

SEQUENCE LISTING

<110> Integragen

<120> Human diabetes susceptibility TNFRSF10A gene

<130> B0579WO

<160> 18

<170> PatentIn version 3.3

<210> 1

<211> 1447

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (23)..(1426)

<400> 1

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Gly Ala Phe Leu Ala Val Thr Pro Asn Pro Gly Ser Ala Ala Ser Gly
                        15             20             25

aca gag gca gcc gcg gcc aca ccc agc aaa gtg tgg ggc tct tcc gcg      148
Thr Glu Ala Ala Ala Ala Thr Pro Ser Lys Val Trp Gly Ser Ser Ala
                        30             35             40

ggg agg att gaa cca cga ggc ggg ggc cga gga gcg ctc cct acc tcc      196
Gly Arg Ile Glu Pro Arg Gly Gly Gly Arg Gly Ala Leu Pro Thr Ser
                        45             50             55

atg gga cag cac gga ccc agt gcc cgg gcc cgg gca ggg cgc gcc cca      244
Met Gly Gln His Gly Pro Ser Ala Arg Ala Arg Ala Gly Arg Ala Pro
                        60             65             70

gga ccc agg ccg gcg cgg gaa gcc agc cct cgg ctc cgg gtc cac aag      292
Gly Pro Arg Pro Ala Arg Glu Ala Ser Pro Arg Leu Arg Val His Lys
                        75             80             85             90

acc ttc aag ttt gtc gtc gtc ggg gtc ctg ctg cag gtc gta cct agc      340
Thr Phe Lys Phe Val Val Val Gly Val Leu Leu Gln Val Val Pro Ser
                        95             100             105

tca gct gca acc atc aaa ctt cat gat caa tca att ggc aca cag caa      388
Ser Ala Ala Thr Ile Lys Leu His Asp Gln Ser Ile Gly Thr Gln Gln
                        110             115             120

tgg gaa cat agc cct ttg gga gag ttg tgt cca cca gga tct cat aga      436
Trp Glu His Ser Pro Leu Gly Glu Leu Cys Pro Pro Gly Ser His Arg
                        125             130             135

tca gaa cat cct gga gcc tgt aac cgg tgc aca gag ggt gtg ggt tac      484
Ser Glu His Pro Gly Ala Cys Asn Arg Cys Thr Glu Gly Val Gly Tyr

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acc aat gct tcc aac aat ttg ttt gct tgc ctc cca tgt aca gct tgt			532
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aaa tca gat gaa gaa gag aga agt ccc tgc acc acg acc agg aac aca			580
Lys Ser Asp Glu Glu Glu Arg Ser Pro Cys Thr Thr Thr Arg Asn Thr			
	175	180	185
gca tgt cag tgc aaa cca gga act ttc cgg aat gac aat tct gct gag			628
Ala Cys Gln Cys Lys Pro Gly Thr Phe Arg Asn Asp Asn Ser Ala Glu			
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atg tgc cgg aag tgc agc aga ggg tgc ccc aga ggg atg gtc aag gtc			676
Met Cys Arg Lys Cys Ser Arg Gly Cys Pro Arg Gly Met Val Lys Val			
	205	210	215
aag gat tgt acg ccc tgg agt gac atc gag tgt gtc cac aaa gaa tca			724
Lys Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser			
	220	225	230
ggc aat gga cat aat ata tgg gtg att ttg gtt gtg act ttg gtt gtt			772
Gly Asn Gly His Asn Ile Trp Val Ile Leu Val Val Thr Leu Val Val			
235	240	245	250
ccg ttg ctg ttg gtg gct gtg ctg att gtc tgt tgt tgc atc ggc tca			820
Pro Leu Leu Leu Val Ala Val Leu Ile Val Cys Cys Cys Ile Gly Ser			
	255	260	265
ggc tgt gga ggg gac ccc aag tgc atg gac agg gtg tgt ttc tgg cgc			868
Gly Cys Gly Gly Asp Pro Lys Cys Met Asp Arg Val Cys Phe Trp Arg			
	270	275	280
ttg ggt ctc cta cga ggg cct ggg gct gag gac aat gct cac aac gag			916
Leu Gly Leu Leu Arg Gly Pro Gly Ala Glu Asp Asn Ala His Asn Glu			
	285	290	295
att ctg agc aac gca gac tcg ctg tcc act ttc gtc tct gag cag caa			964
Ile Leu Ser Asn Ala Asp Ser Leu Ser Thr Phe Val Ser Glu Gln Gln			
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atg gaa agc cag gag ccg gca gat ttg aca ggt gtc act gta cag tcc			1012
Met Glu Ser Gln Glu Pro Ala Asp Leu Thr Gly Val Thr Val Gln Ser			
315	320	325	330
cca ggg gag gca cag tgt ctg ctg gga ccg gca gaa gct gaa ggg tct			1060
Pro Gly Glu Ala Gln Cys Leu Leu Gly Pro Ala Glu Ala Glu Gly Ser			
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cag agg agg agg ctg ctg gtt cca gca aat ggt gct gac ccc act gag			1108
Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Gly Ala Asp Pro Thr Glu			
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act ctg atg ctg ttc ttt gac aag ttt gca aac atc gtg ccc ttt gac			1156
Thr Leu Met Leu Phe Phe Asp Lys Phe Ala Asn Ile Val Pro Phe Asp			
	365	370	375
tcc tgg gac cag ctc atg agg cag ctg gac ctc acg aaa aat gag atc			1204
Ser Trp Asp Gln Leu Met Arg Gln Leu Asp Leu Thr Lys Asn Glu Ile			
	380	385	390

