

TEAP001WO-seq1-000001
SEQUENCE LISTING

<110> Tan, Patrick Boon Ooi
Tan, Puay Hoon

<120> Breast Fibroadenoma Susceptibility Mutations And Use Thereof

<130> TEA-P001WO

<150> SG10201402277X
<151> 2014-05-12

<160> 16

<170> PatentIn version 3.5

<210> 1
<211> 22
<212> DNA
<213> Homo sapiens

<400> 1
tgttctacac ggaaccctcc tc 22

<210> 2
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2
ctgggcaaat gccaatgaga t 21

<210> 3
<211> 22
<212> DNA
<213> Homo sapiens

<400> 3
ttctcctgcc ctactctccc ac 22

<210> 4
<211> 22
<212> DNA
<213> Homo sapiens

<400> 4
caggctgggtt attgaaacct tg 22

<210> 5
<211> 25
<212> DNA
<213> Homo sapiens

<400> 5
ccctaaggaa aaaacaacta aacgc 25

<210> 6
<211> 20
<212> DNA
<213> Homo sapiens

<400> 6
ctgccatgct catccccaga 20

<210> 7
 <211> 23
 <212> DNA
 <213> Homo sapiens

 <400> 7
 cttgttcctt cttttctcct gcc 23

 <210> 8
 <211> 22
 <212> DNA
 <213> Homo sapiens

 <400> 8
 gttttacatt caaggccgtc ag 22

 <210> 9
 <211> 21
 <212> DNA
 <213> Homo sapiens

 <400> 9
 caactaaacg ccgctttcct g 21

 <210> 10
 <211> 22
 <212> DNA
 <213> Homo sapiens

 <400> 10
 aagctgacgt tcttggcact gc 22

 <210> 11
 <211> 23
 <212> DNA
 <213> Homo sapiens

 <400> 11
 gctttcctgc ctcaggatga act 23

 <210> 12
 <211> 22
 <212> DNA
 <213> Homo sapiens

 <400> 12
 ccttggcagg attgaagctg ac 22

 <210> 13
 <211> 24
 <212> DNA
 <213> Homo sapiens

 <400> 13
 gatgaactga cggccttgaa tgta 24

 <210> 14
 <211> 23
 <212> DNA

<213> Homo sapiens

<400> 14

cctggcagag ttgtctcacc ttg

23

<210> 15

<211> 6985

<212> DNA

<213> Homo sapiens

<400> 15

attgtccgat ggttcccggc gtacctcggc ttccctcggg agtttccggc aatggctcag	60
agtttctaac gtgccccctt gttgtctctc ggccgccgtc ctctcaacca ccgccccctt	120
tttcggctcc ctctccccct tcccgttccc ccagtcagcc tggccctgct ggtgcctccg	180
gcgctacggg ctgggcaaga tggcggcctt cgggatcttg agctacgaac accggccccct	240
gaagcggccg cggctggggc ctcccgatgt ttaccctcag gaccccaaac agaaggagga	300
tgaactgacg gccttgaatg taaaacaagg tttcaataac cagcctgctg tctctgggga	360
tgagcatggc agtgccaaga acgtcagctt caatcctgcc aagatcagtt ccaacttcag	420
cagcattatt gcagagaaat tacgttgtaa tacccttcct gacactgggtc gcaggaagcc	480
ccaagtgaac cagaaggata acttctggct ggtgactgca cgatcccaga gtgccattaa	540
cacttggttc actgacttgg ctggcaccaa gccactcacg caactagcca aaaagggtccc	600
cattttcagt aagaaggaag aggtgttttg gtacttagcc aaatacacag tgcctgtgat	660
gcgggctgcc tggctcatta agatgacctg tgcctactat gcagcaatct ctgagaccaa	720
ggttaagaag agacatgttg accctttcat ggaatggact cagatcatca ccaagtactt	780
atgggagcag ttacagaaga tggctgaata ctaccggcca gggcctgcag gaagtggggg	840
ctgtggttcc acgatagggc ccttgcccca tgatgtagag gtggcaatcc ggcagtggga	900
ttacaccgag aagctggcca tgttcatgtt tcaggatgga atgctggaca gacatgagtt	960
cctgacctgg gtgcttgagt gttttgagaa gatccgccct ggagaggatg aattgcttaa	1020
actgctgctg cctctgcttc tccgatactc tggggaattt gttcagtctg catacctgtc	1080
ccgccggctt gcctacttct gtacacggag actggccctg cagctggatg gtgtgagcag	1140
tcactcatct catgttatat ctgctcagtc aacaagcacg ctaccacca cccctgctcc	1200
tcagcccca actagcagca caccctcgac tccctttagt gacctgctta tgtgccctca	1260
gcaccggccc ctggtttttg gcctcagctg taccctacag accatcctcc tgtgctgtcc	1320
tagtgccttg gtttggcact actcactgac tgatagcaga attaagaccg gctcaccact	1380
tgaccacttg cctattgccc cgtccaacct gccatgccca gagggtaaca gtgccttcac	1440
tcagcaggtc cgtgcaaagt tgcgggagat cgagcagcag atcaaggagc ggggacaggc	1500
agttgaagtt cgctggctct tcgataaatg ccaggaagct actgcaggct tcaccattgg	1560
acgggtactt catacttttg aagtgctgga cagccatagt tttgaacgct ctgacttcag	1620
caactctctt gactcccttt gtaaccgaat ctttggattg ggacctagca aggatgggca	1680

