

SEQUENCE LISTING

<110> Bayer BioScience NV
Universiteit Gent
Nagels, Bieke
Weterings, Koen

<120> Production of multi-antennary N-glycan structures in plants

<130> BCS 09-2001

<160> 48

<170> PatentIn version 3.3

<210> 1

<211> 96

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(96)

<400> 1

atg	agt	aaa	cgg	aat	ccg	aag	att	ctg	aag	att	ttt	ctg	tat	atg	tta	48
Met	Ser	Lys	Arg	Asn	Pro	Lys	Ile	Leu	Lys	Ile	Phe	Leu	Tyr	Met	Leu	
1				5				10					15			

ctt	ctc	aac	tct	ctc	ttt	ctc	atc	atc	tac	ttc	gtt	ttt	cac	tca	tcg	96
Leu	Leu	Asn	Ser	Leu	Phe	Leu	Ile	Ile	Tyr	Phe	Val	Phe	His	Ser	Ser	
			20					25					30			

<210> 2

<211> 32

<212> PRT

<213> Arabidopsis thaliana

<400> 2

Met	Ser	Lys	Arg	Asn	Pro	Lys	Ile	Leu	Lys	Ile	Phe	Leu	Tyr	Met	Leu
1				5				10					15		

Leu	Leu	Asn	Ser	Leu	Phe	Leu	Ile	Ile	Tyr	Phe	Val	Phe	His	Ser	Ser
			20					25					30		

<210> 3

<211> 186

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(186)

<400> 3

atg	ggt	gtt	ttc	tcg	aat	ctt	cga	gga	ccc	aga	gcc	gga	gct	acc	cac	48
Met	Gly	Val	Phe	Ser	Asn	Leu	Arg	Gly	Pro	Arg	Ala	Gly	Ala	Thr	His	
1				5				10					15			

gat	gaa	ttt	ccg	gcg	acc	aat	ggc	tct	cct	tcg	tct	tct	tct	tct	cca	96
Asp	Glu	Phe	Pro	Ala	Thr	Asn	Gly	Ser	Pro	Ser	Ser	Ser	Ser	Ser	Pro	
			20					25					30			

tct	tca	tca	atc	aag	cga	aaa	tta	tcg	aat	ttg	tta	cca	ctc	tgc	gtt	144
Ser	Ser	Ser	Ile	Lys	Arg	Lys	Leu	Ser	Asn	Leu	Leu	Pro	Leu	Cys	Val	
		35					40					45				

gct	ctg	gta	gtt	atc	gct	gag	atc	ggg	ttt	ctg	ggg	cgg	ctc			186
Ala	Leu	Val	Val	Ile	Ala	Glu	Ile	Gly	Phe	Leu	Gly	Arg	Leu			
	50					55					60					

<210> 4
 <211> 62
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 4

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

Asp	Glu	Phe	Pro	Ala	Thr	Asn	Gly	Ser	Pro	Ser	Ser	Ser	Ser	Ser	Pro
			20					25					30		

Ser	Ser	Ser	Ile	Lys	Arg	Lys	Leu	Ser	Asn	Leu	Leu	Pro	Leu	Cys	Val
		35					40					45			

Ala	Leu	Val	Val	Ile	Ala	Glu	Ile	Gly	Phe	Leu	Gly	Arg	Leu		
	50					55					60				

<210> 5
 <211> 1527
 <212> DNA
 <213> homo sapiens

<220>
 <221> CDS
 <222> (1)..(1527)

caa	aat	ggg	aaa	gaa	aaa	ctg	att	gct	tat	caa	cga	gaa	ttc	ctt	gct	48
Gln	Asn	Gly	Lys	Glu	Lys	Leu	Ile	Ala	Tyr	Gln	Arg	Glu	Phe	Leu	Ala	
1				5					10					15		

ttg	aaa	gaa	cgt	ctt	cga	ata	gct	gaa	cac	aga	atc	tca	cag	cgc	tct	96
Leu	Lys	Glu	Arg	Leu	Arg	Ile	Ala	Glu	His	Arg	Ile	Ser	Gln	Arg	Ser	
			20					25					30			

tct	gaa	tta	aat	acg	att	gtg	caa	cag	ttc	aag	cgt	gta	gga	gca	gaa	144
Ser	Glu	Leu	Asn	Thr	Ile	Val	Gln	Gln	Phe	Lys	Arg	Val	Gly	Ala	Glu	
		35				40						45				

aca	aat	gga	agt	aag	gat	gcg	ttg	aat	aag	ttt	tca	gat	aat	acc	cta	192
Thr	Asn	Gly	Ser	Lys	Asp	Ala	Leu	Asn	Lys	Phe	Ser	Asp	Asn	Thr	Leu	
	50					55					60					

aag	ctg	tta	aag	gag	tta	aca	agc	aaa	aaa	tct	ctt	caa	gtg	cca	agt	240
Lys	Leu	Leu	Lys	Glu	Leu	Thr	Ser	Lys	Lys	Ser	Leu	Gln	Val	Pro	Ser	
65					70					75					80	

att	tat	tat	cat	ttg	cct	cat	tta	ttg	aaa	aat	gaa	gga	agt	ctt	caa	288
Ile	Tyr	Tyr	His	Leu	Pro	His	Leu	Leu	Lys	Asn	Glu	Gly	Ser	Leu	Gln	
				85					90					95		

cct	gct	gta	cag	att	ggc	aac	gga	aga	aca	gga	gtt	tca	ata	gtc	atg	336
Pro	Ala	Val	Gln	Ile	Gly	Asn	Gly	Arg	Thr	Gly	Val	Ser	Ile	Val	Met	

100				105				110								
ggc Gly	att Ile	ccc Pro 115	aca Thr	gtg Val	aag Lys	aga Arg	gaa Glu 120	gtt Val	aaa Lys	tct Ser	tac Tyr	ctc Leu 125	ata Ile	gaa Glu	act Thr	384
ctt Leu	cat His 130	tcc Ser	ctt Leu	att Ile	gat Asp	aac Asn 135	ctg Leu	tat Tyr	cct Pro	gaa Glu	gag Glu 140	aag Lys	ttg Leu	gac Asp	tgt Cys	432
gtt Val 145	ata Ile	gta Val	gtc Val	ttc Phe	ata Ile 150	gga Gly	gag Glu	aca Thr	gat Asp	att Ile 155	gat Asp	tat Tyr	gta Val	cat His	ggc Gly 160	480
gtt Val	gta Val	gcc Ala	aac Asn	ctg Leu 165	gag Glu	aaa Lys	gaa Glu	ttt Phe	tct Ser 170	aaa Lys	gaa Glu	atc Ile	agt Ser	tct Ser 175	ggc Gly	528
ttg Leu	gtg Val	gaa Glu	gtc Val 180	ata Ile	tca Ser	ccc Pro	cct Pro	gaa Glu 185	agc Ser	tat Tyr	tat Tyr	cct Pro	gac Asp 190	ttg Leu	aca Thr	576
aac Asn	cta Leu	aag Lys 195	gag Glu	aca Thr	ttt Phe	gga Gly	gac Asp 200	tcc Ser	aaa Lys	gaa Glu	aga Arg	gta Val 205	aga Arg	tggt Trp	aga Arg	624
aca Thr	aag Lys 210	caa Gln	aac Asn	cta Leu	gat Asp	tac Tyr 215	tgt Cys	ttt Phe	cta Leu	atg Met	atg Met 220	tat Tyr	gct Ala	caa Gln	gaa Glu	672
aag Lys 225	ggc Gly	ata Ile	tat Tyr	tac Tyr	att Ile 230	cag Gln	ctt Leu	gaa Glu	gat Asp	gat Asp 235	att Ile	att Ile	gtc Val	aaa Lys	caa Gln 240	720
aat Asn	tat Tyr	ttt Phe	aat Asn	acc Thr 245	ata Ile	aaa Lys	aat Asn	ttt Phe	gca Ala 250	ctt Leu	caa Gln	ctt Leu	tct Ser	tct Ser 255	gag Glu	768
gaa Glu	tggt Trp	atg Met	att Ile 260	cta Leu	gag Glu	ttt Phe	tcc Ser	cag Gln 265	ctg Leu	ggc Gly	ttc Phe	att Ile	ggc Gly 270	aaa Lys	atg Met	816
ttt Phe	caa Gln	gcg Ala 275	ccg Pro	gat Asp	ctt Leu	act Thr	ctg Leu 280	att Ile	gta Val	gaa Glu	ttc Phe	ata Ile 285	ttc Phe	atg Met	ttt Phe	864
tac Tyr	aag Lys 290	gag Glu	aaa Lys	ccc Pro	att Ile	gat Asp 295	tggt Trp	ctc Leu	ctg Leu	gac Asp	cat His 300	att Ile	ctc Leu	tggt Trp	gtg Val	912
aaa Lys 305	gtc Val	tcg Cys	aac Asn	cct Pro	gaa Glu 310	aaa Lys	gat Asp	gca Ala	aaa Lys	cat His 315	tgt Cys	gat Asp	aga Arg	cag Gln	aaa Lys 320	960
gca Ala	aat Asn	ctg Leu	cga Arg	att Ile 325	cgc Arg	ttc Phe	aga Arg	cct Pro	tcc Ser 330	ctt Leu	ttc Phe	caa Gln	cat His	gtt Val 335	ggc Gly	1008
ctg Leu	cac His	tca Ser	tca Ser 340	cta Leu	tca Ser	gga Gly	aaa Lys	atc Ile 345	caa Gln	aaa Lys	ctc Leu	acg Thr	gat Asp 350	aaa Lys	gat Asp	1056
tat Tyr	atg Met	aaa Lys 355	cca Pro	tta Leu	ctt Leu	ctt Leu	aaa Lys 360	atc Ile	cat His	gta Val	aac Asn	cca Pro 365	cct Pro	gcg Ala	gag Glu	1104
gta Val	tct Ser 370	act Thr	tcc Ser	ttg Leu	aag Lys	gtc Val 375	tac Tyr	caa Gln	ggg Gly	cat His	acg Thr 380	ctg Leu	gag Glu	aaa Lys	act Thr	1152

tac atg gga gag gat ttc ttc tgg gct atc aca ccg ata gct gga gac	1200
Tyr Met Gly Glu Asp Phe Phe Trp Ala Ile Thr Pro Ile Ala Gly Asp	
385 390 395 400	
tac atc ttg ttt aaa ttt gat aaa cca gtc aat gta gaa agt tat ttg	1248
Tyr Ile Leu Phe Lys Phe Asp Lys Pro Val Asn Val Glu Ser Tyr Leu	
405 410 415	
ttc cat agc ggc aac caa gaa cat cct gga gat att ctg cta aac aca	1296
Phe His Ser Gly Asn Gln Glu His Pro Gly Asp Ile Leu Leu Asn Thr	
420 425 430	
act gtg gaa gtt ttg cct ttt aag agt gaa ggt ttg gaa ata agc aaa	1344
Thr Val Glu Val Leu Pro Phe Lys Ser Glu Gly Leu Glu Ile Ser Lys	
435 440 445	
gaa acc aaa gac aaa cga tta gaa gat ggc tat ttc aga ata gga aaa	1392
Glu Thr Lys Asp Lys Arg Leu Glu Asp Gly Tyr Phe Arg Ile Gly Lys	
450 455 460	
ttt gag aat ggt gtt gca gaa gga atg gtg gat cca agt ctc aat ccc	1440
Phe Glu Asn Gly Val Ala Glu Gly Met Val Asp Pro Ser Leu Asn Pro	
465 470 475 480	
att tca gcc ttt cga ctt tca gtt att cag aat tct gct gtt tgg gcc	1488
Ile Ser Ala Phe Arg Leu Ser Val Ile Gln Asn Ser Ala Val Trp Ala	
485 490 495	
att ctt aat gag att cat att aaa aaa gcc acc aac tga	1527
Ile Leu Asn Glu Ile His Ile Lys Lys Ala Thr Asn	
500 505	

<210> 6
 <211> 508
 <212> PRT
 <213> homo sapiens

<400> 6

Gln Asn Gly Lys Glu Lys Leu Ile Ala Tyr Gln Arg Glu Phe Leu Ala
1 5 10 15
Leu Lys Glu Arg Leu Arg Ile Ala Glu His Arg Ile Ser Gln Arg Ser
20 25 30
Ser Glu Leu Asn Thr Ile Val Gln Gln Phe Lys Arg Val Gly Ala Glu
35 40 45
Thr Asn Gly Ser Lys Asp Ala Leu Asn Lys Phe Ser Asp Asn Thr Leu
50 55 60
Lys Leu Leu Lys Glu Leu Thr Ser Lys Lys Ser Leu Gln Val Pro Ser
65 70 75 80
Ile Tyr Tyr His Leu Pro His Leu Leu Lys Asn Glu Gly Ser Leu Gln
85 90 95
Pro Ala Val Gln Ile Gly Asn Gly Arg Thr Gly Val Ser Ile Val Met
100 105 110

Gly Ile Pro Thr Val Lys Arg Glu Val Lys Ser Tyr Leu Ile Glu Thr
 115 120 125
 Leu His Ser Leu Ile Asp Asn Leu Tyr Pro Glu Glu Lys Leu Asp Cys
 130 135 140
 Val Ile Val Val Phe Ile Gly Glu Thr Asp Ile Asp Tyr Val His Gly
 145 150 155 160
 Val Val Ala Asn Leu Glu Lys Glu Phe Ser Lys Glu Ile Ser Ser Gly
 165 170 175
 Leu Val Glu Val Ile Ser Pro Pro Glu Ser Tyr Tyr Pro Asp Leu Thr
 180 185 190
 Asn Leu Lys Glu Thr Phe Gly Asp Ser Lys Glu Arg Val Arg Trp Arg
 195 200 205
 Thr Lys Gln Asn Leu Asp Tyr Cys Phe Leu Met Met Tyr Ala Gln Glu
 210 215 220
 Lys Gly Ile Tyr Tyr Ile Gln Leu Glu Asp Asp Ile Ile Val Lys Gln
 225 230 235 240
 Asn Tyr Phe Asn Thr Ile Lys Asn Phe Ala Leu Gln Leu Ser Ser Glu
 245 250 255
 Glu Trp Met Ile Leu Glu Phe Ser Gln Leu Gly Phe Ile Gly Lys Met
 260 265 270
 Phe Gln Ala Pro Asp Leu Thr Leu Ile Val Glu Phe Ile Phe Met Phe
 275 280 285
 Tyr Lys Glu Lys Pro Ile Asp Trp Leu Leu Asp His Ile Leu Trp Val
 290 295 300
 Lys Val Cys Asn Pro Glu Lys Asp Ala Lys His Cys Asp Arg Gln Lys
 305 310 315 320
 Ala Asn Leu Arg Ile Arg Phe Arg Pro Ser Leu Phe Gln His Val Gly
 325 330 335
 Leu His Ser Ser Leu Ser Gly Lys Ile Gln Lys Leu Thr Asp Lys Asp
 340 345 350
 Tyr Met Lys Pro Leu Leu Leu Lys Ile His Val Asn Pro Pro Ala Glu
 355 360 365
 Val Ser Thr Ser Leu Lys Val Tyr Gln Gly His Thr Leu Glu Lys Thr
 370 375 380
 Tyr Met Gly Glu Asp Phe Phe Trp Ala Ile Thr Pro Ile Ala Gly Asp

385 390 395 400
 Tyr Ile Leu Phe Lys Phe Asp Lys Pro Val Asn Val Glu Ser Tyr Leu
 405 410 415
 Phe His Ser Gly Asn Gln Glu His Pro Gly Asp Ile Leu Leu Asn Thr
 420 425 430
 Thr Val Glu Val Leu Pro Phe Lys Ser Glu Gly Leu Glu Ile Ser Lys
 435 440 445
 Glu Thr Lys Asp Lys Arg Leu Glu Asp Gly Tyr Phe Arg Ile Gly Lys
 450 455 460
 Phe Glu Asn Gly Val Ala Glu Gly Met Val Asp Pro Ser Leu Asn Pro
 465 470 475 480
 Ile Ser Ala Phe Arg Leu Ser Val Ile Gln Asn Ser Ala Val Trp Ala
 485 490 495
 Ile Leu Asn Glu Ile His Ile Lys Lys Ala Thr Asn
 500 505

<210> 7
 <211> 1548
 <212> DNA
 <213> homo sapiens

<220>
 <221> CDS
 <222> (1)..(1548)

