

SEQUENCES

SEQ ID NO: 1

Description of Artificial Sequence: vector pSS1

5	1	GGGTACCGGG	CCCCCCTCG	AGGTCGACGG	TATCGATAAG	CTTGATATCG	AATTCGAGCT
	61	CGGTACCCGG	GGGCGCGCCG	GATCTCGACA	TTGATTATTG	ACTAGTTATT	AATAGTAATC
	121	AATTACGGGG	TCATTAGTTC	ATAGCCCATATA	TATGGAGTTC	CGCGTTACAT	AACCTACGGT
	181	AAATGGCCCG	CCTGGCTGAC	CGCCCAACGA	CCCCCGCCCA	TTGACGTCAA	TAATGACGTA
	241	TGTTCCCATATA	GTAACGCCAA	TAGGGACTTT	CCATTGACGT	CAATGGGTGG	ACTATTTAGC
10	301	GTAAACTGCC	CACTTGGCAG	TACATCAAGT	GTATCATATG	CCAAGTACGC	CCCCTATTGA
	361	CGTCAATGAC	GGTAAATGGC	CCGCTTGGA	TTATGCCAG	TACATGACCT	TATGGGACTT
	421	TCCTACTTGG	CAGTACATCT	ACGTATTAGT	CATCGCTATT	ACCATGGGTC	GAGGTGAGCC
	481	CCACGTTCTG	CTTCACTCTC	CCCATCTCCC	CCCCCTCCCC	ACCCCCAATT	TTGTATTTAT
	541	TTATTTTTTA	ATTATTTTGT	GCAGCGATGG	GGGCGGGGGG	GGGGGGGGCG	CGCGCCAGGC
15	601	GGGCGGGGAG	GGGCGGAGGG	GGCGGGCGGG	GCGAGGCGGA	GAGGTGCGGC	GGCAGCCAAT
	661	CAGAGCGGCG	CGCTCCGAAA	GTTTCCTTTT	ATGGCGAGGC	GGCGGCGGCG	CGGCGCCTAT
	721	AAAAGCGGAA	GCGCGCGGCG	GGCGGGAGTC	GCTGCGTTGC	CTTCGCCCCG	TGCCCGCGTC
	781	CGCGCCGCTT	CGCGCCGCCC	GCCCGGCTCT	TGACTGACCG	CGTTACTCCC	ACAGGTGAGC
	841	GGGCGGGGAG	CCCTTCTCCC	TCCGGGCTGT	AATTAGCGCT	TGGTTAATG	ACGGCTCGTT
20	901	TCCTTTCTGT	GGCTGCGTGA	AAGCCTTAAA	GGGCTCCGGG	AGGGCCCTTT	GTGCGGGGGG
	961	GAGCGGCTCG	GGGGGTGCGT	CGGTGTGTGT	GTGCGTGCGG	AGCGCGCGCT	CGCGCCCGCG
	1021	CTGCCCGGCG	GCTGTGAGCG	CTGCGGGCGC	GGCGCGGGGC	TTTGTGCGCT	CCGCGTGTGC
	1081	GCGAGGGGAG	GCGGCGGGGG	GGCGGTGCCC	CGCGGTGCGG	GGGGGCTGCG	AGGGGAACAA
	1141	AGGCTGCGTG	CGGGGTGTGT	GCGTGGGGGG	GTGAGCAGGG	GGTGTGGGCG	CGGCGGTCGG
25	1201	GCTGTAACCC	CCCCCTGCAC	CCCCCTCCCC	GAGTTGCTGA	GCACGGCCCG	GCTTCGGGTG
	1261	CGGGGCTCCG	TGCGGGGCGT	GGCGCGGGGC	TGCGCTTGCC	GGGCGGGGGG	TGGCGGAGAG
	1321	TGGGGGTGCG	GGGCGGGGCG	GGGCGGCTCT	GGGCGGGGGA	GGGCTCGGGG	GAGGGGCGCG
	1381	GCGGCCCGCG	AGCGCCGGCG	GCTGTGAGAG	CGCGGCGAGC	CGCAGCCATT	GCCTTTTATG
	1441	GTAATCGTGC	GAGAGGGCGC	AGGGACTTCC	TTTGTCCCAA	ATCTGGCGGA	GCCGAAATCT
30	1501	GGAGGCGGCG	CCCGCACCCC	CTCTAGCGGG	CGCGGGCGAA	GCGGTGCGGC	GCCGCGAGGA
	1561	AGGAAATGGG	CGGGGAGGGC	CTTCGTGCGT	CGCCGCGCGG	CCGTCCCCTT	CTCCCTCTCC
	1621	AGCCTCGGGG	CTGTCCGCGG	GGGGACGGCT	GCCTTCGGGG	GGGACGGGGG	AGGGCGGGGT
	1681	TCGGCTTCTG	GCGTGTGACC	GGCGGCTCTA	GAGCCTCTGC	TAACCATGTT	CATGCCTTCT
	1741	TCCTTTTCTG	ACAGATCCTT	AATTAAGTCT	AGAGTCGACT	GTTTAATTCC	ACCATGTCCA
35	1801	ATTTACTGAC	CGTACACCAA	AATTTGCCTG	CATTACCGGT	CGATGCAACG	AGTGATGAGG
	1861	TTCCGAAGAA	CCTGATGGAC	ATGTTTCAGG	ATCGCCAGGC	GTTTTCTGAG	CATACCTGGA
	1921	AAATGCTTCT	GTCCGTTTGC	CGGTCTGTGG	CGGCATGGTG	CAAGTTGAAT	AACCGGAAAT
	1981	GGTTTCCCGC	AGAACCTGAA	GATGTTTCGC	ATTATCTTCT	ATATCTTCAG	GCGCGCGGTC
	2041	TGGCAGTAAA	AACTATCCAG	CAACATTGGG	GCCAGCTAAA	CATGCTTCAT	CGTCGGTCCG
40	2101	GGCTGCCACG	ACCAAGTGAC	AGCAATGCTG	TTTCACTGGT	TATGCGGCGG	ATCCGAAAAG
	2161	AAAACGTTGA	TGCCGGTGAA	CGTGCAAAAC	AGGCTCTAGC	GTTGCAACGC	ACTGATTTCT
	2221	ACCAGGTTTC	TTCACTCATG	GAAATAGCGG	ATCGCTGCCA	GGATATACGT	AATCTGGCAT
	2281	TTCTGGGGAT	TGCTTATAAC	ACCCTGTTAC	GTATAGCCGA	AATTGCCAGG	ATCAGGGTTA
	2341	AAGATATCTC	ACGTAAGTAC	GGTGGGAGAA	TGTTAATCCA	TATTGGCAGA	ACGAAAACGC
45	2401	TGGTTAGCAC	CGCAGGTGTA	GAGAAGGCAC	TAGCCTGGG	GGTAAGTAAA	CTGGTCGAGC
	2461	GATGGATTTC	CGTCTCTGGT	GATGCTGATG	ATCCGAATAA	CTACCTGTTT	TGCCGGGCTA
	2521	GAAAAAATGG	TGTTGCCGCG	CCATCTGCCA	CCAGCCAGCT	ATCAACTCGC	GCCCTGGAAG
	2581	GGATTTTTTA	AGCAACTCAT	CGATTGATTT	ACGGCGCTAA	GGATGACTCT	GGTCAGAGAT
	2641	ACCTGGCCTG	GTCTGGACAC	AGTGCCCGTG	TCGGAGCCGC	GCGAGATATG	GCCCGCGCTG
50	2701	GAGTTTCAAT	ACCGGAGATC	ATGCAAGCTG	GTGGCTGGAC	CAATGTAAAT	ATTGTCTAGA
	2761	ACTATATCCG	TAACTGGAT	AGTGAACAG	GGGCAATGGT	GCGCTGCTG	GAAGATGGCG
	2821	ATCTCGAGCC	ATCTGCTGGA	GACATGAGAG	CTGCCAACCT	TTGGCCAAGC	CCGCTCATGA
	2881	TCAAACGCTC	TAAGAAGAAC	AGCCTGGCCT	TGTCCTTGAC	GGCCGACCAG	ATGGTCAGTG
	2941	CCTTGTTGGA	TGCTGAGCCC	CCCATACTCT	ATTCCGAGTA	TGATCCTACC	AGACCCCTCA
55	3001	GTGAAGCTTC	GATGATGGGC	TTACTGACCA	ACCTGGCAGA	CAGGGAGCTG	GTTACATAGA
	3061	TCAACTGGGC	GAAGAGGGTG	CCAGGCTTGT	TGGATTGAC	CCTCCATGAT	CAGGTCCACC
	3121	TTGTAGAATG	TGCTTGGCTA	GAGATCCTGA	TGATTGGTCT	CGTCTGGCGC	TCCATGGAGC
	3181	ACCCAGTGAA	GCTACTGTTT	GCTCCTAAT	TGCTCTTGGA	CAGGAACCAG	GGAAAAATGT
	3241	TAGAGGGCAT	GGTGGAGATC	TTGACATGCG	TGCTGGCTAC	ATCATCTCGG	TTCCGCATGA
60	3301	TGAATCTGCA	GGGAGAGGAG	TTTGTGTGCC	TCAAATCTAT	TATTTTGCTT	AATCTGGGAG
	3361	TGTACACATT	TCTGTCCAGC	ACCCTGAAGT	CTCTGGAAGA	GAAGGACCAT	ATCCACCGAG
	3421	TCCTGGACAA	GATCACAGAC	ACTTTGATCC	ACCTGATGGC	CAAGGCAGGC	CTGACCCTGC
	3481	AGCAGCAGCA	CCAGCGGCTG	GCCCAGCTCC	TCTCATCCT	CTCCACATC	AGGCACATGA
	3541	GTAACAAAGG	CATGGAGCAT	CTGTACAGCA	TGAAGTGCAA	GAACGTGGTG	CCCCCTCTAT
65	3601	ACCTGCTGGT	GGAGGCGGCG	GACGCCCAAC	GCTTACATGC	GCCCACTAGC	CGTGGAGGGG
	3661	CATCCGTGGA	GGAGACGGAC	CAAAGCCACT	TGGCCACTGC	GGGCTCTACT	TCATCGCATT
	3721	CCTTGCAAAA	GTATTACATC	ACGGGGGAGG	CAGAGGGTTT	CCCTGCCACA	GCTTGATGAA
	3781	GATCTGAGCT	CCCTGGCGGA	ATTGCGTAAA	TGATTGCAGA	TCCACTAGTT	CTAGAGCTCG
	3841	CTGATCGACC	TCGACTGTGC	CTTCTAGTTG	CCAGCCATCT	GTTGTTTGCC	CCTCCCCCTG
70	3901	GCCTTCCTTG	ACCCTGGAAG	GTGCCACTCC	CACTGTCTTT	TCCTAATAAA	ATGAGGAAAT
	3961	TGCATCGCAT	TGTCTGAGTA	GGTGTCAATC	TATTCTGGGG	GGTGGGGTGG	GGCAGGACAG
	4021	CAAGGGGGAG	GATTGGGAAG	ACAATAGCAG	GCATGCTGGG	GATGCGGTGG	GCTCTATGGC
	4081	TTCTGAGGCG	GAAAGAAGCA	GCTGGGGCTC	GAGATCCACT	AGTTCTAGCC	TCGAGGCTAG

