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<110> ENCODED GENOMICS, INC.

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<151> 2017-04-03

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ttctccctga ttgcggcggt tacagctgat tattctcccc tcacccaaac agtgctgctt	300
cctggcaagg tgccaccag aggagccggc tgggggcccc tggggacagg ggaggactgg	360
attagtaa at gggcatctat cgaatggctt tcatatgtgt ggctggaagg gagaagggtta	420
gggccaggaa tgggtggcagc aagggccag gtagcaatga gggttcttct aaccaccat	480
ttagggatag cgatcagaaa agggccctcg aggaggtgac cttaa atgtgt gtagaagctg	540
acggccacta cacacacaca cacacacata cacaagcatc cttgtccttg	600
gagtcggtca gcatgagcaa gagaaagatg ttcccagtg ccatgagagt ggagccctcc	660
tccctactta catccagggt ggatggccag gagatcctga gatccttcaa gactcc	716

<210> 21
 <211> 147
 <212> DNA
 <213> Mus musculus

<400> 21	
aagccacatc ctgggtggaa atatatggct tcaattccca ctcttccgga tgacctctgt	60
ggggagccct ggcttcacct tgggtccagct tcatccctta gcctcgctgc caggaaggca	120
gtgaggtcag aggctggtgc tggcgtg	147

<210> 22
 <211> 297
 <212> DNA
 <213> Mus musculus

<400> 22	
cctacctggt gcccgccaac atctgggggc catcctggcc agcgccagcg tgggtggtgaa	60
ggcactgtgc gccgtggtac tgtttctcta cctgctttcc ttcgctgtgg acacgggctg	120
cctggccgtc accccaggct accttttccc acccaacttc tggatctgga ccctggccac	180
ccacgggctc atggaacagc acgtgtggga cgtggccatt agcctggcca cagtggttgt	240
ggccgggcga ttactggagc ccctctgggg agccttggag ctgctcatct tcttctc	297

<210> 23
 <211> 101
 <212> DNA
 <213> Homo sapiens

<400> 23
 aaacggacgg gcctccgctg aaccagttag gccccagacg tgcgcataaa taaccctgc 60
 gtgctgcacc acctggggag agggggagga ccacggtaaa t 101

<210> 24
 <211> 101
 <212> DNA
 <213> Homo sapiens

<400> 24
 ggagcgagcg catagcaaaa gggacgcggg gtccttttct ctgccggtgg cactgggtag 60
 ctgtggccag gtgtggtact ttgatggggc ccagggtgg a 101

<210> 25
 <211> 101
 <212> DNA
 <213> Homo sapiens

<400> 25
 gctcaaggaa gcgtcgcagg gtcacagatc tgggggaacc ccggggaaaa gcactgaggc 60
 aaaaccgccg ctcgtctcct acaatatatg ggagggggag g 101

<210> 26
 <211> 547
 <212> DNA
 <213> Homo sapiens

<400> 26
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 gagctggatt tataatcgcc ctataaagct ccagaggcgg tcaggcacct gcagaggagc 120
 cccgccgctc cgccgactag ctgccccgc gagcaacggc ctcgtgattt cccgccgat 180
 ccggtccccg cctccccact ctgccccgc ctaccccgga gccgtgcagc cgcctctccg 240
 aatctctctc ttctcctggc gtcgcgtgc gagagggaac tagcgagaac gaggaagcag 300
 ctggaggtga cgccgggcag attacgcctg tcagggccga gccgagcgga tcgctgggcg 360
 ctgtgcagag gaaaggcggg agtgcccggc tcgctgtcgc agagccgagg tgggtaagct 420

agcgaccacc tggacttccc agcgcccaac cgtggctttt cagccaggtc ctctcctccc 480
gcggcttctc aaccaacccc atcccagcgc cggccacca acctcccga atgagtgctt 540
cctgccc 547

<210> 27
<211> 101
<212> DNA
<213> Homo sapiens

<400> 27
cagcagccga aggcgctact aggaacggtc acctgttact tttccagggg ccgtagtcga 60
cccgctgccc gagttgctgt gcgactgcgc gcgcggggct a 101

<210> 28
<211> 201
<212> DNA
<213> Homo sapiens

<400> 28
gagtgaagg tgactgtggt tcttctctgg ccaagtccga gggagaacgt aaagatatgg 60
gcctttttcc ccctctcacc ttgtctcacc aaagtcccta gtccccggag cagttagcct 120
ctttctttcc aggggaattag ccagacacaa caacgggaac cagacaccga accagacatg 180
cccgccccgt gcgccctccc c 201

<210> 29
<211> 199
<212> DNA
<213> Homo sapiens

<400> 29
gctcgtgcc tttcctccct cttgtctctc cagagccgga tcttcaaggg gagcctccgt 60
gccccgggt gctcagtcct tccggtgtgc aggaccccg aagtcctccc cgcacagctc 120
tcgcttctct ttgcagcctg tttctgcgcc ggaccagtcg aggactctgg acagtagagg 180
ccccgggacg accgagctg 199

<210> 30
<211> 1351
<212> DNA
<213> Homo sapiens

<400> 30
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agggacgcgg ggtccttttc tctgccggtg gacttgggta gctgtggcca ggtgtggtac 180
tttgatgggg cccagggctg gagctcaagg aagcgtcgca gggtcacaga tctgggggaa 240
ccccggggaa aagcactgag gcaaaaccgc cgctcgtctc ctacaatata tgggaggggg 300
aggttgagta cgttctggat tactcataag accttttttt tttccttccg ggcgcaaaac 360
cgtgagctgg atttataatc gccctataaa gctccagagg cggtcaggca cctgcagagg 420
agccccgccg ctccgccgac tagctgcccc cgcgagcaac ggctcgtga tttccccgcc 480
gatccggtcc ccgcctcccc actctgcccc cgctaccccc ggagccgtgc agccgcctct 540
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gcgctgtgca gaggaaaggc gggagtggcc ggctcgtgt cgagagccg aggtgggtaa 720
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cttctgccc cagcagccga aggcgctact aggaacggta acctgttact tttccagggg 900
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gtgactgtgg ttcttctctg gccaagtccg agggagaacg taaagatatg ggcctttttc 1020
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caggggaatta gccagacaca acaacgggaa ccagacaccg aaccagacat gcccggccc 1140
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gggagcctcc gtgccccggg ctgctcagtc cctccggtgt gcaggacccc ggaagtcctc 1260
cccgcacagc tctcgcttct ctttgagcc tgtttctgcg ccggaccagt cgaggactct 1320
ggacagtaga ggccccggga cgaccgagct g 1351