TEAP001WO-seq1-000001

tgagatctcc	tcagatgatg	atgctgtggt	gtcattgcta	tgtgaatggg	ctgtcagctg	1740
caagcgttct	ggtcggcatc	gtgctatggt	ggtagccaag	ctcctggaga	agagacaggc	1800
ggagattgag	gctgagcggt	gtggagaatc	agaagccgca	gatgagaagg	gttccatcgc	1860
ctctggctcc	ctttctgctc	ccagtgtctc	cattttccag	gatgtcctcc	tgcagtttct	1920
ggatacacag	gctcccatgc	tgacggaccc	tcgaagttag	agttagcggg	tggaattctt	1980
taacttagta	ctgctgttct	gtgaactgat	tcgacatgat	gttttctccc	acaacatgta	2040
tacttgact	ctcatctccc	gaggggacct	tgcctttgga	gccctggtc	cccggcctcc	2100
ctctcccttt	gatgatcctg	ccgatgaccc	agagcacaag	gaggctgaag	gcagcagcag	2160
cagcaagctg	gaagatccag	ggctctcaga	atctatggac	attgacccta	gttccagtgt	2220
tctctttgag	gacatggaga	agcctgattt	ctcattgttc	tcccctacta	tgccctgtga	2280
ggggaagggc	agtccatccc	ctgagaagcc	agatgtcgag	aaggaggtga	agccccacc	2340
caaggagaag	attgaaggga	cccttggggt	tctttacgac	cagccacgac	acgtgcagta	2400
cgccacccat	tttcccatcc	cccaggagga	gtcatgcagc	catgagtgca	accagcggtt	2460
ggtcgtactg	tttgggggtg	gaaagcagcg	agatgatgcc	cgccatgcca	tcaagaaaat	2520
caccaaggat	atcttgaagg	ttctgaaccg	caaagggaca	gcagaaactg	accagcttgc	2580
tcctattgtg	cctctgaatc	ctggagacct	gacattctta	ggtggggagg	atgggcagaa	2640
gcggcgacgc	aaccggcctg	aagccttccc	cactgctgaa	gatatctttg	ctaagttcca	2700
gcacctttca	cattatgacc	aacaccaggt	cacggctcag	gtctcccgga	atgttctgga	2760
gcagatcacg	agctttgccc	ttggcatgtc	ataccacttg	cctctggtgc	agcatgtgca	2820
gttcatcttc	gacctcatgg	aatattcact	cagcatcagt	ggcctcatcg	actttgccat	2880
tcagctgctg	aatgaactga	gtgtagttga	ggctgagctg	cttctcaaata	cctcggatct	2940
ggtgggcagc	tacactacta	gcctgtgcct	gtgcatcgtg	gctgtcctgc	ggcactatca	3000
tgcctgcctc	atcctcaacc	aggaccagat	ggcacaggct	tttgaggggc	tgtgtggcgt	3060
cgtgaagcat	gggatgaacc	ggtccgatgg	ctcctctgca	gagcgctgta	tccttgctta	3120
tctctatgat	ctgtacacct	cctgtagcca	tttaaagaac	aaatttgggg	agctcttcag	3180
cgacttttgc	tcaaagggtga	agaacaccat	ctactgcaac	gtggagccat	cggaatcaaa	3240
tatgcgctgg	gcacctgagt	tcatgatcga	cactctagag	aaccctgcag	ctcacacctt	3300
cacctacacg	gggctaggca	agagtcttag	tgagaaccct	gctaaccgct	acagctttgt	3360
ctgcaatgcc	cttatgcacg	tctgtgtggg	gcacatgat	cccgataggg	tgaatgacat	3420
cgcaatcctg	tgtgcagagc	tgaccggcta	ttgcaagtca	ctgagtgcag	aatggctagg	3480
agtgcctaag	gccttgtgct	gctcctctaa	caatggcact	tgtggtttca	acgatctcct	3540
ctgcaatgtt	gatgtcagtg	acctatcttt	tcatgactcg	ctggctactt	ttgttgccat	3600
cctcatcgct	cggcagtggt	tgctcctgga	agatctgatt	cgctgtgctg	ccatcccttc	3660
actccttaat	gctgcttgta	gtgaacagga	ctctgagcca	ggggcccggc	ttacctgccg	3720

