SEQUENCE LISTING

<110> ATGen Co. Ltd.

<120> METHOD OF DIAGNOSING CANCER AND DIAGNOSIS KIT USING MEASUREMENT OF NK CELL ACTIVITY

<130> 08921046WO

<150> KR 2011-0012983
<151> 2011-02-14

<160> 29

<170> PatentIn version 3.5

<210> 1
<211> 474
<212> DNA
<213> Artificial Sequence

<220>
<223> SP-hIL2 fusion coding sequence

<400> 1
atggaccctg acaatgaggc ttatgaaatg ccttctgagg aagggtatca agactacgaa 60

cctgaagccg gatcccctac ttcaagttct acaaagaaaa cacagctaca actggagcat 120

ttactgctgg atttacagat gattttgaat ggaattaata attacaagaa tcccaaactc 180

accaggatgc tcacatttaa gttttacatg cccaagaagg ccacagaact gaaacatctt 240

cagtgtctag aagaagaact caaacctctg gaggaagtgc taaatttagc tcaaagcaaa 300

aactttcact taagacccag ggacttaatc agcaatatca acgtaatagt tctggaacta 360

aagggatctg aaacaacatt catgtgtgaa tatgctgatg agacagcaac cattgtagaa 420

tttctgaaca gatggattac cttttgtcaa agcatcatct caacactgac ttga 474

<210> 2
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> SP-hIL2 fusion polypeptide

<400> 2

Met Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro Ser Glu Glu Gly Tyr
1 5 10 15

Gln Asp Tyr Glu Pro Glu Ala Gly Ser Pro Thr Ser Ser Ser Thr Lys
20 25 30

Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile
35 40 45

Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu
50 55 60

Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu
65 70 75 80

Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu
85 90 95

Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn
100 105 110

Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met
115 120 125

Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg
130 135 140

Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr
145 150 155

<210> 3
<211> 1014
<212> DNA
<213> Artificial Sequence

<220>
<223> SP-hIL12p40 fusion coding sequence

<400> 3
atggaccctg acaatgaggc ttatgaaatg ccttctgagg aagggtatca agactacgaa 60

cctgaagccg gatccatatg ggaactgaag aaagatgttt atgtcgtaga attggattgg 120

tatccggatg cccctggaga aatggtggtc ctcacctgtg acacccctga agaagatggt 180

atcacctgga ccttggacca gagcagtgag gtcttaggct ctggcaaaac cctgaccatc 240

caagtcaaag agtttggaga tgctggccag tacacctgtc acaaaggagg cgaggttcta 300

agccattcgc tcctgctgct tcacaaaaag gaagatggaa tttggtccac tgatatttta 360

aaggaccaga aagaacccaa aaataagacc tttctaagat gcgaggccaa gaattattct 420

ggacgtttca cctgctggtg gctgacgaca atcagtactg atttgacatt cagtgtcaaa 480

agcagcagag gctcttctga cccccaaggg gtgacgtgcg gagctgctac actctctgca 540

gagagagtca gaggggacaa caaggagtat gagtactcag tggagtgcca ggaggacagt 600

gcctgcccag ctgctgagga gagtctgccc attgaggtca tggtggatgc cgttcacaag 660

ctcaagtatg aaaactacac cagcagcttc ttcatcaggg acatcatcaa acctgaccca 720

cccaagaact tgcagctgaa gccattaaag aattctcggc aggtggaggt cagctgggag 780

taccctgaca cctggagtac tccacattcc tacttctccc tgacattctg cgttcaggtc 840

cagggcaaga gcaagagaga aaagaaagat agagtcttca cggacaagac ctcagccacg 900

gtcatctgcc gcaaaaatgc cagcattagc gtgcgggccc aggaccgcta ctatagctca 960

tcttggagcg aatgggcatc tgtgccctgc agtcatcatc accatcacca ctga 1014

<210> 4
<211> 337
<212> PRT
<213> Artificial Sequence

<220>
<223> SP-hIL12p40 fusion polypeptide

<400> 4

Met Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro Ser Glu Glu Gly Tyr
1 5 10 15

Gln Asp Tyr Glu Pro Glu Ala Gly Ser Ile Trp Glu Leu Lys Lys Asp
20 25 30

Val Tyr Val Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met
35 40 45

Val Val Leu Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr
50 55 60

Leu Asp Gln Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile
65 70 75 80

Gln Val Lys Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly
85 90 95

Gly Glu Val Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp
100 105 110

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

Lys Thr Phe Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr
130 135 140

Cys Trp Trp Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys
145 150 155 160