<210> 31
<211> 2051
<212> DNA
<213> Homo sapiens

<400> 31

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atdddgaagt tctgttgaca taaagaatca tgatattaat gcccattgga atgaaagggc	120
gatcaacact atggtttgaa aaggggggaaa ttgtagagca cagatgtgtt cgtgtggcag	180
tgtgctgtct ctagcaatac tcagagaaga gagagaacaa tgaaattctg attggcccca	240
gtgtgagccc agatgagggt cagctgccaa ctttctcttt cacatcttat gaaagtcatt	300
taagcacaac taactttttt tttttttttt tttttttgag acagagtctt gctctgttgc	360
ccaggacaga gtgcagtagt gactcaatct cggctcactg cagcctccac ctctaggct	420
caaacgggcc tcctgcatca gcctcccaag tagctggaat tacaggagtg gccaccattg	480
cccagctaatt ttttgtattt ttaatagata cgggggtttc accatatcac ccaggctggt	540
ctcgaactcc tggcctcaag tgatccacct gcctcggcct cccaaagtgc tgggattata	600
ggcgtcagcc actatgccc aaccgaccaa ctttttttaa aataaatatt taaaaaattg	660
gtatttcaca tatatactag tattttacatt tatccacaca aaacggacgg gcctccgctg	720
aaccagttag gccccagacg tgcgcataaa taaccctgcg gtgctgcacc acctggggag	780
aggggggagga ccacggtaaa tggagcgagc gcatagcaaa agggacgcgg ggtccttttc	840
tctgccggtg gcactgggta gctgtggcca ggtgtggtac tttgatgggg cccagggtg	900
gagctcaagg aagcgtcgca gggtcacaga tctgggggaa ccccggggaa aagcactgag	960
gcaaaaccgc cgctcgtctc ctacaatata tgggaggggg aggttgagta cgttctggat	1020
tactcataag acctttttt tttccttcg ggcgcaaac cgtgagctgg atttataatc	1080
gccctataaa gctccagagg cggtcaggca cctgcagagg agccccgcc ctccgccgac	1140
tagctgcccc cgcgagcaac ggctcgtga tttccccgcc gatccggtcc ccgcctcccc	1200
actctgcccc cgcctacccc ggagccgtgc agccgcctct ccgaatctct ctcttctcct	1260
ggcgctcgcg tgcgagaggg aactagcgag aacgaggaag cagctggagg tgacgccggg	1320
cagattacgc ctgtcagggc cgagccgagc ggatcgtgg gcgctgtgca gaggaaggc	1380
gggagtggcc ggctcgtgt cgagagccg aggtgggtaa gctagcgacc acctggactt	1440
cccagcgccc aaccgtggct tttcagccag gtcctctcct cccgcggctt ctcaaccaac	1500
cccatcccag cgccggccac ccaacctccc gaaatgagtg cttcctgccc cagcagccga	1560

aggcgctact aggaacggta acctgttact tttccagggg ccgtagtcga cccgctgccc	1620
gagttgctgt gcgactgcgc gcgcggggct agagtgaag gtgactgtgg ttctttctctg	1680
gccaagtccg agggagaacg taaagatatg ggcctttttc cccctctcac cttgtctcac	1740
caaagtcctt agtccccgga gcagttagcc tctttctttc cagggaatta gccagacaca	1800
acaacgggaa ccagacaccg aaccagacat gcccgccccg tgcgccctcc ccgctcgctg	1860
cctttcctcc ctcttgtctc tccagagccg gatcttcaag gggagcctcc gtgccccgg	1920
ctgctcagtc cctccggtgt gcaggacccc ggaagtcctc cccgcacagc tctcgcttct	1980
ctttgcagcc tgtttctgcg ccggaccagt cgaggactct ggacagtaga ggccccggga	2040
cgaccgagct g	2051

<210> 32
 <211> 1878
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown:
 RE sequence

<400> 32	
tcaacagggg gacacttggg aaagaaggat ggggacagag ccgagaggac tgttacacat	60
tagagaaaca tcagtgactg tgccagcttt ggggtagact gcacaaaagc cctgaggcag	120
cacaggcagg atccagtctg ctggtcccag gaagctaacc gtctcagaca gagcaciaag	180
caccgagaca tgtgccacaa ggcttgtgta gagaggtcag aggacagcgt acaggtccca	240
gagatcaaac tcaacctcac caggcttggc agcaagcctt taccaacca cccccaccc	300
acccaccctg cacgcgcccc tctcccctcc ccatgggtctc ccatggctat ctacttggc	360
cctaaaatgt ttaaggatga cactggctgc tgagtggaaa tgagacagca gaagtcaaca	420
gtagatttta ggaaagccag agaaaaaggc ttgtgctgtt tttagaaagc caagggacaa	480
gctaagatag ggcccaagta atgctagtat ttacatttat ccacacaaaa cggacgggcc	540
tccgctgaac cagtgaggcc ccagacgtgc gcataaataa cccctgcgtg ctgcaccacc	600
tggggagagg gggaggacca cggtaaattg agcgagcgca tagcaaaagg gacgcggggt	660
ccttttctct gccggtggca ctgggtagct gtggccaggt gtggtacttt gatggggccc	720

agggctggag ctcaaggaag cgtcgcaggg tcacagatct gggggaaccc cggggaaaag	780
cactgaggca aaaccgccgc tcgtctccta caatatatgg gagggggagg ttgagtacgt	840
tctggattac tcataagacc tttttttttt ctttccgggc gcaaaaccgt gagctggatt	900
tataatcgcc ctataaagct ccagaggcgg tcaggcacct gcagaggagc cccgccgctc	960
cgccgactag ctgccccgc gagcaacggc ctcgtgattt ccccgccgat ccggtccccg	1020
cctccccact ctgccccgc ctaccccgga gccgtgcagc gcctctccg aatctctctc	1080
ttctcctggc gctcgcgtgc gagagggaac tagcgagaac gaggaagcag ctggaggtga	1140
cgccgggcag attacgcctg tcagggccga gccgagcggg tcgctgggcg ctgtgcagag	1200
gaaaggcggg agtgcccgcc tcgctgtcgc agagccgagg tgggtaagct agcgaccacc	1260
tggacttccc agcgcccaac cgtggctttt cagccaggtc ctctcctccc gcggcttctc	1320
aaccaacccc atcccagcgc cggccacca acctcccga atgagtgtt cctgccccag	1380
cagccgaagg cgctactagg aacggtaacc tgttactttt ccaggggccg tagtcgaccc	1440
gctgccccgag ttgctgtgcg actgcgcgcg cggggctaga gtgcaaggtg actgtggttc	1500
ttctctggcc aagtccgagg gagaacgtaa agatatgggc ctttttcccc ctctcacctt	1560
gtctcaccaa agtccctagt ccccgagca gttagcctct ttctttccag ggaattagcc	1620
agacacaaca acgggaacca gacaccgaac cagacatgcc cgccccgtgc gccctccccg	1680
ctcgtgcct ttctccctc ttgtctctcc agagccggat cttcaagggg agcctccgtg	1740
ccccgggtg ctcagtcctt ccggtgtgca ggaccccgga agtcctcccc gcacagctct	1800
cgcttctctt tgcagcctgt ttctgcgccg gaccagtcga ggactctgga cagtagaggc	1860
cccgggacga ccgagctg	1878

<210> 33

<211> 19

<212> DNA

<213> Homo sapiens

<400> 33

atttacattt atccacaca

19

<210> 34

<211> 800

<212> DNA

<213> Mus musculus

<400> 34

tgccgctgga ctctcttcca aggaactagg agaaccaaga tccgtttttc tgccaagggc	60
tgcccccccc acgcccccaa cccctcacc ccatcccca cagaaagaaa tcttgaggta	120
gctggagctt cttctgtggg tgtgacagga ctgccattct cctctgtagt ctgcagaagc	180
ctgccattcc accatttaaa cctgtgactc caggccttaa gcctgttgaa ggtcagagtc	240
cagaagggtc atatgtgcaa ctgcctaggg agagtccca ctcgcagggc caagaggagt	300
cccccggtct gaggtgtggg ggcggggacg tgcactgggc gctgggacca cggctggggc	360
tcaggactcg cgagcttgga ttcggatcgg tttgcgcgag ccagtagggc aggctccggg	420
gtgaacgggg acgagggggc cgcgggcaca ggcgggcgcg tgaccgcggc gggggcgcgc	480
ggaggcgggc cggccaagga gagggaggga gggaatgagg gagggagcga caggggaggg	540
cggcgccggc aggttggcgg cggccgctat ttgagcgag gtcccgggcc aggcgctcaa	600
agcgcttgga gccagcgcg cggggagatc gctgcgcgca gcccgcagag gcgctgcggc	660
cagtgcagcc ccggaggccc cgcgcggaga aggaggtgga gaagaggccg gctttccgcc	720
cgccgcccgc gccccccac ctccatccc cgcgccgt cccccctccc tccccgcggc	780
gccgcatctt gaatgaaac	800