TEAP001WO-seq1-000001

catcctcctt	caccttttca	agacaccgca	gctcaatcct	tgccagtctg	atggaaacaa	3780
gcctacagta	ggaatccgct	cctcctgcga	ccgccacctg	ctggctgcct	cccagaaccg	3840
catcgtggat	ggagccgtgt	ttgctgttct	caaggctgtg	tttgtacttg	gggatgcgga	3900
actgaaaggt	tcaggcttca	ctgtgacagg	aggaacagaa	gaacttccag	aggaggaggg	3960
aggaggtggc	agtggtggtc	ggaggcaggg	tggccgcaac	atctctgtgg	agacagccag	4020
tctggatgtc	tatgccaagt	acgtgctgcg	cagcatctgc	caacaggaat	gggtaggaga	4080
acgttgccct	aagtctctgt	gtgaggacag	caatgacctg	caagaccag	tgttgagtag	4140
tgcccaggcg	cagcgcctca	tgcagctcat	ttgctatcca	catcgactgc	tggacaatga	4200
ggatggggaa	aacccccagc	ggcagcgcat	aaagcgcat	ctccagaact	tggaccagtg	4260
gaccatgctc	cagtcttcct	tggagctgca	gctcatgatc	aagcagaccc	ctaacaatga	4320
gatgaactcc	ctcttgagga	acatcgccaa	ggccacaatc	gaggttttcc	aacagtcagc	4380
agagacaggg	tcattcttctg	gaagtactgc	aagcaacatg	cccagcagca	gcaagaccaa	4440
gcctgtgctc	agctctctag	agcgtctctg	tgtatggctg	gtggccccc	tcattgctaa	4500
actgcccacc	tcagtccagg	gacatgtgtt	aaaggctgct	ggggaagaat	tggagaaggg	4560
tcagcacctg	ggttcctctt	cacgcaaaga	acgtgatcga	caaagcaga	agagcatgtc	4620
cctattgagc	cagcagccct	tcttatcgct	ggtgctaaca	tgtctgaaag	ggcaggatga	4680
acaacgcgag	ggactcctta	cctccctcta	cagccagggtg	caccagattg	tgaataattg	4740
gcgagatgac	cagtacttag	atgattgcaa	accaaagcag	cttatgcatg	aggcactcaa	4800
actgcggctc	aacctggtgg	ggggcatgtt	tgacacggtg	cagcgcagca	cccagcagac	4860
cacggagtgg	gccatgctcc	tcctggagat	catcatcagc	ggcactgtcg	acatgcagtc	4920
caacaatgag	ctcttcacta	ctgtgtttga	catgctgagc	gtgctcatca	atgggacatt	4980
ggctgcagac	atgtctagca	tctcgcaagg	tagcatggag	gaaaacaagc	gtgcatacat	5040
gaacctggcg	aagaagttgc	agaaggagtt	gggggagcgc	cagtcagaca	gtctggaaaa	5100
ggttcgccag	ctgctgccac	tgcccaagca	gacccgagat	gtcatcacgt	gtgagccaca	5160
gggtccctt	atcgatacca	agggcaacaa	gattgctggc	ttcgattcca	tcttcaagaa	5220
ggaggggtcta	caggttttcca	ccaaacagaa	gatctcgccc	tgggatcttt	ttgagggggt	5280
gaagccgtca	gcaccactct	cttggggctg	gtttggaaca	gtccgagtgg	accggcgagt	5340
ggctcgagga	gaggagcagc	agcggttgct	gctctaccac	acacacctga	ggccccggcc	5400
ccgcgcctat	tacctggagc	cactgccact	gccccagaa	gatgaggagc	cgctgctcc	5460
tacctgcta	gagcctgaga	aaaaggctcc	agagccccc	aaaactgaca	aaccgggggc	5520
tgctccaccc	agtactgagg	aacgcaagaa	gaagtccacc	aagggaaga	aacgcagcca	5580
gccagctacc	aagacagagg	actatggaat	gggcccgggt	cggagcggcc	cttatggtgt	5640
gacagtgcct	ccggacctcc	tgcaccaccc	aaaccctggt	tctataacac	accttaacta	5700
caggcaaggc	tccataggcc	tgtacaccca	gaaccagcca	ctacctgcag	gtggccctcg	5760