5 4141 AGCGGCCGCC ACCGCGGTGG AGCTCCAATT CGCCCTATAG TGAGTCGTAT TACAATTAC  
4201 TGCCCGTCGT TTTACAACGT CGTGACTGGG AAAACCCCTGG CGTTACCCAA CTTAATCGCC  
4261 TTGCAGCACA TCCCCCTTTC GCCAGCTGGC GTAATAGCGA AGAGGCCCGC ACCGATCGCC  
4321 CTTCCCAACA GTTGCGCAGC CTGAATGGCG AATGGGACGC GCCCTGTAGC GCGCATTA  
4381 GCGCGCGGG TGTGGTGGTT ACGCGCAGCG TGACCGCTAC ACTTGCCAGC GCCCTAGCGC  
4441 CCCTCCTTT CGCTTTCTTC CTTCTCTTTC TCGCCACGTT CGCCGGCTTT CCCCGTCAAG  
4501 CTCTAAATCG GGGGCTCCCT TTAGGGTTCC GATTTAGTGC TTTACGGCAC CTCGACCCCA  
4561 AAAAATTGA TTAGGGTGAT GGTTCACGTA GTGGGCCATC GCCCTGATAG ACGGTTTTTC  
10 4621 GCCCTTTGAC GTTGGAGTCC ACGTTCTTTA ATAGTGGACT CTTGTTCCAA ACTGGAACAA  
4681 CACTCAACCC TATCTCGGTC TATTCTTTTG ATTTATAAGG GATTTTGCCG ATTTCGGCCT  
4741 ATTGGTTAAA AAATGAGCTG ATTTAACAAA AATTTAACGC GAATTTTAA AAAATATTAA  
4801 CCGTTACAA TTAGGTGGCA CTTTTCGGG AAATGTGCGC GGAACCCCTA TTTGTTTTAT  
4861 TTTCTAAATA CATTCAAATA TGTATCCGCT CATGAGACAA TAACCCTGAT AAATGCTTCA  
4921 ATAATATTGA AAAAGGAAGA GTATGAGTAT TCAACATTTC CGTGTGCGCC TTATTCCTT  
15 4981 TTTTGCGGCA TTTTGCCCTC CTGTTTTTGC TCACCAGAA ACGTGGTGA AAGTAAAGA  
5041 TGCTGAAGAT CAGTTGGGTG CACGAGTGGG TTACATCGAA CTGGATCTCA ACAGCGGTAA  
5101 GATCCTTGAG AGTTTTCGCC CCGAAGAACG TTTTCCAATG ATGAGCACTT TTAAGTTCT  
5161 GCTATGTGGC GCGGTATTAT CCCGTATTGA CGCCGGGCAA GAGCAACTCG GTCGCGCAT  
20 5221 ACACGAGCTT CAGAATGACT TGGTTGAGTA CTCACCAGTC ACAGAAAAGC ATCTTACGGA  
5281 TGGCATGACA GTAAGAGAAT TATGCAGTGC TGCCATAACC ATGAGTGATA ACGTGCAGC  
5341 CAACTTACTT CTGACAACGA TCGGAGGACC GAAGGAGCTA ACCGCTTTTT TGACAACAT  
5401 GGGGGATCAT GTAACCTGCC TTGATCGTTG GGAACCGGAG CTGAATGAAG CCATACCAA  
5461 CGACGAGCTT GAGACACGTA TGCCTGTAGC AATGGCAACA ACGTTGCGCA AACTATTAA  
25 5521 TGGCGAATA CTTACTCTAG CTTCCCGGCA ACAATTAATA GACTGGATGG AGGCGGATAA  
5581 AGTTGCAGGA CCACTTCTGC GCTCGGCCCT TCCGCTGGC TGGTTTATTG CTGATAAATC  
5641 TGGAGCCGGT GAGCGTGGT CTCGCGGTAT CATTGCAGCA CTGGGGCCAG ATGGTAAGCC  
5701 CTCCTGATC GTAGTTATCT ACACGACGGG GAGTCAGGCA ACTATGGATG AACGAAATAG  
5761 ACAGATCGCT GAGATAGGTG CCTCACTGAT TAAGCATTGG TAACTGTCAG ACCAAGTTTA  
5821 CTATATATA CTTTAGATTG ATTTAAACT TCATTTTAA TTTAAAAGGA TCTAGGTGAA  
30 5881 GATCCTTTTT GATAATCTCA TGACCAAAAT CCCTTAACGT GAGTTTTCGT TCCACTGAGC  
5941 GTACAGACCC GTAGAAAAGA TCAAAGGATC TTCTTGAGAT CCTTTTTTTC TCGCGTAAAT  
6001 CTGCTGCTTG CAAACAAAAA AACCACCGCT ACCAGCGGTG GTTTGTTTGC CGGATCAAGA  
6061 GCTACCAACT CTTTTTCCGA AGGTAACCTG CTTACGAGA GCGCAGATAC CAAATACTGT  
35 6121 CCTTCTAGT TAGCCGTAGT TAGGCCACCA CTTCAAGAAC TCTGTAGCAC CGCTACATA  
6181 CCTCGTCTG CTAATCTGT TACCAGTGGC TGCTGCCAGT GCGGATAAGT CGTGTCTTAC  
6241 CGGGTTGGAC TCAAGACGAT AGTTACCGGA TAAGGCGCAG CGGTGCGGCT GAACGGGGGG  
6301 TTCGTGCACA CAGCCAGCT TGGAGCGAAC GACCTACACC GAAGTGAAT ACCTACAGCG  
6361 TGAGCTATGA GAAAGCGCCA CGCTTCCCGA AGGGAGAAAG GCGGACAGGT ATCCGGTAAG  
40 6421 CCGCAGGGTC GGAACAGGAG AGCGCACGAG GGAGCTTCCA GGGGAAACG CCTGGTATCT  
6481 TTATAGTCCT GTCGGGTTC GCCACCTCTG ACTTGAGCGT CGATTTTGTG GATGCTCGTC  
6541 AGGGGGGCGG AGCCTATGGA AAAACGCCAG CAACGCGGCC TTTTACGGT TCCTGGCCTT  
6601 TTGCTGGCCT TTTGCTCACA TGTTCTTCC TGCGTTATCC CCGTATTCTG TGGATAACCG  
6661 TATTACCGCC TTTGAGTGAG CTGATACCGC TCGCCGACG CGAACGACCG AGCGCAGCGA  
45 6721 GTCAGTGAGC GAGGAAGCGG AAGAGCGCCC AATACGCAAA CCGCTCTCC CCGCGCTTG  
6781 CCGGATTCAAT TAATGCAGCT GGCACGACAG GTTTCCCGAC TGGAAAGCGG GCAGTGAGCG  
6841 CAACGCAATT AATGTGAGTT AGCTCACTCA TTAGGCACCC CAGGCTTTAC ACTTTATGCT  
6901 TCCGCTCTCG ATGTTGTGTG GAATTGTGAG CGGATAACAA TTTACACAG GAAACAGCTA  
6961 TGACCATGAT TACGCCAAGC GCGCAATTAA CCCTCACTAA AGGGAACAAA AGCT

50 SEQ ID NO: 2  
Description of Artificial Sequence: vector pCAG-C31Int(NLS)-bpa

1 TCGCGCGTTT CGGTGATGAC GGTGAAAC TCTGACACAT GCAGCTCCCG GAGACGGTCA  
61 CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGCGGGTG  
121 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC  
55 181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGGCGCC  
241 ATTGCGCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC TCTTCGCTAT  
301 TACGCCAGCT GCGGAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA ACGCCAGGAT  
361 TTTCCAGTC ACGACGTTGT AAAACGACGG CAGTGAATT CGAGCTCGGT ACCCGGGGCG  
421 GCGCCGGATC TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAATT ACGGGGTCTAT  
60 481 TAGTTCATAG CCCATATATG GAGTTCCGCG TTACATAACT TACGGTAAAT GGCCCGCCTG  
541 GGTGACCGCC CAACGACCCC CGCCATTGA CGTCAATAAT GACGTATGTT CCCATAGTAA  
601 CGGCAATAGG GACTTTCCAT TGACGTCAAT GGGTGGACTA TTTACGGTAA ACTGCCACT  
661 TGGCAGTACA TCAAGTGAT CATATGCCAA GTACGCCCC TATTGACGTC AATGACGGTA  
721 AATGGCCCCG CTGGCATTAT GCGCAGTACA TGACCTTATG GGACTTTCCT ACTTGGCAGT  
65 781 ACATCTACGT ATTAGTCATC GTATTACCA TGGGTGAGG TGAGCCCGAC GTTCTGCTTC  
841 ACTCTCCCCA TCTCCCCCCC CTCCCCACCC CCAATTTTGT ATTTATTAT TTTTAAATTA  
901 TTTTGTGCAG CGATGGGGGG GGGGGGGGGG GGGGCGCGCG CCAGGCGGGG CCGGGCGGGG  
961 CGAGGGGGCG GCGGGGGCGA GCGGAGAGG TGCGGCGGCA GCCAATCAGA GCGGCGCGCT  
1021 CCGAAAGTTT CTTTATATG CGAGGCGGCG GCGGCGGCGC CCCTATAAAA AGCGAAGCGC  
70 1081 GCGGCGGGCG GGAGTCGCTG CGTTGCCTTC GCCCGTGCC CCGCTCCGCG CCGCTCGCG  
1141 CCGCCCGCCC CGCTCTGAC TGACCGCGTT ACTCCACAG GTGAGCGGGG GGGACGGCCC  
1201 TTCTCTCCG GGTGTAATT AGCGTTGGT TTAATGACGG CTCGTTTCTT TTCTGTGGCT  
1261 GCGTGAAAGC CTTAAAGGGC TCCGGGAGGG CCCTTTGTGC GGGGGGAGC GGCTCGGGG