<210> 35

<211> 1335

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 35

gagtaattca taaaaagga ctgcccctg cttggggaa tcccaggac cgtcgtaaa	60
ctcccactaa ctagaacc agatcgct gcgttccgc cccctaccc gccgctctc	120
gtcatcactg aggtggagaa gagcatcgt gaggtccgg tgcccgtcag tgggcagagc	180
gcacatgcc cacagtcccc gagaagttgg ggggaggggt cggcaattga accggtgcct	240
agagaagggt gcgcggggta aactgggaaa gtgatgtcgt gtactggctc cgccttttc	300
ccgagggtgg gggagaaccg tatataagt cagtagtcgc cgtgaacgtt ctttttcgca	360

acgggtttgc cgccagaaca caggttaagt ccgtgtgtgg ttcccgcggg cctggcctct	420
ttacgggtta tggcccttgc gtgccttgaa ttactttcac gcccctggct gcagtacgtg	480
attcttgatc ccgagcttcg ggttggaagt ggggtgggaga gttcgaggcc ttgcgcttaa	540
ggagccccctt cgcctcgtgc ttgagttgag gcctggcttg ggcgctgggg ccgccgcgtg	600
cgaatctggg ggcaccttcg cgcctgtctc gctgctttcg ataagtctct agccatttaa	660
aatttttgat gacctgctgc gacgcttttt ttctggcaag atagtcttgt aaatgcgggc	720
caagatctgc aacttggtat ttcggttttt ggggccgcgg gcggcgacgg ggcccgtgcg	780
tcccagcgca catgttcggc gaggcggggc ctgcgagcgc ggccaccgag aatcggacgg	840
gggtagtctc aagctggccg gcctgctctg gtgcctggcc tcgcgccgcc gtgtatcgcc	900
ccgccctggg cggcaaggct ggcccggtcg gcaccagttg cgtgagcgga aagatggccg	960
cttcccggcc ctgctgcagg gagctcaaaa tggaggacgc ggcgctcggg agagcgggcg	1020
ggtgagtcac ccacacaaag gaaaagggcc tttccgtcct cagccgtcgc ttcatgtgac	1080
tccacggagt accgggcgcc gtccaggcac ctcgattagt tctcgagctt ttggagtacg	1140
tcgtctttag gttgggggga ggggttttat gcgatggagt ttccccacac tgagtgggtg	1200
gagactgaag ttaggccagc ttggcacttg atgtaattct ctttgaatt tgcccttttt	1260
gagtttggat cttggttcat tctcaagcct cagacagtgg ttcaaagttt ttttcttcca	1320
tttcaggtgt cgtga	1335

<210> 36

<211> 222

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 36

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5				10					15		

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
			20					25					30		

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
210 215 220

<210> 37

<211> 218

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
SCN1B sequence

<400> 37

Met Gly Thr Leu Leu Ala Leu Val Val Gly Ala Ala Leu Val Ser Ser
1 5 10 15

Ala Trp Gly Gly Cys Val Glu Val Asp Ser Asp Thr Glu Ala Val Tyr
20 25 30

Gly Met Thr Phe Lys Ile Leu Cys Ile Ser Cys Lys Arg Arg Ser Glu
35 40 45

Thr Thr Ala Glu Thr Phe Thr Glu Trp Thr Phe Arg Gln Lys Gly Thr
50 55 60

Glu Glu Phe Val Lys Ile Leu Arg Tyr Glu Asn Glu Val Leu Gln Leu
65 70 75 80

Glu Glu Asp Glu Arg Phe Glu Gly Arg Val Val Trp Asn Gly Ser Arg
85 90 95

Gly Thr Lys Asp Leu Gln Asp Leu Ser Ile Phe Ile Thr Asn Val Thr
100 105 110

Tyr Asn His Ser Gly Asp Tyr Glu Cys His Val Tyr Arg Leu Leu Phe
115 120 125

Phe Asp Asn Tyr Glu His Asn Thr Ser Val Val Lys Lys Ile His Leu
130 135 140

Glu Val Val Asp Lys Ala Asn Arg Asp Met Ala Ser Ile Val Ser Glu
145 150 155 160

Ile Met Met Tyr Val Leu Ile Val Val Leu Thr Ile Trp Leu Val Ala
165 170 175

Glu Met Val Tyr Cys Tyr Lys Lys Ile Ala Ala Ala Thr Glu Ala Ala
180 185 190

Ala Gln Glu Asn Ala Ser Glu Tyr Leu Ala Ile Thr Ser Glu Ser Lys
195 200 205

Glu Asn Cys Thr Gly Val Gln Val Ala Glu
210 215

<210> 38
<211> 215
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
SCN2B sequence

<400> 38
Met His Arg Asp Ala Trp Leu Pro Arg Pro Ala Phe Ser Leu Thr Gly
1 5 10 15

Leu Ser Leu Phe Phe Ser Leu Val Pro Pro Gly Arg Ser Met Glu Val
20 25 30

Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp Ala Arg Leu
35 40 45

Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His Lys Gln Phe Ser
50 55 60

Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys Ser Glu Glu Met Phe
65 70 75 80

Leu Gln Phe Arg Met Lys Ile Ile Asn Leu Lys Leu Glu Arg Phe Gln
85 90 95

Asp Arg Val Glu Phe Ser Gly Asn Pro Ser Lys Tyr Asp Val Ser Val
100 105 110

Met Leu Arg Asn Val Gln Pro Glu Asp Glu Gly Ile Tyr Asn Cys Tyr
115 120 125

Ile Met Asn Pro Pro Asp Arg His Arg Gly His Gly Lys Ile His Leu
130 135 140

Gln Val Leu Met Glu Glu Pro Pro Glu Arg Asp Ser Thr Val Ala Val
 145 150 155 160

Ile Val Gly Ala Ser Val Gly Gly Phe Leu Ala Val Val Ile Leu Val
 165 170 175

Leu Met Val Val Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser
 180 185 190

Thr Asp Asp Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly
 195 200 205

Asn Pro Asp Asp Gly Ala Lys
 210 215

<210> 39
 <211> 2009
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 SCN1A sequence

<400> 39
 Met Glu Gln Thr Val Leu Val Pro Pro Gly Pro Asp Ser Phe Asn Phe
 1 5 10 15