<400> 7	
gac gtt gtg gac gtt tac cag cgg gag ttc ctg gcg ctg cgc gat cgg	48
Asp Val Val Asp Val Tyr Gln Arg Glu Phe Leu Ala Leu Arg Asp Arg	
1 5 10 15	
ttg cac gca gct gag cag gag agc ctc aag cgc tcc aag gag ctc aac	96
Leu His Ala Ala Glu Gln Glu Ser Leu Lys Arg Ser Lys Glu Leu Asn	
20 25 30	
ctg gtg ctg gac gag atc aag agg gcc gtg tca gaa agg cag gcg ctg	144
Leu Val Leu Asp Glu Ile Lys Arg Ala Val Ser Glu Arg Gln Ala Leu	
35 40 45	
cga gac gga gac ggc aat cgc acc tgg ggc cgc cta aca gag gac ccc	192
Arg Asp Gly Asp Gly Asn Arg Thr Trp Gly Arg Leu Thr Glu Asp Pro	
50 55 60	
cga ttg aag ccg tgg aac ggc tca cac cgg cac gtg ctg cac ctg ccc	240
Arg Leu Lys Pro Trp Asn Gly Ser His Arg His Val Leu His Leu Pro	
65 70 75 80	
acc gtc ttc cat cac ctg cca cac ctg ctg gcc aag gag agc agt ctg	288
Thr Val Phe His His Leu Pro His Leu Leu Ala Lys Glu Ser Ser Leu	
85 90 95	
cag ccc gcg gtg cgc gtg ggc cag ggc cgc acc gga gtg tcg gtg gtg	336
Gln Pro Ala Val Arg Val Gly Gln Gly Arg Thr Gly Val Ser Val Val	
100 105 110	

atg ggc atc ccg agc gtg cgg cgc gag gtg cac tcg tac ctg act gac Met Gly Ile Pro Ser Val Arg Arg Glu Val His Ser Tyr Leu Thr Asp 115 120 125	384
act ctg cac tcg ctc atc tcc gag ctg agc ccg cag gag aag gag gac Thr Leu His Ser Leu Ile Ser Glu Leu Ser Pro Gln Glu Lys Glu Asp 130 135 140	432
tcg gtc atc gtg gtg ctg atc gcc gag act gac tca cag tac act tcg Ser Val Ile Val Val Leu Ile Ala Glu Thr Asp Ser Gln Tyr Thr Ser 145 150 155 160	480
gca gtg aca gag aac atc aag gcc ttg ttc ccc acg gag atc cat tct Ala Val Thr Glu Asn Ile Lys Ala Leu Phe Pro Thr Glu Ile His Ser 165 170 175	528
ggg ctc ctg gag gtc atc tca ccc tcc ccc cac ttc tac cct gac ttc Gly Leu Leu Glu Val Ile Ser Pro Ser Pro His Phe Tyr Pro Asp Phe 180 185 190	576
tcc cgc ctc cga gag tcc ttt ggg gag ccc aag gag aga gtc agg tgg Ser Arg Leu Arg Glu Ser Phe Gly Asp Pro Lys Glu Arg Val Arg Trp 195 200 205	624
agg acc aaa cag aac ctc gat tac tgc ttc ctc atg atg tac gcg cag Arg Thr Lys Gln Asn Leu Asp Tyr Cys Phe Leu Met Met Tyr Ala Gln 210 215 220	672
tcc aaa ggc atc tac tac gtg cag ctg gag gat gac atc gtg gcc aag Ser Lys Gly Ile Tyr Tyr Val Gln Leu Glu Asp Asp Ile Val Ala Lys 225 230 235 240	720
ccc aac tac ctg agc acc atg aag aac ttt gca ctg cag cag cct tca Pro Asn Tyr Leu Ser Thr Met Lys Asn Phe Ala Leu Gln Gln Pro Ser 245 250 255	768
gag gac tgg atg atc ctg gag ttc tcc cag ctg ggc ttc att ggt aag Glu Asp Trp Met Ile Leu Glu Phe Ser Gln Leu Gly Phe Ile Gly Lys 260 265 270	816
atg ttc aag tcg ctg gac ctg agc ctg att gta gag ttc att ctc atg Met Phe Lys Ser Leu Asp Leu Ser Leu Ile Val Glu Phe Ile Leu Met 275 280 285	864
ttc tac cgg gac aag ccc atc gac tgg ctc ctg gac cat att ctg tgg Phe Tyr Arg Asp Lys Pro Ile Asp Trp Leu Leu Asp His Ile Leu Trp 290 295 300	912
gtg aaa gtc tgc aac ccc gag aag gat gcg aag cac tgt gac cgg cag Val Lys Val Cys Asn Pro Glu Lys Asp Ala Lys His Cys Asp Arg Gln 305 310 315 320	960
aaa gcc aac ctg cgg atc cgc ttc aaa ccg tcc ctc ttc cag cac gtg Lys Ala Asn Leu Arg Ile Arg Phe Lys Pro Ser Leu Phe Gln His Val 325 330 335	1008
ggc act cac tcc tcg ctg gct ggc aag atc cag aaa ctg aag gac aaa Gly Thr His Ser Ser Leu Ala Gly Lys Ile Gln Lys Leu Lys Asp Lys 340 345 350	1056
gac ttt gga aag cag gcg ctg cgg aag gag cat gtg aac ccg cca gca Asp Phe Gly Lys Gln Ala Leu Arg Lys Glu His Val Asn Pro Pro Ala 355 360 365	1104
gag gtg agc acg agc ctg aag aca tac cag cac ttc acc ctg gag aaa Glu Val Ser Thr Ser Leu Lys Thr Tyr Gln His Phe Thr Leu Glu Lys 370 375 380	1152

gcc Ala 385	tac Tyr	ctg Leu	cgc Arg	gag Glu	gac Asp 390	ttc Phe	ttc Phe	tgg Trp	gcc Ala	ttc Phe 395	acc Thr	cct Pro	gcc Ala	gcg Ala	ggg Gly 400	1200
gac Asp	ttc Phe	atc Ile	cgc Arg	ttc Phe 405	cgc Arg	ttc Phe	ttc Phe	caa Gln	cct Pro 410	cta Leu	aga Arg	ctg Leu	gag Glu	cgg Arg 415	ttc Phe	1248
ttc Phe	ttc Phe	cgc Arg	agt Ser 420	ggg Gly	aac Asn	atc Ile	gag Glu	cac His 425	ccg Pro	gag Glu	gac Asp	aag Lys	ctc Leu 430	ttc Phe	aac Asn	1296
acg Thr	tct Ser	gtg Val 435	gag Glu	gtg Val	ctg Leu	ccc Pro	ttc Phe 440	gac Asp	aac Asn	cct Pro	cag Gln	tca Ser 445	gac Asp	aag Lys	gag Glu	1344
gcc Ala 450	ctg Leu	cag Gln	gag Glu	ggc Gly	cgc Arg	acc Thr 455	gcc Ala	acc Thr	ctc Leu	cgg Arg	tac Tyr 460	cct Pro	cgg Arg	agc Ser	ccc Pro	1392
gac Asp 465	ggc Gly	tac Tyr	ctc Leu	cag Gln	atc Ile 470	ggc Gly	tcc Ser	ttc Phe	tac Tyr	aag Lys 475	gga Gly	gtg Val	gca Ala	gag Glu	gga Gly 480	1440
gag Glu	gtg Val	gac Asp	cca Pro	gcc Ala 485	ttc Phe	ggc Gly	cct Pro	ctg Leu	gaa Glu 490	gca Ala	ctg Leu	cgc Arg	ctc Leu	tcg Ser 495	atc Ile	1488
cag Gln	acg Thr	gac Asp	tcc Ser 500	cct Pro	gtg Val	tgg Trp	gtg Val	att Ile 505	ctg Leu	agc Ser	gag Glu	atc Ile	ttc Phe 510	ctg Leu	aaa Lys	1536
aag Lys	gcc Ala	gac Asp 515	taa													1548

<210> 8
 <211> 515
 <212> PRT
 <213> homo sapiens

<400> 8

Asp 1	Val	Val	Asp	Val	Tyr	Gln	Arg	Glu	Phe	Leu	Ala	Leu	Arg	Asp 15	Arg
Leu	His	Ala	Ala 20	Glu	Gln	Glu	Ser	Leu 25	Lys	Arg	Ser	Lys	Glu 30	Leu	Asn
Leu	Val	Leu 35	Asp	Glu	Ile	Lys	Arg	Ala 40	Val	Ser	Glu	Arg 45	Gln	Ala	Leu
Arg	Asp 50	Gly	Asp	Gly	Asn	Arg 55	Thr	Trp	Gly	Arg	Leu 60	Thr	Glu	Asp	Pro
Arg 65	Leu	Lys	Pro	Trp	Asn 70	Gly	Ser	His	Arg	His 75	Val	Leu	His	Leu	Pro 80
Thr	Val	Phe	His	His 85	Leu	Pro	His	Leu	Leu 90	Ala	Lys	Glu	Ser	Ser 95	Leu
Gln	Pro	Ala	Val	Arg	Val	Gly	Gln	Gly	Arg	Thr	Gly	Val	Ser	Val	Val

100					105					110					
Met	Gly	Ile	Pro	Ser	Val	Arg	Arg	Glu	Val	His	Ser	Tyr	Leu	Thr	Asp
		115					120					125			
Thr	Leu	His	Ser	Leu	Ile	Ser	Glu	Leu	Ser	Pro	Gln	Glu	Lys	Glu	Asp
	130					135					140				
Ser	Val	Ile	Val	Val	Leu	Ile	Ala	Glu	Thr	Asp	Ser	Gln	Tyr	Thr	Ser
145					150					155					160
Ala	Val	Thr	Glu	Asn	Ile	Lys	Ala	Leu	Phe	Pro	Thr	Glu	Ile	His	Ser
				165					170					175	
Gly	Leu	Leu	Glu	Val	Ile	Ser	Pro	Ser	Pro	His	Phe	Tyr	Pro	Asp	Phe
			180					185					190		
Ser	Arg	Leu	Arg	Glu	Ser	Phe	Gly	Asp	Pro	Lys	Glu	Arg	Val	Arg	Trp
		195					200					205			
Arg	Thr	Lys	Gln	Asn	Leu	Asp	Tyr	Cys	Phe	Leu	Met	Met	Tyr	Ala	Gln
	210					215					220				
Ser	Lys	Gly	Ile	Tyr	Tyr	Val	Gln	Leu	Glu	Asp	Asp	Ile	Val	Ala	Lys
225					230					235					240
Pro	Asn	Tyr	Leu	Ser	Thr	Met	Lys	Asn	Phe	Ala	Leu	Gln	Gln	Pro	Ser
				245					250					255	
Glu	Asp	Trp	Met	Ile	Leu	Glu	Phe	Ser	Gln	Leu	Gly	Phe	Ile	Gly	Lys
			260					265					270		
Met	Phe	Lys	Ser	Leu	Asp	Leu	Ser	Leu	Ile	Val	Glu	Phe	Ile	Leu	Met
		275					280					285			
Phe	Tyr	Arg	Asp	Lys	Pro	Ile	Asp	Trp	Leu	Leu	Asp	His	Ile	Leu	Trp
	290					295					300				
Val	Lys	Val	Cys	Asn	Pro	Glu	Lys	Asp	Ala	Lys	His	Cys	Asp	Arg	Gln
305					310					315					320
Lys	Ala	Asn	Leu	Arg	Ile	Arg	Phe	Lys	Pro	Ser	Leu	Phe	Gln	His	Val
				325					330					335	
Gly	Thr	His	Ser	Ser	Leu	Ala	Gly	Lys	Ile	Gln	Lys	Leu	Lys	Asp	Lys
			340					345					350		
Asp	Phe	Gly	Lys	Gln	Ala	Leu	Arg	Lys	Glu	His	Val	Asn	Pro	Pro	Ala
		355					360					365			
Glu	Val	Ser	Thr	Ser	Leu	Lys	Thr	Tyr	Gln	His	Phe	Thr	Leu	Glu	Lys
	370					375					380				

Ala Tyr Leu Arg Glu Asp Phe Phe Trp Ala Phe Thr Pro Ala Ala Gly
385 390 395 400

Asp Phe Ile Arg Phe Arg Phe Phe Gln Pro Leu Arg Leu Glu Arg Phe
405 410 415

Phe Phe Arg Ser Gly Asn Ile Glu His Pro Glu Asp Lys Leu Phe Asn
420 425 430

Thr Ser Val Glu Val Leu Pro Phe Asp Asn Pro Gln Ser Asp Lys Glu
435 440 445

Ala Leu Gln Glu Gly Arg Thr Ala Thr Leu Arg Tyr Pro Arg Ser Pro
450 455 460

Asp Gly Tyr Leu Gln Ile Gly Ser Phe Tyr Lys Gly Val Ala Glu Gly
465 470 475 480

Glu Val Asp Pro Ala Phe Gly Pro Leu Glu Ala Leu Arg Leu Ser Ile
485 490 495

Gln Thr Asp Ser Pro Val Trp Val Ile Leu Ser Glu Ile Phe Leu Lys
500 505 510

Lys Ala Asp
515

<210> 9
<211> 2109
<212> DNA
<213> Artificial

<220>
<223> catalytic domain of Homo sapiens Gnt-Va sequence which is codon
optimized for Nicotiana benthamiana

<220>
<221> CDS
<222> (1)..(2109)

<400> 9
cct gag tca tct tct atg ctc aga gag cag atc ctt gat ctc tct aag 48
Pro Glu Ser Ser Ser Met Leu Arg Glu Gln Ile Leu Asp Leu Ser Lys
1 5 10 15

aga tat atc aag gct ctc gct gaa gag aac aga aac gtg gtg gat gga 96
Arg Tyr Ile Lys Ala Leu Ala Glu Asn Arg Asn Val Val Asp Gly
20 25 30

cct tat gct ggt gtt atg act gct tac gat ctc aag aaa act ctt gct 144
Pro Tyr Ala Gly Val Met Thr Ala Tyr Asp Leu Lys Lys Thr Leu Ala
35 40 45

gtg ctc ctc gat aac atc ctt cag aga atc gga aag ctc gag tct aaa 192
Val Leu Leu Asp Asn Ile Leu Gln Arg Ile Gly Lys Leu Glu Ser Lys
50 55 60

gtg Val 65	gat Asp	aac Asn	ctc Leu	gtg Val 70	gtt Val 75	aac Asn	gga Gly	act Thr	gga Gly	act Thr 75	aac Asn	tct Ser	aca Thr	aac Asn	tct Ser 80	240
act Thr	act Thr	gct Ala	gtg Val	cct Pro 85	tct Ser	ctt Leu	gtt Val	gct Ala	ctc Leu 90	gag Glu	aag Lys	atc Ile	aac Asn	gtg Val 95	gct Ala	288
gat Asp	atc Ile	atc Ile	aat Asn 100	ggt Gly	gct Ala	caa Gln	gag Glu	aag Lys 105	tgt Cys	gtt Val	ctc Leu	cct Pro	cct Pro 110	atg Met	gat Asp	336
gga Gly	tat Tyr	cct Pro 115	cac His	tgt Cys	gag Glu	gga Gly	aag Lys 120	atc Ile	aag Lys	tgg Trp	atg Met	aag Lys 125	gat Asp	atg Met	tgg Trp	384
aga Arg 130	tct Ser	gat Asp	cct Pro	tgc Cys	tac Tyr	gct Ala 135	gat Asp	tac Tyr	ggt Gly	gtt Val	gat Asp 140	gga Gly	tct Ser	act Thr	tgc Cys	432
tct Ser 145	ttc Phe	ttc Phe	atc Ile	tac Tyr	ctc Leu 150	tca Ser	gag Glu	gtt Val	gaa Glu	aac Asn 155	tgg Trp	tgt Cys	cct Pro	cat His	ctt Leu 160	480
cct Pro	tgg Trp	aga Arg	gct Ala	aag Lys 165	aac Asn	cct Pro	tac Tyr	gaa Glu	gag Glu 170	gct Ala	gat Asp	cac His	aat Asn	tct Ser 175	ctc Leu	528
gct Ala	gag Glu	atc Ile	aga Arg 180	aca Thr	gat Asp	ttc Phe	aac Asn	atc Ile 185	ctc Leu	tac Tyr	tct Ser	atg Met	atg Met 190	aag Lys	aag Lys	576
cac His	gaa Glu	gag Glu 195	ttc Phe	aga Arg	tgg Trp	atg Met	aga Arg 200	ctc Leu	aga Arg	atc Ile	aga Arg	aga Arg 205	atg Met	gct Ala	gac Asp	624
gct Ala	tgg Trp 210	ata Ile	caa Gln	gca Ala	atc Ile	aag Lys 215	tca Ser	ctt Leu	gct Ala	gag Glu	aag Lys 220	cag Gln	aac Asn	ctc Leu	gag Glu	672
aag Lys 225	aga Arg	aag Lys	aga Arg	aag Lys	aag Lys 230	gtt Val	ctc Leu	gtt Val	cat His	ctt Leu 235	gga Gly	ctc Leu	ctc Leu	aca Thr	aaa Lys 240	720
gag Glu	tct Ser	gga Gly	ttc Phe	aag Lys 245	atc Ile	gct Ala	gag Glu	act Thr	gct Ala 250	ttt Phe	tct Ser	ggt Gly	gga Gly	cct Pro 255	ctt Leu	768
gga Gly	gaa Glu	ctt Leu	gtt Val 260	cag Gln	tgg Trp	agt Ser	gat Asp	ctc Leu 265	atc Ile	act Thr	tca Ser	ctc Leu	tac Tyr 270	ctc Leu	ctc Leu	816
gga Gly	cac His	gat Asp 275	att Ile	aga Arg	atc Ile	tct Ser	gct Ala 280	tct Ser	ctc Leu	gca Ala	gag Glu	ctt Leu 285	aaa Lys	gaa Glu	atc Ile	864
atg Met	aag Lys 290	aaa Lys	gtg Val	gtg Val	ggt Gly	aac Asn 295	aga Arg	tct Ser	gga Gly	tgt Cys	cct Pro 300	act Thr	gtg Val	gga Gly	gat Asp	912
aga Arg 305	atc Ile	gtg Val	gag Glu	ctt Leu	atc Ile 310	tac Tyr	atc Ile	gat Asp	atc Ile	gtg Val 315	ggt Gly	ctt Leu	gct Ala	cag Gln	ttc Phe 320	960
aaa Lys	aag Lys	act Thr	ctc Leu	gga Gly 325	cct Pro	tct Ser	tgg Trp	gtt Val	cac His 330	tac Tyr	cag Gln	tgc Cys	atg Met	ctt Leu 335	aga Arg	1008
gtg	ctc	gat	tct	ttc	gga	act	gag	cct	gag	ttt	aac	cac	gct	aac	tac	1056

Val	Leu	Asp	Ser 340	Phe	Gly	Thr	Glu	Pro 345	Glu	Phe	Asn	His	Ala 350	Asn	Tyr	
gct Ala	caa Gln	tct Ser 355	aag Lys	gga Gly	cat His	aag Lys	aca Thr 360	cct Pro	tgg Trp	gga Gly	aag Lys	tgg Trp 365	aac Asn	ctt Leu	aac Asn	1104
cct Pro	cag Gln 370	cag Gln	ttc Phe	tac Tyr	act Thr	atg Met 375	ttc Phe	cct Pro	cac His	act Thr	cct Pro 380	gat Asp	aac Asn	tca Ser	ttc Phe	1152
ctc Leu 385	gga Gly	ttc Phe	gtt Val	gtt Val	gag Glu 390	cag Gln	cac His	ctc Leu	aac Asn	tct Ser 395	tca Ser	gat Asp	atc Ile	cac His	cac His 400	1200
atc Ile	aac Asn	gag Glu	atc Ile	aag Lys 405	aga Arg	cag Gln	aac Asn	cag Gln	tct Ser 410	ctt Leu	gtg Val	tac Tyr	gga Gly	aaa Lys 415	gtg Val	1248
gat Asp	tct Ser	ttc Phe	tgg Trp 420	aag Lys	aac Asn	aag Lys	aag Lys	atc Ile 425	tac Tyr	ctc Leu	gat Asp	atc Ile	atc Ile 430	cac His	act Thr	1296
tac Tyr	atg Met	gaa Glu 435	gtt Val	cac His	gct Ala	act Thr	gtg Val 440	tac Tyr	gga Gly	tct Ser	tct Ser	act Thr 445	aag Lys	aac Asn	atc Ile	1344
cct Pro	tct Ser 450	tac Tyr	gtg Val	aag Lys	aac Asn	cac His 455	gga Gly	atc Ile	ctc Leu	tca Ser	gga Gly 460	aga Arg	gat Asp	ctt Leu	cag Gln	1392
ttc Phe 465	ctc Leu	ctc Leu	aga Arg	gag Glu	act Thr 470	aag Lys	ctc Leu	ttc Phe	gtt Val	ggt Gly 475	ctt Leu	gga Gly	ttt Phe	cct Pro	tat Tyr 480	1440
gag Glu	gga Gly	cct Pro	gct Ala	cct Pro 485	ctt Leu	gaa Glu	gct Ala	atc Ile	gct Ala 490	aac Asn	gga Gly	tgt Cys	gct Ala	ttc Phe 495	ctc Leu	1488
aac Asn	cct Pro	aag Lys	ttc Phe 500	aac Asn	cct Pro	cct Pro	aag Lys	tca Ser 505	tct Ser	aag Lys	aac Asn	act Thr	gat Asp 510	ttc Phe	ttc Phe	1536
atc Ile	gga Gly	aag Lys 515	cct Pro	act Thr	ctc Leu	aga Arg	gag Glu 520	ctt Leu	act Thr	tct Ser	cag Gln	cat His 525	cct Pro	tac Tyr	gct Ala	1584
gag Glu	gtt Val 530	ttc Phe	atc Ile	ggt Gly	aga Arg	cct Pro 535	cat His	gtt Val	tgg Trp	act Thr	gtg Val 540	gat Asp	ctc Leu	aac Asn	aac Asn	1632
cag Gln 545	gaa Glu	gag Glu	gtt Val	gag Glu	gac Asp 550	gct Ala	gtt Val	aag Lys	gct Ala	atc Ile 555	ctc Leu	aac Asn	cag Gln	aaa Lys	atc Ile 560	1680
gaa Glu	cct Pro	tac Tyr	atg Met	cct Pro 565	tac Tyr	gag Glu	ttc Phe	act Thr	tgt Cys 570	gag Glu	gga Gly	atg Met	ctc Leu	cag Gln 575	agg Arg	1728
atc Ile	aac Asn	gct Ala	ttc Phe 580	atc Ile	gag Glu	aag Lys	cag Gln	gat Asp 585	ttc Phe	tgt Cys	cat His	gga Gly	cag Gln 590	gtt Val	atg Met	1776
tgg Trp	cct Pro	cct Pro 595	ctt Leu	tct Ser	gct Ala	ctt Leu	cag Gln 600	gtt Val	aag Lys	ctt Leu	gct Ala	gaa Glu 605	cct Pro	gga Gly	caa Gln	1824
tct Ser	tgc Cys	aag Lys	caa Gln	gtg Val	tgc Cys	caa Gln	gag Glu	tct Ser	cag Gln	ctt Leu	atc Ile	tgc Cys	gag Glu	cct Pro	tct Ser	1872