5	1321	GTGCGTGCCT	GTGTGTGTGC	GTGGGGAGCG	CCGCGTGCCT	CCCGCGCTGC	CCGGCGGCTG
	1381	TGAGCGCTGC	GGGCGCGGCG	CGGGGCTTTG	TGCGCTCCGC	GTGTGCGCGA	GGGGAGCGCG
	1441	GCCGGGGGCG	GTGCCCCGCG	GTGCGGGGGG	GCTGCGAGGG	GAACAAAGGC	TGCGTGCGGG
	1501	GTGTGTGCGT	GGGGGGGTGA	GCAGGGGGTG	TGGGCGCGGC	GGTCGGGCTG	TAACCCCCCC
	1561	CTGCACCCCC	CTCCCCGAGT	TGCTGAGCAC	GGCCCGGCTT	CGGGTGCGGG	GCTCCGTGCG
10	1621	GGGCGTGGCG	CGGGGCTCGC	CGTGCCGGGC	GGGGGTTGGC	GGCAGGTGGG	GGTGCCGGGC
	1681	GGGGCGGGGC	CGCCTCGGGC	CGGGGAGGGC	TCGGGGGAGG	GGCGCGGCGG	CCCCGAGCGG
	1741	CCGGCGGCTG	TCGAGGCGCG	GCGAGCCGCA	GCCATTGCCT	TTTATGGTAA	TCGTGCGAGA
	1801	GGGCGCAGGG	ACTTCCTTTG	TCCCAAATCT	GGCGGAGCCG	AAATCTGGGA	GGCGCCGCGG
	1861	CACCCCCCT	AGCGGGCGCG	GGCGAAGCGG	TGCGGCGCCG	GCAGGAAGGA	AATGGGCGGG
15	1921	GAGGGCCTTC	GTGCGTCGCG	GCGCGCCCGT	CCCCTTCTCC	ATCTCCAGCC	TCGGGGCTGC
	1981	CAGCAGGGGA	CGGCTGCCTT	CGGGGGGGAC	GGGGCAGGGC	GGGGTTTCGG	TTCTGGCGTG
	2041	TGACCGGGCG	CTCTAGAGCC	TCTGTAAACC	ATGTTTCATG	CTTCTCTTTT	TTCTACAGAG
	2101	TCCTTAATTA	AGTCTAGACC	GATATGACAC	AAGGGGTTGT	GACCGGGGTG	GACACGTACG
	2161	CGGGTGCTTA	GACCCGTGAG	TGCGCGGAGC	GCGAGAATTG	GAGCGCAGCA	AGCCAGCGGA
20	2221	CACAGCGTAG	CGCCAACGAA	GACAAGGCGG	CCGACCTTCA	GCGCGAAGTC	GAGCGCGACG
	2281	GGGGCCGGTT	CAGGTTTCGT	GGGCATTTCG	GCGAAGCGCC	GGGCACGTGC	GCGTTCGGGA
	2341	CGGCGGAGCG	CCCGGAGTTC	GAACGCATCC	TGAACGAATG	CCGCGCCGGG	CGGCTCAACA
	2401	TGATCAGTTC	CTATGACGTG	TGCGCGCTTC	CGCGCTTGA	GGTCATGGAC	GCGATTCCGA
	2461	TTGTCTCGGA	ATTGCTCGCC	CTGGGCGTGA	CGATTGTTTC	CACTCAGGAA	GGCGTCTTCC
25	2521	GGCAGGGAAA	CGTCATGGAC	CTGATTCAAC	TGATTATGCG	GCTCGACGCG	TGCGACAAAG
	2581	AATCTTCGCT	GAAGTCGGCG	AAGATTCTCG	ACACGAAGAA	CCTTCAGCGC	GAATTGGGCG
	2641	GGTACGCTCG	CGGGAAGGCG	CCTTACGGCT	TCGAGCTTGT	TTTCGAGACG	AAGGAGATCA
	2701	CGCGCAACGG	CCGAATGGTC	AATGTCGTCA	TCAACAAGCT	TGCGCACTCG	ACCACTCCCC
	2761	TTACCGGACC	CTTCGAGTTC	GAGCCCCGAC	TAATCCGGTG	GTGGTGCGCT	GAGATCAAGA
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	2881	CGGGGCTTTG	TAAGCGCATG	GACGCTGACG	CCGTGCGGAC	CCGGGGCGAG	ACGATTGGGA
	2941	AGAAGACCGC	TTCAAGCGCC	TGGGACCCGG	CAACCGTTAT	GCGAATCCTT	CGGGACCCGC
	3001	GTATTGCGGG	CTTCGCGGCT	GAGGTGATCT	ACAAGAAGAA	GCCGGACGGC	ACGCCGACCA
	3061	CAGAAGTTGA	GGGTTACCGC	ATTCAGCGCG	ACCCGATCAC	GCTCCGGCCG	GTGAGCTTTG
35	3121	ATTGCGGACC	GATCATCGAG	CCCGCTGAGT	GGTATGAGCT	TCAGGCGTGG	TTGGACGGCA
	3181	GGGGGCGCGG	CAAGGGGCTT	TCCCGGGGGC	AAGCCATTCT	GTCCGCCATG	GACAAGCTGT
	3241	ACTGCGAGTG	TGGCGCCGTC	ATGACTTCGA	AGCGCGGGGA	AGAATCGATC	AAGGACTCTT
	3301	ACCGCTGCGC	TCGCGCGAAG	GTGGTCGACC	CGTCCGCACC	TGGGCAGCAC	GAAGGCACGT
	3361	GCAACGCTAG	CATGGCGGCA	CTCGACAAGT	TCGTTGCGGA	ACGCATCTTC	AACAAGATCA
40	3421	GGCAGCCCGA	AGGCGACGAA	GAGACGTTGG	CGCTTCTGTG	GGAAGCCGCC	CGACGCTTCG
	3481	GCAAGCTCAC	TGAGGCGCCT	GAGAAGAGCG	GCGAACGGGC	GAACCTTGTT	GCGGAGCGCG
	3541	CGACGCGCCT	GAACGCCCTT	GAAGAGCTGT	ACGAAGACCG	CGCGGCAGGC	GCGTACGACG
	3601	GACCCGTTGG	CAGGAAGCAC	TTCCGGGAAG	AACAGGCAGC	GCTGACGCTC	CGGCAGCAAG
	3661	GGGCGGAAGA	GCGGCTTGCC	GAACCTGAAG	CCGCCGAAGC	CCCGAAGCTT	CCCTTGAGCC
45	3721	AATGGTTTCC	CGAAGACGCC	GACGCTGACC	CGACCGGCCC	TAAGTCGTGG	TGGGGGCGCG
	3781	CGTCAGTAGA	GCACAAGCGC	GTGTTCTGTC	GGCTCTCTGT	AGACAAGATC	GTTGTACAGA
	3841	AGTCGACTAC	GGGCGAGGGG	CAGGGAACGC	CCATCGAGAA	GCGCGCTTCG	ATCACGTGGG
	3901	CGAAGCCGCC	GACCGACGAC	GACGAAGACG	ACGCCCAGGA	CGGCACGGAA	GACGTAGCGG
	3961	GCCCTAAGAA	GAAGAGGAAG	GTTTAGTCTA	GAGTCGACTG	TTTCTAGAGC	TCGTGTATCA
50	4021	GCTCTGAGTA	TGCCTTCTAG	TGCGCAGCCA	TCTGTTGTTT	GCCCCCTCCC	CGTGCTTCCC
	4081	TTGACCCCTG	AAGGTGCCAC	TCCCACTGTC	CTTTCCTAAT	AAAATGAGGA	AATTGCATCG
	4141	CATTGTCTGA	GTAGGTGTCA	TTCTATTCTG	GGGGGTGGGG	TGGGCGAGGA	CAGCAAGGGG
	4201	GAGGATTGGG	AAGACAATAG	CAGGCATGCT	GGGGATGCGG	TGGGCTCTAT	GGCTTCTGAG
	4261	NNNGAAAGAA	CCAGCTGGGG	CTCGAGATCC	ACTAGTTCTA	GCTTCGAGGC	TAGAGCGGGC
55	4321	AAACCTGCAG	GCATGCAAGC	TTGGCGTAAT	CATGGTCATA	GCTGTTTCTT	GTGTGAAATT
	4381	GTATATCCGT	CACAATTCCA	CACAACATAC	GAGCCGGAAG	CATAAAGTGT	AAAGCCTGGG
	4441	GTGCCTAATG	AGTGAGCTAA	CTCACATTAA	TTGCGTTGCG	CTCACTGCCC	GCTTTCCAGT
	4501	CGGGAACCTT	GTGCTGCCAG	CTGCATTAA	GAATCGGCCA	ACGCGCGGGG	AGAGCGGGTT
	4561	TGCGTATTGG	GCGCTCTTCC	GCTTCTCTCG	TCACTGACTC	GCTGCGCTCG	GTCGTTCCGG
60	4621	TGCGGCGAGC	GGTATCAGCT	CACTCAAAGG	CGGTAATACG	GTTATCCACA	GAATCAGGGG
	4681	ATAACGCAGG	AAAGAACATG	TGAGCAAAAG	GCCAGCAAAA	GGCCAGGAAC	CGTAAAAAGG
	4741	CCGCGTTGCT	GGCGTTTTC	CATAGGCTCC	GCCCCCTGTA	CGAGCATCAC	AAAAATCGAC
	4801	GCTCAAGTCA	GAGGTGGCGA	AACCCGACAG	GACTATAAAG	ATACCAGGCG	TTTCCCCCTG
	4861	GAAGCTCCCT	CGTGCGCTCT	CCTGTTCCGA	CCCTGCGGCT	TACCGGATAC	CTGTCCGCCT
65	4921	TTCTCCCTTC	GGGAAGCGTG	GCGCTTTCTC	ATAGCTCAGC	CTGTAGGTAT	CTCAGTTCCG
	4981	TGTAGGTCCT	TCGCTCCAAG	CTGGGCTGTG	TGCACGAACC	CCCCGTTTCA	CCCGACCGCT
	5041	GCGCCTTATC	CGGTAACAT	CGTCTTGAGT	CCAACCCGGT	AAGACACGAC	TTATCGCCAC
	5101	TGGCAGCAGC	CACTGGTAAC	AGGATTAGCA	GAGCGAGGTA	TGTAGGCGGT	GCTACAGAGT
	5161	TCCTGAAGTG	GTGGCTTAAC	TACGGCTACA	CTAGAAGGAC	AGTATTGGT	ATCTGCGCTC
70	5221	TGCTGAAGCC	AGTTACCTTC	GGAAAAAGAG	TTGGTAGCTC	TTGATCCGGC	AAACAAACCA
	5281	CCGCTGGTAG	CGGTGGTTTT	TTTGTGTTGA	AGCAGCAGAT	TACGCGCAGA	AAAAAGGGAT
	5341	CTCAAGAAGA	TCCTTTGATC	TTTTCTACGG	GGTCTGACGC	TCAGTGGAAC	GAAACTCAGT
	5401	GTTAAGGGAT	TTTGGTCATG	AGATTATCAA	AAAGGATCTT	CACCTAGATC	CTTTTAAATT
	5461	AAAAATGAAG	TTTTAAATCA	ATCTAAAGTA	TATATGAGTA	AACTTGGTCT	GACAGTTACC
	5521	AATGCTTAAT	CAGTGAGGCA	CCTATCTCAG	CGATCTGTCT	ATTTCTGTTA	TCCATAGTTG
	5581	CCTGACTCCC	CGTCGTGTAG	ATAACTACGA	TACGGGAGGG	CTTACCATCT	GGCCCCAGTG
	5641	CTGCAATGAT	ACGCGGAGAC	CCACGCTCAC	CGGCTCCAGA	TTTATCAGCA	ATAAACACAG

5701	CAGCCGGAAG	GGCCGAGCGC	AGAAGTGGTC	CTGCAACTTT	ATCCGCCTCC	ATCCAGTCTA
5761	TTAATTGTTG	CCGGGAAGCT	AGAGTAAGTA	GTTCCGCCAGT	TAATAGTTTG	CGCAACGTTG
5821	TTGCCATTGC	TACAGGCATC	GTGGTGTAC	GCTCGTCTG	TGGTATGGCT	TCATTACAGCT
5881	CCGGTTCCCA	ACGATCAAGG	CGAGTTACAT	GATCCCCCAT	GTTGTGCAAA	AAAGCGGTTA
5941	GCTCCTTCGG	TCCTCCGATC	GTTGTGAGAA	GTAAGTTGGC	CGCAGTGTTA	TCATCATGCG
6001	TTATGGCAGC	ACTGCATAAT	TCTCTTACTG	TCATGCCATC	CGTAAGATGC	TTTTCTGTGA
6061	CTGGTGAGTA	CTCAACCAAG	TCATTCTGAG	AATAGTGTAT	CGCGCGACCG	AGTTGCTCTT
6121	GCCCCGGGTC	AATACGGGAT	AATACCGCGC	CACATAGCAG	AACTTTAAAA	GTGCTCATCA
6181	TTGGAACACG	TTCTTCGGGG	CGAAACTCT	CAAGGATCTT	ACCGCTGTTG	AGATCCAGTT
6241	CGATGTAAAC	CACTCGTGCA	CCCAACTGAT	CTTCAGCATC	TTTTACTTTC	ACCAGCGTTT
6301	CTGGGTGAGC	AAAAACAGGA	AGGCAAAATG	CCGCAAAAAA	GGGAATAAGG	CGGACACGGA
6361	AATGTTGAAT	ACTCATACTC	TTCCTTTTTT	AATATTATTG	AAGCATTAT	CAGGGTTATT
6421	GTCTCATGAG	CGGATACATA	TTTGAATGTA	TTTAGAAAAA	TAAACAAATA	GGGGTTCGCG
6481	GCACATTTC	CCGAAAAGTG	CCACCTGACG	TCTAAGAAAC	CATTATTATC	ATGACATTAA
6541	CCTATAAAAA	TAGGCGTATC	ACGAGGCCCT	TTCGTC		