Phe Thr Arg Glu Ser Leu Ala Ala Ile Glu Arg Arg Ile Ala Glu Glu
 20 25 30

Lys Ala Lys Asn Pro Lys Pro Asp Lys Lys Asp Asp Asp Glu Asn Gly
 35 40 45

Pro Lys Pro Asn Ser Asp Leu Glu Ala Gly Lys Asn Leu Pro Phe Ile
 50 55 60

Tyr Gly Asp Ile Pro Pro Glu Met Val Ser Glu Pro Leu Glu Asp Leu
 65 70 75 80

Asp Pro Tyr Tyr Ile Asn Lys Lys Thr Phe Ile Val Leu Asn Lys Gly

85

90

95

Lys Ala Ile Phe Arg Phe Ser Ala Thr Ser Ala Leu Tyr Ile Leu Thr
 100 105 110

Pro Phe Asn Pro Leu Arg Lys Ile Ala Ile Lys Ile Leu Val His Ser
 115 120 125

Leu Phe Ser Met Leu Ile Met Cys Thr Ile Leu Thr Asn Cys Val Phe
 130 135 140

Met Thr Met Ser Asn Pro Pro Asp Trp Thr Lys Asn Val Glu Tyr Thr
 145 150 155 160

Phe Thr Gly Ile Tyr Thr Phe Glu Ser Leu Ile Lys Ile Ile Ala Arg
 165 170 175

Gly Phe Cys Leu Glu Asp Phe Thr Phe Leu Arg Asp Pro Trp Asn Trp
 180 185 190

Leu Asp Phe Thr Val Ile Thr Phe Ala Tyr Val Thr Glu Phe Val Asp
 195 200 205

Leu Gly Asn Val Ser Ala Leu Arg Thr Phe Arg Val Leu Arg Ala Leu
 210 215 220

Lys Thr Ile Ser Val Ile Pro Gly Leu Lys Thr Ile Val Gly Ala Leu
 225 230 235 240

Ile Gln Ser Val Lys Lys Leu Ser Asp Val Met Ile Leu Thr Val Phe
 245 250 255

Cys Leu Ser Val Phe Ala Leu Ile Gly Leu Gln Leu Phe Met Gly Asn
 260 265 270

Leu Arg Asn Lys Cys Ile Gln Trp Pro Pro Thr Asn Ala Ser Leu Glu
 275 280 285

Glu His Ser Ile Glu Lys Asn Ile Thr Val Asn Tyr Asn Gly Thr Leu
 290 295 300

Ile Asn Glu Thr Val Phe Glu Phe Asp Trp Lys Ser Tyr Ile Gln Asp
 305 310 315 320

Ser Arg Tyr His Tyr Phe Leu Glu Gly Phe Leu Asp Ala Leu Leu Cys
 325 330 335

Gly Asn Ser Ser Asp Ala Gly Gln Cys Pro Glu Gly Tyr Met Cys Val
 340 345 350

Lys Ala Gly Arg Asn Pro Asn Tyr Gly Tyr Thr Ser Phe Asp Thr Phe
 355 360 365

Ser Trp Ala Phe Leu Ser Leu Phe Arg Leu Met Thr Gln Asp Phe Trp
 370 375 380

Glu Asn Leu Tyr Gln Leu Thr Leu Arg Ala Ala Gly Lys Thr Tyr Met
 385 390 395 400

Ile Phe Phe Val Leu Val Ile Phe Leu Gly Ser Phe Tyr Leu Ile Asn
 405 410 415

Leu Ile Leu Ala Val Val Ala Met Ala Tyr Glu Glu Gln Asn Gln Ala
 420 425 430

Thr Leu Glu Glu Ala Glu Gln Lys Glu Ala Glu Phe Gln Gln Met Ile
 435 440 445

Glu Gln Leu Lys Lys Gln Gln Glu Ala Ala Gln Gln Ala Ala Thr Ala
 450 455 460

Thr Ala Ser Glu His Ser Arg Glu Pro Ser Ala Ala Gly Arg Leu Ser
 465 470 475 480

Asp Ser Ser Ser Glu Ala Ser Lys Leu Ser Ser Lys Ser Ala Lys Glu
 485 490 495

Arg Arg Asn Arg Arg Lys Lys Arg Lys Gln Lys Glu Gln Ser Gly Gly
 500 505 510

Glu Glu Lys Asp Glu Asp Glu Phe Gln Lys Ser Glu Ser Glu Asp Ser
515 520 525

Ile Arg Arg Lys Gly Phe Arg Phe Ser Ile Glu Gly Asn Arg Leu Thr
530 535 540

Tyr Glu Lys Arg Tyr Ser Ser Pro His Gln Ser Leu Leu Ser Ile Arg
545 550 555 560

Gly Ser Leu Phe Ser Pro Arg Arg Asn Ser Arg Thr Ser Leu Phe Ser
565 570 575

Phe Arg Gly Arg Ala Lys Asp Val Gly Ser Glu Asn Asp Phe Ala Asp
580 585 590

Asp Glu His Ser Thr Phe Glu Asp Asn Glu Ser Arg Arg Asp Ser Leu
595 600 605

Phe Val Pro Arg Arg His Gly Glu Arg Arg Asn Ser Asn Leu Ser Gln
610 615 620

Thr Ser Arg Ser Ser Arg Met Leu Ala Val Phe Pro Ala Asn Gly Lys
625 630 635 640

Met His Ser Thr Val Asp Cys Asn Gly Val Val Ser Leu Val Gly Gly
645 650 655

Pro Ser Val Pro Thr Ser Pro Val Gly Gln Leu Leu Pro Glu Val Ile
660 665 670

Ile Asp Lys Pro Ala Thr Asp Asp Asn Gly Thr Thr Thr Glu Thr Glu
675 680 685

Met Arg Lys Arg Arg Ser Ser Ser Phe His Val Ser Met Asp Phe Leu
690 695 700

Glu Asp Pro Ser Gln Arg Gln Arg Ala Met Ser Ile Ala Ser Ile Leu
705 710 715 720

Thr Asn Thr Val Glu Glu Leu Glu Glu Ser Arg Gln Lys Cys Pro Pro
725 730 735

Cys Trp Tyr Lys Phe Ser Asn Ile Phe Leu Ile Trp Asp Cys Ser Pro
740 745 750

Tyr Trp Leu Lys Val Lys His Val Val Asn Leu Val Val Met Asp Pro
755 760 765

Phe Val Asp Leu Ala Ile Thr Ile Cys Ile Val Leu Asn Thr Leu Phe
770 775 780

Met Ala Met Glu His Tyr Pro Met Thr Asp His Phe Asn Asn Val Leu
785 790 795 800

Thr Val Gly Asn Leu Val Phe Thr Gly Ile Phe Thr Ala Glu Met Phe
805 810 815

Leu Lys Ile Ile Ala Met Asp Pro Tyr Tyr Tyr Phe Gln Glu Gly Trp
820 825 830

Asn Ile Phe Asp Gly Phe Ile Val Thr Leu Ser Leu Val Glu Leu Gly
835 840 845

Leu Ala Asn Val Glu Gly Leu Ser Val Leu Arg Ser Phe Arg Leu Leu
850 855 860