610	615	620	
ttc ttc cag cat ctc aac aag gat aag gat atg ctc aag tac aag gtg Phe Phe Gln His Leu Asn Lys Asp Lys Asp Met Leu Lys Tyr Lys Val 625 630 635 640			1920
aca tgc cag tca tct gag ctt gct aag gat atc ctc gtg cct tct ttc Thr Cys Gln Ser Ser Glu Leu Ala Lys Asp Ile Leu Val Pro Ser Phe 645 650 655			1968
gat cct aag aac aag cac tgt gtg ttc cag ggt gat ctt ctt ctt ttc Asp Pro Lys Asn Lys His Cys Val Phe Gln Gly Asp Leu Leu Leu Phe 660 665 670			2016
tct tgc gct ggt gct cat cct aga cat cag aga gtt tgc cct tgc aga Ser Cys Ala Gly Ala His Pro Arg His Gln Arg Val Cys Pro Cys Arg 675 680 685			2064
gat ttc atc aag gga caa gtg gct ctc tgt aag gat tgc ctc tga Asp Phe Ile Lys Gly Gln Val Ala Leu Cys Lys Asp Cys Leu 690 695 700			2109

<210> 10
 <211> 702
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 10

Pro Glu Ser Ser Ser Met Leu Arg Glu Gln Ile Leu Asp Leu Ser Lys 1 5 10 15
Arg Tyr Ile Lys Ala Leu Ala Glu Glu Asn Arg Asn Val Val Asp Gly 20 25 30
Pro Tyr Ala Gly Val Met Thr Ala Tyr Asp Leu Lys Lys Thr Leu Ala 35 40 45
Val Leu Leu Asp Asn Ile Leu Gln Arg Ile Gly Lys Leu Glu Ser Lys 50 55 60
Val Asp Asn Leu Val Val Asn Gly Thr Gly Thr Asn Ser Thr Asn Ser 65 70 75 80
Thr Thr Ala Val Pro Ser Leu Val Ala Leu Glu Lys Ile Asn Val Ala 85 90 95
Asp Ile Ile Asn Gly Ala Gln Glu Lys Cys Val Leu Pro Pro Met Asp 100 105 110
Gly Tyr Pro His Cys Glu Gly Lys Ile Lys Trp Met Lys Asp Met Trp 115 120 125
Arg Ser Asp Pro Cys Tyr Ala Asp Tyr Gly Val Asp Gly Ser Thr Cys 130 135 140

Ser Phe Phe Ile Tyr Leu Ser Glu Val Glu Asn Trp Cys Pro His Leu
145 150 155 160

Pro Trp Arg Ala Lys Asn Pro Tyr Glu Glu Ala Asp His Asn Ser Leu
165 170 175

Ala Glu Ile Arg Thr Asp Phe Asn Ile Leu Tyr Ser Met Met Lys Lys
180 185 190

His Glu Glu Phe Arg Trp Met Arg Leu Arg Ile Arg Arg Met Ala Asp
195 200 205

Ala Trp Ile Gln Ala Ile Lys Ser Leu Ala Glu Lys Gln Asn Leu Glu
210 215 220

Lys Arg Lys Arg Lys Lys Val Leu Val His Leu Gly Leu Leu Thr Lys
225 230 235 240

Glu Ser Gly Phe Lys Ile Ala Glu Thr Ala Phe Ser Gly Gly Pro Leu
245 250 255

Gly Glu Leu Val Gln Trp Ser Asp Leu Ile Thr Ser Leu Tyr Leu Leu
260 265 270

Gly His Asp Ile Arg Ile Ser Ala Ser Leu Ala Glu Leu Lys Glu Ile
275 280 285

Met Lys Lys Val Val Gly Asn Arg Ser Gly Cys Pro Thr Val Gly Asp
290 295 300

Arg Ile Val Glu Leu Ile Tyr Ile Asp Ile Val Gly Leu Ala Gln Phe
305 310 315 320

Lys Lys Thr Leu Gly Pro Ser Trp Val His Tyr Gln Cys Met Leu Arg
325 330 335

Val Leu Asp Ser Phe Gly Thr Glu Pro Glu Phe Asn His Ala Asn Tyr
340 345 350

Ala Gln Ser Lys Gly His Lys Thr Pro Trp Gly Lys Trp Asn Leu Asn
355 360 365

Pro Gln Gln Phe Tyr Thr Met Phe Pro His Thr Pro Asp Asn Ser Phe
370 375 380

Leu Gly Phe Val Val Glu Gln His Leu Asn Ser Ser Asp Ile His His
385 390 395 400

Ile Asn Glu Ile Lys Arg Gln Asn Gln Ser Leu Val Tyr Gly Lys Val
405 410 415

Asp Ser Phe Trp Lys Asn Lys Lys Ile Tyr Leu Asp Ile Ile His Thr

420										425					430				
Tyr	Met	Glu	Val	His	Ala	Thr	Val	Tyr	Gly	Ser	Ser	Thr	Lys	Asn	Ile				
		435					440					445							
Pro	Ser	Tyr	Val	Lys	Asn	His	Gly	Ile	Leu	Ser	Gly	Arg	Asp	Leu	Gln				
	450					455					460								
Phe	Leu	Leu	Arg	Glu	Thr	Lys	Leu	Phe	Val	Gly	Leu	Gly	Phe	Pro	Tyr				
465					470					475					480				
Glu	Gly	Pro	Ala	Pro	Leu	Glu	Ala	Ile	Ala	Asn	Gly	Cys	Ala	Phe	Leu				
				485					490					495					
Asn	Pro	Lys	Phe	Asn	Pro	Pro	Lys	Ser	Ser	Lys	Asn	Thr	Asp	Phe	Phe				
			500					505					510						
Ile	Gly	Lys	Pro	Thr	Leu	Arg	Glu	Leu	Thr	Ser	Gln	His	Pro	Tyr	Ala				
		515					520					525							
Glu	Val	Phe	Ile	Gly	Arg	Pro	His	Val	Trp	Thr	Val	Asp	Leu	Asn	Asn				
	530					535					540								
Gln	Glu	Glu	Val	Glu	Asp	Ala	Val	Lys	Ala	Ile	Leu	Asn	Gln	Lys	Ile				
545					550					555					560				
Glu	Pro	Tyr	Met	Pro	Tyr	Glu	Phe	Thr	Cys	Glu	Gly	Met	Leu	Gln	Arg				
				565					570					575					
Ile	Asn	Ala	Phe	Ile	Glu	Lys	Gln	Asp	Phe	Cys	His	Gly	Gln	Val	Met				
			580					585					590						
Trp	Pro	Pro	Leu	Ser	Ala	Leu	Gln	Val	Lys	Leu	Ala	Glu	Pro	Gly	Gln				
		595					600					605							
Ser	Cys	Lys	Gln	Val	Cys	Gln	Glu	Ser	Gln	Leu	Ile	Cys	Glu	Pro	Ser				
	610					615					620								
Phe	Phe	Gln	His	Leu	Asn	Lys	Asp	Lys	Asp	Met	Leu	Lys	Tyr	Lys	Val				
625					630					635					640				
Thr	Cys	Gln	Ser	Ser	Glu	Leu	Ala	Lys	Asp	Ile	Leu	Val	Pro	Ser	Phe				
				645					650					655					
Asp	Pro	Lys	Asn	Lys	His	Cys	Val	Phe	Gln	Gly	Asp	Leu	Leu	Leu	Phe				
			660					665					670						
Ser	Cys	Ala	Gly	Ala	His	Pro	Arg	His	Gln	Arg	Val	Cys	Pro	Cys	Arg				
		675					680					685							
Asp	Phe	Ile	Lys	Gly	Gln	Val	Ala	Leu	Cys	Lys	Asp	Cys	Leu						
	690					695					700								

<210> 11
 <211> 1623
 <212> DNA
 <213> Artificial

<220>
 <223> nucleotide sequence of hybrid GnT-IVa (xylosyltransferase localization signal derived from A. thaliana fused to catalytic domain of GnT-IVa derived from Homo sapiens), codon optimized for Nicotiana benthamiana

<220>
 <221> CDS
 <222> (1)..(1623)

<400> 11
 atg tcc aaa cgg aac ccg aaa att ctc aag att ttc ctt tac atg ctg 48
 Met Ser Lys Arg Asn Pro Lys Ile Leu Lys 10 Ile Phe Leu Tyr Met Leu 15
 1 5
 ctt cta aac tcc ttg ttc ctc att ata tac ttc gtc ttc cat tct agc 96
 Leu Leu Asn Ser Leu Phe Leu Ile Ile Tyr Phe Val Phe His Ser Ser 20 25 30
 caa aat gga aag gaa aag ctg att gca tac caa aga gag ttt ctt gca 144
 Gln Asn Gly Lys Glu Lys Leu Ile Ala Tyr Gln Arg Glu Phe Leu Ala 35 40 45
 cta aag gaa agg ctt aga att gct gaa cac aga att tct cag aga tcc 192
 Leu Lys Glu Arg Leu Arg Ile Ala Glu His Arg Ile Ser Gln Arg Ser 50 55 60
 tct gaa ctg aat acg att gtt cag caa ttt aaa cgc gta ggt gct gaa 240
 Ser Glu Leu Asn Thr Ile Val Gln Gln Phe Lys Arg Val Gly Ala Glu 65 70 75 80
 act aat ggt tct aag gat gct cta aac aag ttt agc gac aat acc ttg 288
 Thr Asn Gly Ser Lys Asp Ala Leu Asn Lys Phe Ser Asp Asn Thr Leu 85 90 95
 aag ttg ctc aag gaa ttg acc tct aaa aag tca ctt caa gtc cct agt 336
 Lys Leu Leu Lys Glu Leu Thr Ser Lys Lys Ser Leu Gln Val Pro Ser 100 105 110
 atc tac tat cat ctt cca cac ttg ctt aag aat gaa gga tca ctt caa 384
 Ile Tyr Tyr His Leu Pro His Leu Leu Lys Asn Glu Gly Ser Leu Gln 115 120 125
 cca gca gta caa att ggt aat ggt aga aca gga gtt tct ata gtc atg 432
 Pro Ala Val Gln Ile Gly Asn Gly Arg Thr Gly Val Ser Ile Val Met 130 135 140
 ggt att cct act gtt aag agg gaa gtt aag agt tac ctc att gag aca 480
 Gly Ile Pro Thr Val Lys Arg Glu Val Lys Ser Tyr Leu Ile Glu Thr 145 150 155 160
 ttg cac tca ctt atc gac aat ctt tat cct gaa gag aaa ctt gat tgc 528
 Leu His Ser Leu Ile Asp Asn Leu Tyr Pro Glu Glu Lys Leu Asp Cys 165 170 175
 gta atc gtt gtt ttc att gga gag act gac ata gat tat gtt cat ggt 576
 Val Ile Val Val Phe Ile Gly Glu Thr Asp Ile Asp Tyr Val His Gly 180 185 190
 gtc gtt gca aat ctc gaa aag gaa ttt agt aag gag atc tcc tct ggt 624
 Val Val Ala Asn Leu Glu Lys Glu Phe Ser Lys Glu Ile Ser Ser Gly

195					200					205										
ctt Leu	gtt Val 210	gaa Glu	gtt Val	ata Ile	tct Ser	cca Pro 215	cct Pro	gag Glu	tct Ser	tat Tyr	tat Tyr 220	ccg Pro	gat Asp	ctt Leu	acc Thr	672				
aac Asn 225	cta Leu	aag Lys	gaa Glu	act Thr	ttt Phe 230	ggt Gly	gac Asp	tca Ser	aag Lys	gaa Glu 235	aga Arg	gtt Val	aga Arg	tgg Trp	aga Arg 240	720				
aca Thr	aag Lys	cag Gln	aac Asn	ctc Leu 245	gat Asp	tat Tyr	tgt Cys	ttc Phe	ctg Leu 250	atg Met	atg Met	tat Tyr	gct Ala	cag Gln 255	gaa Glu	768				
aag Lys	gga Gly	atc Ile	tac Tyr 260	tac Tyr	att Ile	caa Gln	ctt Leu	gag Glu 265	gac Asp	gat Asp	ata Ile	atc Ile	gtc Val 270	aag Lys	cag Gln	816				
aac Asn	tac Tyr	ttt Phe 275	aac Asn	acg Thr	atc Ile	aag Lys	aac Asn 280	ttt Phe	gcc Ala	ttg Leu	caa Gln	ctt Leu 285	agt Ser	tct Ser	gaa Glu	864				
gaa Glu	tgg Trp 290	atg Met	atc Ile	ctt Leu	gag Glu	ttt Phe 295	agt Ser	caa Gln	ctt Leu	gga Gly	ttc Phe 300	att Ile	ggc Gly	aag Lys	atg Met	912				
ttt Phe 305	caa Gln	gca Ala	cct Pro	gat Asp	cta Leu 310	act Thr	ctc Leu	ata Ile	gtg Val	gag Glu 315	ttt Phe	atc Ile	ttc Phe	atg Met	ttc Phe 320	960				
tac Tyr	aag Lys	gag Glu	aaa Lys	ccc Pro 325	att Ile	gat Asp	tgg Trp	cta Leu	ctt Leu 330	gat Asp	cac His	ata Ile	ctt Leu	tgg Trp 335	gtt Val	1008				
aag Lys	gtt Val	tgt Cys	aac Asn 340	cca Pro	gaa Glu	aag Lys	gat Asp	gca Ala 345	aag Lys	cat His	tgt Cys	gat Asp	aga Arg 350	caa Gln	aag Lys	1056				
gct Ala	aat Asn	ctt Leu 355	cga Arg	atc Ile	cgt Arg	ttt Phe	aga Arg 360	cca Pro	tca Ser	ttg Leu	ttc Phe	caa Gln 365	cat His	gtt Val	gga Gly	1104				
ttg Leu	cat His 370	tca Ser	tct Ser	ttg Leu	tct Ser	ggg Gly 375	aag Lys	att Ile	caa Gln	aaa Lys	ctt Leu 380	acc Thr	gat Asp	aag Lys	gac Asp	1152				
tat Tyr 385	atg Met	aaa Lys	cca Pro	ctg Leu	ctt Leu 390	ctg Leu	aag Lys	att Ile	cat His	gta Val 395	aat Asn	cct Pro	cca Pro	gcc Ala	gaa Glu 400	1200				
gtt Val	tct Ser	aca Thr	agt Ser	ctt Leu 405	aag Lys	gta Val	tat Tyr	cag Gln	ggt Gly 410	cat His	aca Thr	ctc Leu	gaa Glu	aag Lys 415	act Thr	1248				
tat Tyr	atg Met	gga Gly	gag Glu 420	gat Asp	ttt Phe	ttc Phe	tgg Trp	gct Ala 425	att Ile	act Thr	cct Pro	att Ile	gct Ala 430	gga Gly	gat Asp	1296				
tat Tyr	atc Ile	ctg Leu 435	ttc Phe	aag Lys	ttt Phe	gac Asp	aag Lys 440	cct Pro	gtg Val	aat Asn	gtt Val	gag Glu 445	agt Ser	tac Tyr	ctt Leu	1344				
ttt Phe	cac His 450	tct Ser	ggt Gly	aat Asn	caa Gln	gaa Glu 455	cat His	cca Pro	ggt Gly	gat Asp	ata Ile 460	ctg Leu	ctt Leu	aac Asn	aca Thr	1392				
acg Thr 465	gtt Val	gaa Glu	gtt Val	ctt Leu	cct Pro 470	ttt Phe	aag Lys	tca Ser	gaa Glu	ggc Gly 475	ttg Leu	gaa Glu	att Ile	tca Ser	aag Lys 480	1440				

gag act aag gac aag aga ctt gaa gat ggt tat ttc cga ata ggc aag	1488
Glu Thr Lys Asp Lys Arg Leu Glu Asp Gly Tyr Phe Arg Ile Gly Lys	
485 490 495	
ttt gaa aat ggt gtt gct gag ggt atg gtt gat cct tct ctt aat ccc	1536
Phe Glu Asn Gly Val Ala Glu Gly Met Val Asp Pro Ser Leu Asn Pro	
500 505 510	
ata tca gct ttt cgt ctc agt gtt atc caa aat tct gca gtt tgg gct	1584
Ile Ser Ala Phe Arg Leu Ser Val Ile Gln Asn Ser Ala Val Trp Ala	
515 520 525	
att ctg aat gag att cac atc aag aag gct aca aat tga	1623
Ile Leu Asn Glu Ile His Ile Lys Lys Ala Thr Asn	
530 535 540	

<210> 12
 <211> 540
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 12

Met Ser Lys Arg Asn Pro Lys Ile Leu Lys Ile Phe Leu Tyr Met Leu
1 5 10 15
Leu Leu Asn Ser Leu Phe Leu Ile Ile Tyr Phe Val Phe His Ser Ser
20 25 30
Gln Asn Gly Lys Glu Lys Leu Ile Ala Tyr Gln Arg Glu Phe Leu Ala
35 40 45
Leu Lys Glu Arg Leu Arg Ile Ala Glu His Arg Ile Ser Gln Arg Ser
50 55 60
Ser Glu Leu Asn Thr Ile Val Gln Gln Phe Lys Arg Val Gly Ala Glu
65 70 75 80
Thr Asn Gly Ser Lys Asp Ala Leu Asn Lys Phe Ser Asp Asn Thr Leu
85 90 95
Lys Leu Leu Lys Glu Leu Thr Ser Lys Lys Ser Leu Gln Val Pro Ser
100 105 110
Ile Tyr Tyr His Leu Pro His Leu Leu Lys Asn Glu Gly Ser Leu Gln
115 120 125
Pro Ala Val Gln Ile Gly Asn Gly Arg Thr Gly Val Ser Ile Val Met
130 135 140
Gly Ile Pro Thr Val Lys Arg Glu Val Lys Ser Tyr Leu Ile Glu Thr
145 150 155 160
Leu His Ser Leu Ile Asp Asn Leu Tyr Pro Glu Glu Lys Leu Asp Cys