SEQ ID NO: 3

Description of Artificial Sequence: vector pCAG-Cre-ER(T2)-bpa

1	TCGCGCGTTT	CGGTGATGAC	GGTGAAAACC	TCTGACACAT	GCAGCTCCCG	GAGACGGTCA
61	CAGCTTGTCT	GTAAGCGGAT	GCCGGGAGCA	GACAAGCCCG	TCAGGGCGCG	TCAGCGGGTG
121	TTGGCGGGTG	TCGGGGCTGG	CTTAACATATG	CGGCATCAGA	GCAGATTGTA	CTGAGAGTGC
181	ACCATATGCG	GTGTGAAATA	CCGCACAGAT	GCGTAAGGAG	AAAATACCGC	ATCAGGCGCC
241	ATTFCGCCATT	CAGGCTGCGC	AAGTGTGGG	AAGGCGGATC	GTTGCGGGCC	TCTCGCTAT
301	TACGCCAGCT	GGCGAAAGGG	GGATGTGCTG	CAAGGCGATT	AAGTTGGGTA	ACGCCAGGGT
361	TTTCCCAGTC	ACGACGTTGT	AAAACGACGG	CCAGTGAAAT	CGAGCTCGGT	ACCGGGGGGC
421	GCGCCGGATC	TCGACATTGA	TTATTGACTA	GTTATTAATA	GTAATCAATT	ACGGGGTCAT
481	TAGTTCATAG	CCCATATATG	GAGTTCCGCG	TTACATAACT	TACGGTAAAT	GGCCCGCGTG
541	GCTGACCGCC	CAACGACCCC	CGCCCATGTA	CGTCAATAAT	GACGTATGTT	CCCATAGTAA
601	CGCCAATAGG	GACTTTCCAT	TGACGTCAAT	GGGTGGACTA	TTTACGGTAA	ACTGCCCACT
661	TGGCAGTACA	TCAAGTGTAT	CATATGCCAA	GTACGCCCCC	TATTGACGTC	AATGACGGTA
721	AATGGCCCGC	CTGGCATTAT	GCCAGTACA	TGACCTTATG	GGACTTTTCT	ACTTGGCAGT
781	ACATCTACGT	ATTAGTCATC	GCTATTACCA	TGGGTGAGG	TGAGCCCCAC	GTTCTGCTTC
841	ACTCTCCCA	TCTCCCCCCC	CTCCCCACCC	CCAAATTTGT	ATTTATTTAT	TTTTTAATTA
901	TTTTGTGAC	CGATGGGGGG	GGGGGGGGGG	GGGGCGCGCG	CCAGGCGGGG	CGGGCGGGGG
961	CGAGGGGCGG	CGGGGGGCGA	GGCGGAGAGG	TGCGGCGGCA	GCCAATCAGA	CGGGCGGCGT
1021	CCGAAAGTTT	CCTTTTATGG	CGAGGGGCGG	GCGGGGCGGG	CCCTATAAAA	AGCGAAGCGC
1081	CGGGCGGGCG	GGAGTCGCTG	CGTTGCTTTC	GCCCCGTGCC	CCGCTCCGCG	CCGCCTCGCG
1141	CCGCCCGCCC	CGCCTCTGAC	TGACCGCGTT	ACTCCACAG	GTGAGCGGGC	GGGACGGCCC
1201	TTCTCTCCCG	GGCTGTAATT	AGCGCTTGGT	TTAATGACGG	CTCGTTTCTT	TTCTGTGGCT
1261	GCGTGAAAGC	CTTAAAGGGC	TCCGGGAGGG	CCCTTTGTGC	GGGGGGGAGC	GGCTCGGGGG
1321	TGCGGTGCGT	GTGTGTGTGC	GTGGGGAGCG	CCGCGTGC	CCCGCGCTGC	CCGGCGGGTG
1381	TGAGCGCTGC	GGGCGCGGCG	CGGGGCTTTG	TGCGCTCCGC	GTGTGCGCGA	GGGAGCGCGC
1441	GCCGGGGGCG	GTGCCCCGCG	GTGCGGGGGG	GCTGCGAGGG	GAACAAAGGC	TGCGTGCGGG
1501	GTGTGTGCGT	GGGGGGGTGA	GCAGGGGGTG	TGGGCGCGGC	GGTCGGGGTG	TAACCCCCCC
1561	CTGCACCCCC	CTCCCCGAGT	TGCTGAGCAC	GGCCCGGCTT	CGGGTGC	GCTCCGTGCG
1621	GGCCCTCTCT	CGGGGCTGCG	CGTGCCGGGC	GGGGGTTGGC	GGCAGGTGGG	GGTGCCGGGC
1681	GGGGCGGGGC	CGCCTCGGGC	CGGGGAGGGC	TCGGGGGAGG	GGCGCGGCGG	CCCCGGAGCG
1741	CCGGCGGGTG	TCGAGGCGCG	GCGAGCCGCA	GCCATTGCCT	TTTATGGTAA	TCGTGCGAGA
1801	GGGCGCAGGG	ACTTCTTTTG	TCCCAAATCT	GGCGGAGCCG	AAATCTGGGA	GGCGCCGGCG
1861	CACCCCTCT	AGCGGGGCGG	GGCGAAGCGG	TGCGGCGCGG	GCAGGAAGGA	AATGGGCGGG
1921	GAGGGCTTTC	GTGCGTGC	GCGCCGCCGT	CCCCTTCTCC	ATCTCCAGCC	TCGGGGCTGC
1981	CGCAGGGGGA	CGGCTGCCTT	CGGGGGGGAC	GGGGCAGGGC	GGGGTTCGCG	TTCTGGCGTG
2041	TGACCGGCGG	CTCTAGAGCC	TCTGCTAACC	ATGTTTCATG	CTTCTTCTTT	TTCTACAGA
2101	TCCTTAATTA	AGTCTAGAGT	CGACTGTTTA	ATTCCACCAT	GTCCAATTTA	CTGACCGTAC
2161	ACCAAAATTT	GCCTGCATTA	CCGGTCGATG	CAACGAGTGA	TGAGGTTGCG	AAGAACCCTGA
2221	TGGACATGTT	CAGGGATCGC	CAGGCGTTTT	CTGAGCATAC	CTGGAAAAATG	CTTCTGTCCG
2281	TTTGCCGGTC	GTGGGCGGCA	TGGTGCAAGT	TGAATAACCG	GAAATGGTTT	CCCGCAGAAC
2341	CTGAAGATGT	TCGCGATTAT	CTTCTATATC	TTCAGGCGCG	CGGTCTGGCA	GTAATAACTA
2401	TCCAGCAACA	TTTGGGCCAG	CTAAACATGC	TTCATCGTCG	GTCCGGGCTG	CCACGACCAA
2461	GTGACAGCAA	TGCTGTTTCA	CTGGTTATGC	GGCGGATCCG	AAAAGAAAAC	GTTGATGCCG
2521	GTGAACGTGC	AAAACAGGCT	CTAGCGTTTC	AACGCACTGA	TTTCGACCG	GTTGCTTCAC
2581	TCATGGAAAA	TAGCGATCGC	TGCCAGGATA	TACGTAATCT	GGCATTTCTG	GGGATTGCTT
2641	ATAACACCTT	GTTACGTATA	GCCGAAATTG	CCAGGATCAG	GGTTAAAGAT	ATCTCACGTA
2701	CTGACGGTGG	GAGAATGTTA	ATCCATATTG	GCAGAACGAA	AACGCTGGTT	AGCACCGGAG
2761	GTGTAGAGAA	GGCACTTAGC	CTGGGGGTAA	CTAAACTGGT	CGAGCGATGG	ATTTCGCTCT
2821	CTGGGTAGC	TGATGATCCG	AATAACTACC	TGTTTTGCGG	GGTCAGAAAA	AATGGTGTTC
2881	CCGCGCCATC	TGCCACAGCG	CAGCTATCAA	CTCGCGCCCT	GGAAGGGATT	TTTGAAGCAA
2941	CTCATCGATT	GATTTACGGC	GCTAAGGATG	ACTCTGGTCA	GAGATACCTG	GCCTGGTCTG
3001	GACACAGTGC	CCGTGTGCGA	GCCGCGCGAG	ATATGGCCCG	CGCTGGAGTT	TCAATACCGG
3061	AGATCATGCA	AGCTGGTGGC	TGGACCAATG	TAAATATTGT	CATGAACAT	ATCCGTAACC
3121	TGATAGTGA	AACAGGGGCA	ATGGTGC	TGCTGGAAGA	TGGCGATCTC	GAGCCATCTG
3181	CTGGAGACAT	GAGAGCTGCC	AACCTTTGGC	CAAGCCCGCT	CATGATCAAA	CGCTCTAAGA
3241	AGAACAGCCT	GGCCTTGTC	CTGACGGCCG	ACCAGATGGT	CAGTGCCTTG	TTGGATGCTG

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3301 AGCCCCCAT ACTCTATTC GAGTATGATC CTACCAGACC CTTCACTGAA GCTTCGATGA
3361 TGGGCTTACT GACCAACCTG GCAGACAGGG AGCTGGTTCA CATGATCAAC TGGGCGAAGA
3421 GGGTGCCAGG CTTTGTGGAT TTGACCCTCC ATGATCAGGT CCACCTTCTA GAATGTGCGT
3481 GGCTAGAGAT CCTGATGATT GGTCTCGTCT GCGCTCCAT GGAGCACCCA GTGAAGCTAC
5 3541 TGTTTGCTCC TAACTTGCTC TTGGACAGGA ACCAGGGAAA ATGTGTAGAG GGCATGGTGG
3601 AGATCTTCGA CATGCTGCTG GCTACATCAT CTCGGTTCCG CATGATGAAT CTGCAGGGAG
3661 AGGAGTTTGT GTGCCCTCAA TCTATTATTT TGCTTAATTC TGGAGTGTAC ACATTTCTGT
3721 CCAGCACCTT GAAGTCTCTG GAAGAGAAGG ACCATATCCA CCGAGTCCCTG GACAAGATCA
10 3781 CAGACACTTT GATCCACCTG ATGGCCAAGG CAGGCCTGAC CCTGCAGCAG CAGCACCAGC
3841 GGCTGGCCCA GTCCTCTCTC ATCCTCTCCC ACATCAGGCA CATGAGTAAC AAAGGCATGG
3901 AGCATCTGTA CAGCATGAAG TGCAAGAAGC TGGTGCCCTT CTATGACCTG CTGCTGGAGG
3961 CGGCGGACGC CCACCGCCTA CATGCGCCCA CTAGCCGTGG AGGGGCATCC GTGGAGGAGA
4021 CGGACCAAAG CCACTTGGCC ACTGCGGGCT CTACTTCATC GCATTCCTTG CAAAAGTATT
4081 ACATCACGGG GGAGGCAGAG GGTTCCTCTG CCACAGCTTG ATGAAGATCT GAGCTCCCTG
15 4141 GCGGAATTCG GTAAATGATT GCAGATCCAC TAGTTCTAGA GCTCGCTGAT CAGCCTCGAC
4201 TGTGCTTCTT AGTTGCCAGC CATCTGTTGT TTGCCCCCTC CCCGTGCTTT CTTGACCCCT
4261 GGAAGGTGCC ACTCCCACTG TCCTTTCCTA ATAAATGAG GAAATTGCAT CGCATTTGTCT
4321 GAGTAGGTGT CATTCTATTC TGGGGGGTGG GGTGGGGCAG GACAGCAAGG GGGAGGATTG
4381 GGAAGACAAT AGCAGGATGC CTGGGGATGC GGTGGGCTCT ATGGCTTCTG AGGCGGAAG
20 4441 AACCAGAAGC TTGGCGTAAT CATGGTCATA GCTGTTTCCT GTGTGAAATT GTTATCCGCT
4501 CACAATTCAC CACAACATAC GAGCCGGAAG CATAAAGTGT AAAGCCTGGG GTGCCTAATG
4561 AGTGAGCTAA CTCACATTAA TTGCGTTGCG CTCACTGCCC GCTTTCCAGT CGGGAAACCT
4621 TCGTGTCCAG CTGCAATTAAT GAATCGGCCA ACGCGCGGGG AGAGGCGGTT TCGGTATTGG
4681 GCGCTCTTCC GCTTCTCTCG TCACTGACTC GCTGCGCTCG GTCGTTCCGC TCGCGCGAGC
25 4741 GGTATCAGCT CACTCAAAGG CGGTAATACG GTTATCCACA GAATCAGGGG ATACGCGAGG
4801 AAAGAACATG TGAGCAAAAG GCCAGCAAAA GGCCAGGAAC CGTAAAAAGG CCGCGTTGCT
4861 GCGCTTTTTC CATAGGCTCC GCCCCCTGA CGAGCATCAC AAAAATCGAC GCTCAAGTCA
4921 GAGGTGGCGA AACCCGACAG GACTATAAAG ATACCAGGCG TTTCCCCCTG GAAGCTCCCT
4981 CGTGCGCTCT CCGTGTCCGA CCCTGCCGCT TACCGGATAC CTGTCCGCTT TTCTCCCTTC
30 5041 GGAAGCGGTG GCGCTTTCTC ATAGCTCAGC CTGTAGGTAT CTCAGTTCGG TGTAGGTCGT
5101 TCGTCCCAAG CTGGGCTGTG TGACGAACCC CCCCCTTCAG CCGGACCGCT GCGCTTATC
5161 CGGTAACATC CGTCTTGAGT CCAACCCGGT AAGACACGAC TTATCGCCAC TGGCAGCAGC
5221 CACTGGTAAC AGGATTAGCA GAGCGAGGTA TGTAAGCGGT GCTACAGAGT TCTTGAAGTG
5281 TGGCCCTAAC TACGGCTACA CTAGAAGGAC AGTATTGGT ATCTGCGCTC TGCTGAAGCC
35 5341 AGTTACTTTC GGAAAAAGAG TTGGTAGCTC TTGATCCGGC AAACAAACCA CCGCTGGTAG
5401 CGGTGGTTTT TTTGTTTGCA AGCAGCAGAT TACGCGCAGA AAAAAAGGAT CTCAGAAGA
5461 TCCTTTGATC TTTTCTACGG GGTCTGACGC TCAGTGGAAC GAAAACTCAC GTTAAGGGAT
5521 TTTGGTCATG AGATTATCAA AAAGGATCTT CACCTAGATC CTTTAAAT AAATTAAG
40 5581 TTTTAAATCA ATCTAAAGTA TATATGAGTA AACTTGGTCT GACAGTTACC AATGCTTAAT
5641 CAGTGAGGCA CCTATCTCAG CGATCTGTCT ATTTCTGTTCA TCCATAGTTG CCTGACTCCC
5701 CGTCGTGTAG ATAACACGAC TACGGGAGGG CTTACCATCT GGGCCAGTG CTGCAATGAT
5761 ACCGCGAGAC CACGCTCAC CCGCTCCAGA TTTATCAGCA ATAAACCAGC CAGCCGGAAG
5821 GGGCGAGCGC AGAAGTGGTC CTGCAACTTT ATCCGCTCTC ATCCAGTCTA TTAATTGTTG
45 5881 CCGGAAGCT AGAGTAAGTA GTTCGCCAGT TAATAGTTTG CGCAACGTTG TTGCCATTGC
5941 TACAGGCATC GTGGTGTAC GCTCGTCGTT TGGTATGGCT TCATTAGCTC CCGGTTCCCA
6001 ACCATCAAGG CGAGTTACAT GATCCCCCAT GTTGTGCAAA AAAGCGGTTA GCTCCTTCGG
6061 TCCTCCGATC GTTGTGAGAA GTAAGTTGGC CGCAGTGTTA TCACTCATGG TTATGGCAGC
6121 ACTGCATAAT TCTCTTACTG TCATGCCATC CGTAAGATGC TTTTCTGTGA CTGGTGAGTA
50 6181 CTCAACCAAG TCATTCTGAG AATAGTGTAT GCGCGGACCG AGTTGCTCTT GCCCGGCGTC
6241 AATACGGGAT AATACCGCGC CACATAGCAG AACTTTAAAA GTGCTCATCA TTGGAAAAACG
6301 TTCTTCGGGG CGAAAACTCT CAAGGATCTT ACCGCTGTTG AGATCCAGTT CGATGTAACC
6361 CACTCGTGCA CCCAACTGAT CTTCAGCATC TTTTACTTTC ACCAGCGTTT CTGGGTGAGC
6421 AAAAACAGGA AGGCAAAATG CCGCAAAAAA GGGAATAAGG GCGACACGGA AATGTTGAAT
6481 ACTCATACTC TTCCTTTTTC AATATTATTG AAGCATTTAT CAGGGTTATT GTCTCATGAG
55 6541 CGGATACATA TTTGAATGTA TTTAGAAAAA TAAACAAATA GGGGTTCGCG GCACATTTC
6601 CCGAAAAGTG CCACCTGACG TCTAAGAAAC CATTATTATC ATGACATTAA CCTATAAAAA
6661 TAGGCGTATC ACGAGGCCCT TTCGTC

