

SEQUENCE LISTING

<110> Ngee Ann Polytechnic

<120> D-PSICOSE PRODUCTION USING PROBIOTIC MICROORGANISMS

<130> P114208

<160> 4

<170> PatentIn version 3.5

<210> 1

<211> 289

<212> PRT

<213> Agrobacterium tumefaciens

<400> 1

Met Lys His Gly Ile Tyr Tyr Ser Tyr Trp Glu His Glu Trp Ser Ala
1 5 10 15

Lys Phe Gly Pro Tyr Ile Glu Lys Val Ala Lys Leu Gly Phe Asp Ile
20 25 30

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

Ala Thr Ile Arg Lys Ser Ala Lys Asp Asn Gly Ile Ile Leu Thr Ala
50 55 60

Gly Ile Gly Pro Ser Lys Thr Lys Asn Leu Ser Ser Glu Asp Ala Ala
65 70 75 80

Val Arg Ala Ala Gly Lys Ala Phe Phe Glu Arg Thr Leu Ser Asn Val
85 90 95

Ala Lys Leu Asp Ile His Thr Ile Gly Gly Ala Leu His Ser Tyr Trp
100 105 110

Pro Ile Asp Tyr Ser Gln Pro Val Asp Lys Ala Gly Asp Tyr Ala Arg
115 120 125

Gly Val Glu Gly Ile Asn Gly Ile Ala Asp Phe Ala Asn Asp Leu Gly
130 135 140

Ile Asn Leu Cys Ile Glu Val Leu Asn Arg Phe Glu Asn His Val Leu
145 150 155 160

Asn Thr Ala Ala Glu Gly Val Ala Phe Val Lys Asp Val Gly Lys Asn
165 170 175

Asn Val Lys Val Met Leu Asp Thr Phe His Met Asn Ile Glu Glu Asp
180 185 190

Ser Phe Gly Asp Ala Ile Arg Thr Ala Gly Pro Leu Leu Gly His Phe
195 200 205

His Thr Gly Glu Ser Asn Arg Arg Val Pro Gly Lys Gly Arg Met Pro
210 215 220

Trp His Glu Ile Gly Leu Ala Leu Arg Asp Ile Asn Tyr Thr Gly Ala
225 230 235 240

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

Ile Lys Val Trp Arg Asp Leu Ser Gly Gly Ala Asp Ile Ala Lys Met
260 265 270

Asp Glu Asp Ala Arg Asn Ala Leu Ala Phe Ser Arg Phe Val Leu Gly
275 280 285

Gly

<210> 2
<211> 289
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 2

Met Lys His Gly Ile Tyr Tyr Ser Tyr Trp Glu His Glu Trp Ser Ala
1 5 10 15

Lys Phe Gly Pro Tyr Ile Glu Lys Val Ala Lys Leu Gly Phe Asp Ile
20 25 30

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

Ala Thr Ile Arg Lys Ser Ala Lys Asp Asn Gly Ile Ile Leu Thr Ala
50 55 60

Gly Ile Gly Pro Ser Lys Thr Lys Asn Leu Ser Ser Glu Asp Ala Ala
65 70 75 80

Val Arg Ala Ala Gly Lys Ala Phe Phe Glu Arg Thr Leu Ser Asn Val
85 90 95

Ala Lys Leu Asp Ile His Thr Ile Gly Gly Ala Leu His Ser Tyr Trp
100 105 110

Pro Ile Asp Tyr Ser Gln Pro Val Asp Lys Ala Gly Asp Tyr Ala Arg
115 120 125

Gly Val Glu Gly Ile Asn Gly Ile Ala Asp Phe Ala Asn Asp Leu Gly
130 135 140

Ile Asn Leu Cys Ile Glu Val Leu Asn Arg Phe Glu Asn His Val Leu
145 150 155 160

Asn Thr Ala Ala Glu Gly Val Ala Phe Val Lys Asp Val Gly Lys Asn
165 170 175

Asn Val Lys Val Met Leu Asp Thr Phe His Met Asn Ile Glu Glu Asp
180 185 190

Ser Phe Gly Asp Ala Ile Arg Thr Ala Gly Pro Leu Leu Gly His Phe
195 200 205

His Thr Gly Glu Cys Asn Arg Arg Val Pro Gly Lys Gly Arg Met Pro
210 215 220

Trp His Glu Ile Gly Leu Ala Leu Arg Asp Ile Asn Tyr Thr Gly Ala

225		230		235		240									
Val	Ile	Met	Glu	Pro	Phe	Val	Lys	Thr	Gly	Gly	Thr	Ile	Gly	Ser	Asp
				245					250					255	

Ile	Lys	Val	Trp	Arg	Asp	Leu	Ser	Gly	Gly	Ala	Asp	Ile	Ala	Lys	Met
			260					265					270		

