

# SEQUENCE LISTING

<110> Icon Genetics GmbH  
 Weterings, Koen  
 van Eldik, Gerben

<120> Nicotiana benthamiana plants deficient in fucosyltransferase activity

<130> PCT-15780

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<170> PatentIn version 3.5

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cta cct cta gta gtt gga ctt gtg gtt tta gtg gaa att gca ttt ctg Leu Pro Leu Val Val Gly Leu Val Val Leu Val Glu Ile Ala Phe Leu 35 40 45	144
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370

375

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Ala Glu Tyr Asp Ile Met Ala Pro Val Gln Pro Lys Thr Glu Asn Ala  
                             210                            215                            220

Leu Ala Ala Ala Phe Ile Ser Asn Cys Gly Ala Cys Asn Phe Arg Leu  
 225                            230                            235                            240

Gln Ala Leu Glu Val Leu Glu Arg Ala Asn Ile Lys Ile Asp Ser Phe  
                             245                            250                            255

Gly Ser Cys His Arg Asn Arg Asp Gly Asn Val Asp Lys Val Glu Thr  
                             260                            265                            270

Leu Lys Cys Tyr Lys Phe Ser Phe Ala Phe Glu Asn Ser Asn Glu Glu  
                             275                            280                            285

Asp Tyr Val Thr Glu Lys Phe Phe Gln Ser Leu Val Ala Gly Ser Val  
                             290                            295                            300

Pro Val Val Ile Gly Ala Pro Asn Ile Leu Asp Phe Ala Pro Ser Pro  
 305                            310                            315                            320

Asn Ser Leu Leu His Ile Lys Glu Leu Lys Asp Ala Ala Ser Val Ala  
                             325                            330                            335

Lys Ile Met Lys Tyr Leu Ala Glu His Pro Ser Ala Tyr Asn Glu Ser  
                             340                            345                            350

Leu Ser Trp Lys Phe Glu Gly Pro Ser Asp Ser Phe Lys Ala Leu Val  
                             355                            360                            365

Asp Met Ala Ala Val His Ser Ser Cys Arg Leu Cys Ile Phe Leu Ala  
                             370                            375                            380

Thr Ser Ile Arg Glu Lys Glu Glu Lys Ser Pro Lys Phe Thr Lys Arg  
 385                            390                            395                            400

Pro Cys Lys Cys Thr Arg Gly Ser Glu Thr Val Tyr His Val Tyr Val  
                             405                            410                            415

Arg Glu Arg Gly Arg Phe Asp Met Glu Ser Val Phe Leu Arg Ser Ser  
                             420                            425                            430

Asn Leu Ser Leu Glu Ala Phe Glu Ser Ala Val Leu Ser Lys Phe Lys  
 435 440 445

Ser Leu Lys His Val Pro Ile Trp Lys Glu Glu Arg Pro Gln Ile Leu  
 450 455 460

Arg Gly Gly Asp Glu Leu Lys Leu Tyr Arg Val Tyr Pro Leu Gly Met  
 465 470 475 480

Thr Gln Arg Gln Ala Leu Tyr Thr Phe Lys Phe Lys Gly Asp Ala Asp  
 485 490 495

Phe Arg Asn His Ile Glu Ser His Pro Cys Ala Asn Phe Glu Ala Ile  
 500 505 510

Phe Val

<210> 13  
 <211> 1536  
 <212> DNA  
 <213> Nicotiana benthamiana

<220>  
 <221> CDS  
 <222> (1)..(1536)

<220>  
 <221> Variation  
 <222> (910)..(910)  
 <223> G to A substitution in FucT003