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SEQ ID NOS: 4 and 5

60 Description of Artificial Sequence: DNA sequence (SEQ ID NO: 4) coding for fusion protein Cre-ER(T2) (SEQ ID NO: 5)

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Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
2139 ATG TCC AAT TTA CTG ACC GTA CAC CAA AAT TTG CCT GCA TTA CCG GTC

65 Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
2187 GAT GCA ACG AGT GAT GAG GTT CGC AAG AAC CTG ATG GAC ATG TTC AGG

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
2235 GAT CGC CAG GCG TTT TCT GAG CAT ACC TGG AAA ATG CTT CTG TCC GTT

70 Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
2283 TGC CGG TCG TGG GCG GCA TGG TGC AAG TTG AAT AAC CGG AAA TGG TTT

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5	2331	Pro	Ala	Glu	Pro	Glu	Asp	Val	Arg	Asp	Tyr	Leu	Leu	Tyr	Leu	Gln	Ala
		CCC	GCA	GAA	CCT	GAA	GAT	GTT	CGC	GAT	TAT	CTT	CTA	TAT	CTT	CAG	GCG
	2379	Arg	Gly	Leu	Ala	Val	Lys	Thr	Ile	Gln	Gln	His	Leu	Gly	Gln	Leu	Asn
10		CGC	GGT	CTG	GCA	GTA	AAA	ACT	ATC	CAG	CAA	CAT	TTG	GGC	CAG	CTA	AAC
	2427	Met	Leu	His	Arg	Arg	Ser	Gly	Leu	Pro	Arg	Pro	Ser	Asp	Ser	Asn	Ala
		ATG	CTT	CAT	CGT	CGG	TCC	GGG	CTG	CCA	CGA	CCA	AGT	GAC	AGC	AAT	GCT
15	2475	Val	Ser	Leu	Val	Met	Arg	Arg	Ile	Arg	Lys	Glu	Asn	Val	Asp	Ala	Gly
		GTT	TCA	CTG	GTT	ATG	CGG	CGG	ATC	CGA	AAA	GAA	AAC	GTT	GAT	GCC	GGT
	2523	Glu	Arg	Ala	Lys	Gln	Ala	Leu	Ala	Phe	Glu	Arg	Thr	Asp	Phe	Asp	Gln
20		GAA	CGT	GCA	AAA	CAG	GCT	CTA	GCG	TTC	GAA	CGC	ACT	GAT	TTC	GAC	CAG
	2571	Val	Arg	Ser	Leu	Met	Glu	Asn	Ser	Asp	Arg	Cys	Gln	Asp	Ile	Arg	Asn
		GTT	CGT	TCA	CTC	ATG	GAA	AAT	AGC	GAT	CGC	TGC	CAG	GAT	ATA	CGT	AAT
25	2619	Leu	Ala	Phe	Leu	Gly	Ile	Ala	Tyr	Asn	Thr	Leu	Leu	Arg	Ile	Ala	Glu
		CTG	GCA	TTT	CTG	GGG	ATT	GCT	TAT	AAC	ACC	CTG	TTA	CGT	ATA	GCC	GAA
	2667	Ile	Ala	Arg	Ile	Arg	Val	Lys	Asp	Ile	Ser	Arg	Thr	Asp	Gly	Gly	Arg
30		ATT	GCC	AGG	ATC	AGG	GTT	AAA	GAT	ATC	TCA	CGT	ACT	GAC	GGT	GGG	AGA
	2715	Met	Leu	Ile	His	Ile	Gly	Arg	Thr	Lys	Thr	Leu	Val	Ser	Thr	Ala	Gly
		ATG	TTA	ATC	CAT	ATT	GGC	AGA	ACG	AAA	ACG	CTG	GTT	AGC	ACC	GCA	GGT
35	2763	Val	Glu	Lys	Ala	Leu	Ser	Leu	Gly	Val	Thr	Lys	Leu	Val	Glu	Arg	Trp
		GTA	GAG	AAG	GCA	CTT	AGC	CTG	GGG	GTA	ACT	AAA	CTG	GTC	GAG	CGA	TGG
	2811	Ile	Ser	Val	Ser	Gly	Val	Ala	Asp	Asp	Pro	Asn	Asn	Tyr	Leu	Phe	Cys
40		ATT	TCC	GTC	TCT	GGT	GTA	GCT	GAT	GAT	CCG	AAT	AAC	TAC	CTG	TTT	TGC
	2859	Arg	Val	Arg	Lys	Asn	Gly	Val	Ala	Ala	Pro	Ser	Ala	Thr	Ser	Gln	Leu
		CGG	GTC	AGA	AAA	AAT	GGT	GTT	GCC	GCG	CCA	TCT	GCC	ACC	AGC	CAG	CTA
45	2907	Ser	Thr	Arg	Ala	Leu	Glu	Gly	Ile	Phe	Glu	Ala	Thr	His	Arg	Leu	Ile
		TCA	ACT	CGC	GCC	CTG	GAA	GGG	ATT	TTT	GAA	GCA	ACT	CAT	CGA	TTG	ATT
	2955	Tyr	Gly	Ala	Lys	Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly
50		TAC	GGC	GCT	AAG	GAT	GAC	TCT	GGT	CAG	AGA	TAC	CTG	GCC	TGG	TCT	GGA
	3003	His	Ser	Ala	Arg	Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val
		CAC	AGT	GCC	CGT	GTC	GGA	GCC	GCG	CGA	GAT	ATG	GCC	CGC	GCT	GGA	GTT
55	3051	Ser	Ile	Pro	Glu	Ile	Met	Gln	Ala	Gly	Gly	Trp	Thr	Asn	Val	Asn	Ile
		TCA	ATA	CCG	GAG	ATC	ATG	CAA	GCT	GGT	GGC	TGG	ACC	AAT	GTA	AAT	ATT
	3099	Val	Met	Asn	Tyr	Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val
60		GTC	ATG	AAC	TAT	ATC	CGT	AAC	CTG	GAT	AGT	GAA	ACA	GGG	GCA	ATG	GTG
	3147	Arg	Leu	Leu	Glu	Asp	Gly	Asp	Leu	Glu	Pro	Ser	Ala	Gly	Asp	Met	Arg
		CGC	CTG	CTG	GAA	GAT	GGC	GAT	CTC	GAG	CCA	TCT	GCT	GGA	GAC	ATG	AGA
65	3195	Ala	Ala	Asn	Leu	Trp	Pro	Ser	Pro	Leu	Met	Ile	Lys	Arg	Ser	Lys	Lys
		GCT	GCC	AAC	CTT	TGG	CCA	AGC	CCG	CTC	ATG	ATC	AAA	CGC	TCT	AAG	AAG
	3243	Asn	Ser	Leu	Ala	Leu	Ser	Leu	Thr	Ala	Asp	Gln	Met	Val	Ser	Ala	Leu
70		AAC	AGC	CTG	GCC	TTG	TCC	CTG	ACG	GCC	GAC	CAG	ATG	GTC	AGT	GCC	TTG
	3291	Leu	Asp	Ala	Glu	Pro	Pro	Ile	Leu	Tyr	Ser	Glu	Tyr	Asp	Pro	Thr	Arg
		TTG	GAT	GCT	GAG	CCC	CCC	ATA	CTC	TAT	TCC	GAG	TAT	GAT	CCT	ACC	AGA
75	3339	Pro	Phe	Ser	Glu	Ala	Ser	Met	Met	Gly	Leu	Leu	Thr	Asn	Leu	Ala	Asp
		CCC	TTC	AGT	GAA	GCT	TCG	ATG	ATG	GGC	TTA	CTG	ACC	AAC	CTG	GCA	GAC
	3387	Arg	Glu	Leu	Val	His	Met	Ile	Asn	Trp	Ala	Lys	Arg	Val	Pro	Gly	Phe
80		AGG	GAG	CTG	GTT	CAC	ATG	ATC	AAC	TGG	GCG	AAG	AGG	GTG	CCA	GGC	TTT
	3435	Val	Asp	Leu	Thr	Leu	His	Asp	Gln	Val	His	Leu	Leu	Glu	Cys	Ala	Trp
		GTG	GAT	TTG	ACC	CTC	CAT	GAT	CAG	GTC	CAC	CTT	CTA	GAA	TGT	GCC	TGG
		Leu	Glu	Ile	Leu	Met	Ile	Gly	Leu	Val	Trp	Arg	Ser	Met	Glu	His	Pro

3483 CTA GAG ATC CTG ATG ATT GGT CTC GTC TGG CGC TCC ATG GAG CAC CCA

5 3531 Val Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly  
GTG AAG CTA CTG TTT GCT CCT AAC TTG CTC TTG GAC AGG AAC CAG GGA

3579 Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr  
AAA TGT GTA GAG GGC ATG GTG GAG ATC TTC GAC ATG CTG CTG GCT ACA

10 3627 Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys  
TCA TCT CGG TTC CGC ATG ATG AAT CTG CAG GGA GAG GAG TTT GTG TGC

3675 Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser  
CTC AAA TCT ATT ATT TTG CTT AAT TCT GGA GTG TAC ACA TTT CTG TCC

15 3723 Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu  
AGC ACC CTG AAG TCT CTG GAA GAG AAG GAC CAT ATC CAC CGA GTC CTG

20 3771 Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu  
GAC AAG ATC ACA GAC ACT TTG ATC CAC CTG ATG GCC AAG GCA GGC CTG

3819 Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu  
ACC CTG CAG CAG CAG CAC CAG CGG CTG GCC CAG CTC CTC CTC ATC CTC

25 3867 Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser  
TCC CAC ATC AGG CAC ATG AGT AAC AAA GGC ATG GAG CAT CTG TAC AGC

3915 Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala  
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30 3963 Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser  
GCG GAC GCC CAC CGC CTA CAT GCG CCC ACT AGC CGT GGA GGG GCA TCC

35 4011 Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser  
GTG GAG GAG ACG GAC CAA AGC CAC TTG GCC ACT GCG GGC TCT ACT TCA

4059 Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe  
TCG CAT TCC TTG CAA AAG TAT TAC ATC ACG GGG GAG GCA GAG GGT TTC

40 4107 Pro Ala Thr Ala \*\*\*  
CCT GCC ACA GCT TGA

**SEQ ID NO: 6**

**Description of Artificial Sequence: primer fas1ER-A**

45 1 ATCCTTAATT AAATTCCACC ATGGGCTACC CCTACGACGT GCCCGACTAC GCCACCAGCA ATACAACTG CAGG

**SEQ ID NO: 7**

**Description of Artificial Sequence: primer fasER-B**

1 GGGTCGACCA GACATTGTCC TTCATTTTC

**SEQ ID NO: 8**

**Description of Artificial Sequence: primer fas2ER-A**

50 1 CCTTAATTAA ATCCACCAT GCTGTGGATC TGGGCTGTCC TGCCTCTGGT GCTTGCTGGC TCACAGTTAA  
GAGTTCATAC TACCAGCAAT ACAAACCTGCA  
101 GG