165										170					175				
Val	Ile	Val	Val	Phe	Ile	Gly	Glu	Thr	Asp	Ile	Asp	Tyr	Val	His	Gly				
			180					185					190						
Val	Val	Ala	Asn	Leu	Glu	Lys	Glu	Phe	Ser	Lys	Glu	Ile	Ser	Ser	Gly				
		195					200					205							
Leu	Val	Glu	Val	Ile	Ser	Pro	Pro	Glu	Ser	Tyr	Tyr	Pro	Asp	Leu	Thr				
	210					215					220								
Asn	Leu	Lys	Glu	Thr	Phe	Gly	Asp	Ser	Lys	Glu	Arg	Val	Arg	Trp	Arg				
225					230					235					240				
Thr	Lys	Gln	Asn	Leu	Asp	Tyr	Cys	Phe	Leu	Met	Met	Tyr	Ala	Gln	Glu				
				245					250					255					
Lys	Gly	Ile	Tyr	Tyr	Ile	Gln	Leu	Glu	Asp	Asp	Ile	Ile	Val	Lys	Gln				
			260					265					270						
Asn	Tyr	Phe	Asn	Thr	Ile	Lys	Asn	Phe	Ala	Leu	Gln	Leu	Ser	Ser	Glu				
		275					280					285							
Glu	Trp	Met	Ile	Leu	Glu	Phe	Ser	Gln	Leu	Gly	Phe	Ile	Gly	Lys	Met				
	290					295					300								
Phe	Gln	Ala	Pro	Asp	Leu	Thr	Leu	Ile	Val	Glu	Phe	Ile	Phe	Met	Phe				
305					310					315					320				
Tyr	Lys	Glu	Lys	Pro	Ile	Asp	Trp	Leu	Leu	Asp	His	Ile	Leu	Trp	Val				
				325					330					335					
Lys	Val	Cys	Asn	Pro	Glu	Lys	Asp	Ala	Lys	His	Cys	Asp	Arg	Gln	Lys				
			340					345					350						
Ala	Asn	Leu	Arg	Ile	Arg	Phe	Arg	Pro	Ser	Leu	Phe	Gln	His	Val	Gly				
		355					360					365							
Leu	His	Ser	Ser	Leu	Ser	Gly	Lys	Ile	Gln	Lys	Leu	Thr	Asp	Lys	Asp				
	370					375					380								
Tyr	Met	Lys	Pro	Leu	Leu	Leu	Lys	Ile	His	Val	Asn	Pro	Pro	Ala	Glu				
385					390					395					400				
Val	Ser	Thr	Ser	Leu	Lys	Val	Tyr	Gln	Gly	His	Thr	Leu	Glu	Lys	Thr				
				405					410					415					
Tyr	Met	Gly	Glu	Asp	Phe	Phe	Trp	Ala	Ile	Thr	Pro	Ile	Ala	Gly	Asp				
			420					425					430						
Tyr	Ile	Leu	Phe	Lys	Phe	Asp	Lys	Pro	Val	Asn	Val	Glu	Ser	Tyr	Leu				
		435					440					445							

Phe His Ser Gly Asn Gln Glu His Pro Gly Asp Ile Leu Leu Asn Thr
 450 455 460
 Thr Val Glu Val Leu Pro Phe Lys Ser Glu Gly Leu Glu Ile Ser Lys
 465 470 475 480
 Glu Thr Lys Asp Lys Arg Leu Glu Asp Gly Tyr Phe Arg Ile Gly Lys
 485 490 495
 Phe Glu Asn Gly Val Ala Glu Gly Met Val Asp Pro Ser Leu Asn Pro
 500 505 510
 Ile Ser Ala Phe Arg Leu Ser Val Ile Gln Asn Ser Ala Val Trp Ala
 515 520 525
 Ile Leu Asn Glu Ile His Ile Lys Lys Ala Thr Asn
 530 535 540

<210> 13
 <211> 1713
 <212> DNA
 <213> Artificial

<220>
 <223> nucleotide sequence of hybrid GnT-IVa (fucosyltransferase B localization signal derived from *A. thaliana* fused to catalytic domain of GnT-IVa derived from *Homo sapiens*), codon optimized for *Nicotiana benthamiana*

<220>
 <221> CDS
 <222> (1)..(1713)

<400> 13
 atg gga gtc ttt tca aac tta aga ggt cca aga gct ggt gca aca cat 48
 Met Gly Val Phe Ser Asn Leu Arg Gly Pro Arg Ala Gly Ala Thr His
 1 5 10 15
 gat gaa ttt cct gct act aat ggt tct cct tct agt tct tca tct ccc 96
 Asp Glu Phe Pro Ala Thr Asn Gly Ser Pro Ser Ser Ser Ser Ser Pro
 20 25 30
 agt tct tct att aag cgt aag ctc tct aat ctt ctt ccg ctt tgt gtt 144
 Ser Ser Ser Ile Lys Arg Lys Leu Ser Asn Leu Leu Pro Leu Cys Val
 35 40 45
 gct ctt gtt gtg att gct gaa att ggc ttt cta gga cga ctt caa aat 192
 Ala Leu Val Val Ile Ala Glu Ile Gly Phe Leu Gly Arg Leu Gln Asn
 50 55 60
 gga aag gaa aag ctg att gca tac caa aga gag ttt ctt gca cta aag 240
 Gly Lys Glu Lys Leu Ile Ala Tyr Gln Arg Glu Phe Leu Ala Leu Lys
 65 70 75 80
 gaa agg ctt aga att gct gaa cac aga att tct cag aga tcc tct gaa 288
 Glu Arg Leu Arg Ile Ala Glu His Arg Ile Ser Gln Arg Ser Ser Glu
 85 90 95
 ctg aat acg att gtt cag caa ttt aaa cgc gta ggt gct gaa act aat 336
 Leu Asn Thr Ile Val Gln Gln Phe Lys Arg Val Gly Ala Glu Thr Asn

100				105				110								
ggt	tct	aag	gat	gct	cta	aac	aag	ttt	agc	gac	aat	acc	ttg	aag	ttg	384
Gly	Ser	Lys	Asp	Ala	Leu	Asn	Lys	Phe	Ser	Asp	Asn	Thr	Leu	Lys	Leu	
		115					120					125				
ctc	aag	gaa	ttg	acc	tct	aaa	aag	tca	ctt	caa	gtc	cct	agt	atc	tac	432
Leu	Lys	Glu	Leu	Thr	Ser	Lys	Lys	Ser	Leu	Gln	Val	Pro	Ser	Ile	Tyr	
	130					135					140					
tat	cat	ctt	cca	cac	ttg	ctt	aag	aat	gaa	gga	tca	ctt	caa	cca	gca	480
Tyr	His	Leu	Pro	His	Leu	Leu	Lys	Asn	Glu	Gly	Ser	Leu	Gln	Pro	Ala	
145					150					155					160	
gta	caa	att	ggt	aat	ggt	aga	aca	gga	gtt	tct	ata	gtc	atg	ggt	att	528
Val	Gln	Ile	Gly	Asn	Gly	Arg	Thr	Gly	Val	Ser	Ile	Val	Met	Gly	Ile	
				165				170						175		
cct	act	gtt	aag	agg	gaa	gtt	aag	agt	tac	ctc	att	gag	aca	ttg	cac	576
Pro	Thr	Val	Lys	Arg	Glu	Val	Lys	Ser	Tyr	Leu	Ile	Glu	Thr	Leu	His	
			180					185					190			
tca	ctt	atc	gac	aat	ctt	tat	cct	gaa	gag	aaa	ctt	gat	tgc	gta	atc	624
Ser	Leu	Ile	Asp	Asn	Leu	Tyr	Pro	Glu	Glu	Lys	Leu	Asp	Cys	Val	Ile	
		195					200					205				
gtt	gtt	ttc	att	gga	gag	act	gac	ata	gat	tat	gtt	cat	ggt	gtc	gtt	672
Val	Val	Phe	Ile	Gly	Glu	Thr	Asp	Ile	Asp	Tyr	Val	His	Gly	Val	Val	
	210					215					220					
gca	aat	ctc	gaa	aag	gaa	ttt	agt	aag	gag	atc	tcc	tct	ggt	ctt	gtt	720
Ala	Asn	Leu	Glu	Lys	Glu	Phe	Ser	Lys	Glu	Ile	Ser	Ser	Gly	Leu	Val	
225					230					235					240	
gaa	gtt	ata	tct	cca	cct	gag	tct	tat	tat	ccg	gat	ctt	acc	aac	cta	768
Glu	Val	Ile	Ser	Pro	Pro	Glu	Ser	Tyr	Tyr	Pro	Asp	Leu	Thr	Asn	Leu	
				245					250					255		
aag	gaa	act	ttt	ggt	gac	tca	aag	gaa	aga	gtt	aga	tgg	aga	aca	aag	816
Lys	Glu	Thr	Phe	Gly	Asp	Ser	Lys	Glu	Arg	Val	Arg	Trp	Arg	Thr	Lys	
			260					265					270			
cag	aac	ctc	gat	tat	tgt	ttc	ctg	atg	atg	tat	gct	cag	gaa	aag	gga	864
Gln	Asn	Leu	Asp	Tyr	Cys	Phe	Leu	Met	Met	Tyr	Ala	Gln	Glu	Lys	Gly	
		275					280					285				
atc	tac	tac	att	caa	ctt	gag	gac	gat	ata	atc	gtc	aag	cag	aac	tac	912
Ile	Tyr	Tyr	Ile	Gln	Leu	Glu	Asp	Asp	Ile	Ile	Val	Lys	Gln	Asn	Tyr	
	290					295					300					
ttt	aac	acg	atc	aag	aac	ttt	gcc	ttg	caa	ctt	agt	tct	gaa	gaa	tgg	960
Phe	Asn	Thr	Ile	Lys	Asn	Phe	Ala	Leu	Gln	Leu	Ser	Ser	Glu	Glu	Trp	
305					310					315					320	
atg	atc	ctt	gag	ttt	agt	caa	ctt	gga	ttc	att	ggc	aag	atg	ttt	caa	1008
Met	Ile	Leu	Glu	Phe	Ser	Gln	Leu	Gly	Phe	Ile	Gly	Lys	Met	Phe	Gln	
				325				330						335		
gca	cct	gat	cta	act	ctc	ata	gtg	gag	ttt	atc	ttc	atg	ttc	tac	aag	1056
Ala	Pro	Asp	Leu	Thr	Leu	Ile	Val	Glu	Phe	Ile	Phe	Met	Phe	Tyr	Lys	
			340					345					350			
gag	aaa	ccc	att	gat	tgg	cta	ctt	gat	cac	ata	ctt	tgg	gtt	aag	gtt	1104
Glu	Lys	Pro	Ile	Asp	Trp	Leu	Leu	Asp	His	Ile	Leu	Trp	Val	Lys	Val	
		355				360						365				
tgt	aac	cca	gaa	aag	gat	gca	aag	cat	tgt	gat	aga	caa	aag	gct	aat	1152
Cys	Asn	Pro	Glu	Lys	Asp	Ala	Lys	His	Cys	Asp	Arg	Gln	Lys	Ala	Asn	
	370					375					380					

ctt Leu 385	cga Arg	atc Ile	cgt Arg	ttt Phe	aga Arg 390	cca Pro	tca Ser	ttg Leu	ttc Phe	caa Gln 395	cat His	gtt Val	gga Gly	ttg Leu	cat His 400	1200
tca Ser	tct Ser	ttg Leu	tct Ser	ggg Gly 405	aag Lys	att Ile	caa Gln	aaa Lys	ctt Leu 410	acc Thr	gat Asp	aag Lys	gac Asp	tat Tyr 415	atg Met	1248
aaa Lys	cca Pro	ctg Leu	ctt Leu 420	ctg Leu	aag Lys	att Ile	cat His	gta Val 425	aat Asn	cct Pro	cca Pro	gcc Ala	gaa Glu 430	gtt Val	tct Ser	1296
aca Thr	agt Ser	ctt Leu 435	aag Lys	gta Val	tat Tyr	cag Gln	ggg Gly 440	cat His	aca Thr	ctc Leu	gaa Glu	aag Lys 445	act Thr	tat Tyr	atg Met	1344
gga Gly	gag Glu 450	gat Asp	ttt Phe	ttc Phe	tgg Trp	gct Ala 455	att Ile	act Thr	cct Pro	att Ile	gct Ala 460	gga Gly	gat Asp	tat Tyr	atc Ile	1392
ctg Leu 465	ttc Phe	aag Lys	ttt Phe	gac Asp	aag Lys 470	cct Pro	gtg Val	aat Asn	gtt Val	gag Glu 475	agt Ser	tac Tyr	ctt Leu	ttt Phe	cac His 480	1440
tct Ser	ggg Gly	aat Asn	caa Gln	gaa Glu 485	cat His	cca Pro	ggg Gly	gat Asp	ata Ile 490	ctg Leu	ctt Leu	aac Asn	aca Thr	acg Thr 495	gtt Val	1488
gaa Glu	gtt Val	ctt Leu	cct Pro 500	ttt Phe	aag Lys	tca Ser	gaa Glu	ggc Gly 505	ttg Leu	gaa Glu	att Ile	tca Ser	aag Lys 510	gag Glu	act Thr	1536
aag Lys	gac Asp	aag Lys 515	aga Arg	ctt Leu	gaa Glu	gat Asp	ggg Gly 520	tat Tyr	ttc Phe	cga Arg	ata Ile	ggc Gly 525	aag Lys	ttt Phe	gaa Glu	1584
aat Asn 530	ggg Gly	gtt Val	gct Ala	gag Glu	ggg Gly	atg Met 535	gtt Val	gat Asp	cct Pro	tct Ser	ctt Leu 540	aat Asn	ccc Pro	ata Ile	tca Ser	1632
gct Ala 545	ttt Phe	cgt Arg	ctc Leu	agt Ser	gtt Val 550	atc Ile	caa Gln	aat Asn	tct Ser	gca Ala 555	gtt Val	tgg Trp	gct Ala	att Ile	ctg Leu 560	1680
aat Asn	gag Glu	att Ile	cac His	atc Ile 565	aag Lys	aag Lys	gct Ala	aca Thr	aat Asn 570	tga						1713

<210> 14
 <211> 570
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 14

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

Asp Glu Phe Pro Ala Thr Asn Gly Ser Pro Ser Ser Ser Ser Ser Pro
20 25 30

Ser Ser Ser Ile Lys Arg Lys Leu Ser Asn Leu Leu Pro Leu Cys Val

35					40					45					
Ala	Leu	Val	Val	Ile	Ala	Glu	Ile	Gly	Phe	Leu	Gly	Arg	Leu	Gln	Asn
	50					55					60				
Gly	Lys	Glu	Lys	Leu	Ile	Ala	Tyr	Gln	Arg	Glu	Phe	Leu	Ala	Leu	Lys
65				70						75				80	
Glu	Arg	Leu	Arg	Ile	Ala	Glu	His	Arg	Ile	Ser	Gln	Arg	Ser	Ser	Glu
				85					90					95	
Leu	Asn	Thr	Ile	Val	Gln	Gln	Phe	Lys	Arg	Val	Gly	Ala	Glu	Thr	Asn
			100					105					110		
Gly	Ser	Lys	Asp	Ala	Leu	Asn	Lys	Phe	Ser	Asp	Asn	Thr	Leu	Lys	Leu
		115					120					125			
Leu	Lys	Glu	Leu	Thr	Ser	Lys	Lys	Ser	Leu	Gln	Val	Pro	Ser	Ile	Tyr
	130					135					140				
Tyr	His	Leu	Pro	His	Leu	Leu	Lys	Asn	Glu	Gly	Ser	Leu	Gln	Pro	Ala
145					150					155					160
Val	Gln	Ile	Gly	Asn	Gly	Arg	Thr	Gly	Val	Ser	Ile	Val	Met	Gly	Ile
				165					170					175	
Pro	Thr	Val	Lys	Arg	Glu	Val	Lys	Ser	Tyr	Leu	Ile	Glu	Thr	Leu	His
			180					185					190		
Ser	Leu	Ile	Asp	Asn	Leu	Tyr	Pro	Glu	Glu	Lys	Leu	Asp	Cys	Val	Ile
		195					200					205			
Val	Val	Phe	Ile	Gly	Glu	Thr	Asp	Ile	Asp	Tyr	Val	His	Gly	Val	Val
	210					215					220				
Ala	Asn	Leu	Glu	Lys	Glu	Phe	Ser	Lys	Glu	Ile	Ser	Ser	Gly	Leu	Val
225					230					235					240
Glu	Val	Ile	Ser	Pro	Pro	Glu	Ser	Tyr	Tyr	Pro	Asp	Leu	Thr	Asn	Leu
				245					250					255	
Lys	Glu	Thr	Phe	Gly	Asp	Ser	Lys	Glu	Arg	Val	Arg	Trp	Arg	Thr	Lys
			260					265					270		
Gln	Asn	Leu	Asp	Tyr	Cys	Phe	Leu	Met	Met	Tyr	Ala	Gln	Glu	Lys	Gly
		275					280					285			
Ile	Tyr	Tyr	Ile	Gln	Leu	Glu	Asp	Asp	Ile	Ile	Val	Lys	Gln	Asn	Tyr
	290					295					300				
Phe	Asn	Thr	Ile	Lys	Asn	Phe	Ala	Leu	Gln	Leu	Ser	Ser	Glu	Glu	Trp
305					310					315					320

Met Ile Leu Glu Phe Ser Gln Leu Gly Phe Ile Gly Lys Met Phe Gln
 325 330 335
 Ala Pro Asp Leu Thr Leu Ile Val Glu Phe Ile Phe Met Phe Tyr Lys
 340 345 350
 Glu Lys Pro Ile Asp Trp Leu Leu Asp His Ile Leu Trp Val Lys Val
 355 360 365
 Cys Asn Pro Glu Lys Asp Ala Lys His Cys Asp Arg Gln Lys Ala Asn
 370 375 380
 Leu Arg Ile Arg Phe Arg Pro Ser Leu Phe Gln His Val Gly Leu His
 385 390 395 400
 Ser Ser Leu Ser Gly Lys Ile Gln Lys Leu Thr Asp Lys Asp Tyr Met
 405 410 415
 Lys Pro Leu Leu Leu Lys Ile His Val Asn Pro Pro Ala Glu Val Ser
 420 425 430
 Thr Ser Leu Lys Val Tyr Gln Gly His Thr Leu Glu Lys Thr Tyr Met
 435 440 445
 Gly Glu Asp Phe Phe Trp Ala Ile Thr Pro Ile Ala Gly Asp Tyr Ile
 450 455 460
 Leu Phe Lys Phe Asp Lys Pro Val Asn Val Glu Ser Tyr Leu Phe His
 465 470 475 480
 Ser Gly Asn Gln Glu His Pro Gly Asp Ile Leu Leu Asn Thr Thr Val
 485 490 495
 Glu Val Leu Pro Phe Lys Ser Glu Gly Leu Glu Ile Ser Lys Glu Thr
 500 505 510
 Lys Asp Lys Arg Leu Glu Asp Gly Tyr Phe Arg Ile Gly Lys Phe Glu
 515 520 525
 Asn Gly Val Ala Glu Gly Met Val Asp Pro Ser Leu Asn Pro Ile Ser
 530 535 540
 Ala Phe Arg Leu Ser Val Ile Gln Asn Ser Ala Val Trp Ala Ile Leu
 545 550 555 560
 Asn Glu Ile His Ile Lys Lys Ala Thr Asn
 565 570