Asp	Glu	Asp	Ala	Arg	Asn	Ala	Leu	Ala	Phe	Ser	Arg	Phe	Val	Leu	Gly
		275					280					285			

Gly

<210> 3
 <211> 401
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 3

Met	Ser	Asp	Ser	Glu	Val	Asn	Gln	Glu	Ala	Lys	Pro	Glu	Val	Lys	Pro
1				5					10					15	

Glu	Val	Lys	Pro	Glu	Thr	His	Ile	Asn	Leu	Lys	Val	Ser	Asp	Gly	Ser
			20					25					30		

Ser	Glu	Ile	Phe	Phe	Lys	Ile	Lys	Lys	Thr	Thr	Pro	Leu	Arg	Arg	Leu
		35					40					45			

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

Phe	Leu	Tyr	Asp	Gly	Ile	Arg	Ile	Gln	Ala	Asp	Gln	Thr	Pro	Glu	Asp
65					70					75					80

Leu	Asp	Met	Glu	Asp	Asn	Asp	Ile	Ile	Glu	Ala	His	Arg	Glu	Gln	Ile
				85					90					95	

Gly	Gly	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
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100	105	110																	
Ser	Lys	His	Gly	Ile	Tyr	Tyr	Ser	Tyr	Trp	Glu	His	Glu	Trp	Ser	Ala				
	115						120					125							
Lys	Phe	Gly	Pro	Tyr	Ile	Glu	Lys	Val	Ala	Lys	Leu	Gly	Phe	Asp	Ile				
	130					135					140								
Leu	Glu	Val	Ala	Ala	His	His	Ile	Asn	Glu	Tyr	Ser	Asp	Ala	Glu	Leu				
145					150					155					160				
Ala	Thr	Ile	Arg	Lys	Ser	Ala	Lys	Asp	Asn	Gly	Ile	Ile	Leu	Thr	Ala				
				165					170					175					
Gly	Ile	Gly	Pro	Ser	Lys	Thr	Lys	Asn	Leu	Ser	Ser	Glu	Asp	Ala	Ala				
			180					185					190						
Val	Arg	Ala	Ala	Gly	Lys	Ala	Phe	Phe	Glu	Arg	Thr	Leu	Ser	Asn	Val				
	195						200					205							
Ala	Lys	Leu	Asp	Ile	His	Thr	Ile	Gly	Gly	Ala	Leu	His	Ser	Tyr	Trp				
	210					215					220								
Pro	Ile	Asp	Tyr	Ser	Gln	Pro	Val	Asp	Lys	Ala	Gly	Asp	Tyr	Ala	Arg				
225					230					235					240				
Gly	Val	Glu	Gly	Ile	Asn	Gly	Ile	Ala	Asp	Phe	Ala	Asn	Asp	Leu	Gly				
				245					250					255					
Ile	Asn	Leu	Cys	Ile	Glu	Val	Leu	Asn	Arg	Phe	Glu	Asn	His	Val	Leu				
			260					265					270						
Asn	Thr	Ala	Ala	Glu	Gly	Val	Ala	Phe	Val	Lys	Asp	Val	Gly	Lys	Asn				
		275					280					285							
Asn	Val	Lys	Val	Met	Leu	Asp	Thr	Phe	His	Met	Asn	Ile	Glu	Glu	Asp				
	290					295					300								
Ser	Phe	Gly	Asp	Ala	Ile	Arg	Thr	Ala	Gly	Pro	Leu	Leu	Gly	His	Phe				
305					310					315					320				

His Thr Gly Glu Cys Asn Arg Arg Val Pro Gly Lys Gly Arg Met Pro
325 330 335

Trp His Glu Ile Gly Leu Ala Leu Arg Asp Ile Asn Tyr Thr Gly Ala
340 345 350

Val Ile Met Glu Pro Phe Val Lys Thr Gly Gly Thr Ile Gly Ser Asp
355 360 365

Ile Lys Val Trp Arg Asp Leu Ser Gly Gly Ala Asp Ile Ala Lys Met
370 375 380

Asp Glu Asp Ala Arg Asn Ala Leu Ala Phe Ser Arg Phe Val Leu Gly
385 390 395 400

Gly

<210> 4
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 4

Met Ser Asp Ser Glu Val Asn Gln Glu Ala Lys Pro Glu Val Lys Pro
1 5 10 15

Glu Val Lys Pro Glu Thr His Ile Asn Leu Lys Val Ser Asp Gly Ser
20 25 30

Ser Glu Ile Phe Phe Lys Ile Lys Lys Thr Thr Pro Leu Arg Arg Leu
35 40 45

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

Phe Leu Tyr Asp Gly Ile Arg Ile Gln Ala Asp Gln Thr Pro Glu Asp
65 70 75 80

Leu Asp Met Glu Asp Asn Asp Ile Ile Glu Ala His Arg Glu Gln Ile
85 90 95

Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
100 105 110

Ser