**SEQ ID NO: 9**

**Description of Artificial Sequence: vector pCAG-HAFas-ER(T2)-bpa**

1 TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA  
60 61 CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGCGGGTG  
121 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC  
181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGGCGCC  
241 ATTGCCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC TCTTCGCTAT  
301 TACGCCAGCT GCGGAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA ACGCCAGGGT  
361 TTTCCCAGTC ACGACGTTGT AAAACGACGG CCAAGTGAATT CGAGCTCGGT ACCCGGGGGC  
65 421 GCGCCGGATC TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAATT ACGGGGTCAT  
481 TAGTTCATAG CCCATATATG GAGTTCCGCG TTACATAACT TACGGTAAAT GGCCCGCTG  
541 GCTGACCGCC CAACGACCCC CGCCCATGTA CGTCAATAAT GACGTATGTT CCCATAGTAA  
601 CGCCAATAGG GACTTTCCAT TGACGTCAAT GGGTGGACTA TTTACGGTAA ACTGCCACT  
661 TGGCAGTACA TCAAGTGTAT CATATGCCAA GTACGCCCC TATTGACGTC AATGACGGTA  
70 721 AATGGCCCGC CTGGCATTAT GCCCAGTACA TGACCTTATG GGACTTTCCT ACTTGGCAGT  
781 ACATCTACGT ATTAGTCATC GCTATTACCA TGGGTCGAGG TGAGCCCCAC GTTCTGCTTC  
841 ACTCTCCCCA TCTCCCCCCC CTCCCCACCC CCAATTTTGT ATTTATTTAT TTTTAAATTA  
901 TTTTGTGCAG CGATGGGGGC GGGGGGGGGG GGGGCGCGCG CCAGGCGGGG CGGGGCGGGG

	961	CGAGGGGCGG	GGCGGGGCGA	GGCGGAGAGG	TGCGGCGGCA	GCCAATCAGA	GCGGCGCGCT
	1021	CCGAAAGTTT	CCTTTTATGG	CGAGGCGGCG	GCGGCGGCGG	CCCTATAAAA	AGCGAAGCGC
	1081	GCGGCGGGCG	GGAGTCGCTG	CGTTGCCTTC	GCCCCGTGCC	CCGCTCCGCG	CCGCCTCGCG
	1141	CCGCCCCGCC	CGGCTCTGAC	TGACCGCGTT	ACTCCCACAG	GTGAGCGGGC	GGGACGGCCC
5	1201	TTCTCCTCCG	GGCTGTAATT	AGCGCTTGGT	TTAATGACGG	CTCGTTTCTT	TTCTGTGGCT
	1261	GCGTGAAAGC	CTTAAAGGGC	TCCGGGAGGG	CCCTTTGTGC	GGGGGGGAGC	GGCTCGGGGG
	1321	GTGCGTGCGT	GTGTGTGTGC	GTGGGGAGCG	CCGCGTGCCG	CCCGCGCTGC	CCGGCGGCTG
	1381	TGAGCGCTGC	GGGCGCGGCG	CGGGGCTTTG	TGCGCTCCGC	GTGTGCGCGA	GGGGAGCGCG
	1441	GCCGGGGGCG	GTGCCCCGCG	GTGCGGGGGG	GCTGCGAGGG	GAACAAAGGC	TGCGTGCGGG
10	1501	GTGTGTGCGT	GGGGGGGTGA	GCAGGGGGTG	TGGGCGCGGC	GGTCGGGCTG	TAACCCCCCG
	1561	CTGCACCCCG	CTCCCCGAGT	TGCTGAGCAC	GGCCCGGCTT	CGGGTGCGGG	GCTCCGTGCG
	1621	GGGCGTGGCG	CGGGGCTCGC	CGTGCCGGGC	GGGGGGTGGC	GGCAGGTGGG	GGTGCCGGGC
	1681	GGGGCGGGGC	CGCCTCGGGC	CGGGGAGGGC	TCGGGGGAGG	GGCGCGGCGG	CCCCGGAGCG
	1741	CCGGCGGCTG	TCGAGGCGCG	GCGAGCCGCA	GCCATTGCCT	TTTATGGTAA	TCGTGCGAGA
15	1801	GACCCAGAGG	ATTTCCTTTG	TCCCAATCT	GGCGGAGCCG	AAATCTGGGA	GCGGCCCGCG
	1861	CACCCCCCTC	AGCGGGCGCG	GGCGAAGCGG	TGCGGCGCCG	GCAGGAAGGA	AATGGGCGGG
	1921	GAGGGCCTTC	GTGCGTCGCC	GCGCCGCCGT	CCCCTTCTCC	ATCTCCAGCC	TCGGGGCTCG
	1981	CGCAGGGGGA	CGGCTGCCTT	CGGGGGGGAC	GGGGCAGGGC	GGGGTTTCGG	TTCTGGCGTG
	2041	TGACCGGCGG	CTCTAGAGCC	TCTGCTAACC	ATGTTTCATG	CTTCTTCTTT	TTCTACAGA
20	2101	TCCTTAATTA	AATTCCACCA	TGGGCTACCC	CTACGACGTG	CCCAGCTACG	CCACCAGCAA
	2161	TACAAACTGC	AGGAAACAAA	GTCCCAAGAA	TCGCTATATG	TTGTTGACCA	TCCTTGTTTT
	2221	CTTAATTCCA	CTTGATTTTA	TATATCGAAA	GTACCGGAAA	AGAAAGTGCT	GGAAAGGAG
	2281	ACAGGATGAC	CCTGAATCTA	GAACCTCCAG	TCGTGAAACC	ATACCAATGA	ATGCCTCAAA
	2341	TCCTAGCTTG	AGTAAATACA	TCCCAGAGAT	TGCTGAAGAC	ATGACAATCC	AGGAAGCTAA
25	2401	AAAAATTTGCT	CGAGAAAAATA	ACATCAAGGA	GGGCAAGATA	GATGAGATCA	TGCATGACAG
	2461	CATCCAAGAC	ACAGCTGAGC	AGAAAGTCCA	GCTGCTCCTG	TGCTGGTACC	AATCTCATGG
	2521	GAAGAGTGAT	GCATATCAAG	ATTTAATCAA	GGGTCTCAAA	AAAGCCGAAT	GTGCGAGAAC
	2581	CTTAGATAAA	TTTCAGGACA	TGGTCCAGAA	GGACCTTGGA	AAATCAACCC	CAGACACTGG
	2641	AAATGAAAAA	GAAGGACAAT	GTCTGGTCTG	GCCATCTGCT	GGAGACATGA	GAGCTGCCAA
30	2701	CCTTTGGCCA	AGCCCGCTCA	TGATCAAACG	CTCTAAGAAG	AACAGCCTGG	CCTGTGCCCT
	2761	GACGGCCGAC	CAGATGGTCA	GTGCCTTGTT	GGATGCTGAG	CCCCCCTAC	TCTATTCCGA
	2821	GTATGATCCT	ACCAGACCCCT	TCAGTGAAGC	TTCGATGATG	GGCTTACTGA	CCAACCTGGC
	2881	AGACAGGGAG	CTGGTTCACA	TGATCAACTG	GGCGAAGAGG	GTGCCAGGCT	TTGTGGATTT
	2941	GACCCCTCAT	GATCAGGTCC	ACCTTCTAGA	ATGTGCCTGG	CTAGAGATCC	TGATGATTGG
35	3001	TCTCGTCTGG	CGCTCCATGG	AGCACCCAGT	GAAGCTACTG	TTTGCTCCTA	ACTTGCTCTT
	3061	GGACAGGAAC	CAGGGAAAAT	GTGTAGAGGG	CATGGTGGAG	ATCTTCGACA	TGCTGCTGGC
	3121	TACATCATCT	CGGTTCGCCA	TGATGAATCT	GCAGGGAGAG	GAGTTTGTGT	GCCTCAAATC
	3181	TATTATTTTG	CTTAATTTCT	GAGTGTACAC	ATTTCTGTCC	AGCACCTTGA	AGTCTCTGGA
	3241	AGAGAAGGAC	CATATCCACC	GAGTCCCTGA	CAAGATCACA	GACACTTTGA	TCCACCTGAT
40	3301	GGCCAAGGCA	GGCCTGACCC	TGCAGCAGCA	GCACCAGCGG	CTGGCCCAGC	TCCTCCTCAT
	3361	CCTCTCCAC	ATCAGGCACA	TGAGTAACAA	AGGCATGGAG	CATCTGTACA	GCATGAAGTG
	3421	CAGCAACCTG	TGCCCCCTCT	ATGACCTGCT	GCTGGAGGCG	GCGGACGCCC	ACCGCCTACA
	3481	TGCGCCCACT	AGCCGTGGAG	GGGCATCCGT	GGAGGAGACG	GACCAAAGCC	ACTTGGCCAC
	3541	TGCGGGGCTCT	ACTTCATCGC	ATTCCCTTGA	AAAGTATTAC	ATCACGGGGG	AGGCAGAGGG
45	3601	TTTCCCTGCC	ACAGCTTGAT	GAAGATCTGA	GCTCCCTGGC	GGAATTGCGT	AAATGATTGC
	3661	AGATCCACTA	GTTCCTAGAG	TCGCTGATCA	GCCTCGACTG	TGCCTTCTAG	TTGCCAGCCA
	3721	TCTGTTGTTT	GCCCTCCTCC	CGTGCCTTCC	TTGACCTTGG	AAGTGCCAC	TCCCACTGTC
	3781	CTTCTCTAAT	AAAATGAGGA	AATTGCATCG	CATTGTCTGA	GATAGTGTCA	TTCTATTCTG
50	3841	GGGGGTGGGG	TGGGGCAGGA	CAGCAAGGGG	GAGGATTGGG	AAGACAATAG	CAGGCATGCT
	3901	GGGGATGCGG	TGGGCTCTAT	GGCTTCTGAG	GCGGAAAGAA	CCAGAAGCTT	GGCGTAATCA
	3961	TGGTCATAGC	TGTTTCTGTG	GTGAAATTGT	TATCCGCTCA	CAATCCACA	CAACATACGA
	4021	GCCGGAAGCA	TAAAGTGTA	AGCCTGGGGT	GCCTAATGAG	TGAGCTAACT	CACATTAATT
	4081	GCGTTGCGCT	CACTGCCCGC	TTTCCAGTCG	GGAAACCTGT	CGTGCCAGCT	GCATTAATGA
55	4141	ATCGGCCAAC	GCGCGGGGAG	AGGCGGTTTG	CGTATTGGGC	GCTCTTCCGC	TTCTCGCTC
	4201	ACTGACTCGC	TGCGCTCGGT	CGTTCGGCTG	CGGCGAGCGG	TATCAGCTCA	CTCAAAGGCG
	4261	GTAATACCGT	TATCCACAGA	ATCAGGGGAT	AACGCAGGAA	AGAACATGTG	AGCAAAAGGC
	4321	CAGCAAAAGG	CCAGGAACCG	TAAAAAGGCC	GCGTTGCTGG	CGTTTTCCTA	TAGGCTCCGC
	4381	CCCCCTGACG	AGCATCACAA	AAATCGACGC	TCAAGTCAGA	GGTGGCGAAA	CCCCACAGGA
	4441	CTATAAAGAT	ACCAGGCGTT	TCCCCCTGGA	AGCTCCCTCG	TGCGCTCTCC	TGTTCCGACC
60	4501	CTGCCGCTTA	CCGGATACCT	GTCCGCCTTT	CTCCCTTCGG	GAAGCGTGGC	GCTTCTCAT
	4561	AGCTCACGCT	GTAGGTATCT	CAGTTCGGTG	TAGGTCGTTT	GCTCCAAGCT	GGGCTGTGTG
	4621	CACGAACCCC	CCGTTACAGC	CGACCGCTGC	GCCTTATCCG	GTAACATACG	TCTTGAGTCC
	4681	AACCCGGTAA	GACACGACTT	ATCGCCACTG	GCAGCAGCCA	CTGGTAACAG	GATTAGCAGA
	4741	GCGAGGTATG	TAGGCGGTGC	TACAGAGTTC	TTGAAGTGGT	GGCCTAACTA	CGGCTACACT
65	4801	AGAAGGACAG	TATTTGGTAT	CTGCGCTCTG	CTGAAGCCAG	TTACCTTCGG	AAAAAGGATT
	4861	GGTAGCTCTT	GATCCGGCAA	ACAAACCACC	GCTGGTAGCG	GTGGTTTTTT	TGTTTGCAAG
	4921	CAGCAGATTA	GCGCAGAGAA	AAAAGGATCT	CAAGAAGATC	CTTTGATCTT	TTCTACGGGG
	4981	TCTGACGCTC	AGTGGAACGA	AAACTCACGT	TAAGGGATTT	TGGTCATGAG	ATTATCAAAA
	5041	AGGATCTTCA	CCTAGATCCT	TTTAAATTAA	AAATGAAGTT	TTAAATCAAT	CTAAAGTATA
70	5101	TATGAGTAAA	CTTGGTCTGA	CAGTTACCAA	TGCTTAATCA	GTAGGACACC	TATCTCAGCG
	5161	ATCTGTCTAT	TTGTTTATC	CATAGTTGCC	TGACTCCCCG	TCGTGTAGAT	AACTACGATA
	5221	CGGGAGGGCT	TACCATCTGG	CCCCAGTGCT	GCAATGATAC	CGCGAGACCC	ACGCTCACCG
	5281	GCTCCAGATT	TATCAGCAAT	AAACAGCCAA	GCCGGAAGGG	CCGAGCGCAG	AAGTGGTCCT