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 Met Glu Thr Val Ile Pro Ile Gln Arg Ile Pro Arg Phe Glu Gly Val  
 1 5 10 15  
 ggg tca tca tcc cct aca aac gtt ccc caa aag aaa tgg tcc aat tgg 96  
 Gly Ser Ser Ser Pro Thr Asn Val Pro Gln Lys Lys Trp Ser Asn Trp  
 20 25 30  
 tta cct cta ata gtt gca ctt gtg gtt ata gtt gaa att gca ttt ctg 144  
 Leu Pro Leu Ile Val Ala Leu Val Val Ile Val Glu Ile Ala Phe Leu  
 35 40 45  
 ggt cga ctg gag atg gct gaa aaa gcc aac ctg gtc aac tct tgg act 192  
 Gly Arg Leu Glu Met Ala Glu Lys Ala Asn Leu Val Asn Ser Trp Thr  
 50 55 60  
 gac tca ttt tac cag ttt acg acg tcg ttt tgg tca acc tcc aaa gtg 240  
 Asp Ser Phe Tyr Gln Phe Thr Thr Ser Phe Trp Ser Thr Ser Lys Val  
 65 70 75 80  
 gaa att aat gag gct ggg ttg ggt gtg ttg agg agt agt gag gtt gat 288  
 Glu Ile Asn Glu Ala Gly Leu Gly Val Leu Arg Ser Ser Glu Val Asp  
 85 90 95  
 cgg aat ttg gca act ggg agc tgt gag gag tgg ttg gaa aag gaa gat 336

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

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

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 <212> PRT  
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<400> 14

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

Arg Asn Leu Ala Thr Gly Ser Cys Glu Glu Trp Leu Glu Lys Glu Asp  
 100 105 110

Ser Val Glu Tyr Ser Arg Asp Phe Asp Lys Asp Pro Ile Phe Val His  
 115 120 125

Gly Gly Glu Lys Asp Trp Lys Ser Cys Ala Val Gly Cys Asn Ile Gly  
 130 135 140

Val Asp Ser Asp Lys Lys Pro Asp Ala Ala Phe Gly Thr Pro Gln Gln  
 145 150 155 160

Ala Gly Thr Ala Ser Val Leu Arg Ser Met Glu Ser Ala Gln Tyr Tyr  
 165 170 175

Pro Glu Asn Asn Ile Val Thr Ala Arg Arg Arg Gly Tyr Asp Ile Val  
 180 185 190

Met Thr Thr Ser Leu Ser Ser Asp Val Pro Val Gly Tyr Phe Ser Trp  
 195 200 205

Ala Glu Tyr Asp Ile Met Ala Pro Val Gln Pro Lys Thr Glu Asn Ala  
 210 215 220

Leu Ala Ala Ala Phe Ile Ser Asn Cys Gly Ala Arg Asn Phe Arg Leu  
 225 230 235 240

Gln Ala Leu Glu Val Leu Glu Arg Ala Asn Ile Lys Ile Asp Ser Phe  
 245 250 255

Gly Ser Cys His Arg Asn Arg Asp Gly Asn Val Asp Lys Val Glu Thr  
 260 265 270

Leu Lys Arg Tyr Lys Phe Ser Phe Ala Phe Glu Asn Ser Asn Glu Asp  
 275 280 285

Thr Glu Lys Phe Phe Gln Ser Leu Val Ala Gly Ser Val Pro Val Val  
 290 295 300

Ile Gly Ala Pro Asn Ile Leu Asp Phe Ala Pro Ser Pro Asn Ser Leu  
 305 310 315 320

Leu His Ile Lys Glu Leu Lys Asp Ala Ala Ser Val Ala Lys Thr Met  
 325 330 335

Lys Tyr Leu Ala Glu Asn Pro Ser Ala Tyr Asn Glu Ser Leu Arg Trp  
 340 345 350

Lys Phe Glu Gly Pro Ser Asp Ser Phe Lys Ala Leu Val Asp Met Ala  
 355 360 365



Ala Val His Ser Ser Cys Arg Leu Cys Ile Phe Leu Ala Thr Ser Ile  
370 375 380

Arg Glu Lys Glu Glu Lys Ser Pro Lys Phe Thr Lys Arg Pro Cys Lys  
385 390 395 400

Cys Thr Arg Gly Ser Glu Thr Val Tyr His Val Tyr Val Arg Glu Arg  
405 410 415

Gly Arg Phe Asp Met Glu Ser Ile Phe Leu Arg Ser Ser Asn Leu Ser  
420 425 430

Leu Glu Ala Phe Glu Ser Ala Val Leu Ser Lys Phe Lys Ser Leu Lys  
435 440 445

His Val Pro Ile Trp Lys Glu Glu Arg Pro Gln Ile Leu Arg Gly Gly  
450 455 460

Glu Glu Leu Lys Leu Tyr Arg Val Tyr Pro Leu Gly Met Thr Gln Arg  
465 470 475 480