Arg Val Phe Lys Leu Ala Lys Ser Trp Pro Thr Leu Asn Met Leu Ile
865 870 875 880

Lys Ile Ile Gly Asn Ser Val Gly Ala Leu Gly Asn Leu Thr Leu Val
885 890 895

Leu Ala Ile Ile Val Phe Ile Phe Ala Val Val Gly Met Gln Leu Phe
900 905 910

Gly Lys Ser Tyr Lys Asp Cys Val Cys Lys Ile Ala Ser Asp Cys Gln
915 920 925

Leu Pro Arg Trp His Met Asn Asp Phe Phe His Ser Phe Leu Ile Val

930

935

940

Phe Arg Val Leu Cys Gly Glu Trp Ile Glu Thr Met Trp Asp Cys Met
 945 950 955 960

Glu Val Ala Gly Gln Ala Met Cys Leu Thr Val Phe Met Met Val Met
 965 970 975

Val Ile Gly Asn Leu Val Val Leu Asn Leu Phe Leu Ala Leu Leu Leu
 980 985 990

Ser Ser Phe Ser Ala Asp Asn Leu Ala Ala Thr Asp Asp Asp Asn Glu
 995 1000 1005

Met Asn Asn Leu Gln Ile Ala Val Asp Arg Met His Lys Gly Val
 1010 1015 1020

Ala Tyr Val Lys Arg Lys Ile Tyr Glu Phe Ile Gln Gln Ser Phe
 1025 1030 1035

Ile Arg Lys Gln Lys Ile Leu Asp Glu Ile Lys Pro Leu Asp Asp
 1040 1045 1050

Leu Asn Asn Lys Lys Asp Ser Cys Met Ser Asn His Thr Ala Glu
 1055 1060 1065

Ile Gly Lys Asp Leu Asp Tyr Leu Lys Asp Val Asn Gly Thr Thr
 1070 1075 1080

Ser Gly Ile Gly Thr Gly Ser Ser Val Glu Lys Tyr Ile Ile Asp
 1085 1090 1095

Glu Ser Asp Tyr Met Ser Phe Ile Asn Asn Pro Ser Leu Thr Val
 1100 1105 1110

Thr Val Pro Ile Ala Val Gly Glu Ser Asp Phe Glu Asn Leu Asn
 1115 1120 1125

Thr Glu Asp Phe Ser Ser Glu Ser Asp Leu Glu Glu Ser Lys Glu
 1130 1135 1140

Lys Leu Asn Glu Ser Ser Ser Ser Ser Glu Gly Ser Thr Val Asp
 1145 1150 1155

 Ile Gly Ala Pro Val Glu Glu Gln Pro Val Val Glu Pro Glu Glu
 1160 1165 1170

 Thr Leu Glu Pro Glu Ala Cys Phe Thr Glu Gly Cys Val Gln Arg
 1175 1180 1185

 Phe Lys Cys Cys Gln Ile Asn Val Glu Glu Gly Arg Gly Lys Gln
 1190 1195 1200

 Trp Trp Asn Leu Arg Arg Thr Cys Phe Arg Ile Val Glu His Asn
 1205 1210 1215

 Trp Phe Glu Thr Phe Ile Val Phe Met Ile Leu Leu Ser Ser Gly
 1220 1225 1230

 Ala Leu Ala Phe Glu Asp Ile Tyr Ile Asp Gln Arg Lys Thr Ile
 1235 1240 1245

 Lys Thr Met Leu Glu Tyr Ala Asp Lys Val Phe Thr Tyr Ile Phe
 1250 1255 1260

 Ile Leu Glu Met Leu Leu Lys Trp Val Ala Tyr Gly Tyr Gln Thr
 1265 1270 1275

 Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp Phe Leu Ile Val Asp
 1280 1285 1290

 Val Ser Leu Val Ser Leu Thr Ala Asn Ala Leu Gly Tyr Ser Glu
 1295 1300 1305

 Leu Gly Ala Ile Lys Ser Leu Arg Thr Leu Arg Ala Leu Arg Pro
 1310 1315 1320

 Leu Arg Ala Leu Ser Arg Phe Glu Gly Met Arg Val Val Val Asn
 1325 1330 1335

Ala	Leu	Leu	Gly	Ala	Ile	Pro	Ser	Ile	Met	Asn	Val	Leu	Leu	Val
1340						1345					1350			
Cys	Leu	Ile	Phe	Trp	Leu	Ile	Phe	Ser	Ile	Met	Gly	Val	Asn	Leu
1355						1360					1365			
Phe	Ala	Gly	Lys	Phe	Tyr	His	Cys	Ile	Asn	Thr	Thr	Thr	Gly	Asp
1370						1375					1380			
Arg	Phe	Asp	Ile	Glu	Asp	Val	Asn	Asn	His	Thr	Asp	Cys	Leu	Lys
1385						1390					1395			
Leu	Ile	Glu	Arg	Asn	Glu	Thr	Ala	Arg	Trp	Lys	Asn	Val	Lys	Val
1400						1405					1410			
Asn	Phe	Asp	Asn	Val	Gly	Phe	Gly	Tyr	Leu	Ser	Leu	Leu	Gln	Val
1415						1420					1425			
Ala	Thr	Phe	Lys	Gly	Trp	Met	Asp	Ile	Met	Tyr	Ala	Ala	Val	Asp
1430						1435					1440			
Ser	Arg	Asn	Val	Glu	Leu	Gln	Pro	Lys	Tyr	Glu	Glu	Ser	Leu	Tyr
1445						1450					1455			
Met	Tyr	Leu	Tyr	Phe	Val	Ile	Phe	Ile	Ile	Phe	Gly	Ser	Phe	Phe
1460						1465					1470			
Thr	Leu	Asn	Leu	Phe	Ile	Gly	Val	Ile	Ile	Asp	Asn	Phe	Asn	Gln
1475						1480					1485			
Gln	Lys	Lys	Lys	Phe	Gly	Gly	Gln	Asp	Ile	Phe	Met	Thr	Glu	Glu
1490						1495					1500			
Gln	Lys	Lys	Tyr	Tyr	Asn	Ala	Met	Lys	Lys	Leu	Gly	Ser	Lys	Lys
1505						1510					1515			
Pro	Gln	Lys	Pro	Ile	Pro	Arg	Pro	Gly	Asn	Lys	Phe	Gln	Gly	Met
1520						1525					1530			

Val Phe Asp Phe Val Thr Arg Gln Val Phe Asp Ile Ser Ile Met
1535 1540 1545

Ile Leu Ile Cys Leu Asn Met Val Thr Met Met Val Glu Thr Asp
1550 1555 1560

Asp Gln Ser Glu Tyr Val Thr Thr Ile Leu Ser Arg Ile Asn Leu
1565 1570 1575

Val Phe Ile Val Leu Phe Thr Gly Glu Cys Val Leu Lys Leu Ile
1580 1585 1590

Ser Leu Arg His Tyr Tyr Phe Thr Ile Gly Trp Asn Ile Phe Asp
1595 1600 1605

Phe Val Val Val Ile Leu Ser Ile Val Gly Met Phe Leu Ala Glu
1610 1615 1620

Leu Ile Glu Lys Tyr Phe Val Ser Pro Thr Leu Phe Arg Val Ile
1625 1630 1635

Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg Leu Ile Lys Gly Ala
1640 1645 1650