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

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

Ser Val Glu Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser
195 200 205

Leu Pro Ile Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu
210 215 220

Asn Tyr Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro
225 230 235 240

Pro Lys Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu
245 250 255

Val Ser Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe
260 265 270

Ser Leu Thr Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys
275 280 285

Lys Asp Arg Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg
290 295 300

Lys Asn Ala Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser
305 310 315 320

Ser Trp Ser Glu Trp Ala Ser Val Pro Cys Ser His His His His His
325 330 335

His

<210> 5
<211> 687
<212> DNA
<213> Artificial Sequence

<220>
<223> SP-hIL12p35 fusion coding sequence

<400> 5
atggaccctg acaatgaggc ttatgaaatg ccttctgagg aagggtatca agactacgaa 60

cctgaagccg gatccagaaa cctccccgtg gccactccag acccaggaat gttcccatgc 120

cttcaccact cccaaaacct gctgagggcc gtcagcaaca tgctccagaa ggccagacaa 180

actctagaat tttacccttg cacttctgaa gagattgatc atgaagatat cacaaaagat 240

aaaaccagca cagtggaggc ctgtttacca ttggaattaa ccaagaatga aagctgtctt 300

aactcaagag aaacttcatt tatcacaaac ggtagttgcc tggcctccag aaagacctct 360

tttatgatgg ccctgtgcct tagtagtatt tatgaagact tgaagatgta ccaggtggag 420

ttcaagacca tgaatgcaaa gcttctgatg gaccctaaga ggcaaatctt tctagatcaa 480

aacatgctgg cagttattga tgagctgatg caggccctga atttcaacag tgagactgtg 540

ccacaaaaat cctcccttga agaaccggat ttttataaaa ctaaaatcaa gctctgcata 600

cttcttcatg ctttcagaat tcgggcagtg actattgata gagtgatgag ctatctgaat 660

gcttcccatc atcaccatca ccactga 687

<210> 6
<211> 228
<212> PRT
<213> Artificial Sequence

<220>
<223> SP-hIL12p35 fusion polypeptide

<400> 6

Met Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro Ser Glu Glu Gly Tyr
1 5 10 15

Gln Asp Tyr Glu Pro Glu Ala Gly Ser Arg Asn Leu Pro Val Ala Thr
20 25 30

Pro Asp Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu
35 40 45

Arg Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe
50 55 60

Tyr Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn
85 90 95

Glu Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser
100 105 110

Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser
115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met
130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln

145 150 155 160

Asn Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn
165 170 175

Ser Glu Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
195 200 205

Ala Val Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser His His
210 215 220

His His His His
225

<210> 7
<211> 420
<212> DNA
<213> Artificial Sequence

<220>
<223> hIL15-SP fusion coding sequence

<400> 7
atgaactggg tgaatgtaat aagtgatttg aaaaaaattg aagatcttat tcaatctatg 60

catattgatg ctactttata tacggaaagt gatgttcacc ccagttgcaa agtaacagca 120

atgaagtgct ttctcttgga gttacaagtt atttcacttg agtccggaga tgcaagtatt 180

catgatacag tagaaaatct gatcatccta gcaaacaaca gtttgtcttc taatgggaat 240

gtaacagaat ctggatgcaa agaatgtgag gaactggagg aaaaaaatat taaagaattt 300

ttgcagagtt ttgtacatat tgtccaaatg ttcatcaaca cttctggatc cgatcctgac 360

aatgaggctt atgaaatgcc ttctgaggaa gggtatcaag actacgaacc tgaagcctaa 420

<210> 8
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> hIL15-SP fusion polypeptide

<400> 8

Met Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu
1 5 10 15

Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val
20 25 30

His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu
35 40 45

Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val
50 55 60

Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn
65 70 75 80

Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn
85 90 95

Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile
100 105 110

Asn Thr Ser Gly Ser Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro Ser
115 120 125

Glu Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala
130 135

<210> 9
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> SP-hIL18 fusion coding sequence