TEAP001WO-seq1-000001

tgtggacca taccgtcctg tgcgcttacc aatgcagaag ctgcccaccc gaccaactta 5820
 ccctggagtg ctgcccacaa ccatgactgg cgtcatgggt ttagaacctt cctcttataa 5880
 gacctctgtg taccggcagc agcaacctgc ggtgccccaa ggacagcgcc ttcgccaaca 5940
 gctccagcag agtcagggca tgttgggaca gtcattctgtc catcagatga ctcccagctc 6000
 ttcctacggg ttgcagactt cccaggggcta tactccttat gtttctcatg tgggattgca 6060
 gcaacacaca ggccctgcag gtaccatggg gccccccagc tactccagcc agccttacca 6120
 gagcaccac ctttctacca atcctactct thtagatcct acccgccacc tgcaacagcg 6180
 gccagtgagg tatgtgcacc agcaggcccc cacctatgga catggactga cctccactca 6240
 aaggttttca caccagacac tgcagcagac accatgata agtaccatga ctccaatgag 6300
 tgcccagggc gtccaggcag gcgtccgttc aacagccatc ctacctgagc agcagcagca 6360
 gcagcaacag cagcaacagc aacagcagca gcagcagcaa cagcaacagc agcagcagca 6420
 gcagcagtac cacatccggc agcagcagca gcagcagatc ctgcggcagc agcagcaaca 6480
 gcaacagcag cagcagcagc agcagcaaca gcaacagcag cagcagcaac agcaacaaca 6540
 gcaacaccag cagcaacagc agcaacaggc ggctcctccc caaccccagc cccagtccca 6600
 gccccagttc cagcgccagg ggcttcagca gaccagcag cagcaacaga cagcagcttt 6660
 ggtccggcaa cttcaacaac agctctctaa taccagcca cagcccagta ccaacatatt 6720
 tggacgctac tgagccacct ggaggaactg cttgtgcact ggatgtggcc ccaccctttc 6780
 ctcttaattc ccaatcccat tcctgggcta gcaccagtag tggttggggc cctccccctca 6840
 ggctccattt ttaataagtt tttagtattt ttgttaatgt gaggcattga gctgttgggt 6900
 tttgtatatt atttatatag agaccccaga gctgttgcac ccaatacaca gagcttcttt 6960
 gcaaagggaa aaaaaaaaaa aaaaaa 6985

<210> 16
 <211> 2177
 <212> PRT
 <213> Homo sapiens

<400> 16

Met Ala Ala Phe Gly Ile Leu Ser Tyr Glu His Arg Pro Leu Lys Arg
1 5 10 15

Pro Arg Leu Gly Pro Pro Asp Val Tyr Pro Gln Asp Pro Lys Gln Lys
20 25 30

Glu Asp Glu Leu Thr Ala Leu Asn Val Lys Gln Gly Phe Asn Asn Gln
35 40 45

Pro Ala Val Ser Gly Asp Glu His Gly Ser Ala Lys Asn Val Ser Phe
50 55 60

Asn Pro Ala Lys Ile Ser Ser Asn Phe Ser Ser Ile Ile Ala Glu Lys
65 70 75 80

TEAP001WO-seq1-000001

Leu Arg Cys Asn Thr 85 Leu Pro Asp Thr Gly 90 Arg Arg Lys Pro Gln Val
 Asn Gln Lys Asp 100 Asn Phe Trp Leu Val 105 Thr Ala Arg Ser Gln 110 Ser Ala
 Ile Asn Thr 115 Trp Phe Thr Asp Leu 120 Ala Gly Thr Lys Pro 125 Leu Thr Gln
 Leu Ala 130 Lys Lys Val Pro Ile 135 Phe Ser Lys Lys Glu 140 Glu Val Phe Gly
 Tyr 145 Leu Ala Lys Tyr Thr 150 Val Pro Val Met Arg 155 Ala Ala Trp Leu Ile 160
 Lys Met Thr Cys Ala 165 Tyr Tyr Ala Ala Ile 170 Ser Glu Thr Lys Val 175 Lys
 Lys Arg His Val 180 Asp Pro Phe Met Glu 185 Trp Thr Gln Ile Ile 190 Thr Lys
 Tyr Leu Trp 195 Glu Gln Leu Gln Lys 200 Met Ala Glu Tyr Tyr 205 Arg Pro Gly
 Pro Ala 210 Gly Ser Gly Gly Cys 215 Gly Ser Thr Ile Gly 220 Pro Leu Pro His
 Asp 225 Val Glu Val Ala Ile 230 Arg Gln Trp Asp Tyr 235 Thr Glu Lys Leu Ala 240
 Met Phe Met Phe Gln 245 Asp Gly Met Leu Asp 250 Arg His Glu Phe Leu 255 Thr
 Trp Val Leu Glu 260 Cys Phe Glu Lys Ile 265 Arg Pro Gly Glu Asp 270 Glu Leu
 Leu Lys Leu 275 Leu Leu Pro Leu Leu 280 Leu Arg Tyr Ser Gly 285 Glu Phe Val
 Gln Ser 290 Ala Tyr Leu Ser Arg 295 Arg Leu Ala Tyr Phe 300 Cys Thr Arg Arg
 Leu 305 Ala Leu Gln Leu Asp 310 Gly Val Ser Ser His 315 Ser Ser His Val Ile 320
 Ser Ala Gln Ser Thr 325 Ser Thr Leu Pro Thr 330 Thr Pro Ala Pro Gln 335 Pro
 Pro Thr Ser Ser 340 Thr Pro Ser Thr Pro 345 Phe Ser Asp Leu Leu 350 Met Cys