Lys Gly Ile Arg Thr Leu Leu Phe Ala Leu Met Met Ser Leu Pro
1655 1660 1665

Ala Leu Phe Asn Ile Gly Leu Leu Leu Phe Leu Val Met Phe Ile
1670 1675 1680

Tyr Ala Ile Phe Gly Met Ser Asn Phe Ala Tyr Val Lys Arg Glu
1685 1690 1695

Val Gly Ile Asp Asp Met Phe Asn Phe Glu Thr Phe Gly Asn Ser
1700 1705 1710

Met Ile Cys Leu Phe Gln Ile Thr Thr Ser Ala Gly Trp Asp Gly
1715 1720 1725

Leu Leu Ala Pro Ile Leu Asn Ser Lys Pro Pro Asp Cys Asp Pro

1730						1735						1740			
Asn	Lys	Val	Asn	Pro	Gly	Ser	Ser	Val	Lys	Gly	Asp	Cys	Gly	Asn	
1745						1750					1755				
Pro	Ser	Val	Gly	Ile	Phe	Phe	Phe	Val	Ser	Tyr	Ile	Ile	Ile	Ser	
1760						1765					1770				
Phe	Leu	Val	Val	Val	Asn	Met	Tyr	Ile	Ala	Val	Ile	Leu	Glu	Asn	
1775						1780					1785				
Phe	Ser	Val	Ala	Thr	Glu	Glu	Ser	Ala	Glu	Pro	Leu	Ser	Glu	Asp	
1790						1795					1800				
Asp	Phe	Glu	Met	Phe	Tyr	Glu	Val	Trp	Glu	Lys	Phe	Asp	Pro	Asp	
1805						1810					1815				
Ala	Thr	Gln	Phe	Met	Glu	Phe	Glu	Lys	Leu	Ser	Gln	Phe	Ala	Ala	
1820						1825					1830				
Ala	Leu	Glu	Pro	Pro	Leu	Asn	Leu	Pro	Gln	Pro	Asn	Lys	Leu	Gln	
1835						1840					1845				
Leu	Ile	Ala	Met	Asp	Leu	Pro	Met	Val	Ser	Gly	Asp	Arg	Ile	His	
1850						1855					1860				
Cys	Leu	Asp	Ile	Leu	Phe	Ala	Phe	Thr	Lys	Arg	Val	Leu	Gly	Glu	
1865						1870					1875				
Ser	Gly	Glu	Met	Asp	Ala	Leu	Arg	Ile	Gln	Met	Glu	Glu	Arg	Phe	
1880						1885					1890				
Met	Ala	Ser	Asn	Pro	Ser	Lys	Val	Ser	Tyr	Gln	Pro	Ile	Thr	Thr	
1895						1900					1905				
Thr	Leu	Lys	Arg	Lys	Gln	Glu	Glu	Val	Ser	Ala	Val	Ile	Ile	Gln	
1910						1915					1920				
Arg	Ala	Tyr	Arg	Arg	His	Leu	Leu	Lys	Arg	Thr	Val	Lys	Gln	Ala	
1925						1930					1935				

Ser Phe Thr Tyr Asn Lys Asn Lys Ile Lys Gly Gly Ala Asn Leu
1940 1945 1950

Leu Ile Lys Glu Asp Met Ile Ile Asp Arg Ile Asn Glu Asn Ser
1955 1960 1965

Ile Thr Glu Lys Thr Asp Leu Thr Met Ser Thr Ala Ala Cys Pro
1970 1975 1980

Pro Ser Tyr Asp Arg Val Thr Lys Pro Ile Val Glu Lys His Glu
1985 1990 1995

Gln Glu Gly Lys Asp Glu Lys Ala Lys Gly Lys
2000 2005

<210> 40

<211> 603

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
STXBP1 sequence

<400> 40

Met Ala Pro Ile Gly Leu Lys Ala Val Val Gly Glu Lys Ile Met His
1 5 10 15

Asp Val Ile Lys Lys Val Lys Lys Lys Gly Glu Trp Lys Val Leu Val
20 25 30

Val Asp Gln Leu Ser Met Arg Met Leu Ser Ser Cys Cys Lys Met Thr
35 40 45

Asp Ile Met Thr Glu Gly Ile Thr Ile Val Glu Asp Ile Asn Lys Arg
50 55 60

Arg Glu Pro Leu Pro Ser Leu Glu Ala Val Tyr Leu Ile Thr Pro Ser
65 70 75 80

Glu Lys Ser Val His Ser Leu Ile Ser Asp Phe Lys Asp Pro Pro Thr

85

90

95

Ala Lys Tyr Arg Ala Ala His Val Phe Phe Thr Asp Ser Cys Pro Asp
 100 105 110

Ala Leu Phe Asn Glu Leu Val Lys Ser Arg Ala Ala Lys Val Ile Lys
 115 120 125

Thr Leu Thr Glu Ile Asn Ile Ala Phe Leu Pro Tyr Glu Ser Gln Val
 130 135 140

Tyr Ser Leu Asp Ser Ala Asp Ser Phe Gln Ser Phe Tyr Ser Pro His
 145 150 155 160

Lys Ala Gln Met Lys Asn Pro Ile Leu Glu Arg Leu Ala Glu Gln Ile
 165 170 175

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

Gly Glu Tyr Lys Asp Asn Ala Leu Leu Ala Gln Leu Ile Gln Asp Lys
 195 200 205

Leu Asp Ala Tyr Lys Ala Asp Asp Pro Thr Met Gly Glu Gly Pro Asp
 210 215 220

Lys Ala Arg Ser Gln Leu Leu Ile Leu Asp Arg Gly Phe Asp Pro Ser
 225 230 235 240

Ser Pro Val Leu His Glu Leu Thr Phe Gln Ala Met Ser Tyr Asp Leu
 245 250 255

Leu Pro Ile Glu Asn Asp Val Tyr Lys Tyr Glu Thr Ser Gly Ile Gly
 260 265 270

Glu Ala Arg Val Lys Glu Val Leu Leu Asp Glu Asp Asp Asp Leu Trp
 275 280 285

Ile Ala Leu Arg His Lys His Ile Ala Glu Val Ser Gln Glu Val Thr
 290 295 300

Arg Ser Leu Lys Asp Phe Ser Ser Ser Lys Arg Met Asn Thr Gly Glu
 305 310 315 320

Lys Thr Thr Met Arg Asp Leu Ser Gln Met Leu Lys Lys Met Pro Gln
 325 330 335

Tyr Gln Lys Glu Leu Ser Lys Tyr Ser Thr His Leu His Leu Ala Glu
 340 345 350

Asp Cys Met Lys His Tyr Gln Gly Thr Val Asp Lys Leu Cys Arg Val
 355 360 365

Glu Gln Asp Leu Ala Met Gly Thr Asp Ala Glu Gly Glu Lys Ile Lys
 370 375 380

Asp Pro Met Arg Ala Ile Val Pro Ile Leu Leu Asp Ala Asn Val Ser
 385 390 395 400

Thr Tyr Asp Lys Ile Arg Ile Ile Leu Leu Tyr Ile Phe Leu Lys Asn
 405 410 415

Gly Ile Thr Glu Glu Asn Leu Asn Lys Leu Ile Gln His Ala Gln Ile
 420 425 430

Pro Pro Glu Asp Ser Glu Ile Ile Thr Asn Met Ala His Leu Gly Val
 435 440 445

Pro Ile Val Thr Asp Ser Thr Leu Arg Arg Arg Ser Lys Pro Glu Arg
 450 455 460

Lys Glu Arg Ile Ser Glu Gln Thr Tyr Gln Leu Ser Arg Trp Thr Pro
 465 470 475 480

Ile Ile Lys Asp Ile Met Glu Asp Thr Ile Glu Asp Lys Leu Asp Thr
 485 490 495

Lys His Tyr Pro Tyr Ile Ser Thr Arg Ser Ser Ala Ser Phe Ser Thr
 500 505 510

Thr Ala Val Ser Ala Arg Tyr Gly His Trp His Lys Asn Lys Ala Pro
515 520 525

Gly Glu Tyr Arg Ser Gly Pro Arg Leu Ile Ile Phe Ile Leu Gly Gly
530 535 540

Val Ser Leu Asn Glu Met Arg Cys Ala Tyr Glu Val Thr Gln Ala Asn
545 550 555 560

Gly Lys Trp Glu Val Leu Ile Gly Ser Thr His Ile Leu Thr Pro Thr
565 570 575

Lys Phe Leu Met Asp Leu Arg His Pro Asp Phe Arg Glu Ser Ser Arg
580 585 590

Val Ser Phe Glu Asp Gln Ala Pro Thr Met Glu
595 600

<210> 41
<211> 511
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Kv3.1 sequence