<400> 9
atggaccctg acaatgaggc ttatgaaatg ccttctgagg aagggtatca agactacgaa 60

cctgaagccg gatcctactt tggcaagctt gaatctaaat tatcagtcat aagaaatttg 120

aatgaccaag ttctcttcat tgaccaagga aatcggcctc tatttgaaga tatgactgat 180

tctgactgta gagataatgc accccggacc atatttatta taagtatgta taaagatagc 240

cagcctagag gtatggctgt aactatctct gtgaagtgtg agaaaatttc aactctctcc 300

tgtgagaaca aaattatttc ctttaaggaa atgaatcctc ctgataacat caaggataca 360

aaaagtgaca tcatattctt tcagagaagt gtcccaggac atgataataa gatgcaattt 420

gaatcttcat catacgaagg atactttcta gcttgtgaaa aagagagaga ccttttttaaa 480

ctcattttga aaaaagagga tgaattgggg gatagatcta taatgttcac tgttcaaaac 540

gaagactag 549

<210> 10
<211> 182
<212> PRT

<213> Artificial Sequence

<220>
<223> SP-hIL18 fusion polypeptide

<400> 10

Met Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro Ser Glu Glu Gly Tyr
1 5 10 15

Gln Asp Tyr Glu Pro Glu Ala Gly Ser Tyr Phe Gly Lys Leu Glu Ser
20 25 30

Lys Leu Ser Val Ile Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp
35 40 45

Gln Gly Asn Arg Pro Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg
50 55 60

Asp Asn Ala Pro Arg Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser
65 70 75 80

Gln Pro Arg Gly Met Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile
85 90 95

Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn
100 105 110

Pro Pro Asp Asn Ile Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln
115 120 125

Arg Ser Val Pro Gly His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser
130 135 140

Tyr Glu Gly Tyr Phe Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys
145 150 155 160

Leu Ile Leu Lys Lys Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe
165 170 175

Thr Val Gln Asn Glu Asp
180

<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> IL2-22-BamH1 forward primer

<400> 11
acaggatccc ctacttcaag ttct 24

<210> 12
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> IL2-153-Xho reverse primer

<400> 12
cactctcgag tcaagtcagt gttgagat 28

<210> 13
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> IL12-p40-23-BamH1 forward primer

<400> 13
gtggatccat atgggaactg aagaaagatg 30

<210> 14
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> IL12-p40-328-CT-His reverse primer

<400> 14
atggtgatga tgactgcagg gcacagatgc cc 32

<210> 15
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> IL12-p35-23-BamH1 forward primer

<400> 15
gtggatccag aaacctcccc gtggc 25

<210> 16
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> IL12-p35-219-CT-His reverse primer

<400> 16
atggtgatga tgggaagcat tcagatagc 29

<210> 17
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> IL15-49-Nde forward primer

<400> 17
gagtcaagca tatgaactgg gtgaatgtaa 30

<210> 18
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> IL15-162-BamH1 reverse primer

<400> 18
gtggatccag aagtgttgat gaac 24

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> IL18-37-BamH1 forward primer

<400> 19
gtggatccta ctttggcaag cttg 24

<210> 20
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> IL18-193-EcoR1 reverse primer

<400> 20
agactggaat tcctagtctt cgttttg 27

<210> 21
<211> 140
<212> PRT
<213> Homo Sapien

<220>
<223> human alpha synuclein

<400> 21

Met Asp Val Phe Met Lys Gly Leu Ser Lys Ala Lys Glu Gly Val Val
1 5 10 15

Ala Ala Ala Glu Lys Thr Lys Gln Gly Val Ala Glu Ala Ala Gly Lys
20 25 30

Thr Lys Glu Gly Val Leu Tyr Val Gly Ser Lys Thr Lys Glu Gly Val
35 40 45

Val His Gly Val Ala Thr Val Ala Glu Lys Thr Lys Glu Gln Val Thr
50 55 60

Asn Val Gly Gly Ala Val Val Thr Gly Val Thr Ala Val Ala Gln Lys
65 70 75 80

Thr Val Glu Gly Ala Gly Ser Ile Ala Ala Ala Thr Gly Phe Val Lys
85 90 95

Lys Asp Gln Leu Gly Lys Asn Glu Glu Gly Ala Pro Gln Glu Gly Ile
100 105 110

Leu Glu Asp Met Pro Val Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro
115 120 125

Ser Glu Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala
130 135 140

<210> 22
<211> 13
<212> PRT
<213> Homo Sapien

<220>
<223> human alpha synuclein / C-terminal acidic tail domain residues 103-115

<400> 22

Asn Glu Glu Gly Ala Pro Gln Glu Gly Ile Leu Glu Asp
1 5 10

<210> 23
<211> 23
<212> PRT
<213> Homo Sapien

<220>
<223> human alpha synuclein / C-terminal acidic tail domain residues 114-126