gat gtg gtc aga gct ggt aca gca ggc cca ggg gat gcc ttg tat gca 1252
 Asp Val Val Arg Ala Gly Thr Ala Gly Pro Gly Asp Ala Leu Tyr Ala
 395 400 405 410

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 Met Leu Met Lys Trp Val Asn Lys Thr Gly Arg Asn Ala Ser Ile His
 415 420 425

acc ctg ctg gat gcc ttg gag agg atg gaa gag aga cat gca aaa gag 1348
 Thr Leu Leu Asp Ala Leu Glu Arg Met Glu Glu Arg His Ala Lys Glu
 430 435 440

aag att cag gac ctc ttg gtg gac tct gga aag ttc atc tac tta gaa 1396
 Lys Ile Gln Asp Leu Leu Val Asp Ser Gly Lys Phe Ile Tyr Leu Glu
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Thr Pro Ser Lys Val Trp Gly Ser Ser Ala Gly Arg Ile Glu Pro Arg
 35 40 45

Gly Gly Gly Arg Gly Ala Leu Pro Thr Ser Met Gly Gln His Gly Pro
 50 55 60

Ser Ala Arg Ala Arg Ala Gly Arg Ala Pro Gly Pro Arg Pro Ala Arg
 65 70 75 80

Glu Ala Ser Pro Arg Leu Arg Val His Lys Thr Phe Lys Phe Val Val
 85 90 95

Val Gly Val Leu Leu Gln Val Val Pro Ser Ser Ala Ala Thr Ile Lys
 100 105 110

Leu His Asp Gln Ser Ile Gly Thr Gln Gln Trp Glu His Ser Pro Leu
 115 120 125

Gly Glu Leu Cys Pro Pro Gly Ser His Arg Ser Glu His Pro Gly Ala
 130 135 140

Cys Asn Arg Cys Thr Glu Gly Val Gly Tyr Thr Asn Ala Ser Asn Asn
 145 150 155 160

Leu Phe Ala Cys Leu Pro Cys Thr Ala Cys Lys Ser Asp Glu Glu Glu
 165 170 175

Arg Ser Pro Cys Thr Thr Thr Arg Asn Thr Ala Cys Gln Cys Lys Pro
 180 185 190

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

Arg Gly Cys Pro Arg Gly Met Val Lys Val Lys Asp Cys Thr Pro Trp
 210 215 220

Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly Asn Gly His Asn Ile
 225 230 235 240

Trp Val Ile Leu Val Val Thr Leu Val Val Pro Leu Leu Leu Val Ala
 245 250 255

Val Leu Ile Val Cys Cys Cys Ile Gly Ser Gly Cys Gly Gly Asp Pro
 260 265 270

Lys Cys Met Asp Arg Val Cys Phe Trp Arg Leu Gly Leu Leu Arg Gly
 275 280 285

Pro Gly Ala Glu Asp Asn Ala His Asn Glu Ile Leu Ser Asn Ala Asp
 290 295 300

Ser Leu Ser Thr Phe Val Ser Glu Gln Gln Met Glu Ser Gln Glu Pro
 305 310 315 320

Ala Asp Leu Thr Gly Val Thr Val Gln Ser Pro Gly Glu Ala Gln Cys
 325 330 335

Leu Leu Gly Pro Ala Glu Ala Glu Gly Ser Gln Arg Arg Arg Leu Leu
 340 345 350

Val Pro Ala Asn Gly Ala Asp Pro Thr Glu Thr Leu Met Leu Phe Phe
 355 360 365

Asp Lys Phe Ala Asn Ile Val Pro Phe Asp Ser Trp Asp Gln Leu Met

370

375

380

Arg Gln Leu Asp Leu Thr Lys Asn Glu Ile Asp Val Val Arg Ala Gly
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Thr Ala Gly Pro Gly Asp Ala Leu Tyr Ala Met Leu Met Lys Trp Val
 405 410 415