5341 GCAACTTTAT CCGCTCCAT CCAGTCTATT AATTGTTGCC GGAAGCTAG AGTAAGTAGT  
5401 TCGCCAGTTA ATAGTTTGCG CAACGTTGTT GCCATTGCTA CAGGCATCGT GGTGTCACGC  
5461 TCGTCGTTTG GTATGGCTTC ATTCAGCTCC GGTTCCTAAC GATCAAGGCG AGTTACATGA  
5521 TCCCCCATGT TGTGCAAAAA AGCGGTTAGC TCCTTCGGTC CTCCGATCGT TGTGAGAAGT  
5581 AAGTTGGCCG CAGTGTATC ACTCATGGTT ATGGCAGCAC TGCATAATTC TCTTACTGTC  
5641 ATGCCATCCG TAAGATGCTT TTCTGTGACT GGTGAGTACT CAACCAAGTC ATCTGAGAA  
5701 TAGTGTATGC GGCGACCGAG TTGCTCTTGC CCGGCGTCAA TACGGGATAA TACCGCGCCA  
5761 CATAGCAGAA CTTTAAAAGT GCTCATCATT GGAACACGTT CTTGCGGGCG AAAACTCTCA  
5821 AGGATCTTAC CGCTGTTGAG ATCCAGTTTC ATGTAACCCA CTCGTGCACC CAACTGATCT  
5881 TCAGCATCTT TACTTTTCAC CAGCGTTTCT GGGTGAACCA AAACAGGAAG GCAAAATGCC  
5941 GCAAAAAAGG GAATAAGGGC GACACGGAAA TGTGAATAC TCATACTCTT CCTTTTTCAA  
6001 TATTATTGAA GCATTTATCA GGGTTATTGT CTCATGAGCG GATACATATT TGAATGTATT  
6061 TAGAAAAATA AACAAATAGG GGTTCGCGCG ACATTTCGCC GAAAAGTGCC ACCTGACGTC  
6121 TAAGAAACCA TTATTATCAT GACATTAACC TATAAAAAATA GGCATATCAC GAGGCCCTTT  
6181 CGTC

SEQ ID NO: 10

Description of Artificial Sequence: vector pCAG-MFas-ER(T2) -bpa

1 TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA  
20 61 CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGCGGGTG  
121 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC  
181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGGCGCC  
241 ATTCGCCATT CAGGCTGCGC AACTGTTGGG AAGGCGGATC GGTGCGGGCC TCTTCGCTAT  
301 TACGCCAGCT GGCGAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA ACGCCAGGGT  
25 361 TTTCCCGAGT ACGACGTTGT AAAACGACGG CCAGTGAATT CGAGCTCGGT ACCCGGGGGC  
421 GCGCCGGATC TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAATT ACGGGGTCAT  
481 TAGTTCCATG CCCATATATG GAGTTCCGCG TTACATAACT TACGGTAAAT GGCCCGCTG  
541 GCTGACCGCC CAACGACCCC CGCCATTGA CGTCAATAAT GACGTATGTT CCCATAGTAA  
601 CGCCAATAGG GACTTTCCAT TGACGTCAAT GGGTGGACTA TTTACGGTAA ACTGCCACT  
30 661 TGGCAGTACA TCAAGTGTAT CATATGCCAA GTACGCCCC TATTGACGTC AATGACGGTA  
721 AATGGCCCGC CTGGCATTAT GCCAGTACA TGACCTTATG GGACTTTTCT ACTTGGCAGT  
781 ACATCTACGT ATTAGTCATC GCTATTACCA TGGGTCGAGG TGAGCCCCAC GTTCTGCTTC  
841 ACTCTCCCCA TCTCCCCCCC CTCGCCACCC CCAATTTTGT ATTTATTTAT TTTTAAATTA  
901 TTTTGTGACG CGATGGGGGG GGGGGGGGGG GGGGCGCGCG CCAGGCGGGG CGGGCGGGGG  
35 961 CAGAGGGGCG GCGGGGCGGA GCGGAGAGGG TCGGCGGGCA GCCAATCAGA GCGGCGCGCT  
1021 CCGAAAGTTT CCTTTTATGG CGAGGCGGCG GCGGCGGGCG CCTATAAAA AGCGAAGCGC  
1081 GCGGCGGGCG GGAGTCGCTG CGTTGCTTTC GCCCGTGCC CCGCTCCGCG CCGCTCCGCG  
1141 CCGCCCGCCC CGGCTCTGAC TGACCGCGTT ACTCCACAG GTGAGCGGGC GGGACGGCCC  
40 1201 TTTCTCTCCG GCGTGTAAAT AGCGCTTGGT TTAATGACGG CTCGTTTCTT TTTGTGGCT  
1261 GCGTGAAAGC CTTAAAGGGC TCCGGGAGGG CCCTTTGTGC GGGGGGAGC GGCTCGGGGG  
1321 GTGCGTGCCT GTGTGTGTG GTGGGGAGCG CCGCGTGCAG CCCGCGCTGC CCGGCGGGTG  
1381 TGAGCGCTGC GGGCGCGGCG CGGGGCTTTG TCGCTCCGCG GTGTGCGCGA GGGGAGCGCG  
1441 GCGGGGGGCG GTGCCCGGCG GTGCGGGGGG GCTGCGAGGG GAACAAAGGC TCGTGCGGG  
45 1501 GTGTGTGCGT GGGGGGGTGA GCAGGGGGTG TGGGCGCGCG GGTGCGGGTG TAACCCCCC  
1561 GTGCACCCCC CTCCCCGAGT TGCTGAGCAC GGCCCGGCTT CGGGTGCGGG GCTCCGTGCG  
1621 GCGCGTGGCG CGGGGCTCGC CGTGCCGGGC GGGGGGTGGC GGCAGGTGGG GGTGCCGGGC  
1681 GGGGCGGGGC CGCCTCGGGC CGGGGAGGGC TCGGGGAGG GGCAGCGCGG CCGCGGAGCG  
1741 CCGGCGGGTG TCGAGGCGCG GCGAGCGCA GCCATTGCCT TTTATGGTAA TCGTGCAGAA  
50 1801 GGGCGCAGGG ACTTCTTTT TCCCAAATCT GGCGGAGCCG AAATCTGGGA GCGCGCGCG  
1861 CACCCCTCTT AGCGGGCGCG GCGGAAGCGG TCGGCGCGCG GCAGGAAGGA AATGGGCGGG  
1921 GAGGGCCTTC GTGCGTGCCT GCGCGCGCGT CCCCTTCTCC ATCTCCAGCC TCGGGGCTGC  
1981 CGCAGGGGGA CGGCTGCCTT CGGGGGGGAC GGGGAGGGC GGGGTTCGCG TTTGCGCTG  
2041 TGACCGGCGG CTCTAGAGCC TCTGCTAACC ATGTTTCATG CTTCTTCTTT TTCTACAGA  
55 2101 TCCTTAATTA AATTCCACCA TGCTGTGGAT CTGGGCTGTC CTGCTCTGCG TGCTTGTGG  
2161 CTCACAGTTA AGAGTTTATA CTACCAGCAA TACAAACTGC AGGAAACAAA GTCCAGAAA  
2221 TCGCCTATGG TTGTTGACCA TCCTTGTTTT GTTAATTCCA CTTGTATTTA TATATCGAAA  
2281 GTACCGGAAA AGAAAGTGCT GGAAGAGGAG ACAGGATGAC CCTGAATCTA GAACCTCCAG  
2341 TCGTGAAACC ATACCAATGA ATGCCTCAAA TCTTAGCTTG AGTAAATACA TCCCGAGAA  
2401 TGCTGAAGAC ATGACAATCC AGGAAGCTAA AAAATTGCTC CGAGAAAATA ACATCAAGGA  
60 2461 GGGCAAGATA GATGAGATCA TGCATGACAG CATCCAAGAC ACAGCTGAGC AGAAAGTCCA  
2521 GTGCTCCTG TGCTGGTACC AATCTCATGG GAAGAGTGAT GCATATCAAG ATTTAATCAA  
2581 GGTCTTCAAA AAAGCCGAAT GTCGAGAAAC CTTAGATAAA TTTTCAAGAA TGGTCCAGAA  
2641 GGACCTTGA AAATCAACCC CAGACACTGG AAATGAAAAT GAAGGACAA GTCTGGTCGA  
2701 GCCATCTGCT GGAGACATGA GAGCTGCCAA CCTTTGGCCA AGCCCGCTCA TGATCAACAG  
65 2761 CTCTAAGAAG AACAGCCTGC CCTTGTCCCT GACGGCCGAC CAGATGGTCA GTGCTTGTG  
2821 GGATGCTGAG CCCCCATAC TCTATTCCGA GTATGATCCT ACCAGACCTT TCACTGAAGC  
2881 TTCGATGATG GGCTTACTGA CCAACCTGGC AGACAGGGAG CTGGTTTACA TGATCAACTG  
2941 GGGCAAGAGG GTGCCAGGCT TTGTGGATTT GACCTCCAT GATCAGGTCC ACCTTCTAGA  
3001 ATGTGCCTGG CTAGAGATCC AGTGATTGG TCTCGTCTGG CGTCCATGG AGCACCCAGT  
70 3061 GAAGCTACTG TTTGCTCTTA TCTTGCTCTT GGACAGGAAC CAGGGAAAAT GTGTAGAGGG  
3121 CATGGTGGAG ATCTTCGACA TGCTGCTGGC TACATCATCT CCGTTCGCGA TGATGAATCT  
3181 GCAGGGAGAG GAGTTTGTGT GCCTCAAATC TATTATTTTG CTTAATTCGT GAGTGTACAC  
3241 ATTTCTGTCC AGCACCTGTA AGTCTCTGGA AGAGAAGGAC CATATCCACC GAGTCTGGA