<400> 23

Glu Glu Gly Ala Pro Gln Glu Gly Ile Leu Glu Asp Met Pro Val Asp
1 5 10 15

Pro Asp Asn Glu Ala Tyr Glu
20

<210> 24
<211> 22
<212> PRT
<213> Homo Sapien

<220>
<223> human alpha synuclein / C-terminal acidic tail domain residues 119-140

<400> 24

Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro Ser Glu Glu Gly Tyr Gln
1 5 10 15

Asp Tyr Glu Pro Glu Ala
20

<210> 25
<211> 11
<212> PRT
<213> Homo Sapien

<220>
<223> human alpha synuclein / C-terminal acidic tail domain residues 130-140

<400> 25

Glu Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala
1 5 10

<210> 26
<211> 134
<212> PRT
<213> Homo Sapien

<220>
<223> human beta synuclein

<400> 26

Met Asp Val Phe Met Lys Gly Leu Ser Met Ala Lys Glu Gly Val Val
1 5 10 15

Ala Ala Ala Glu Lys Thr Lys Gln Gly Val Thr Glu Ala Ala Glu Lys
20 25 30

Thr Lys Glu Gly Val Leu Tyr Val Gly Ser Lys Thr Arg Glu Gly Val
35 40 45

Val Gln Gly Val Ala Ser Val Ala Glu Lys Thr Lys Glu Gln Ala Ser
50 55 60

His Leu Gly Gly Ala Val Phe Ser Gly Ala Gly Asn Ile Ala Ala Ala
65 70 75 80

Thr Gly Leu Val Lys Arg Glu Glu Phe Pro Thr Asp Leu Lys Pro Glu
85 90 95

Glu Val Ala Gln Glu Ala Ala Glu Glu Pro Leu Ile Glu Pro Leu Met
100 105 110

Glu Pro Glu Gly Glu Ser Tyr Glu Asp Pro Pro Gln Glu Glu Tyr Gln
115 120 125

Glu Tyr Glu Pro Glu Ala
130

<210> 27
<211> 50
<212> PRT
<213> Homo Sapien

<220>
<223> human beta synuclein / C-terminal acidic tail domain residues 85-134

<400> 27

Lys Arg Glu Glu Phe Pro Thr Asp Leu Lys Pro Glu Glu Val Ala Gln
1 5 10 15

Glu Ala Ala Glu Glu Pro Leu Ile Glu Pro Leu Met Glu Pro Glu Gly
20 25 30

Glu Ser Tyr Glu Asp Pro Pro Gln Glu Glu Tyr Gln Glu Tyr Glu Pro
35 40 45

Glu Ala
50

<210> 28
<211> 127
<212> PRT
<213> Homo Sapien

<220>
<223> human gamma synuclein (synoretin)

<400> 28

Met Asp Val Phe Lys Lys Gly Phe Ser Ile Ala Lys Glu Gly Val Val
1 5 10 15

Gly Ala Val Glu Lys Thr Lys Gln Gly Val Thr Glu Ala Ala Glu Lys
20 25 30

Thr Lys Glu Gly Val Met Tyr Val Gly Ala Lys Thr Lys Glu Asn Val
35 40 45

Val Gln Ser Val Thr Ser Val Ala Glu Lys Thr Lys Glu Gln Ala Asn
50 55 60

Ala Val Ser Glu Ala Val Val Ser Ser Val Asn Thr Val Ala Thr Lys
65 70 75 80

Thr Val Glu Glu Ala Glu Asn Ile Ala Val Thr Ser Gly Val Val Arg
85 90 95

Lys Glu Asp Leu Arg Pro Ser Ala Pro Gln Gln Glu Gly Glu Ala Ser
100 105 110

Lys Glu Lys Glu Glu Val Ala Glu Glu Ala Gln Ser Gly Gly Asp
115 120 125

<210> 29
<211> 32
<212> PRT
<213> Homo Sapien

<220>
<223> human gamma synuclein (synoretin) / C-terminal acidic tail domain residues 96-127

<400> 29

Arg Lys Glu Asp Leu Arg Pro Ser Ala Pro Gln Gln Glu Gly Glu Ala
1 5 10 15

Ser Lys Glu Lys Glu Glu Val Ala Glu Glu Ala Gln Ser Gly Gly Asp
20 25 30