Asn Lys Thr Gly Arg Asn Ala Ser Ile His Thr Leu Leu Asp Ala Leu
 420 425 430

Glu Arg Met Glu Glu Arg His Ala Lys Glu Lys Ile Gln Asp Leu Leu
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Val Ser Leu Glu
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<210> 3
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 ctaagcagca ttgggcctga ttagttggtt ctaggtggtg ttctctgcga tgctgtttgg 660

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gatggaagag agacatgcaa ragagaagat tcaggacctc ttggtggact ctggaaagtt 240
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ccaagcaatt ttcaagttca tgtgacttaa gtaaatacctt actaaacaag tcagctttaa 900
aattattggt aaaataagaa aacagaagtg tcttcagaat tgtcagcata catttttgtc 960
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accttcactg aattatctat tggagctaac aaatttcagc catgtgaaca tatttgtaga 180
ctggtgagtt tgtattactg tctcatggag agagttcaaa ggtaaaagct attggatctt 240
tgtgtgtgca tataggtcta gatgtgttta tgtgtatgta catttattat taagttacat 300
gttgtgtcta ccaaattgac ttataagtaa aagagtactc ataaataaag taaataattc 360
caagcaattt tcaagttcat gtgacttaag taaatcctta ctaaacaagt cagctttaaa 420

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ctacaagccc aaccaaaaaca aaatgatctt tgagtcaagc ttttgataag taagattaaa 600
ttaatgtttg ttgttttaag aaaacagctg agtcttctga cttattgggtg aaaatatcta 660
tatatttaac tttgaagctc ttaggtgagc acctgatgtt cactggctat taaaaaatg 720
gctgacaaag aaattaacta actttaaatg atgggtgtcta atatctcaat tttcagaagc 780
aatctggata aacttaaaaa tgaaagaatt gagtaaagt aaatgggatg ttttaagtaa 840
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gtctgaatgt gagaaaaagc atgagtagga gagcaggcct tctcataaag actctgagag 180
acaagacact gatcttacgc aaaaacagtg aaacaaaga aatgttcggt taaaacaatg 240
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saaaatacat gaactggtac aaaccaacac tagggggctg tgtgcatgtg tgtacctgta 360
tgtgtgggta cgtgcatgtg tgtgtgcatg tgtgtacatg catgtgtgtg catgtgctgt 420
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ttggaatcct ccatacaacc atatgcagaa atttgggcag agatttagat ccaaatatgt 540
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 ctgccaatg tccctgagaa ggcgtcaggg gaaggatagt ctctcgtat ctgcaggggg 180
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 tggcctccct gctctggggg cagagctgca gttccaggag cttctgtgc tgggcacaca 300
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 accggttaca ggctccagga ygttctgac tatgagatcc tgggaaggga gagaaaagcc 240
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 ttggccatca gtagacccca gacagagaaa tocatcttc ttggcttggg cttgtcgtca 360
 attctgcatc tatacacacc tctgactggc gctgctgaca gaaatacaat acaaaccaca 420
 tgcaaaattc aaattctatg agagccatat taaaatagta aaaagagaat gaggtcaaat 480
 taattttaac aatgtacttt ttggacctaa aatatccaaa acattagcat ttcaacatgt 540

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aaacaagata aaacattgag atattttctt ttattttgaa tactaagtgt tcgaaacca 600
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ctaatttttt gtattttttag tagagacggg gtttcactag gtttcaccag gatggtctcg 180
atctcctgac ctcatgatcc acctgcctcg gcctcccaa gtgctgggat tacaggagt 240
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ttggagagag aaaggacctt ctcaagtctc cgagaaacta aaaagttgca taaagttaac 540
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tgtgttatga tgatgacact atcgatgata aaaatgtgat tattcagtaa tggcgctggg 180

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<210> 14
<211> 1983
<212> DNA
<213> homo sapiens

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<223> SNP311=C/G

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<213> homo sapiens

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<223> SNP312=C/G

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<220>
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 <223> SNP313=A/G

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 <211> 701
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<223> SNP314=G/T

<220>

<221> misc_feature

<222> (201)..(201)

<223> n is a, c, g, or t

<400> 17

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<210> 18

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<213> homo sapiens

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<223> SNP315=A/T

<400> 18

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