 170																
aga tct aac ggt gct aga ttc aga gct ggt atg aga gct ttc ttg gct	578															
Arg Ser Asn Gly Ala Arg Phe Arg Ala Gly Met Arg Ala Phe Leu Ala																
175 180 185																
ttg aga ggt gac gct gct ttg ttg gct tgg ttc gac gct aac gtt tct	626															
Leu Arg Gly Asp Ala Ala Leu Leu Ala Trp Phe Asp Ala Asn Val Ser																
190 195 200 205																

eolf-seql

tgt cca tct gct atg gtt gac aga atc acc cca aga cca acc gac gac	674
Cys Pro Ser Ala Met Val Asp Arg Ile Thr Pro Arg Pro Thr Asp Asp	
210 215 220	
gtt aga acc aga gtt cac gct gct acc ggt gtt gac gac aga tgt cca	722
Val Arg Thr Arg Val His Ala Ala Thr Gly Val Asp Asp Arg Cys Pro	
225 230 235	
gtt atg ggt gag tct ttc atc cag tgg gtt atc gag gac aac ttc atc	770
Val Met Gly Glu Ser Phe Ile Gln Trp Val Ile Glu Asp Asn Phe Ile	
240 245 250	
gct ggt aga cca gct tgg gag atc gct ggt gct gag atc gtt gct gac	818
Ala Gly Arg Pro Ala Trp Glu Ile Ala Gly Ala Glu Ile Val Ala Asp	
255 260 265	
gtt cac cca tac gag gag gct aag atc aga atc ttg aac gct acc cac	866
Val His Pro Tyr Glu Glu Ala Lys Ile Arg Ile Leu Asn Ala Thr His	
270 275 280 285	
tct tgt atc gct tgg gct ggt acc ttg gct ggt ttg acc tac atc cac	914
Ser Cys Ile Ala Trp Ala Gly Thr Leu Ala Gly Leu Thr Tyr Ile His	
290 295 300	
gag ggt atg aga gac gct gct atc tac aga ttc gct tac gac tac gtt	962
Glu Gly Met Arg Asp Ala Ala Ile Tyr Arg Phe Ala Tyr Asp Tyr Val	
305 310 315	
acc gac gac gtt atc cca tgt ttg acc cca tct cca ttg gac ttg gag	1010
Thr Asp Asp Val Ile Pro Cys Leu Thr Pro Ser Pro Leu Asp Leu Glu	
320 325 330	
aga tac aga gac gtt gtt ttg gag aga ttc ggt aac cca tac gtt ttg	1058
Arg Tyr Arg Asp Val Val Leu Glu Arg Phe Gly Asn Pro Tyr Val Leu	
335 340 345	
gac acc aac cag aga gtt gct gct gac ggt ttc tct aag atc cca ggt	1106
Asp Thr Asn Gln Arg Val Ala Ala Asp Gly Phe Ser Lys Ile Pro Gly	
350 355 360 365	
ttc atc gct cca acc ttg gct gag tgt ttc gct aga ggt gct gac cca	1154
Phe Ile Ala Pro Thr Leu Ala Glu Cys Phe Ala Arg Gly Ala Asp Pro	
370 375 380	
gtt gct acc gct gtt ttg cca gct ttg ttc ttg ggt ttc ttg gag ggt	1202
Val Ala Thr Ala Val Leu Pro Ala Leu Phe Leu Gly Phe Leu Glu Gly	
385 390 395	

eolf-seql

tgg gct aga ggt acc ttg cca tac gtt tac cag gac ggt gtt atg gac	1250
Trp Ala Arg Gly Thr Leu Pro Tyr Val Tyr Gln Asp Gly Val Met Asp	
400 405 410	

ggt gct gct gct aga tct atc gtt gag gct cca gac tct gtt gct gct	1298
Gly Ala Ala Ala Arg Ser Ile Val Glu Ala Pro Asp Ser Val Ala Ala	
415 420 425	

ttc tgt tct gac aga cag ttg tgg ggt tct ttg gct ggt aga gac gct	1346
Phe Cys Ser Asp Arg Gln Leu Trp Gly Ser Leu Ala Gly Arg Asp Ala	
430 435 440 445	