<210> 15
 <211> 1644
 <212> DNA

<213> Artificial

<220>

<223> nucleotide sequence of hybrid GnT-IVb (xylosyltransferase localization signal derived from A. thaliana fused to catalytic domain of GnT-IVb derived from Homo sapiens), codon optimized for Nicotiana benthamiana

<220>

<221> CDS

<222> (1)..(1644)

<400> 15

atg	agt	aag	cga	aat	ccc	aag	atc	ctg	aag	att	ttc	ttg	tac	atg	ctc	48
Met	Ser	Lys	Arg	Asn	Pro	Lys	Ile	Leu	Lys	Ile	Phe	Leu	Tyr	Met	Leu	
1				5				10					15			

ctg	ttg	aac	tct	ctt	ttc	ctc	atc	ata	tac	ttc	gta	ttt	cac	tca	tct	96
Leu	Leu	Asn	Ser	Leu	Phe	Leu	Ile	Ile	Tyr	Phe	Val	Phe	His	Ser	Ser	
			20					25					30			

gac	gtt	gta	gat	gta	tac	caa	cgc	gaa	ttt	ctt	gct	ctt	aga	gat	aga	144
Asp	Val	Val	Asp	Val	Tyr	Gln	Arg	Glu	Phe	Leu	Ala	Leu	Arg	Asp	Arg	
		35					40					45				

ctt	cat	gct	gca	gaa	caa	gaa	tcc	cta	aag	cgc	tcc	aaa	gaa	ctt	aat	192
Leu	His	Ala	Ala	Glu	Gln	Glu	Ser	Leu	Lys	Arg	Ser	Lys	Glu	Leu	Asn	
	50					55					60					

ctt	gtc	cta	gat	gag	att	aag	cgt	gct	gtg	tct	gaa	aga	caa	gct	ctt	240
Leu	Val	Leu	Asp	Glu	Ile	Lys	Arg	Ala	Val	Ser	Glu	Arg	Gln	Ala	Leu	
65					70					75					80	

aga	gac	gga	gat	ggt	aat	aga	aca	tgg	gga	aga	ctt	aca	gaa	gat	cct	288
Arg	Asp	Gly	Asp	Gly	Asn	Arg	Thr	Trp	Gly	Arg	Leu	Thr	Glu	Asp	Pro	
				85					90					95		

agg	ctt	aag	cca	tgg	aat	gga	tct	cat	aga	cat	gta	ctc	cac	tta	cca	336
Arg	Leu	Lys	Pro	Trp	Asn	Gly	Ser	His	Arg	His	Val	Leu	His	Leu	Pro	
			100					105					110			

aca	gtt	ttc	cat	cat	ctt	cct	cac	cta	ctt	gca	aaa	gaa	tct	tca	ttg	384
Thr	Val	Phe	His	His	Leu	Pro	His	Leu	Leu	Ala	Lys	Glu	Ser	Ser	Leu	
		115					120					125				

caa	cct	gct	gtt	aga	gtt	ggt	caa	ggt	aga	act	gga	gtt	tca	gta	gtt	432
Gln	Pro	Ala	Val	Arg	Val	Gly	Gln	Gly	Arg	Thr	Gly	Val	Ser	Val	Val	
	130					135					140					

atg	ggt	att	cca	agc	gtt	aga	aga	gaa	gtt	cac	tct	tat	ctc	act	gat	480
Met	Gly	Ile	Pro	Ser	Val	Arg	Arg	Glu	Val	His	Ser	Tyr	Leu	Thr	Asp	
145					150					155					160	

acc	ctc	cat	tct	ttg	att	tct	gag	ttg	tca	cca	caa	gag	aag	gaa	gat	528
Thr	Leu	His	Ser	Leu	Ile	Ser	Glu	Leu	Ser	Pro	Gln	Glu	Lys	Glu	Asp	
				165					170					175		

tct	gta	att	gtt	gtc	ctt	atc	gct	gag	act	gat	tct	caa	tat	act	tct	576
Ser	Val	Ile	Val	Val	Leu	Ile	Ala	Glu	Thr	Asp	Ser	Gln	Tyr	Thr	Ser	
			180					185					190			

gcc	gtt	act	gag	aac	atc	aaa	gca	ctt	ttc	cca	act	gaa	ata	cac	tct	624
Ala	Val	Thr	Glu	Asn	Ile	Lys	Ala	Leu	Phe	Pro	Thr	Glu	Ile	His	Ser	
		195					200					205				

ggt	tta	ctg	gag	gta	ata	tca	cct	tct	cct	cat	ttt	tac	cca	gac	ttt	672
Gly	Leu	Leu	Glu	Val	Ile	Ser	Pro	Ser	Pro	His	Phe	Tyr	Pro	Asp	Phe	
	210					215					220					

agt Ser 225	agg Arg	ttg Leu	cga Arg	gaa Glu	tct Ser 230	ttt Phe	gga Gly	gat Asp	cct Pro	aaa Lys 235	gaa Glu	aga Arg	gtc Val	aga Arg	tgg Trp 240	720
agg Arg	act Thr	aag Lys	caa Gln	aat Asn 245	ctt Leu	gac Asp	tac Tyr	tgc Cys	ttt Phe 250	ctt Leu	atg Met	atg Met	tat Tyr	gcc Ala 255	caa Gln	768
tcc Ser	aag Lys	gga Gly	atc Ile 260	tat Tyr	tat Tyr	gtt Val	cag Gln	ctt Leu 265	gag Glu	gat Asp	gac Asp	att Ile	gtt Val 270	gct Ala	aaa Lys	816
ccc Pro	aac Asn	tac Tyr 275	ctg Leu	agt Ser	acc Thr	atg Met	aag Lys 280	aat Asn	ttt Phe	gcc Ala	tta Leu	cag Gln 285	caa Gln	cca Pro	agc Ser	864
gaa Glu	gat Asp 290	tgg Trp	atg Met	ata Ile	ctg Leu	gaa Glu 295	ttt Phe	tcc Ser	cag Gln	ctt Leu	ggg Gly 300	ttc Phe	att Ile	ggc Gly	aag Lys	912
atg Met 305	ttc Phe	aag Lys	agc Ser	ctt Leu	gat Asp 310	ctt Leu	agt Ser	ctg Leu	att Ile	gtc Val 315	gag Glu	ttc Phe	atc Ile	ctt Leu	atg Met 320	960
ttc Phe	tac Tyr	cga Arg	gat Asp	aag Lys 325	cca Pro	ata Ile	gat Asp	tgg Trp	ttg Leu 330	ctt Leu	gat Asp	cac His	att Ile	ctc Leu 335	tgg Trp	1008
gtt Val	aag Lys	gtt Val	tgt Cys 340	aat Asn	ccg Pro	gaa Glu	aag Lys	gat Asp 345	gct Ala	aag Lys	cat His	tgt Cys	gat Asp 350	aga Arg	cag Gln	1056
aag Lys	gct Ala	aac Asn 355	ttg Leu	cgt Arg	att Ile	aga Arg	ttc Phe 360	aaa Lys	ccg Pro	tca Ser	ctc Leu	ttt Phe 365	caa Gln	cat His	gtt Val	1104
gga Gly	act Thr 370	cat His	agt Ser	tct Ser	ctc Leu	gct Ala 375	ggg Gly	aag Lys	atc Ile	caa Gln	aag Lys 380	ctg Leu	aag Lys	gat Asp	aag Lys	1152
gat Asp 385	ttt Phe	ggg Gly	aaa Lys	caa Gln	gct Ala 390	ctg Leu	aga Arg	aag Lys	gaa Glu	cat His 395	gtt Val	aat Asn	cct Pro	cca Pro	gca Ala 400	1200
gaa Glu	gtt Val	tct Ser	act Thr	tca Ser 405	cta Leu	aag Lys	acg Thr	tac Tyr	cag Gln 410	cac His	ttt Phe	aca Thr	ctt Leu	gag Glu 415	aag Lys	1248
gct Ala	tat Tyr	ctt Leu	agg Arg 420	gag Glu	gac Asp	ttt Phe	ttt Phe	tgg Trp 425	gca Ala	ttt Phe	aca Thr	cct Pro	gca Ala 430	gct Ala	ggg Gly	1296
gat Asp	ttc Phe	att Ile 435	aga Arg	ttc Phe	cgg Arg	ttt Phe	ttc Phe 440	caa Gln	cca Pro	cta Leu	aga Arg	ctt Leu 445	gaa Glu	cgc Arg	ttt Phe	1344
ttc Phe 450	ttt Phe	cgt Arg	tct Ser	ggc Gly	aat Asn	ata Ile 455	gag Glu	cat His	cct Pro	gaa Glu	gac Asp 460	aag Lys	ttg Leu	ttt Phe	aac Asn	1392
aca Thr 465	tcc Ser	gtt Val	gaa Glu	gtg Val	ttg Leu 470	cct Pro	ttt Phe	gat Asp	aac Asn 475	cct Pro 475	caa Gln	tct Ser	gac Asp	aaa Lys	gaa Glu 480	1440
gca Ala	ctt Leu	caa Gln	gaa Glu	ggg Gly 485	aga Arg	aca Thr	gca Ala	aca Thr	ctt Leu 490	agg Arg	tat Tyr	cct Pro	aga Arg	tca Ser 495	ccc Pro	1488

gac ggt tat ctt caa atc gga tca ttt tat aag gga gtt gca gaa ggt	1536
Asp Gly Tyr Leu Gln Ile Gly Ser Phe Tyr Lys Gly Val Ala Glu Gly	
500 505 510	
gaa gtt gat cca gct ttt ggt cct tta gaa gct cta agg ctt tct att	1584
Glu Val Asp Pro Ala Phe Gly Pro Leu Glu Ala Leu Arg Leu Ser Ile	
515 520 525	
cag act gat tct cct gtc tgg gtt att ctt agc gaa att ttc ctg aag	1632
Gln Thr Asp Ser Pro Val Trp Val Ile Leu Ser Glu Ile Phe Leu Lys	
530 535 540	
aag gcc gac tga	1644
Lys Ala Asp	
545	

<210> 16
 <211> 547
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 16

Met Ser Lys Arg Asn Pro Lys Ile Leu Lys Ile Phe Leu Tyr Met Leu	
1 5 10 15	
Leu Leu Asn Ser Leu Phe Leu Ile Ile Tyr Phe Val Phe His Ser Ser	
20 25 30	
Asp Val Val Asp Val Tyr Gln Arg Glu Phe Leu Ala Leu Arg Asp Arg	
35 40 45	
Leu His Ala Ala Glu Gln Glu Ser Leu Lys Arg Ser Lys Glu Leu Asn	
50 55 60	
Leu Val Leu Asp Glu Ile Lys Arg Ala Val Ser Glu Arg Gln Ala Leu	
65 70 75 80	
Arg Asp Gly Asp Gly Asn Arg Thr Trp Gly Arg Leu Thr Glu Asp Pro	
85 90 95	
Arg Leu Lys Pro Trp Asn Gly Ser His Arg His Val Leu His Leu Pro	
100 105 110	
Thr Val Phe His His Leu Pro His Leu Leu Ala Lys Glu Ser Ser Leu	
115 120 125	
Gln Pro Ala Val Arg Val Gly Gln Gly Arg Thr Gly Val Ser Val Val	
130 135 140	
Met Gly Ile Pro Ser Val Arg Arg Glu Val His Ser Tyr Leu Thr Asp	
145 150 155 160	
Thr Leu His Ser Leu Ile Ser Glu Leu Ser Pro Gln Glu Lys Glu Asp	
165 170 175	

Ser Val Ile Val Val Leu Ile Ala Glu Thr Asp Ser Gln Tyr Thr Ser
 180 185 190

Ala Val Thr Glu Asn Ile Lys Ala Leu Phe Pro Thr Glu Ile His Ser
 195 200 205

Gly Leu Leu Glu Val Ile Ser Pro Ser Pro His Phe Tyr Pro Asp Phe
 210 215 220

Ser Arg Leu Arg Glu Ser Phe Gly Asp Pro Lys Glu Arg Val Arg Trp
 225 230 235 240

Arg Thr Lys Gln Asn Leu Asp Tyr Cys Phe Leu Met Met Tyr Ala Gln
 245 250 255

Ser Lys Gly Ile Tyr Tyr Val Gln Leu Glu Asp Asp Ile Val Ala Lys
 260 265 270

Pro Asn Tyr Leu Ser Thr Met Lys Asn Phe Ala Leu Gln Gln Pro Ser
 275 280 285

Glu Asp Trp Met Ile Leu Glu Phe Ser Gln Leu Gly Phe Ile Gly Lys
 290 295 300

Met Phe Lys Ser Leu Asp Leu Ser Leu Ile Val Glu Phe Ile Leu Met
 305 310 315 320

Phe Tyr Arg Asp Lys Pro Ile Asp Trp Leu Leu Asp His Ile Leu Trp
 325 330 335

Val Lys Val Cys Asn Pro Glu Lys Asp Ala Lys His Cys Asp Arg Gln
 340 345 350

Lys Ala Asn Leu Arg Ile Arg Phe Lys Pro Ser Leu Phe Gln His Val
 355 360 365

Gly Thr His Ser Ser Leu Ala Gly Lys Ile Gln Lys Leu Lys Asp Lys
 370 375 380

Asp Phe Gly Lys Gln Ala Leu Arg Lys Glu His Val Asn Pro Pro Ala
 385 390 395 400

Glu Val Ser Thr Ser Leu Lys Thr Tyr Gln His Phe Thr Leu Glu Lys
 405 410 415

Ala Tyr Leu Arg Glu Asp Phe Phe Trp Ala Phe Thr Pro Ala Ala Gly
 420 425 430

Asp Phe Ile Arg Phe Arg Phe Phe Gln Pro Leu Arg Leu Glu Arg Phe
 435 440 445

Phe Phe Arg Ser Gly Asn Ile Glu His Pro Glu Asp Lys Leu Phe Asn
450 455 460

Thr Ser Val Glu Val Leu Pro Phe Asp Asn Pro Gln Ser Asp Lys Glu
465 470 475 480

Ala Leu Gln Glu Gly Arg Thr Ala Thr Leu Arg Tyr Pro Arg Ser Pro
485 490 495

Asp Gly Tyr Leu Gln Ile Gly Ser Phe Tyr Lys Gly Val Ala Glu Gly
500 505 510

Glu Val Asp Pro Ala Phe Gly Pro Leu Glu Ala Leu Arg Leu Ser Ile
515 520 525

Gln Thr Asp Ser Pro Val Trp Val Ile Leu Ser Glu Ile Phe Leu Lys
530 535 540

Lys Ala Asp
545

<210> 17
<211> 1713
<212> DNA
<213> Artificial

<220>
<223> nucleotide sequence of hybrid GnT-IVb (fucosyltransferase B localization signal derived from A. thaliana fused to catalytic domain of GnT-IVb derived from Homo sapiens), codon optimized for Nicotiana benthamiana

<220>
<221> CDS
<222> (1)..(1713)

<400> 17	
atg gga gtc ttt tca aac tta aga ggt cca aga gct ggt gca aca cat	48
Met Gly Val Phe Ser Asn Leu Arg Gly Pro Arg Ala Gly Ala Thr His	
1 5 10 15	
gat gaa ttt cct gct act aat ggt tct cct tct agt tct tca tct ccc	96
Asp Glu Phe Pro Ala Thr Asn Gly Ser Pro Ser Ser Ser Ser Pro	
20 25 30	
agt tct tct att aag cgt aag ctc tct aat ctt ctt ccg ctt tgt gtt	144
Ser Ser Ser Ile Lys Arg Lys Leu Ser Asn Leu Leu Pro Leu Cys Val	
35 40 45	
gct ctt gtt gtg att gct gaa att ggc ttt cta gga cga ctt caa aat	192
Ala Leu Val Val Ile Ala Glu Ile Gly Phe Leu Gly Arg Leu Gln Asn	
50 55 60	
gga aag gaa aag ctg att gca tac caa aga gag ttt ctt gca cta aag	240
Gly Lys Glu Lys Leu Ile Ala Tyr Gln Arg Glu Phe Leu Ala Leu Lys	
65 70 75 80	
gaa agg ctt aga att gct gaa cac aga att tct cag aga tcc tct gaa	288
Glu Arg Leu Arg Ile Ala Glu His Arg Ile Ser Gln Arg Ser Ser Glu	
85 90 95	