TEAP001WO-seq1-000001

Pro Gln His Arg Pro Leu Val Phe Gly Leu Ser Cys Ile Leu Gln Thr
 355 360 365
 Ile Leu Leu Cys Cys Pro Ser Ala Leu Val Trp His Tyr Ser Leu Thr
 370 375 380
 Asp Ser Arg Ile Lys Thr Gly Ser Pro Leu Asp His Leu Pro Ile Ala
 385 390 395 400
 Pro Ser Asn Leu Pro Met Pro Glu Gly Asn Ser Ala Phe Thr Gln Gln
 405 410 415
 Val Arg Ala Lys Leu Arg Glu Ile Glu Gln Gln Ile Lys Glu Arg Gly
 420 425 430
 Gln Ala Val Glu Val Arg Trp Ser Phe Asp Lys Cys Gln Glu Ala Thr
 435 440 445
 Ala Gly Phe Thr Ile Gly Arg Val Leu His Thr Leu Glu Val Leu Asp
 450 455 460
 Ser His Ser Phe Glu Arg Ser Asp Phe Ser Asn Ser Leu Asp Ser Leu
 465 470 475 480
 Cys Asn Arg Ile Phe Gly Leu Gly Pro Ser Lys Asp Gly His Glu Ile
 485 490 495
 Ser Ser Asp Asp Asp Ala Val Val Ser Leu Leu Cys Glu Trp Ala Val
 500 505 510
 Ser Cys Lys Arg Ser Gly Arg His Arg Ala Met Val Val Ala Lys Leu
 515 520 525
 Leu Glu Lys Arg Gln Ala Glu Ile Glu Ala Glu Arg Cys Gly Glu Ser
 530 535 540
 Glu Ala Ala Asp Glu Lys Gly Ser Ile Ala Ser Gly Ser Leu Ser Ala
 545 550 555 560
 Pro Ser Ala Pro Ile Phe Gln Asp Val Leu Leu Gln Phe Leu Asp Thr
 565 570 575
 Gln Ala Pro Met Leu Thr Asp Pro Arg Ser Glu Ser Glu Arg Val Glu
 580 585 590
 Phe Phe Asn Leu Val Leu Leu Phe Cys Glu Leu Ile Arg His Asp Val
 595 600 605
 Phe Ser His Asn Met Tyr Thr Cys Thr Leu Ile Ser Arg Gly Asp Leu
 610 615 620