ttg gtt cag gct gtt aga gct ggt aga gct aga gtt gag gct tgg aga	1394
Leu Val Gln Ala Val Arg Ala Gly Arg Ala Arg Val Glu Ala Trp Arg	
450 455 460	

gct gct aga aga tga gcatgc	1415
Ala Ala Arg Arg	
465	

<210> 43
 <211> 465
 <212> PRT
 <213> artificial sequence

<220>
 <223> Synthetic Construct

<400> 43

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

Ala Gly Ser Phe His Arg Ala His Gln Ala Trp Tyr Leu His Arg Val
20 25 30

Asn Ala Ala Val Pro Pro Gly Glu Arg Trp Thr Leu Thr Val Gly Asn
35 40 45

Ile Arg Asp Asp Met His Ala Thr Leu Ala Ala Leu Ala Ala Gln Gln
50 55 60

Gly Ala Tyr Thr Leu Glu Thr Val Thr Pro Gln Gly Glu Arg Ala Tyr

eolf-seql

65		70		75		80
Glu Thr Ile Arg Ser Ile Ala Arg Val Leu Pro Trp Ser Ala Asp Leu						
		85		90		95
Ala Ala Leu Ile Asn Thr Gly Ala Asp Pro Ala Cys Arg Ile Val Ser						
		100		105		110
Phe Thr Val Thr Glu Gly Gly Tyr Tyr Leu Asp Glu His Asp Arg Leu						
		115		120		125
Asp Val Thr His Pro Asp Leu Ala Ala Asp Leu Arg Gly Ala Arg Ser						
		130		135		140
Thr Leu Tyr Gly Ala Leu Ala Ala Leu Leu Ala Glu Arg Arg Gln Arg						
		145		150		155
Gly Ala Gly Pro Leu Thr Leu Gln Ser Cys Asp Asn Leu Arg Ser Asn						
		165		170		175
Gly Ala Arg Phe Arg Ala Gly Met Arg Ala Phe Leu Ala Leu Arg Gly						
		180		185		190
Asp Ala Ala Leu Leu Ala Trp Phe Asp Ala Asn Val Ser Cys Pro Ser						
		195		200		205
Ala Met Val Asp Arg Ile Thr Pro Arg Pro Thr Asp Asp Val Arg Thr						
		210		215		220
Arg Val His Ala Ala Thr Gly Val Asp Asp Arg Cys Pro Val Met Gly						
		225		230		235
Glu Ser Phe Ile Gln Trp Val Ile Glu Asp Asn Phe Ile Ala Gly Arg						
		245		250		255
Pro Ala Trp Glu Ile Ala Gly Ala Glu Ile Val Ala Asp Val His Pro						

eolf-seql

260

265

270

Tyr Glu Glu Ala Lys Ile Arg Ile Leu Asn Ala Thr His Ser Cys Ile
275 280 285

Ala Trp Ala Gly Thr Leu Ala Gly Leu Thr Tyr Ile His Glu Gly Met
290 295 300

Arg Asp Ala Ala Ile Tyr Arg Phe Ala Tyr Asp Tyr Val Thr Asp Asp
305 310 315 320

Val Ile Pro Cys Leu Thr Pro Ser Pro Leu Asp Leu Glu Arg Tyr Arg
325 330 335

Asp Val Val Leu Glu Arg Phe Gly Asn Pro Tyr Val Leu Asp Thr Asn
340 345 350

Gln Arg Val Ala Ala Asp Gly Phe Ser Lys Ile Pro Gly Phe Ile Ala
355 360 365

Pro Thr Leu Ala Glu Cys Phe Ala Arg Gly Ala Asp Pro Val Ala Thr
370 375 380

Ala Val Leu Pro Ala Leu Phe Leu Gly Phe Leu Glu Gly Trp Ala Arg
385 390 395 400

Gly Thr Leu Pro Tyr Val Tyr Gln Asp Gly Val Met Asp Gly Ala Ala
405 410 415

Ala Arg Ser Ile Val Glu Ala Pro Asp Ser Val Ala Ala Phe Cys Ser
420 425 430

Asp Arg Gln Leu Trp Gly Ser Leu Ala Gly Arg Asp Ala Leu Val Gln
435 440 445

Ala Val Arg Ala Gly Arg Ala Arg Val Glu Ala Trp Arg Ala Ala Arg

450

455

eolf-seql
460

Arg
465