ctg Leu	aat Asn	acg Thr	att Ile 100	gtt Val	cag Gln	caa Gln	ttt Phe	aaa Lys 105	cgc Arg	gta Val	ggt Gly	gct Ala	gaa Glu 110	act Thr	aat Asn	336
ggt Gly	tct Ser	aag Lys 115	gat Asp	gct Ala	cta Leu	aac Asn	aag Lys 120	ttt Phe	agc Ser	gac Asp	aat Asn	acc Thr 125	ttg Leu	aag Lys	ttg Leu	384
ctc Leu	aag Lys 130	gaa Glu	ttg Leu	acc Thr	tct Ser	aaa Lys 135	aag Lys	tca Ser	ctt Leu	caa Gln	gtc Val 140	cct Pro	agt Ser	atc Ile	tac Tyr	432
tat Tyr 145	cat His	ctt Leu	cca Pro	cac His	ttg Leu 150	ctt Leu	aag Lys	aat Asn	gaa Glu	gga Gly 155	tca Ser	ctt Leu	caa Gln	cca Pro	gca Ala 160	480
gta Val	caa Gln	att Ile	ggt Gly	aat Asn 165	ggt Gly	aga Arg	aca Thr	gga Gly	gtt Val 170	tct Ser	ata Ile	gtc Val	atg Met	ggt Gly 175	att Ile	528
cct Pro	act Thr	gtt Val	aag Lys 180	agg Arg	gaa Glu	gtt Val	aag Lys	agt Ser 185	tac Tyr	ctc Leu	att Ile	gag Glu	aca Thr 190	ttg Leu	cac His	576
tca Ser	ctt Leu	atc Ile 195	gac Asp	aat Asn	ctt Leu	tat Tyr	cct Pro 200	gaa Glu	gag Glu	aaa Lys	ctt Leu	gat Asp 205	tgc Cys	gta Val	atc Ile	624
gtt Val	gtt Val 210	ttc Phe	att Ile	gga Gly	gag Glu	act Thr 215	gac Asp	ata Ile	gat Asp	tat Tyr	gtt Val 220	cat His	ggt Gly	gtc Val	gtt Val	672
gca Ala 225	aat Asn	ctc Leu	gaa Glu	aag Lys	gaa Glu 230	ttt Phe	agt Ser	aag Lys	gag Glu	atc Ile 235	tcc Ser	tct Ser	ggt Gly	ctt Leu	gtt Val 240	720
gaa Glu	gtt Val	ata Ile	tct Ser	cca Pro 245	cct Pro	gag Glu	tct Ser	tat Tyr	tat Tyr 250	ccg Pro	gat Asp	ctt Leu	acc Thr	aac Asn 255	cta Leu	768
aag Lys	gaa Glu	act Thr	ttt Phe 260	ggt Gly	gac Asp	tca Ser	aag Lys	gaa Glu 265	aga Arg	gtt Val	aga Arg	tgg Trp 270	aga Arg	aca Thr	aag Lys	816
cag Gln	aac Asn	ctc Leu 275	gat Asp	tat Tyr	tgt Cys	ttc Phe	ctg Leu 280	atg Met	atg Met	tat Tyr	gct Ala	cag Gln 285	gaa Glu	aag Lys	gga Gly	864
atc Ile	tac Tyr 290	tac Tyr	att Ile	caa Gln	ctt Leu	gag Glu 295	gac Asp	gat Asp	ata Ile	atc Ile	gtc Val 300	aag Lys	cag Gln	aac Asn	tac Tyr	912
ttt Phe 305	aac Asn	acg Thr	atc Ile	aag Lys	aac Asn 310	ttt Phe	gcc Ala	ttg Leu	caa Gln	ctt Leu 315	agt Ser	tct Ser	gaa Glu	gaa Glu	tgg Trp 320	960
atg Met	atc Ile	ctt Leu	gag Glu	ttt Phe 325	agt Ser	caa Gln	ctt Leu	gga Gly	ttc Phe 330	att Ile	ggc Gly	aag Lys	atg Met	ttt Phe 335	caa Gln	1008
gca Ala	cct Pro	gat Asp	cta Leu 340	act Thr	ctc Leu	ata Ile	gtg Val	gag Glu 345	ttt Phe	atc Ile	ttc Phe	atg Met	ttc Phe 350	tac Tyr	aag Lys	1056
gag Glu	aaa Lys	ccc Pro 355	att Ile	gat Asp	tgg Trp	cta Leu	ctt Leu 360	gat Asp	cac His	ata Ile	ctt Leu	tgg Trp 365	gtt Val	aag Lys	gtt Val	1104

tgt	aac	cca	gaa	aag	gat	gca	aag	cat	tgt	gat	aga	caa	aag	gct	aat	1152
Cys	Asn	Pro	Glu	Lys	Asp	Ala	Lys	His	Cys	Asp	Arg	Gln	Lys	Ala	Asn	
	370					375					380					
ctt	cga	atc	cgt	ttt	aga	cca	tca	ttg	ttc	caa	cat	ggt	gga	ttg	cat	1200
Leu	Arg	Ile	Arg	Phe	Arg	Pro	Ser	Leu	Phe	Gln	His	Val	Gly	Leu	His	
	385				390					395					400	
tca	tct	ttg	tct	ggg	aag	att	caa	aaa	ctt	acc	gat	aag	gac	tat	atg	1248
Ser	Ser	Leu	Ser	Gly	Lys	Ile	Gln	Lys	Leu	Thr	Asp	Lys	Asp	Tyr	Met	
				405					410					415		
aaa	cca	ctg	ctt	ctg	aag	att	cat	gta	aat	cct	cca	gcc	gaa	ggt	tct	1296
Lys	Pro	Leu	Leu	Leu	Lys	Ile	His	Val	Asn	Pro	Pro	Ala	Glu	Val	Ser	
			420					425					430			
aca	agt	ctt	aag	gta	tat	cag	ggg	cat	aca	ctc	gaa	aag	act	tat	atg	1344
Thr	Ser	Leu	Lys	Val	Tyr	Gln	Gly	His	Thr	Leu	Glu	Lys	Thr	Tyr	Met	
		435					440					445				
gga	gag	gat	ttt	ttc	tgg	gct	att	act	cct	att	gct	gga	gat	tat	atc	1392
Gly	Glu	Asp	Phe	Phe	Trp	Ala	Ile	Thr	Pro	Ile	Ala	Gly	Asp	Tyr	Ile	
	450					455					460					
ctg	ttc	aag	ttt	gac	aag	cct	gtg	aat	ggt	gag	agt	tac	ctt	ttt	cac	1440
Leu	Phe	Lys	Phe	Asp	Lys	Pro	Val	Asn	Val	Glu	Ser	Tyr	Leu	Phe	His	
	465				470					475					480	
tct	ggt	aat	caa	gaa	cat	cca	ggg	gat	ata	ctg	ctt	aac	aca	acg	ggt	1488
Ser	Gly	Asn	Gln	Glu	His	Pro	Gly	Asp	Ile	Leu	Leu	Asn	Thr	Thr	Val	
				485					490					495		
gaa	ggt	ctt	cct	ttt	aag	tca	gaa	ggc	ttg	gaa	att	tca	aag	gag	act	1536
Glu	Val	Leu	Pro	Phe	Lys	Ser	Glu	Gly	Leu	Glu	Ile	Ser	Lys	Glu	Thr	
			500					505					510			
aag	gac	aag	aga	ctt	gaa	gat	ggg	tat	ttc	cga	ata	ggc	aag	ttt	gaa	1584
Lys	Asp	Lys	Arg	Leu	Glu	Asp	Gly	Tyr	Phe	Arg	Ile	Gly	Lys	Phe	Glu	
		515					520					525				
aat	ggg	ggt	gct	gag	ggg	atg	ggt	gat	cct	tct	ctt	aat	ccc	ata	tca	1632
Asn	Gly	Val	Ala	Glu	Gly	Met	Val	Asp	Pro	Ser	Leu	Asn	Pro	Ile	Ser	
	530					535					540					
gct	ttt	cgt	ctc	agt	ggt	atc	caa	aat	tct	gca	ggt	tgg	gct	att	ctg	1680
Ala	Phe	Arg	Leu	Ser	Val	Ile	Gln	Asn	Ser	Ala	Val	Trp	Ala	Ile	Leu	
	545				550					555					560	
aat	gag	att	cac	atc	aag	aag	gct	aca	aat	tga						1713
Asn	Glu	Ile	His	Ile	Lys	Lys	Ala	Thr	Asn							
				565					570							

<210> 18
 <211> 570
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 18

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

Asp Glu Phe Pro Ala Thr Asn Gly Ser Pro Ser Ser Ser Ser Ser Pro
20 25 30

Ser Ser Ser Ile Lys Arg Lys Leu Ser Asn Leu Leu Pro Leu Cys Val
 35 40 45
 Ala Leu Val Val Ile Ala Glu Ile Gly Phe Leu Gly Arg Leu Gln Asn
 50 55 60
 Gly Lys Glu Lys Leu Ile Ala Tyr Gln Arg Glu Phe Leu Ala Leu Lys
 65 70 75 80
 Glu Arg Leu Arg Ile Ala Glu His Arg Ile Ser Gln Arg Ser Ser Glu
 85 90 95
 Leu Asn Thr Ile Val Gln Gln Phe Lys Arg Val Gly Ala Glu Thr Asn
 100 105 110
 Gly Ser Lys Asp Ala Leu Asn Lys Phe Ser Asp Asn Thr Leu Lys Leu
 115 120 125
 Leu Lys Glu Leu Thr Ser Lys Lys Ser Leu Gln Val Pro Ser Ile Tyr
 130 135 140
 Tyr His Leu Pro His Leu Leu Lys Asn Glu Gly Ser Leu Gln Pro Ala
 145 150 155 160
 Val Gln Ile Gly Asn Gly Arg Thr Gly Val Ser Ile Val Met Gly Ile
 165 170 175
 Pro Thr Val Lys Arg Glu Val Lys Ser Tyr Leu Ile Glu Thr Leu His
 180 185 190
 Ser Leu Ile Asp Asn Leu Tyr Pro Glu Glu Lys Leu Asp Cys Val Ile
 195 200 205
 Val Val Phe Ile Gly Glu Thr Asp Ile Asp Tyr Val His Gly Val Val
 210 215 220
 Ala Asn Leu Glu Lys Glu Phe Ser Lys Glu Ile Ser Ser Gly Leu Val
 225 230 235 240
 Glu Val Ile Ser Pro Pro Glu Ser Tyr Tyr Pro Asp Leu Thr Asn Leu
 245 250 255
 Lys Glu Thr Phe Gly Asp Ser Lys Glu Arg Val Arg Trp Arg Thr Lys
 260 265 270
 Gln Asn Leu Asp Tyr Cys Phe Leu Met Met Tyr Ala Gln Glu Lys Gly
 275 280 285
 Ile Tyr Tyr Ile Gln Leu Glu Asp Asp Ile Ile Val Lys Gln Asn Tyr
 290 295 300

Phe Asn Thr Ile Lys Asn Phe Ala Leu Gln Leu Ser Ser Glu Glu Trp
 305 310 315 320
 Met Ile Leu Glu Phe Ser Gln Leu Gly Phe Ile Gly Lys Met Phe Gln
 325 330 335
 Ala Pro Asp Leu Thr Leu Ile Val Glu Phe Ile Phe Met Phe Tyr Lys
 340 345 350
 Glu Lys Pro Ile Asp Trp Leu Leu Asp His Ile Leu Trp Val Lys Val
 355 360 365
 Cys Asn Pro Glu Lys Asp Ala Lys His Cys Asp Arg Gln Lys Ala Asn
 370 375 380
 Leu Arg Ile Arg Phe Arg Pro Ser Leu Phe Gln His Val Gly Leu His
 385 390 395 400
 Ser Ser Leu Ser Gly Lys Ile Gln Lys Leu Thr Asp Lys Asp Tyr Met
 405 410 415
 Lys Pro Leu Leu Leu Lys Ile His Val Asn Pro Pro Ala Glu Val Ser
 420 425 430
 Thr Ser Leu Lys Val Tyr Gln Gly His Thr Leu Glu Lys Thr Tyr Met
 435 440 445
 Gly Glu Asp Phe Phe Trp Ala Ile Thr Pro Ile Ala Gly Asp Tyr Ile
 450 455 460
 Leu Phe Lys Phe Asp Lys Pro Val Asn Val Glu Ser Tyr Leu Phe His
 465 470 475 480
 Ser Gly Asn Gln Glu His Pro Gly Asp Ile Leu Leu Asn Thr Thr Val
 485 490 495
 Glu Val Leu Pro Phe Lys Ser Glu Gly Leu Glu Ile Ser Lys Glu Thr
 500 505 510
 Lys Asp Lys Arg Leu Glu Asp Gly Tyr Phe Arg Ile Gly Lys Phe Glu
 515 520 525
 Asn Gly Val Ala Glu Gly Met Val Asp Pro Ser Leu Asn Pro Ile Ser
 530 535 540
 Ala Phe Arg Leu Ser Val Ile Gln Asn Ser Ala Val Trp Ala Ile Leu
 545 550 555 560
 Asn Glu Ile His Ile Lys Lys Ala Thr Asn
 565 570

<210> 19
 <211> 2205
 <212> DNA
 <213> Artificial

<220>
 <223> nucleotide sequence of hybrid GnT-Va (xylosyltransferase localization signal derived from A. thaliana fused to catalytic domain of GnT-Va derived from Homo sapiens), codon optimized for Nicotiana benthamiana

<220>
 <221> CDS
 <222> (1)..(2205)

<400> 19
 atg tcc aag aga aac ccc aag ata ctg aag atc ttc cta tat atg ctc 48
 Met Ser Lys Arg Asn Pro Lys Ile Leu Lys Ile Phe Leu Tyr Met Leu
 1 5 10 15
 ctg ctt aat agc ctg ttt ctg atc att tat ttc gtc ttc cac tct agt 96
 Leu Leu Asn Ser Leu Phe Leu Ile Ile Tyr Phe Val Phe His Ser Ser
 20 25 30
 cca gaa tca tct tca atg ctt aga gag caa atc ctc gat ttg tcc aag 144
 Pro Glu Ser Ser Ser Met Leu Arg Glu Gln Ile Leu Asp Leu Ser Lys
 35 40 45
 aga tac att aag gca ctt gct gaa gag aac aga aat gtt gtt gat ggt 192
 Arg Tyr Ile Lys Ala Leu Ala Glu Glu Asn Arg Asn Val Val Asp Gly
 50 55 60
 cct tat gca gga gtt atg act gcc tat gat ctt aag aag aca tta gcc 240
 Pro Tyr Ala Gly Val Met Thr Ala Tyr Asp Leu Lys Lys Thr Leu Ala
 65 70 75 80
 gtt ctg ctt gac aac att cta cag aga ata ggc aag ttg gag agt aag 288
 Val Leu Leu Asp Asn Ile Leu Gln Arg Ile Gly Lys Leu Glu Ser Lys
 85 90 95
 gtt gat aat ctt gtg gtc aat gga acg gga aca aat tca acc aat agc 336
 Val Asp Asn Leu Val Val Asn Gly Thr Gly Thr Asn Ser Thr Asn Ser
 100 105 110
 act aca gct gtt cct tct tta gtt gct ctt gag aag atc aat gtt gcc 384
 Thr Thr Ala Val Pro Ser Leu Val Ala Leu Glu Lys Ile Asn Val Ala
 115 120 125
 gac ata atc aat ggt gca caa gaa aag tgt gta ctt cct cct atg gat 432
 Asp Ile Ile Asn Gly Ala Gln Glu Lys Cys Val Leu Pro Pro Met Asp
 130 135 140
 ggt tac cct cat tgt gaa gga aag atc aag tgg atg aaa gat atg tgg 480
 Gly Tyr Pro His Cys Glu Gly Lys Ile Lys Trp Met Lys Asp Met Trp
 145 150 155 160
 aga tct gat cct tgt tat gct gat tat ggt gtg gat gga agt acc tgc 528
 Arg Ser Asp Pro Cys Tyr Ala Asp Tyr Gly Val Asp Gly Ser Thr Cys
 165 170 175
 tca ttt ttc atc tat ctg tct gaa gtt gag aat tgg tgt cct cat ctt 576
 Ser Phe Phe Ile Tyr Leu Ser Glu Val Glu Asn Trp Cys Pro His Leu
 180 185 190
 cct tgg aga gct aag aat cca tac gaa gag gct gat cat aat tca ttg 624
 Pro Trp Arg Ala Lys Asn Pro Tyr Glu Glu Ala Asp His Asn Ser Leu
 195 200 205

gct Ala 210	gaa Glu 210	atc Ile	agg Arg	acg Thr	gac Asp 215	ttc Phe 215	aat Asn	atc Ile	cta Leu	tac Tyr	tct Ser 220	atg Met	atg Met	aag Lys	aag Lys	672
cac His 225	gaa Glu	gag Glu	ttc Phe	aga Arg	tgg Trp 230	atg Met	aga Arg	ctt Leu	aga Arg	att Ile 235	aga Arg	aga Arg	atg Met	gca Ala	gac Asp 240	720
gcg Ala	tgg Trp	ata Ile	caa Gln	gct Ala 245	att Ile	aag Lys	agt Ser	ctt Leu	gct Ala 250	gag Glu	aag Lys	caa Gln	aac Asn	cta Leu 255	gaa Glu	768
aag Lys	agg Arg	aag Lys	cga Arg 260	aag Lys	aag Lys	gtt Val	ctt Leu	gta Val 265	cat His	ctt Leu	ggt Gly	ttg Leu	ctt Leu 270	acc Thr	aag Lys	816
gag Glu	tct Ser	ggt Gly 275	ttt Phe	aaa Lys	att Ile	gca Ala	gaa Glu 280	act Thr	gcc Ala	ttt Phe	tct Ser	gga Gly 285	ggt Gly	cca Pro	ctt Leu	864
ggt Gly	gaa Glu 290	tta Leu	gta Val	cag Gln	tgg Trp	tca Ser 295	gac Asp	ttg Leu	ata Ile	aca Thr	tct Ser 300	ctc Leu	tac Tyr	ttg Leu	ctt Leu	912
ggc Gly 305	cat His	gac Asp	att Ile	aga Arg	att Ile 310	tct Ser	gct Ala	agt Ser	ctt Leu	gct Ala 315	gag Glu	ttg Leu	aag Lys	gaa Glu	atc Ile 320	960
atg Met	aag Lys	aag Lys	gtt Val	gtt Val 325	ggc Gly	aat Asn	aga Arg	tct Ser	gga Gly 330	tgt Cys	cct Pro	act Thr	gtt Val	ggt Gly 335	gat Asp	1008
cgc Arg	att Ile	gtt Val	gaa Glu 340	ctg Leu	att Ile	tat Tyr	att Ile	gat Asp 345	ata Ile	gtc Val	gga Gly	ctt Leu	gcc Ala 350	cag Gln	ttt Phe	1056
aag Lys	aaa Lys	act Thr 355	tta Leu	ggt Gly	cct Pro	agt Ser	tgg Trp 360	gta Val	cat His	tac Tyr	caa Gln	tgt Cys 365	atg Met	ctg Leu	aga Arg	1104
gta Val 370	ctc Leu	gat Asp	tct Ser	ttt Phe	ggt Gly	act Thr 375	gaa Glu	cct Pro	gaa Glu	ttt Phe	aac Asn 380	cac His	gct Ala	aac Asn	tat Tyr	1152
gct Ala 385	caa Gln	agt Ser	aaa Lys	ggt Gly	cat His 390	aag Lys	aca Thr	cca Pro	tgg Trp	gga Gly 395	aag Lys	tgg Trp	aat Asn	ctt Leu	aac Asn 400	1200
ccc Pro	caa Gln	caa Gln	ttc Phe	tac Tyr 405	aca Thr	atg Met	ttt Phe	cct Pro	cac His 410	act Thr	ccg Pro	gat Asp	aat Asn	agt Ser 415	ttc Phe	1248
ctt Leu	ggc Gly	ttt Phe	gtt Val 420	gtt Val	gaa Glu	cag Gln	cac His	ctt Leu 425	aat Asn	tcc Ser	tct Ser	gac Asp	ata Ile 430	cac His	cac His	1296
att Ile	aat Asn	gaa Glu 435	att Ile	aag Lys	agg Arg	cag Gln	aac Asn 440	caa Gln	agc Ser	ctc Leu	gtt Val	tat Tyr 445	gga Gly	aaa Lys	gtt Val	1344
gac Asp	tcc Ser 450	ttt Phe	tgg Trp	aag Lys	aac Asn	aag Lys 455	aag Lys	atc Ile	tat Tyr	ctg Leu	gat Asp 460	ata Ile	att Ile	cat His	acg Thr	1392
tac Tyr 465	atg Met	gaa Glu	gtt Val	cat His	gct Ala 470	act Thr	gtt Val	tac Tyr	ggg Gly 475	tca Ser	tct Ser	acc Thr	aag Lys	aat Asn	att Ile 480	1440
ccc	tcc	tat	gtc	aag	aat	cat	ggt	ata	ctt	tct	gga	aga	gac	ttg	cag	1488