<400> 41
Met Gly Gln Gly Asp Glu Ser Glu Arg Ile Val Ile Asn Val Gly Gly
1 5 10 15

Thr Arg His Gln Thr Tyr Arg Ser Thr Leu Arg Thr Leu Pro Gly Thr
20 25 30

Arg Leu Ala Trp Leu Ala Glu Pro Asp Ala His Ser His Phe Asp Tyr
35 40 45

Asp Pro Arg Ala Asp Glu Phe Phe Phe Asp Arg His Pro Gly Val Phe
50 55 60

Ala His Ile Leu Asn Tyr Tyr Arg Thr Gly Lys Leu His Cys Pro Ala
65 70 75 80

Asp Val Cys Gly Pro Leu Tyr Glu Glu Glu Leu Ala Phe Trp Gly Ile
85 90 95

Asp Glu Thr Asp Val Glu Pro Cys Cys Trp Met Thr Tyr Arg Gln His
100 105 110

Arg Asp Ala Glu Glu Ala Leu Asp Ser Phe Gly Gly Ala Pro Leu Asp
115 120 125

Asn Ser Ala Asp Asp Ala Asp Ala Asp Gly Pro Gly Asp Ser Gly Asp
130 135 140

Gly Glu Asp Glu Leu Glu Met Thr Lys Arg Leu Ala Leu Ser Asp Ser
145 150 155 160

Pro Asp Gly Arg Pro Gly Gly Phe Trp Arg Arg Trp Gln Pro Arg Ile
165 170 175

Trp Ala Leu Phe Glu Asp Pro Tyr Ser Ser Arg Tyr Ala Arg Tyr Val
180 185 190

Ala Phe Ala Ser Leu Phe Phe Ile Leu Val Ser Ile Thr Thr Phe Cys
195 200 205

Leu Glu Thr His Glu Arg Phe Asn Pro Ile Val Asn Lys Thr Glu Ile
210 215 220

Glu Asn Val Arg Asn Gly Thr Gln Val Arg Tyr Tyr Arg Glu Ala Glu
225 230 235 240

Thr Glu Ala Phe Leu Thr Tyr Ile Glu Gly Val Cys Val Val Trp Phe
245 250 255

Thr Phe Glu Phe Leu Met Arg Val Ile Phe Cys Pro Asn Lys Val Glu
260 265 270

Phe Ile Lys Asn Ser Leu Asn Ile Ile Asp Phe Val Ala Ile Leu Pro
275 280 285

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

Asp Val Leu Gly Phe Leu Arg Val Val Arg Phe Val Arg Ile Leu Arg
305 310 315 320

Ile Phe Lys Leu Thr Arg His Phe Val Gly Leu Arg Val Leu Gly His
325 330 335

Thr Leu Arg Ala Ser Thr Asn Glu Phe Leu Leu Leu Ile Ile Phe Leu
340 345 350

Ala Leu Gly Val Leu Ile Phe Ala Thr Met Ile Tyr Tyr Ala Glu Arg
355 360 365

Ile Gly Ala Gln Pro Asn Asp Pro Ser Ala Ser Glu His Thr His Phe
370 375 380

Lys Asn Ile Pro Ile Gly Phe Trp Trp Ala Val Val Thr Met Thr Thr
385 390 395 400

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

Gly Ala Leu Cys Ala Leu Ala Gly Val Leu Thr Ile Ala Met Pro Val
420 425 430

Pro Val Ile Val Asn Asn Phe Gly Met Tyr Tyr Ser Leu Ala Met Ala
435 440 445

Lys Gln Lys Leu Pro Lys Lys Lys Lys Lys His Ile Pro Arg Pro Pro
450 455 460

Gln Leu Gly Ser Pro Asn Tyr Cys Lys Ser Val Val Asn Ser Pro His
465 470 475 480

His Ser Thr Gln Ser Asp Thr Cys Pro Leu Ala Gln Glu Glu Ile Leu
485 490 495

Glu Ile Asn Arg Ala Gly Arg Lys Pro Leu Arg Gly Met Ser Ile
500 505 510

<210> 42
<211> 639
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Kv3.2 sequence

<400> 42
Met Gly Lys Ile Glu Ser Asn Glu Arg Val Ile Leu Asn Val Gly Gly
1 5 10 15