TEAP001WO-seq1-000001

Ala Phe Gly Ala Pro Gly Pro Arg Pro Pro Ser Pro Phe Asp Asp Pro
625 630 635 640

Ala Asp Asp Pro Glu His Lys Glu Ala Glu Gly Ser Ser Ser Ser Lys
645 650 655

Leu Glu Asp Pro Gly Leu Ser Glu Ser Met Asp Ile Asp Pro Ser Ser
660 665 670

Ser Val Leu Phe Glu Asp Met Glu Lys Pro Asp Phe Ser Leu Phe Ser
675 680 685

Pro Thr Met Pro Cys Glu Gly Lys Gly Ser Pro Ser Pro Glu Lys Pro
690 695 700

Asp Val Glu Lys Glu Val Lys Pro Pro Pro Lys Glu Lys Ile Glu Gly
705 710 715 720

Thr Leu Gly Val Leu Tyr Asp Gln Pro Arg His Val Gln Tyr Ala Thr
725 730 735

His Phe Pro Ile Pro Gln Glu Glu Ser Cys Ser His Glu Cys Asn Gln
740 745 750

Arg Leu Val Val Leu Phe Gly Val Gly Lys Gln Arg Asp Asp Ala Arg
755 760 765

His Ala Ile Lys Lys Ile Thr Lys Asp Ile Leu Lys Val Leu Asn Arg
770 775 780

Lys Gly Thr Ala Glu Thr Asp Gln Leu Ala Pro Ile Val Pro Leu Asn
785 790 795 800

Pro Gly Asp Leu Thr Phe Leu Gly Gly Glu Asp Gly Gln Lys Arg Arg
805 810 815

Arg Asn Arg Pro Glu Ala Phe Pro Thr Ala Glu Asp Ile Phe Ala Lys
820 825 830

Phe Gln His Leu Ser His Tyr Asp Gln His Gln Val Thr Ala Gln Val
835 840 845

Ser Arg Asn Val Leu Glu Gln Ile Thr Ser Phe Ala Leu Gly Met Ser
850 855 860

Tyr His Leu Pro Leu Val Gln His Val Gln Phe Ile Phe Asp Leu Met
865 870 875 880

Glu Tyr Ser Leu Ser Ile Ser Gly Leu Ile Asp Phe Ala Ile Gln Leu
885 890 895

TEAP001WO-seq1-000001

Leu Asn Glu Leu Ser Val Val Glu Ala Glu Leu Leu Leu Lys Ser Ser
 900 905 910
 Asp Leu Val Gly Ser Tyr Thr Thr Ser Leu Cys Leu Cys Ile Val Ala
 915 920 925
 Val Leu Arg His Tyr His Ala Cys Leu Ile Leu Asn Gln Asp Gln Met
 930 935 940
 Ala Gln Val Phe Glu Gly Leu Cys Gly Val Val Lys His Gly Met Asn
 945 950 955 960
 Arg Ser Asp Gly Ser Ser Ala Glu Arg Cys Ile Leu Ala Tyr Leu Tyr
 965 970 975
 Asp Leu Tyr Thr Ser Cys Ser His Leu Lys Asn Lys Phe Gly Glu Leu
 980 985 990
 Phe Ser Asp Phe Cys Ser Lys Val Lys Asn Thr Ile Tyr Cys Asn Val
 995 1000 1005
 Glu Pro Ser Glu Ser Asn Met Arg Trp Ala Pro Glu Phe Met Ile
 1010 1015 1020
 Asp Thr Leu Glu Asn Pro Ala Ala His Thr Phe Thr Tyr Thr Gly
 1025 1030 1035
 Leu Gly Lys Ser Leu Ser Glu Asn Pro Ala Asn Arg Tyr Ser Phe
 1040 1045 1050
 Val Cys Asn Ala Leu Met His Val Cys Val Gly His His Asp Pro
 1055 1060 1065
 Asp Arg Val Asn Asp Ile Ala Ile Leu Cys Ala Glu Leu Thr Gly
 1070 1075 1080
 Tyr Cys Lys Ser Leu Ser Ala Glu Trp Leu Gly Val Leu Lys Ala
 1085 1090 1095
 Leu Cys Cys Ser Ser Asn Asn Gly Thr Cys Gly Phe Asn Asp Leu
 1100 1105 1110
 Leu Cys Asn Val Asp Val Ser Asp Leu Ser Phe His Asp Ser Leu
 1115 1120 1125
 Ala Thr Phe Val Ala Ile Leu Ile Ala Arg Gln Cys Leu Leu Leu
 1130 1135 1140
 Glu Asp Leu Ile Arg Cys Ala Ala Ile Pro Ser Leu Leu Asn Ala
 1145 1150 1155

TEAP001WO-seq1-000001

Ala	Cys	Ser	Glu	Gln	Asp	Ser	Glu	Pro	Gly	Ala	Arg	Leu	Thr	Cys
	1160					1165					1170			
Arg	Ile	Leu	Leu	His	Leu	Phe	Lys	Thr	Pro	Gln	Leu	Asn	Pro	Cys
	1175					1180					1185			
Gln	Ser	Asp	Gly	Asn	Lys	Pro	Thr	Val	Gly	Ile	Arg	Ser	Ser	Cys
	1190					1195					1200			
Asp	Arg	His	Leu	Leu	Ala	Ala	Ser	Gln	Asn	Arg	Ile	Val	Asp	Gly
	1205					1210					1215			
Ala	Val	Phe	Ala	Val	Leu	Lys	Ala	Val	Phe	Val	Leu	Gly	Asp	Ala
	1220					1225					1230			
Glu	Leu	Lys	Gly	Ser	Gly	Phe	Thr	Val	Thr	Gly	Gly	Thr	Glu	Glu
	1235					1240					1245			
Leu	Pro	Glu	Glu	Glu	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Arg	Arg	Gln
	1250					1255					1260			
Gly	Gly	Arg	Asn	Ile	Ser	Val	Glu	Thr	Ala	Ser	Leu	Asp	Val	Tyr
	1265					1270					1275			
Ala	Lys	Tyr	Val	Leu	Arg	Ser	Ile	Cys	Gln	Gln	Glu	Trp	Val	Gly
	1280					1285					1290			
Glu	Arg	Cys	Leu	Lys	Ser	Leu	Cys	Glu	Asp	Ser	Asn	Asp	Leu	Gln
	1295					1300					1305			
Asp	Pro	Val	Leu	Ser	Ser	Ala	Gln	Ala	Gln	Arg	Leu	Met	Gln	Leu
	1310					1315					1320			
Ile	Cys	Tyr	Pro	His	Arg	Leu	Leu	Asp	Asn	Glu	Asp	Gly	Glu	Asn
	1325					1330					1335			
Pro	Gln	Arg	Gln	Arg	Ile	Lys	Arg	Ile	Leu	Gln	Asn	Leu	Asp	Gln
	1340					1345					1350			
Trp	Thr	Met	Arg	Gln	Ser	Ser	Leu	Glu	Leu	Gln	Leu	Met	Ile	Lys
	1355					1360					1365			
Gln	Thr	Pro	Asn	Asn	Glu	Met	Asn	Ser	Leu	Leu	Glu	Asn	Ile	Ala
	1370					1375					1380			
Lys	Ala	Thr	Ile	Glu	Val	Phe	Gln	Gln	Ser	Ala	Glu	Thr	Gly	Ser
	1385					1390					1395			
Ser	Ser	Gly	Ser	Thr	Ala	Ser	Asn	Met	Pro	Ser	Ser	Ser	Lys	Thr
	1400					1405					1410			