Pro	Ser	Tyr	Val	Lys 485	Asn	His	Gly	Ile	Leu 490	Ser	Gly	Arg	Asp	Leu 495	Gln		
ttc	ttg	ctt	aga	gaa	acc	aaa	ctt	ttt	gtc	ggg	ctt	ggg	ttt	cct	tat	1536	
Phe	Leu	Leu	Arg 500	Glu	Thr	Lys	Leu	Phe 505	Val	Gly	Leu	Gly	Phe 510	Pro	Tyr		
gaa	ggg	cct	gca	cca	ctt	gaa	gct	att	gca	aat	gga	tgt	gct	ttt	ctc	1584	
Glu	Gly	Pro 515	Ala	Pro	Leu	Glu	Ala 520	Ile	Ala	Asn	Gly	Cys 525	Ala	Phe	Leu		
aac	cca	aag	ttc	aat	cct	cca	aag	tca	agc	aag	aac	acc	gat	ttc	ttt	1632	
Asn	Pro 530	Lys	Phe	Asn	Pro	Pro 535	Lys	Ser	Ser	Lys	Asn 540	Thr	Asp	Phe	Phe		
att	ggc	aag	cct	aca	cta	aga	gaa	ctt	act	tca	caa	cac	cct	tat	gcc	1680	
Ile	Gly	Lys	Pro	Thr	Leu 550	Arg	Glu	Leu	Thr	Ser 555	Gln	His	Pro	Tyr	Ala 560		
gaa	gtt	ttt	att	gga	aga	cca	cat	gtt	tgg	aca	gtc	gat	ttg	aac	aat	1728	
Glu	Val	Phe	Ile	Gly 565	Arg	Pro	His	Val	Trp 570	Thr	Val	Asp	Leu	Asn 575	Asn		
caa	gag	gaa	gtt	gag	gat	gca	gtt	aag	gct	atc	ctt	aac	cag	aag	att	1776	
Gln	Glu	Glu	Val 580	Glu	Asp	Ala	Val	Lys 585	Ala	Ile	Leu	Asn	Gln 590	Lys	Ile		
gaa	cca	tac	atg	ccc	tac	gaa	ttt	aca	tgt	gaa	ggg	atg	ttg	cag	cgg	1824	
Glu	Pro	Tyr 595	Met	Pro	Tyr	Glu	Phe 600	Thr	Cys	Glu	Gly	Met 605	Leu	Gln	Arg		
att	aac	gca	ttc	att	gaa	aag	cag	gac	ttt	tgt	cat	ggg	caa	gtt	atg	1872	
Ile	Asn 610	Ala	Phe	Ile	Glu	Lys 615	Gln	Asp	Phe	Cys	His 620	Gly	Gln	Val	Met		
tgg	cca	cct	ctt	tca	gct	ctt	caa	gta	aag	tta	gca	gaa	cct	ggg	caa	1920	
Trp	Pro	Pro	Leu	Ser	Ala 630	Leu	Gln	Val	Lys	Leu 635	Ala	Glu	Pro	Gly	Gln 640		
tct	tgt	aag	caa	gtt	tgt	caa	gag	tca	cag	ctt	att	tgc	gaa	cct	tct	1968	
Ser	Cys	Lys	Gln	Val 645	Cys	Gln	Glu	Ser	Gln 650	Leu	Ile	Cys	Glu	Pro 655	Ser		
ttt	ttc	cag	cac	ctc	aat	aag	gat	aag	gat	atg	ctc	aag	tac	aag	gtt	2016	
Phe	Phe	Gln	His 660	Leu	Asn	Lys	Asp	Lys 665	Asp	Met	Leu	Lys	Tyr 670	Lys	Val		
act	tgc	caa	tct	tct	gaa	ctt	gca	aag	gat	ata	ctc	gtt	cca	tct	ttt	2064	
Thr	Cys	Gln 675	Ser	Ser	Glu	Leu	Ala 680	Lys	Asp	Ile	Leu	Val 685	Pro	Ser	Phe		
gac	cca	aag	aat	aag	cat	tgc	gtc	ttc	caa	ggg	gat	ctt	cta	ttg	ttt	2112	
Asp	Pro 690	Lys	Asn	Lys	His	Cys 695	Val	Phe	Gln	Gly	Asp 700	Leu	Leu	Leu	Phe		
agt	tgt	gct	gga	gca	cat	cct	aga	cat	caa	aga	gta	tgt	cca	tgc	aga	2160	
Ser	Cys	Ala	Gly	Ala	His 710	Pro	Arg	His	Gln 715	Arg 715	Val	Cys	Pro	Cys	Arg 720		
gat	ttc	ata	aag	ggg	caa	gta	gct	cta	tgc	aag	gat	tgc	ctt	tga		2205	
Asp	Phe	Ile	Lys	Gly 725	Gln	Val	Ala	Leu	Cys 730	Lys	Asp	Cys	Leu				
<210>	20																
<211>	734																
<212>	PRT																
<213>	Artificial																

<220>

<223> Synthetic Construct

<400> 20

Met Ser Lys Arg Asn Pro Lys Ile Leu Lys Ile Phe Leu Tyr Met Leu
1 5 10 15

Leu Leu Asn Ser Leu Phe Leu Ile Ile Tyr Phe Val Phe His Ser Ser
20 25 30

Pro Glu Ser Ser Ser Met Leu Arg Glu Gln Ile Leu Asp Leu Ser Lys
35 40 45

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

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

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

Val Asp Asn Leu Val Val Asn Gly Thr Gly Thr Asn Ser Thr Asn Ser
100 105 110

Thr Thr Ala Val Pro Ser Leu Val Ala Leu Glu Lys Ile Asn Val Ala
115 120 125

Asp Ile Ile Asn Gly Ala Gln Glu Lys Cys Val Leu Pro Pro Met Asp
130 135 140

Gly Tyr Pro His Cys Glu Gly Lys Ile Lys Trp Met Lys Asp Met Trp
145 150 155 160

Arg Ser Asp Pro Cys Tyr Ala Asp Tyr Gly Val Asp Gly Ser Thr Cys
165 170 175

Ser Phe Phe Ile Tyr Leu Ser Glu Val Glu Asn Trp Cys Pro His Leu
180 185 190

Pro Trp Arg Ala Lys Asn Pro Tyr Glu Glu Ala Asp His Asn Ser Leu
195 200 205

Ala Glu Ile Arg Thr Asp Phe Asn Ile Leu Tyr Ser Met Met Lys Lys
210 215 220

His Glu Glu Phe Arg Trp Met Arg Leu Arg Ile Arg Arg Met Ala Asp
225 230 235 240

Ala Trp Ile Gln Ala Ile Lys Ser Leu Ala Glu Lys Gln Asn Leu Glu
245 250 255

Lys Arg Lys Arg Lys Lys Val Leu Val His Leu Gly Leu Leu Thr Lys
 260 265 270
 Glu Ser Gly Phe Lys Ile Ala Glu Thr Ala Phe Ser Gly Gly Pro Leu
 275 280 285
 Gly Glu Leu Val Gln Trp Ser Asp Leu Ile Thr Ser Leu Tyr Leu Leu
 290 295 300
 Gly His Asp Ile Arg Ile Ser Ala Ser Leu Ala Glu Leu Lys Glu Ile
 305 310 315 320
 Met Lys Lys Val Val Gly Asn Arg Ser Gly Cys Pro Thr Val Gly Asp
 325 330 335
 Arg Ile Val Glu Leu Ile Tyr Ile Asp Ile Val Gly Leu Ala Gln Phe
 340 345 350
 Lys Lys Thr Leu Gly Pro Ser Trp Val His Tyr Gln Cys Met Leu Arg
 355 360 365
 Val Leu Asp Ser Phe Gly Thr Glu Pro Glu Phe Asn His Ala Asn Tyr
 370 375 380
 Ala Gln Ser Lys Gly His Lys Thr Pro Trp Gly Lys Trp Asn Leu Asn
 385 390 395 400
 Pro Gln Gln Phe Tyr Thr Met Phe Pro His Thr Pro Asp Asn Ser Phe
 405 410 415
 Leu Gly Phe Val Val Glu Gln His Leu Asn Ser Ser Asp Ile His His
 420 425 430
 Ile Asn Glu Ile Lys Arg Gln Asn Gln Ser Leu Val Tyr Gly Lys Val
 435 440 445
 Asp Ser Phe Trp Lys Asn Lys Lys Ile Tyr Leu Asp Ile Ile His Thr
 450 455 460
 Tyr Met Glu Val His Ala Thr Val Tyr Gly Ser Ser Thr Lys Asn Ile
 465 470 475 480
 Pro Ser Tyr Val Lys Asn His Gly Ile Leu Ser Gly Arg Asp Leu Gln
 485 490 495
 Phe Leu Leu Arg Glu Thr Lys Leu Phe Val Gly Leu Gly Phe Pro Tyr
 500 505 510
 Glu Gly Pro Ala Pro Leu Glu Ala Ile Ala Asn Gly Cys Ala Phe Leu
 515 520 525
 Asn Pro Lys Phe Asn Pro Pro Lys Ser Ser Lys Asn Thr Asp Phe Phe

530 535 540
 Ile Gly Lys Pro Thr Leu Arg Glu Leu Thr Ser Gln His Pro Tyr Ala
 545 550 555 560
 Glu Val Phe Ile Gly Arg Pro His Val Trp Thr Val Asp Leu Asn Asn
 565 570 575
 Gln Glu Glu Val Glu Asp Ala Val Lys Ala Ile Leu Asn Gln Lys Ile
 580 585 590
 Glu Pro Tyr Met Pro Tyr Glu Phe Thr Cys Glu Gly Met Leu Gln Arg
 595 600 605
 Ile Asn Ala Phe Ile Glu Lys Gln Asp Phe Cys His Gly Gln Val Met
 610 615 620
 Trp Pro Pro Leu Ser Ala Leu Gln Val Lys Leu Ala Glu Pro Gly Gln
 625 630 635 640
 Ser Cys Lys Gln Val Cys Gln Glu Ser Gln Leu Ile Cys Glu Pro Ser
 645 650 655
 Phe Phe Gln His Leu Asn Lys Asp Lys Asp Met Leu Lys Tyr Lys Val
 660 665 670
 Thr Cys Gln Ser Ser Glu Leu Ala Lys Asp Ile Leu Val Pro Ser Phe
 675 680 685
 Asp Pro Lys Asn Lys His Cys Val Phe Gln Gly Asp Leu Leu Leu Phe
 690 695 700
 Ser Cys Ala Gly Ala His Pro Arg His Gln Arg Val Cys Pro Cys Arg
 705 710 715 720
 Asp Phe Ile Lys Gly Gln Val Ala Leu Cys Lys Asp Cys Leu
 725 730

<210> 21
 <211> 2295
 <212> DNA
 <213> Artificial

<220>
 <223> nucleotide sequence of hybrid GnT-Va (fucosyltransferase B
 localization signal derived from A. thaliana fused to catalytic
 domain of GnT-Va derived from Homo sapiens), codon optimized for
 Nicotiana benthamiana

<220>
 <221> CDS
 <222> (1)..(2295)

<400> 21
 atg gga gtt ttc agc aat ctc aga ggt cca aga gct ggt gct act cat

Met 1	Gly	Val	Phe	Ser 5	Asn	Leu	Arg	Gly	Pro 10	Arg	Ala	Gly	Ala	Thr 15	His	
gat Asp	gaa Glu	ttt Phe	cct Pro 20	gct Ala	aca Thr	aat Asn	ggg Gly	tct Ser 25	cct Pro	tct Ser	tct Ser	tct Ser	tct Ser 30	tct Ser	cct Pro	96
tct Ser	tct Ser	tct Ser 35	att Ile	aag Lys	agg Arg	aaa Lys	ctt Leu 40	tct Ser	aat Asn	ctt Leu	ctt Leu	cct Pro 45	ctt Leu	tgt Cys	gtt Val	144
gct Ala	ctt Leu 50	gtt Val	gtt Val	att Ile	gct Ala	gaa Glu 55	atc Ile	ggg Gly	ttt Phe	ctt Leu	ggg Gly 60	aga Arg	ctt Leu	cca Pro	gaa Glu	192
tca Ser 65	tct Ser	tca Ser	atg Met	ctt Leu	aga Arg 70	gag Glu	caa Gln	atc Ile	ctc Leu	gat Asp 75	ttg Leu	tcc Ser	aag Lys	aga Arg	tac Tyr 80	240
att Ile	aag Lys	gca Ala	ctt Leu	gct Ala 85	gaa Glu	gag Glu	aac Asn	aga Arg 90	aat Asn	gtt Val	gtt Val	gat Asp	ggg Gly 95	cct Pro	tat Tyr	288
gca Ala	gga Gly	gtt Val	atg Met 100	act Thr	gcc Ala	tat Tyr	gat Asp	ctt Leu 105	aag Lys	aag Lys	aca Thr	tta Leu	gcc Ala 110	gtt Val	ctg Leu	336
ctt Leu	gac Asp	aac Asn 115	att Ile	cta Leu	cag Gln	aga Arg	ata Ile 120	ggc Gly	aag Lys	ttg Leu	gag Glu	agt Ser 125	aag Lys	gtt Val	gat Asp	384
aat Asn	ctt Leu 130	gtg Val	gtc Val	aat Asn	gga Gly	acg Thr 135	gga Gly	aca Thr	aat Asn	tca Ser	acc Thr 140	aat Asn	agc Ser	act Thr	aca Thr	432
gct Ala 145	gtt Val	cct Pro	tct Ser	tta Leu	gtt Val 150	gct Ala	ctt Leu	gag Glu	aag Lys	atc Ile 155	aat Asn	gtt Val	gcc Ala	gac Asp	ata Ile 160	480
atc Ile	aat Asn	ggg Gly	gca Ala	caa Gln 165	gaa Glu	aag Lys	tgt Cys	gta Val 170	ctt Leu 170	cct Pro	cct Pro	atg Met	gat Asp	ggg Gly 175	tac Tyr	528
cct Pro	cat His	tgt Cys	gaa Glu 180	gga Gly	aag Lys	atc Ile	aag Lys	tgg Trp 185	atg Met	aaa Lys	gat Asp	atg Met	tgg Trp 190	aga Arg	tct Ser	576
gat Asp	cct Pro	tgt Cys 195	tat Tyr	gct Ala	gat Asp	tat Tyr	ggg Gly 200	gtg Val	gat Asp	gga Gly	agt Ser	acc Thr 205	tgc Cys	tca Ser	ttt Phe	624
ttc Phe 210	atc Ile	tat Tyr	ctg Leu	tct Ser	gaa Glu	gtt Val 215	gag Glu	aat Asn	tgg Trp	tgt Cys	cct Pro 220	cat His	ctt Leu	cct Pro	tgg Trp	672
aga Arg 225	gct Ala	aag Lys	aat Asn	cca Pro	tac Tyr 230	gaa Glu	gag Glu	gct Ala	gat Asp	cat His 235	aat Asn	tca Ser	ttg Leu	gct Ala	gaa Glu 240	720
atc Ile	agg Arg	acg Thr	gac Asp	ttc Phe 245	aat Asn	atc Ile	cta Leu	tac Tyr	tct Ser 250	atg Met	atg Met	aag Lys	aag Lys	cac His 255	gaa Glu	768
gag Glu	ttc Phe	aga Arg	tgg Trp 260	atg Met	aga Arg	ctt Leu	aga Arg	att Ile 265	aga Arg	aga Arg	atg Met	gca Ala	gac Asp 270	gag Ala	tgg Trp	816
ata Ile	caa Gln	gct Ala	att Ile	aag Lys	agt Ser	ctt Leu	gct Ala	gag Glu	aag Lys	caa Gln	aac Asn	cta Leu	gaa Glu	aag Lys	agg Arg	864

275					280					285									
aag Lys	cga Arg 290	aag Lys	aag Lys	gtt Val	ctt Leu	gta Val 295	cat His	ctt Leu	ggt Gly	ttg Leu	ctt Leu 300	acc Thr	aag Lys	gag Glu	tct Ser	912			
ggt Gly 305	ttt Phe	aaa Lys	att Ile	gca Ala	gaa Glu 310	act Thr	gcc Ala	ttt Phe	tct Ser	gga Gly 315	ggt Gly	cca Pro	ctt Leu	ggt Gly	gaa Glu 320	960			
tta Leu	gta Val	cag Gln	tgg Trp	tca Ser 325	gac Asp	ttg Leu	ata Ile	aca Thr	tct Ser 330	ctc Leu	tac Tyr	ttg Leu	ctt Leu	ggc Gly 335	cat His	1008			
gac Asp	att Ile	aga Arg	att Ile 340	tct Ser	gct Ala	agt Ser	ctt Leu	gct Ala 345	gag Glu	ttg Leu	aag Lys	gaa Glu	atc Ile 350	atg Met	aag Lys	1056			
aag Lys	gtt Val	gtt Val 355	ggc Gly	aat Asn	aga Arg	tct Ser	gga Gly 360	tgt Cys	cct Pro	act Thr	gtt Val	ggt Gly 365	gat Asp	cgc Arg	att Ile	1104			
gtt Val	gaa Glu 370	ctg Leu	att Ile	tat Tyr	att Ile	gat Asp 375	ata Ile	gtc Val	gga Gly	ctt Leu	gcc Ala 380	cag Gln	ttt Phe	aag Lys	aaa Lys	1152			
act Thr 385	tta Leu	ggt Gly	cct Pro	agt Ser	tgg Trp 390	gta Val	cat His	tac Tyr	caa Gln	tgt Cys 395	atg Met	ctg Leu	aga Arg	gta Val	ctc Leu 400	1200			
gat Asp	tct Ser	ttt Phe	ggt Gly	act Thr 405	gaa Glu	cct Pro	gaa Glu	ttt Phe	aac Asn 410	cac His	gct Ala	aac Asn	tat Tyr	gct Ala 415	caa Gln	1248			
agt Ser	aaa Lys	ggt Gly	cat His 420	aag Lys	aca Thr	cca Pro	tgg Trp	gga Gly 425	aag Lys	tgg Trp	aat Asn	ctt Leu	aac Asn 430	ccc Pro	caa Gln	1296			
caa Gln	ttc Phe	tac Tyr 435	aca Thr	atg Met	ttt Phe	cct Pro	cac His 440	act Thr	ccg Pro	gat Asp	aat Asn	agt Ser 445	ttc Phe	ctt Leu	ggc Gly	1344			
ttt Phe	gtt Val 450	gtt Val	gaa Glu	cag Gln	cac His	ctt Leu 455	aat Asn	tcc Ser	tct Ser	gac Asp	ata Ile 460	cac His	cac His	att Ile	aat Asn	1392			
gaa Glu 465	att Ile	aag Lys	agg Arg	cag Gln	aac Asn 470	caa Gln	agc Ser	ctc Leu	gtt Val	tat Tyr 475	gga Gly	aaa Lys	gtt Val	gac Asp	tcc Ser 480	1440			
ttt Phe	tgg Trp	aag Lys	aac Asn	aag Lys 485	aag Lys	atc Ile	tat Tyr	ctg Leu	gat Asp 490	ata Ile	att Ile	cat His	acg Thr	tac Tyr 495	atg Met	1488			
gaa Glu	gtt Val	cat His	gct Ala 500	act Thr	gtt Val	tac Tyr	ggg Gly	tca Ser 505	tct Ser	acc Thr	aag Lys	aat Asn	att Ile 510	ccc Pro	tcc Ser	1536			
tat Tyr	gtc Val	aag Lys 515	aat Asn	cat His	ggt Gly	ata Ile	ctt Leu 520	tct Ser	gga Gly	aga Arg	gac Asp	ttg Leu 525	cag Gln	ttc Phe	ttg Leu	1584			
ctt Leu	aga Arg 530	gaa Glu	acc Thr	aaa Lys	ctt Leu	ttt Phe 535	gtc Val	ggt Gly	ctt Leu	ggt Gly	ttt Phe 540	cct Pro	tat Tyr	gaa Glu	ggt Gly	1632			
cct Pro 545	gca Ala	cca Pro	ctt Leu	gaa Glu	gct Ala 550	att Ile	gca Ala	aat Asn	gga Gly	tgt Cys 555	gct Ala	ttt Phe	ctc Leu	aac Asn	cca Pro 560	1680			