Thr Arg His Glu Thr Tyr Arg Ser Thr Leu Lys Thr Leu Pro Gly Thr
20 25 30

Arg Leu Ala Leu Leu Ala Ser Ser Glu Pro Gln Gly Asp Cys Leu Thr
35 40 45

Ala Ala Gly Asp Lys Leu Gln Pro Leu Pro Pro Pro Leu Ser Pro Pro
50 55 60

Pro Arg Pro Pro Pro Leu Ser Pro Val Pro Ser Gly Cys Phe Glu Gly
65 70 75 80

Gly Ala Gly Asn Cys Ser Ser His Gly Gly Asn Gly Gly Asn Gly Gly
85 90 95

Ser Asp His Pro Gly Gly Gly Arg Glu Phe Phe Phe Asp Arg His Pro
100 105 110

Gly Val Phe Ala Tyr Val Leu Asn Tyr Tyr Arg Thr Gly Lys Leu His
115 120 125

Cys Pro Ala Asp Val Cys Gly Pro Leu Phe Glu Glu Glu Leu Ala Phe
130 135 140

Trp Gly Ile Asp Glu Thr Asp Val Glu Pro Cys Cys Trp Met Thr Tyr
145 150 155 160

Arg Gln His Arg Asp Ala Glu Glu Ala Leu Asp Ile Phe Glu Thr Pro
165 170 175

Asp Leu Ile Gly Gly Asp Pro Gly Asp Asp Glu Asp Leu Ala Ala Lys
180 185 190

Arg Leu Gly Ile Glu Asp Ala Ala Gly Leu Gly Gly Pro Asp Gly Lys
195 200 205

Ser Gly Arg Trp Arg Lys Leu Gln Pro Arg Met Trp Ala Leu Phe Glu
210 215 220

Asp Pro Tyr Ser Ser Arg Ala Ala Arg Phe Ile Ala Phe Ala Ser Leu
225 230 235 240

Phe Phe Ile Leu Val Ser Ile Thr Thr Phe Cys Leu Glu Thr His Glu
245 250 255

Ala Phe Asn Ile Val Lys Asn Lys Thr Glu Pro Val Ile Asn Gly Thr
260 265 270

Ser Pro Val Leu Gln Tyr Glu Ile Glu Thr Asp Pro Ala Leu Thr Tyr
275 280 285

Val Glu Gly Val Cys Val Val Trp Phe Thr Phe Glu Phe Leu Val Arg
290 295 300

Ile Val Phe Ser Pro Asn Lys Leu Glu Phe Ile Lys Asn Leu Leu Asn
305 310 315 320

Ile Ile Asp Phe Val Ala Ile Leu Pro Phe Tyr Leu Glu Val Gly Leu
325 330 335

Ser Gly Leu Ser Ser Lys Ala Ala Lys Asp Val Leu Gly Phe Leu Arg
340 345 350

Val Val Arg Phe Val Arg Ile Leu Arg Ile Phe Lys Leu Thr Arg His
355 360 365

Phe Val Gly Leu Arg Val Leu Gly His Thr Leu Arg Ala Ser Thr Asn
 370 375 380

Glu Phe Leu Leu Leu Ile Ile Phe Leu Ala Leu Gly Val Leu Ile Phe
 385 390 395 400

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

Pro Ser Ala Ser Glu His Thr Gln Phe Lys Asn Ile Pro Ile Gly Phe
 420 425 430

Trp Trp Ala Val Val Thr Met Thr Thr Leu Gly Tyr Gly Asp Met Tyr
 435 440 445

Pro Gln Thr Trp Ser Gly Met Leu Val Gly Ala Leu Cys Ala Leu Ala
 450 455 460

Gly Val Leu Thr Ile Ala Met Pro Val Pro Val Ile Val Asn Asn Phe
 465 470 475 480

Gly Met Tyr Tyr Ser Leu Ala Met Ala Lys Gln Lys Leu Pro Arg Lys
 485 490 495

Arg Lys Lys His Ile Pro Pro Ala Pro Leu Ala Ser Ser Pro Thr Phe
 500 505 510

Cys Lys Thr Glu Leu Asn Met Ala Cys Asn Ser Thr Gln Ser Asp Thr
 515 520 525

Cys Leu Gly Lys Glu Asn Arg Leu Leu Glu His Asn Arg Ser Val Leu
 530 535 540

Ser Gly Asp Asp Ser Thr Gly Ser Glu Pro Pro Leu Ser Pro Pro Glu
 545 550 555 560

Arg Leu Pro Ile Arg Arg Ser Ser Thr Arg Asp Lys Asn Arg Arg Gly
 565 570 575

Glu Thr Cys Phe Leu Leu Thr Thr Gly Asp Tyr Thr Cys Ala Ser Asp

580

585

590

Gly Gly Ile Arg Lys Ala Ser Thr Leu Glu Pro Met Glu Ser Thr Ala
 595 600 605

Gln Thr Lys Gly Asp Thr Arg Pro Glu Ala His Trp Asn Cys Ala His
 610 615 620

Leu Leu Asn Phe Gly Cys Pro Thr Gly Ser Ser Phe Pro Thr Leu
 625 630 635

<210> 43

<211> 757

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 Kv3.3 sequence

<400> 43

Met Leu Ser Ser Val Cys Val Ser Ser Phe Arg Gly Arg Gln Gly Ala
 1 5 10 15

Ser Lys Gln Gln Pro Ala Pro Pro Pro Gln Pro Pro Glu Ser Pro Pro
 20 25 30

Pro Pro Pro Leu Pro Pro Gln Gln Gln Gln Pro Ala Gln Pro Gly Pro
 35 40 45

Ala Ala Ser Pro Ala Gly Pro Pro Ala Pro Arg Gly Pro Gly Asp Arg
 50 55 60

Arg Ala Glu Pro Cys Pro Gly Leu Pro Ala Ala Ala Met Gly Arg His
 65 70 75 80

Gly Gly Gly Gly Gly Asp Ser Gly Lys Ile Val Ile Asn Val Gly Gly
 85 90 95

Val Arg His Glu Thr Tyr Arg Ser Thr Leu Arg Thr Leu Pro Gly Thr
 100 105 110

Arg Leu Ala Gly Leu Thr Glu Pro Glu Ala Ala Ala Arg Phe Asp Tyr
115 120 125

Asp Pro Gly Ala Asp Glu Phe Phe Phe Asp Arg His Pro Gly Val Phe
130 135 140

Ala Tyr Val Leu Asn Tyr Tyr Arg Thr Gly Lys Leu His Cys Pro Ala
145 150 155 160

Asp Val Cys Gly Pro Leu Phe Glu Glu Glu Leu Gly Phe Trp Gly Ile
165 170 175

Asp Glu Thr Asp Val Glu Ala Cys Cys Trp Met Thr Tyr Arg Gln His
180 185 190

Arg Asp Ala Glu Glu Ala Leu Asp Ser Phe Glu Ala Pro Asp Pro Ala
195 200 205

Gly Ala Ala Asn Ala Ala Asn Ala Ala Gly Ala His Asp Gly Gly Leu
210 215 220

Asp Asp Glu Ala Gly Ala Gly Gly Gly Gly Leu Asp Gly Ala Gly Gly
225 230 235 240

Glu Leu Lys Arg Leu Cys Phe Gln Asp Ala Gly Gly Gly Ala Gly Gly
245 250 255

Pro Pro Gly Gly Ala Gly Gly Ala Gly Gly Thr Trp Trp Arg Arg Trp
260 265 270

Gln Pro Arg Val Trp Ala Leu Phe Glu Asp Pro Tyr Ser Ser Arg Ala
275 280 285

Ala Arg Tyr Val Ala Phe Ala Ser Leu Phe Phe Ile Leu Ile Ser Ile
290 295 300

Thr Thr Phe Cys Leu Glu Thr His Glu Gly Phe Ile His Ile Ser Asn
305 310 315 320

Lys Thr Val Thr Gln Ala Ser Pro Ile Pro Gly Ala Pro Pro Glu Asn

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

Tyr Tyr Ser Leu Ala Met Ala Lys Gln Lys Leu Pro Lys Lys Lys Asn
545 550 555 560

Lys His Ile Pro Arg Pro Pro Gln Pro Gly Ser Pro Asn Tyr Cys Lys
565 570 575

Pro Asp Pro Pro Pro Pro Pro Pro Pro His Pro His His Gly Ser Gly
580 585 590

Gly Ile Ser Pro Pro Pro Pro Ile Thr Pro Pro Ser Met Gly Val Thr
595 600 605

Val Ala Gly Ala Tyr Pro Ala Gly Pro His Thr His Pro Gly Leu Leu
610 615 620

Arg Gly Gly Ala Gly Gly Leu Gly Ile Met Gly Leu Pro Pro Leu Pro
625 630 635 640

Ala Pro Gly Glu Pro Cys Pro Leu Ala Gln Glu Glu Val Ile Glu Ile
645 650 655

Asn Arg Ala Asp Pro Arg Pro Asn Gly Asp Pro Ala Ala Ala Ala Leu
660 665 670

Ala His Glu Asp Cys Pro Ala Ile Asp Gln Pro Ala Met Ser Pro Glu
675 680 685

Asp Lys Ser Pro Ile Thr Pro Gly Ser Arg Gly Arg Tyr Ser Arg Asp
690 695 700

Arg Ala Cys Phe Leu Leu Thr Asp Tyr Ala Pro Ser Pro Asp Gly Ser
705 710 715 720

Ile Arg Lys Ala Thr Gly Ala Pro Pro Leu Pro Pro Gln Asp Trp Arg
725 730 735

Lys Pro Gly Pro Pro Ser Phe Leu Pro Asp Leu Asn Ala Asn Ala Ala
740 745 750

Ala Trp Ile Ser Pro
755