TEAP001WO-seq1-000001

Lys	Pro	Val	Leu	Ser	Ser	Leu	Glu	Arg	Ser	Gly	Val	Trp	Leu	Val
	1415					1420					1425			
Ala	Pro	Leu	Ile	Ala	Lys	Leu	Pro	Thr	Ser	Val	Gln	Gly	His	Val
	1430					1435					1440			
Leu	Lys	Ala	Ala	Gly	Glu	Glu	Leu	Glu	Lys	Gly	Gln	His	Leu	Gly
	1445					1450					1455			
Ser	Ser	Ser	Arg	Lys	Glu	Arg	Asp	Arg	Gln	Lys	Gln	Lys	Ser	Met
	1460					1465					1470			
Ser	Leu	Leu	Ser	Gln	Gln	Pro	Phe	Leu	Ser	Leu	Val	Leu	Thr	Cys
	1475					1480					1485			
Leu	Lys	Gly	Gln	Asp	Glu	Gln	Arg	Glu	Gly	Leu	Leu	Thr	Ser	Leu
	1490					1495					1500			
Tyr	Ser	Gln	Val	His	Gln	Ile	Val	Asn	Asn	Trp	Arg	Asp	Asp	Gln
	1505					1510					1515			
Tyr	Leu	Asp	Asp	Cys	Lys	Pro	Lys	Gln	Leu	Met	His	Glu	Ala	Leu
	1520					1525					1530			
Lys	Leu	Arg	Leu	Asn	Leu	Val	Gly	Gly	Met	Phe	Asp	Thr	Val	Gln
	1535					1540					1545			
Arg	Ser	Thr	Gln	Gln	Thr	Thr	Glu	Trp	Ala	Met	Leu	Leu	Leu	Glu
	1550					1555					1560			
Ile	Ile	Ile	Ser	Gly	Thr	Val	Asp	Met	Gln	Ser	Asn	Asn	Glu	Leu
	1565					1570					1575			
Phe	Thr	Thr	Val	Leu	Asp	Met	Leu	Ser	Val	Leu	Ile	Asn	Gly	Thr
	1580					1585					1590			
Leu	Ala	Ala	Asp	Met	Ser	Ser	Ile	Ser	Gln	Gly	Ser	Met	Glu	Glu
	1595					1600					1605			
Asn	Lys	Arg	Ala	Tyr	Met	Asn	Leu	Ala	Lys	Lys	Leu	Gln	Lys	Glu
	1610					1615					1620			
Leu	Gly	Glu	Arg	Gln	Ser	Asp	Ser	Leu	Glu	Lys	Val	Arg	Gln	Leu
	1625					1630					1635			
Leu	Pro	Leu	Pro	Lys	Gln	Thr	Arg	Asp	Val	Ile	Thr	Cys	Glu	Pro
	1640					1645					1650			
Gln	Gly	Ser	Leu	Ile	Asp	Thr	Lys	Gly	Asn	Lys	Ile	Ala	Gly	Phe
	1655					1660					1665			