aag ttc aat cct cca aag tca agc aag aac acc gat ttc ttt att ggc Lys Phe Asn Pro Pro 565 Lys Ser Ser Lys Asn 570 Thr Asp Phe Phe Ile 575 Gly	1728
aag cct aca cta aga gaa ctt act tca caa cac cct tat gcc gaa gtt Lys Pro Thr 580 Leu Arg Glu Leu Thr Ser 585 Gln His Pro Tyr Ala 590 Glu Val	1776
ttt att gga aga cca cat gtt tgg aca gtc gat ttg aac aat caa gag Phe Ile 595 Gly Arg Pro His Val Trp 600 Thr Val Asp Leu Asn 605 Asn Gln Glu	1824
gaa gtt gag gat gca gtt aag gct atc ctt aac cag aag att gaa cca Glu Val 610 Glu Asp Ala Val Lys 615 Ala Ile Leu Asn Gln 620 Lys Ile Glu Pro	1872
tac atg ccc tac gaa ttt aca tgt gaa ggt atg ttg cag cgg att aac Tyr Met Pro Tyr Glu Phe 630 Thr Cys Glu Gly Met 635 Leu Gln Arg Ile Asn 640	1920
gca ttc att gaa aag cag gac ttt tgt cat ggt caa gtt atg tgg cca Ala Phe Ile Glu Lys 645 Gln Asp Phe Cys His 650 Gly Gln Val Met Trp 655 Pro	1968
cct ctt tca gct ctt caa gta aag tta gca gaa cct ggt caa tct tgt Pro Leu Ser 660 Ala Leu Gln Val Lys 665 Ala Glu Pro Gly Gln 670 Ser Cys	2016
aag caa gtt tgt caa gag tca cag ctt att tgc gaa cct tct ttt ttc Lys Gln Val 675 Cys Gln Glu Ser Gln 680 Leu Ile Cys Glu Pro 685 Ser Phe Phe	2064
cag cac ctc aat aag gat aag gat atg ctc aag tac aag gtt act tgc Gln His 690 Leu Asn Lys Asp Lys 695 Asp Met Leu Lys Tyr 700 Lys Val Thr Cys	2112
caa tct tct gaa ctt gca aag gat ata ctc gtt cca tct ttt gac cca Gln Ser Ser Glu Leu Ala 710 Lys Asp Ile Leu Val 715 Pro Ser Phe Asp Pro 720	2160
aag aat aag cat tgc gtc ttc caa ggt gat ctt cta ttg ttt agt tgt Lys Asn Lys His 725 Cys Val Phe Gln Gly Asp 730 Leu Leu Phe 735 Ser Cys	2208
gct gga gca cat cct aga cat caa aga gta tgt cca tgc aga gat ttc Ala Gly Ala His 740 Pro Arg His Gln Arg 745 Val Cys Pro Cys Arg 750 Asp Phe	2256
ata aag ggt caa gta gct cta tgc aag gat tgc ctt tga Ile Lys 755 Gln Val Ala Leu Cys 760 Lys Asp Cys Leu	2295

<210> 22
 <211> 764
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 22

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

Asp Glu Phe Pro Ala Thr Asn Gly Ser Pro Ser Ser Ser Ser Pro

20					25					30					
Ser	Ser	Ser	Ile	Lys	Arg	Lys	Leu	Ser	Asn	Leu	Leu	Pro	Leu	Cys	Val
		35					40					45			
Ala	Leu	Val	Val	Ile	Ala	Glu	Ile	Gly	Phe	Leu	Gly	Arg	Leu	Pro	Glu
	50					55					60				
Ser	Ser	Ser	Met	Leu	Arg	Glu	Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr
65					70					75					80
Ile	Lys	Ala	Leu	Ala	Glu	Glu	Asn	Arg	Asn	Val	Val	Asp	Gly	Pro	Tyr
				85					90					95	
Ala	Gly	Val	Met	Thr	Ala	Tyr	Asp	Leu	Lys	Lys	Thr	Leu	Ala	Val	Leu
			100					105					110		
Leu	Asp	Asn	Ile	Leu	Gln	Arg	Ile	Gly	Lys	Leu	Glu	Ser	Lys	Val	Asp
		115					120					125			
Asn	Leu	Val	Val	Asn	Gly	Thr	Gly	Thr	Asn	Ser	Thr	Asn	Ser	Thr	Thr
	130					135					140				
Ala	Val	Pro	Ser	Leu	Val	Ala	Leu	Glu	Lys	Ile	Asn	Val	Ala	Asp	Ile
145						150				155					160
Ile	Asn	Gly	Ala	Gln	Glu	Lys	Cys	Val	Leu	Pro	Pro	Met	Asp	Gly	Tyr
				165					170					175	
Pro	His	Cys	Glu	Gly	Lys	Ile	Lys	Trp	Met	Lys	Asp	Met	Trp	Arg	Ser
			180					185					190		
Asp	Pro	Cys	Tyr	Ala	Asp	Tyr	Gly	Val	Asp	Gly	Ser	Thr	Cys	Ser	Phe
		195					200					205			
Phe	Ile	Tyr	Leu	Ser	Glu	Val	Glu	Asn	Trp	Cys	Pro	His	Leu	Pro	Trp
	210					215					220				
Arg	Ala	Lys	Asn	Pro	Tyr	Glu	Glu	Ala	Asp	His	Asn	Ser	Leu	Ala	Glu
225					230					235					240
Ile	Arg	Thr	Asp	Phe	Asn	Ile	Leu	Tyr	Ser	Met	Met	Lys	Lys	His	Glu
				245					250					255	
Glu	Phe	Arg	Trp	Met	Arg	Leu	Arg	Ile	Arg	Arg	Met	Ala	Asp	Ala	Trp
			260					265					270		
Ile	Gln	Ala	Ile	Lys	Ser	Leu	Ala	Glu	Lys	Gln	Asn	Leu	Glu	Lys	Arg
		275					280					285			
Lys	Arg	Lys	Lys	Val	Leu	Val	His	Leu	Gly	Leu	Leu	Thr	Lys	Glu	Ser
	290					295					300				

Gly Phe Lys Ile Ala Glu Thr Ala Phe Ser Gly Gly Pro Leu Gly Glu
 305 310 315 320
 Leu Val Gln Trp Ser Asp Leu Ile Thr Ser Leu Tyr Leu Leu Gly His
 325 330 335
 Asp Ile Arg Ile Ser Ala Ser Leu Ala Glu Leu Lys Glu Ile Met Lys
 340 345 350
 Lys Val Val Gly Asn Arg Ser Gly Cys Pro Thr Val Gly Asp Arg Ile
 355 360 365
 Val Glu Leu Ile Tyr Ile Asp Ile Val Gly Leu Ala Gln Phe Lys Lys
 370 375 380
 Thr Leu Gly Pro Ser Trp Val His Tyr Gln Cys Met Leu Arg Val Leu
 385 390 395 400
 Asp Ser Phe Gly Thr Glu Pro Glu Phe Asn His Ala Asn Tyr Ala Gln
 405 410 415
 Ser Lys Gly His Lys Thr Pro Trp Gly Lys Trp Asn Leu Asn Pro Gln
 420 425 430
 Gln Phe Tyr Thr Met Phe Pro His Thr Pro Asp Asn Ser Phe Leu Gly
 435 440 445
 Phe Val Val Glu Gln His Leu Asn Ser Ser Asp Ile His His Ile Asn
 450 455 460
 Glu Ile Lys Arg Gln Asn Gln Ser Leu Val Tyr Gly Lys Val Asp Ser
 465 470 475 480
 Phe Trp Lys Asn Lys Lys Ile Tyr Leu Asp Ile Ile His Thr Tyr Met
 485 490 495
 Glu Val His Ala Thr Val Tyr Gly Ser Ser Thr Lys Asn Ile Pro Ser
 500 505 510
 Tyr Val Lys Asn His Gly Ile Leu Ser Gly Arg Asp Leu Gln Phe Leu
 515 520 525
 Leu Arg Glu Thr Lys Leu Phe Val Gly Leu Gly Phe Pro Tyr Glu Gly
 530 535 540
 Pro Ala Pro Leu Glu Ala Ile Ala Asn Gly Cys Ala Phe Leu Asn Pro
 545 550 555 560
 Lys Phe Asn Pro Pro Lys Ser Ser Lys Asn Thr Asp Phe Phe Ile Gly
 565 570 575

Lys Pro Thr Leu Arg Glu Leu Thr Ser Gln His Pro Tyr Ala Glu Val
 580 585 590
 Phe Ile Gly Arg Pro His Val Trp Thr Val Asp Leu Asn Asn Gln Glu
 595 600 605
 Glu Val Glu Asp Ala Val Lys Ala Ile Leu Asn Gln Lys Ile Glu Pro
 610 615 620
 Tyr Met Pro Tyr Glu Phe Thr Cys Glu Gly Met Leu Gln Arg Ile Asn
 625 630 635 640
 Ala Phe Ile Glu Lys Gln Asp Phe Cys His Gly Gln Val Met Trp Pro
 645 650 655
 Pro Leu Ser Ala Leu Gln Val Lys Leu Ala Glu Pro Gly Gln Ser Cys
 660 665 670
 Lys Gln Val Cys Gln Glu Ser Gln Leu Ile Cys Glu Pro Ser Phe Phe
 675 680 685
 Gln His Leu Asn Lys Asp Lys Asp Met Leu Lys Tyr Lys Val Thr Cys
 690 695 700
 Gln Ser Ser Glu Leu Ala Lys Asp Ile Leu Val Pro Ser Phe Asp Pro
 705 710 715 720
 Lys Asn Lys His Cys Val Phe Gln Gly Asp Leu Leu Leu Phe Ser Cys
 725 730 735
 Ala Gly Ala His Pro Arg His Gln Arg Val Cys Pro Cys Arg Asp Phe
 740 745 750
 Ile Lys Gly Gln Val Ala Leu Cys Lys Asp Cys Leu
 755 760

<210> 23
 <211> 609
 <212> DNA
 <213> Artificial

<220>
 <223> nucleotide sequence of aranesp (human erythropoietin), including
 secretion signal and HIS tag - codon optimized for Nicotiana
 benthamiana

<220>
 <221> CDS
 <222> (1)..(606)

<400> 23
 atg gcg aac aaa cac ttg tcc ctc tcc ctc ttc ctc gtc ctc ctt ggc
 Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
 1 5 10 15

48

ctg tcg gcc agc ttg gcc tca ggt gca cct cct cgt ctg att tgc gat	96
Leu Ser Ala Ser 20 Leu Ala Ser Gly 25 Ala Pro Pro Arg Leu 30 Ile Cys Asp	
tct cgc gtt ttg gaa cgg tac tta ctg gaa gct aag gag gct gag aat	144
Ser Arg Val 35 Leu Glu Arg Tyr Leu 40 Leu Glu Ala Lys 45 Glu Ala Glu Asn	
ata aca acg ggc tgt aat gag act tgc tcc cta aat gag aat ata act	192
Ile Thr 50 Thr Gly Cys Asn 55 Glu Thr Cys Ser Leu 60 Asn Glu Asn Ile Thr	
gtc ccc gat aca aaa gta aat ttc tac gct tgg aag cga atg gaa gtt	240
Val 65 Pro Asp Thr Lys 70 Val Asn Phe Tyr Ala Trp 75 Lys Arg Met Glu Val 80	
gga cag caa gct gtg gaa gtg tgg caa gga ttg gca ttg ctt agc gaa	288
Gly Gln Gln Ala 85 Val Glu Val Trp Gln 90 Gly Leu Ala Leu Leu 95 Ser Glu	
gct gtc tta agg gga caa gca ctg ctc gta aat agt agt caa gtt aac	336
Ala Val Leu 100 Arg Gly Gln Ala Leu 105 Leu Val Asn Ser Ser 110 Gln Val Asn	
gag aca ctt cag ctg cac gtt gac aag gct gtt tct gga ctt cgt tct	384
Glu Thr 115 Leu Gln Leu His Val Asp 120 Lys Ala Val Ser 125 Gly Leu Arg Ser	
cta acc aca cta ttg agg gca ctc ggg gct cag aaa gaa gct att tca	432
Leu Thr 130 Thr Leu Leu Arg Ala 135 Leu Gly Ala Gln Lys 140 Glu Ala Ile Ser	
ccg cct gac gcc gca tct gca gct cca ctt cga act atc act gct gat	480
Pro 145 Pro Asp Ala Ala 150 Ser Ala Ala Pro Leu Arg 155 Thr Ile Thr Ala Asp 160	
acc ttt aga aag ctc ttt agg gtg tat tca aac ttt ctt aga ggg aag	528
Thr Phe Arg Lys 165 Phe Arg Val Tyr Ser 170 Asn Phe Leu Arg Gly Lys 175	
ctt aaa ctc tat acg gga gag gcc tgt aga act ggt gat cgt tta gtt	576
Leu Lys Leu 180 Thr Gly Glu Ala Cys 185 Arg Thr Gly Asp 190 Arg Leu Val	
cca aga ggc tca cat cat cat cat cat cac tag	609
Pro Arg Gly 195 Ser His His His His His	

<210> 24
 <211> 202
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 24

Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
1 5 10 15
Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Pro Arg Leu Ile Cys Asp
20 25 30
Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn
35 40 45

Ile Thr Thr Gly Cys Asn Glu Thr Cys Ser Leu Asn Glu Asn Ile Thr
50 55 60

Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val
65 70 75 80

Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu
85 90 95

Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Val Asn
100 105 110

Glu Thr Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser
115 120 125

Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser
130 135 140

Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp
145 150 155 160

Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys
165 170 175

Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Leu Val
180 185 190

Pro Arg Gly Ser His His His His His His
195 200

<210> 25
<211> 33
<212> DNA
<213> artificial

<220>
<223> oligonucleotide

<400> 25
caccggtctc aaatgagtaa acggaatccg aag

33

<210> 26
<211> 36
<212> DNA
<213> artificial

<220>
<223> oligonucleotide

<400> 26
caccggtctc atacccgatg agtgaaaaac gaagta

36

<210> 27
<211> 34
<212> DNA

<213> artificial
 <220>
 <223> oligonucleotide
 <400> 27
 caccggtctc aaatgggtgt tttctcgaat cttc 34

<210> 28
 <211> 35
 <212> DNA
 <213> artificial
 <220>
 <223> oligonucleotide
 <400> 28
 caatggtctc ataccgagcc gaccagaaa cccga 35

<210> 29
 <211> 39
 <212> DNA
 <213> artificial
 <220>
 <223> oligonucleotide
 <400> 29
 caccggtctc aaggtcaaaa tgggaaagaa aaactgatt 39

<210> 30
 <211> 39
 <212> DNA
 <213> artificial
 <220>
 <223> oligonucleotide
 <400> 30
 caccggtctc aaagctcagt tgggtggcttt tttaatatg 39

<210> 31
 <211> 36
 <212> DNA
 <213> artificial
 <220>
 <223> oligonucleotide
 <400> 31
 caacggtctc aaggtgacgt tgtggacgtt taccag 36

<210> 32
 <211> 36
 <212> DNA
 <213> artificial
 <220>
 <223> oligonucleotide
 <400> 32
 caccggtctc aaagcttagt cggccttttt caggaa 36

<210>	33	
<211>	36	
<212>	DNA	
<213>	artificial	
<220>		
<223>	oligonucleotide	
<400>	33	
	caacggtctc aaggtcctga gtcattcttct atgctc	36
<210>	34	
<211>	36	
<212>	DNA	
<213>	artificial	
<220>		
<223>	oligonucleotide	
<400>	34	
	caacggtctc aaagctcaga ggcaatcctt acagag	36
<210>	35	
<211>	19	
<212>	DNA	
<213>	artificial	
<220>		
<223>	primer	
<400>	35	
	tcttgctgtg gttgccctc	19
<210>	36	
<211>	20	
<212>	DNA	
<213>	artificial	
<220>		
<223>	Reverse primer	
<400>	36	
	ccaggaagcc acgtctctga	20
<210>	37	
<211>	19	
<212>	DNA	
<213>	artificial	
<220>		
<223>	epsps probe	
<400>	37	
	ttgccgatgg cccgacagc	19
<210>	38	
<211>	20	
<212>	DNA	
<213>	artificial	
<220>		
<223>	forward primer xylg19b	
<400>	38	

gcctctctgc ctttttgat 20

<210> 39
 <211> 26
 <212> DNA
 <213> artificial

<220>
 <223> Reverse primer xylTg19b

<400> 39
 aaaggcattt actcgaatta caacaa 26

<210> 40
 <211> 27
 <212> DNA
 <213> artificial

<220>
 <223> probe xylTg19b

<400> 40
 tacgtgtacc atccccagac cccactc 27

<210> 41
 <211> 24
 <212> DNA
 <213> artificial

<220>
 <223> Forward primer EF1alfa

<400> 41
 gctgactgtg ctgtcctgat tatt 24

<210> 42
 <211> 21
 <212> DNA
 <213> artificial

<220>
 <223> Reverse primer EF1alfa

<400> 42
 tcacgggtct gtccatcctt a 21

<210> 43
 <211> 22
 <212> DNA
 <213> artificial

<220>
 <223> forward GnTIV target primer

<400> 43
 acaagcctgt gaatgttgag ag 22

<210> 44
 <211> 22
 <212> DNA
 <213> artificial

<220>

<223> Reverse GnT-IV target primer
 <400> 44
 cacctggatg ttcttgatta cc 22

 <210> 45
 <211> 22
 <212> DNA
 <213> artificial

 <220>
 <223> Forward GnT-IVb target primer
 <400> 45
 ccaacagttt tccatcatct tc 22

 <210> 46
 <211> 22
 <212> DNA
 <213> artificial

 <220>
 <223> Reverse GnT-IVb target primer
 <400> 46
 actctaacag caggttgcaa tg 22

 <210> 47
 <211> 20
 <212> DNA
 <213> artificial

 <220>
 <223> Forward GnT-Va target primer
 <400> 47
 tgcaccactt gaagctattg 20

 <210> 48
 <211> 20
 <212> DNA
 <213> artificial

 <220>
 <223> Reverse GnT-Va target primer
 <400> 48
 aatcggtgtt cttgcttgac 20