Gln Ala Leu Tyr Thr Phe Lys Phe Lys Gly Asp Ala Asp Phe Arg Asn  
485 490 495

His Ile Glu Ser His Pro Cys Ala Asn Phe Glu Ala Ile Phe Val  
500 505 510

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20

<210> 16  
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<212> DNA  
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acctccctct ttcacgtac

19

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<212> DNA  
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<400> 17  
cttctcttgg gctgagtatg 20

<210> 18  
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<220>  
<223> Primer VH034

<400> 18  
ttaggagaag gcgcaaagtc 20

<210> 19  
<211> 1066  
<212> DNA  
<213> artificial

<220>  
<223> sequence encoding FucT silencing RNA

<220>  
<221> misc\_feature  
<222> (1)..(426)  
<223> part of the Nicotiana benthamiana FucT cDNA sequence in sense orientation

<220>  
<221> Intron  
<222> (427)..(644)  
<223> second intron of the A. thaliana XylT gene

<220>  
<221> misc\_feature  
<222> (647)..(1066)  
<223> part of the Nicotiana benthamiana FucT cDNA sequence in antisense orientation

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ctagaggatc cttggcagcg gctttcattt ctaattgtgg tgctcgcaac ttccgtttgc 60  
aagcttttaga agcccttgaa agggcaaata tcagaattga ctcttatgga agttgtcatc 120  
ataacaggga tggaagagtt gacaaagtgg cagcactgaa gcgttaccag tttagcctgg 180  
cttttgggaa ttctaattgag gaggactatg taactgaaaa attctttcag tctctggtag 240  
ctgggtcaat ccctgtggtg gttggtgctc caaacatcca agactttgcg ctttctccta 300  
attcagtttt acacattaaa gagataaaaag atgctgaatc aattgccaat accatgaagt 360  
accttgetca aaaccctatt gcatataatg agtcattaag gtggaagttt gagggcccat 420  
ctgatggatc cactgcacgg tatgctcctc ttcttgttca tggatcatgat ccttatatga 480  
gcaggggaaag tccagtttag acttgtagtt agttactctt cgttatagga tttggatttc 540  
ttgcgtgttt atgggttttag tttccctcct ttgatgaata aaattgaatc ttgtatgagt 600  
ttcatatcca tgttgtgaat ctttttgcag acgcagctag gtaccggatc catcagatgg 660

gccctcaaac ttccacctta atgactcatt atatgcaata gggttttgag caagggtactt	720
catgggtattg gcaattgatt cagcatcttt tatctcttta atgtgtaaaa ctgaattagg	780
agaaggcgca aagtcttgga tgtttgagc accaaccacc acagggattg acccagctac	840
cagagactga aagaatTTTT cagttacata gtcctcctca ttagaattcc caaaagccag	900
gctaaactgg taacgcttca gtgctgccac tttgtcaact cttccatccc tgttatgatg	960
acaacttcca taagagtcaa ttctgatatt tgccctttca agggttcta aagcttgcaa	1020
acggaagttg cgagcaccac aattagaaat gaaagccgct gccaat	1066

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 <211> 83  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Part of the Nicotiana benthamiana FucTB coding sequence from 1183 to 1265

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gaaactgtct atcatgtata tgtacgtgaa agagggaggt ttgagatgga ttccattttc	60
ttaaggtcga gtgatttgtc ttt	83

<210> 21  
 <211> 390  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Sequence encoding FucT silencing RNA

<400> 21	
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ttaaggtcga gtgatttgtc tttgatccac tgcacgggat gtcctcttc ttgttcattg	120
tcatgatcct tatatgagca gggaaagtcc agtttagact tgtagttagt tactcttcgt	180
tataggattt ggatttcttg cgtgtttatg gttttagttt cctcctttg atgaataaaa	240
ttgaatcttg tatgagtttc atatccatgt tgtgaatctt ttgcagacg cagctaggta	300
ccggatcaaa gacaaatcac tcgaccttaa gaaaatggaa tccatctcaa acctccctct	360
ttcacgtaca tatacatgat agacagtttc	390