TEAP001WO-seq1-000001

Asp	Ser	Ile	Phe	Lys	Lys	Glu	Gly	Leu	Gln	Val	Ser	Thr	Lys	Gln
	1670					1675					1680			
Lys	Ile	Ser	Pro	Trp	Asp	Leu	Phe	Glu	Gly	Leu	Lys	Pro	Ser	Ala
	1685					1690					1695			
Pro	Leu	Ser	Trp	Gly	Trp	Phe	Gly	Thr	Val	Arg	Val	Asp	Arg	Arg
	1700					1705					1710			
Val	Ala	Arg	Gly	Glu	Glu	Gln	Gln	Arg	Leu	Leu	Leu	Tyr	His	Thr
	1715					1720					1725			
His	Leu	Arg	Pro	Arg	Pro	Arg	Ala	Tyr	Tyr	Leu	Glu	Pro	Leu	Pro
	1730					1735					1740			
Leu	Pro	Pro	Glu	Asp	Glu	Glu	Pro	Pro	Ala	Pro	Thr	Leu	Leu	Glu
	1745					1750					1755			
Pro	Glu	Lys	Lys	Ala	Pro	Glu	Pro	Pro	Lys	Thr	Asp	Lys	Pro	Gly
	1760					1765					1770			
Ala	Ala	Pro	Pro	Ser	Thr	Glu	Glu	Arg	Lys	Lys	Lys	Ser	Thr	Lys
	1775					1780					1785			
Gly	Lys	Lys	Arg	Ser	Gln	Pro	Ala	Thr	Lys	Thr	Glu	Asp	Tyr	Gly
	1790					1795					1800			
Met	Gly	Pro	Gly	Arg	Ser	Gly	Pro	Tyr	Gly	Val	Thr	Val	Pro	Pro
	1805					1810					1815			
Asp	Leu	Leu	His	His	Pro	Asn	Pro	Gly	Ser	Ile	Thr	His	Leu	Asn
	1820					1825					1830			
Tyr	Arg	Gln	Gly	Ser	Ile	Gly	Leu	Tyr	Thr	Gln	Asn	Gln	Pro	Leu
	1835					1840					1845			
Pro	Ala	Gly	Gly	Pro	Arg	Val	Asp	Pro	Tyr	Arg	Pro	Val	Arg	Leu
	1850					1855					1860			
Pro	Met	Gln	Lys	Leu	Pro	Thr	Arg	Pro	Thr	Tyr	Pro	Gly	Val	Leu
	1865					1870					1875			
Pro	Thr	Thr	Met	Thr	Gly	Val	Met	Gly	Leu	Glu	Pro	Ser	Ser	Tyr
	1880					1885					1890			
Lys	Thr	Ser	Val	Tyr	Arg	Gln	Gln	Gln	Pro	Ala	Val	Pro	Gln	Gly
	1895					1900					1905			
Gln	Arg	Leu	Arg	Gln	Gln	Leu	Gln	Gln	Ser	Gln	Gly	Met	Leu	Gly
	1910					1915					1920			

TEAP001WO-seq1-000001

Gln Ser Ser Val His Gln Met Thr Pro Ser Ser Ser Tyr Gly Leu
 1925 1930 1935
 Gln Thr Ser Gln Gly Tyr Thr Pro Tyr Val Ser His Val Gly Leu
 1940 1945 1950
 Gln Gln His Thr Gly Pro Ala Gly Thr Met Val Pro Pro Ser Tyr
 1955 1960 1965
 Ser Ser Gln Pro Tyr Gln Ser Thr His Pro Ser Thr Asn Pro Thr
 1970 1975 1980
 Leu Val Asp Pro Thr Arg His Leu Gln Gln Arg Pro Ser Gly Tyr
 1985 1990 1995
 Val His Gln Gln Ala Pro Thr Tyr Gly His Gly Leu Thr Ser Thr
 2000 2005 2010
 Gln Arg Phe Ser His Gln Thr Leu Gln Gln Thr Pro Met Ile Ser
 2015 2020 2025
 Thr Met Thr Pro Met Ser Ala Gln Gly Val Gln Ala Gly Val Arg
 2030 2035 2040
 Ser Thr Ala Ile Leu Pro Glu Gln Gln Gln Gln Gln Gln Gln
 2045 2050 2055
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 2060 2065 2070
 Gln Gln Gln Tyr His Ile Arg Gln Gln Gln Gln Gln Gln Ile Leu
 2075 2080 2085
 Arg Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 2090 2095 2100
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His Gln Gln
 2105 2110 2115
 Gln Gln Gln Gln Gln Ala Ala Pro Pro Gln Pro Gln Pro Gln Ser
 2120 2125 2130
 Gln Pro Gln Phe Gln Arg Gln Gly Leu Gln Gln Thr Gln Gln Gln
 2135 2140 2145
 Gln Gln Thr Ala Ala Leu Val Arg Gln Leu Gln Gln Gln Leu Ser
 2150 2155 2160
 Asn Thr Gln Pro Gln Pro Ser Thr Asn Ile Phe Gly Arg Tyr
 2165 2170 2175

TEAP001wo-seq1-000001