	3301	CAAGATCACA	GACACTTTGA	TCCACCTGAT	GGCCAAGGCA	GGCCTGACCC	TGCAGCAGCA
	3361	GCACCAGCGG	CTGGCCCCAGC	TCCTCCTCAT	CCTCTCCCAC	ATCAGGCACA	TGAGTAACAA
	3421	AGGCATGGAG	CATCTGTACA	GCATGAAGTG	CAAGAACGTG	GTGCCCTCT	ATGACCTGCT
	3481	GCTGGAGGCG	GCGGACGCCC	ACCGCCTACA	TGCGCCCACT	AGCCGTGGAG	GGGCATCCGT
5	3541	GGAGGAGACG	GACCAAAGCC	ACTTGCCAC	TGCGGGCTCT	ACTTCATCGC	ATTCTTTGCA
	3601	AAAGTATTAC	ATCACGGGGG	AGGCAGAGGG	TTTCCTGCC	ACAGCTTGAT	GAAGATCTGA
	3661	GCTCCCTGGC	GGAAATTGCGT	AAATGATTGC	AGATCCACTA	GTTCTAGAGC	TCGCTGATCA
	3721	GCCTCGACTG	TGCCTTCTAG	TTGCCAGCCA	TCTGTTGTTT	GCCCTCCCC	CGTGCCTTCC
	3781	TTGACCCCTG	AAGGTGCCAC	TCCCCTGTC	CTTTCCTAAT	AAAATGAGGA	AATGTCATCG
10	3841	CATTGTCTGA	GTAGGTGTCA	TTCTATTCTG	GGGGGTGGGG	TGGGGCAGGA	CAGCAAGGGG
	3901	GAGGATTGGG	AAGACAATAG	CAGGCATGCT	GGGGATGCGG	TGGGCTCTAT	GGCTTCTGAG
	3961	GCGGAAAGAA	CCAGAAGCTT	GGCGTAATCA	TGGTCATAGC	TGTTTCTCTG	GTGAAATTGT
	4021	TATCCGCTCA	CAATTCCACA	CAACATACGA	GCCGGAAGCA	TAAAGTGTA	AGCCTGGGGT
	4081	GCCTAATGAG	TGAGCTAACT	CACATTAATT	GCGTTGCGCT	CACTGCCCCG	TTTCCAGTCG
15	4141	GGAAACCTGT	CTTGCCAGCT	GCATTAATGA	ATCGGCCAAC	GCGCGGGGAG	AGGCGGTTTG
	4201	CGTATTGGGC	GCTCTTCCGC	TTCCTCGCTC	ACTGACTCGC	TGCGCTCGGT	CGTTCGGCTG
	4261	CGGCGAGCGG	TATCAGCTCA	CTCAAAGGCG	GTAATACGGT	TATCCACAGA	ATCAGGGGAT
	4321	AACGCAGGAA	AGAACATGTG	AGCAAAAGGC	CAGCAAAAGG	CCAGGAACCG	TAAAAAGGCC
	4381	TAGGTGCTGG	GCTTTTCCCA	TAGGCTCCGC	CCCCCTGACG	AGCATCACAA	AAATCGACGC
20	4441	TCAAGTCAGA	GGTGGCGAAA	CCCGACAGGA	CTATAAAGAT	ACCAGGCGTT	TCCCCCTGGA
	4501	AGTCCCTCG	TGCGCTCTCC	TGTTCCGACC	CTGCCGCTTA	CCGGATACCT	GTCCGCCTTT
	4561	CTCCCTTCGG	GAAGCGTGGC	GCTTCTCAT	AGCTCACGCT	GTAGGTATCT	CAGTTCGGTG
	4621	TAGGTGCTGG	GCTCCAAGCT	GGGCTGTGTG	CACGAACCCC	CCGTTACAGC	CGACCGCTGC
	4681	GCCTTATCCG	GTAACATATC	TCTTGAGTCC	AACCCGGTAA	GACACGACTT	ATCGCCACTG
25	4741	GCAGCAGCCA	CTGGTAACAG	GATTAGCAGA	GCGAGGTATG	TAGGCGGTGC	TACAGAGTTC
	4801	TTGAAGTGGT	GGCCTAACTA	CGGCTACACT	AGAAGGACAG	TATTTGGTAT	CTGCGCTCTG
	4861	CTGAAGCCAG	TTACCTTCGG	AAAAAGAGTT	GGTAGCTCTT	GATCCGGCAA	ACAAACCACC
	4921	GCTGGTAGCG	GTGGTTTTTT	TGTTTGCAAG	CAGCAGATTA	CGCGCAGAAA	AAAAGGATCT
	4981	CAAGAAGATC	CTTTGATCTT	TTCTACGGGG	TCTGACGCTC	AGTGGAACGA	AAACTCACGT
30	5041	TAAGGGATT	TGGTCATGAG	ATTATCAAAA	AGGATCTTCA	CCTAGATCCT	TTTAAATTAA
	5101	AAATGAAGTT	TTAAATCAAT	CTAAAGTATA	TATGAGTAAA	CTTGGTCTGA	CAGTTACCAA
	5161	TGCTTAATCA	GTGAGGCACC	TATCTCAGCG	ATCTGTCTAT	TTCGTTTCATC	CATAGTTGCC
	5221	TGACTCCCCG	TCGTGTAGAT	AACATACGATA	CGGGAGGGCT	TACCATCTGG	CCCCAGTGCT
	5281	GCATGATAC	GCGGAGACCC	ACGCTCACCG	GCTCCAGATT	TATCAGCAAT	AAACGAGCCA
35	5341	GCCGGAAGGG	CCGAGCGCAG	AAGTGGTCTT	GCAACTTTAT	CCGCCTCCAT	CCAGTCTATT
	5401	AAATGTTGCC	GGGAAGCTAG	AGTAAGTAGT	TCGCCAGTTA	ATAGTTTGCG	CAACGTTGTT
	5461	GCCATTGCTA	CAGGCATCGT	GGTGTACGCG	TCGTGCTTTG	GTATGGCTTC	ATTCAGTCC
	5521	GGTCCCAAC	GATCAAGGCG	AGTTACATGA	TCCCCCATGT	TGTGCAAAAA	AGCGGTTAGC
	5581	TCCTTCGGTC	CTCCGATCGT	TGTCAGAAGT	AAGTTGGCCG	CAGTGTATC	ACTCATGGTT
40	5641	ATGGCAGCAC	TGCATAATTC	TCTTACTGTC	ATGCCATCCG	TAAGATGCTT	TTCTGTGACT
	5701	GGTGAGTACT	CAACCAAGTC	ATTCTGAGAA	TAGTGTATGC	GGCGACCGAG	TTGCTCTTGC
	5761	CCGCGCTCAA	TACGGGATAA	TACCGCGCCA	CATAGCAGAA	CTTTAAAAAGT	GCTCATCATT
	5821	GGAAAACGTT	CTTCGGGGCG	AAAACCTCTCA	AGGATCTTAC	CGCTGTTGAG	ATCCAGTTCTG
	5881	ATGTAACCCA	CTCGTGACCC	CAACTGATCT	TCAGCATCTT	TTACTTTTAC	CAGCGTTTCT
45	5941	GGGTGAGCAA	AAACAGGAAG	GCAAAATGCC	GCAAAAAAGG	GAATAAGGGC	GACACGGAAA
	6001	TGTTGAATAC	TCATACTCTT	CCTTTTCAA	TATTATTGAA	GCATTTATCA	GGGTATTGT
	6061	CTCATGAGCG	GATACATATT	TGAATGTATT	TAGAAAAATA	AACAAATAGG	GGTCCGCGC
	6121	ACATTTCCCC	GAAAAGTGCC	ACCTGACGTC	TAAGAAACCA	TTATTATCAT	GACATTAACC
50	6181	TATAAAAAATA	GGCGTATCAC	GAGGCCCTTT	CGTC		

SEQ ID NOS: 11 and 12

Description of Artificial Sequence: DNA sequence (SEQ ID NO: 11) coding for fusion protein HAFas-ER(T2) (SEQ ID NO: 12)

		Met	Gly	Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala	Thr	Ser	Asn	Thr	Asn
55	2120	ATG	GGC	TAC	CCC	TAC	GAC	GTG	CCC	GAC	TAC	GCC	ACC	AGC	AAT	ACA	AAC
		Cys	Arg	Lys	Gln	Ser	Pro	Arg	Asn	Arg	Leu	Trp	Leu	Leu	Thr	Ile	Leu
	2168	TGC	AGG	AAA	CAA	AGT	CCC	AGA	AAT	CGC	CTA	TGG	TTG	TTG	ACC	ATC	CTT
60		Val	Leu	Leu	Ile	Pro	Leu	Val	Phe	Ile	Tyr	Arg	Lys	Tyr	Arg	Lys	Arg
	2216	GTT	TTG	TTA	ATT	CCA	CTT	GTA	TTT	ATA	TAT	CGA	AAG	TAC	CGG	AAA	AGA
		Lys	Cys	Trp	Lys	Arg	Arg	Gln	Asp	Asp	Pro	Glu	Ser	Arg	Thr	Ser	Ser
65	2264	AAG	TGC	TGG	AAA	AGG	AGA	CAG	GAT	GAC	CCT	GAA	TCT	AGA	ACC	TCC	AGT
		Arg	Glu	Thr	Ile	Pro	Met	Asn	Ala	Ser	Asn	Leu	Ser	Leu	Ser	Lys	Tyr
	2312	CGT	GAA	ACC	ATA	CCA	ATG	AAT	GCC	TCA	AAT	CTT	AGC	TTG	AGT	AAA	TAC
		Ile	Pro	Arg	Ile	Ala	Glu	Asp	Met	Thr	Ile	Gln	Glu	Ala	Lys	Lys	Phe
70	2360	ATC	CCG	AGA	ATT	GCT	GAA	GAC	ATG	ACA	ATC	CAG	GAA	GCT	AAA	AAA	TTT
		Ala	Arg	Glu	Asn	Asn	Ile	Lys	Glu	Gly	Lys	Ile	Asp	Glu	Ile	Met	His
	2408	GCT	CGA	GAA	AAT	AAC	ATC	AAG	GAG	GGC	AAG	ATA	GAT	GAG	ATC	ATG	CAT

	2456	Asp Ser Ile Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Leu Cys
		GAC AGC ATC CAA GAC ACA GCT GAG CAG AAA GTC CAG CTG CTC CTG TGC
5		
	2504	Trp Tyr Gln Ser His Gly Lys Ser Asp Ala Tyr Gln Asp Leu Ile Lys
		TGG TAC CAA TCT CAT GGG AAG AGT GAT GCA TAT CAA GAT TTA ATC AAG
10		
	2552	Gly Leu Lys Lys Ala Glu Cys Arg Arg Thr Leu Asp Lys Phe Gln Asp
		GGT CTC AAA AAA GCC GAA TGT CGC AGA ACC TTA GAT AAA TTT CAG GAC
	2600	Met Val Gln Lys Asp Leu Gly Lys Ser Thr Pro Asp Thr Gly Asn Glu
		ATG GTC CAG AAG GAC CTT GGA AAA TCA ACC CCA GAC ACT GGA AAT GAA
15		
	2648	Asn Glu Gly Gln Cys Leu Val Glu Pro Ser Ala Gly Asp Met Arg Ala
		AAT GAA GGA CAA TGT CTG GTC GAG CCA TCT GCT GGA GAC ATG AGA GCT
	2696	Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn
		GCC AAC CTT TGG CCA AGC CCG CTC ATG ATC AAA CGC TCT AAG AAG AAC
20		
	2744	Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu
		AGC CTG GCC TTG TCC CTG ACG GCC GAC CAG ATG GTC AGT GCC TTG TTG
	2792	Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro
		GAT GCT GAG CCC CCC ATA CTC TAT TCC GAG TAT GAT CCT ACC AGA CCC
25		
	2840	Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg
		TTC AGT GAA GCT TCG ATG ATG GGC TTA CTG ACC AAC CTG GCA GAC AGG
30		
	2888	Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val
		GAG CTG GTT CAC ATG ATC AAC TGG GCG AAG AGG GTG CCA GGC TTT GTG
	2936	Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu
		GAT TTG ACC CTC CAT GAT CAG GTC CAC CTT CTA GAA TGT GCC TGG CTA
35		
	2984	Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Val
		GAG ATC CTG ATG ATT GGT CTC GTC TGG CGC TCC ATG GAG CAC CCA GTG
40		
	3032	Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys
		AAG CTA CTG TTT GCT CCT AAC TTG CTC TTG GAC AGG AAC CAG GGA AAA
	3080	Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser
		TGT GTA GAG GGC ATG GTG GAG ATC TTC GAC ATG CTG CTG GCT ACA TCA
45		
	3128	Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu
		TCT CGG TTC CGC ATG ATG AAT CTG CAG GGA GAG GAG TTT GTG TGC CTC
	3176	Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser
		AAA TCT ATT ATT TTG CTT AAT TCT GGA GTG TAC ACA TTT CTG TCC AGC
50		
	3224	Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp
		ACC CTG AAG TCT CTG GAA GAG AAG GAC CAT ATC CAC CGA GTC CTG GAC
	3272	Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr
		AAG ATC ACA GAC ACT TTG ATC CAC CTG ATG GCC AAG GCA GGC CTG ACC
55		
	3320	Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser
		CTG CAG CAG CAG CAC CAG CGG CTG GCC CAG CTC CTC CTC ATC CTC TCC
60		
	3368	His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met
		CAC ATC AGG CAC ATG AGT AAC AAA GGC ATG GAG CAT CTG TAC AGC ATG
	3416	Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala Ala
		AAG TGC AAG AAC GTG GTG CCC CTC TAT GAC CTG CTG CTG GAG GCG GCG
65		
	3464	Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val
		GAC GCC CAC CGC CTA CAT GCG CCC ACT AGC CGT GGA GGG GCA TCC GTG
	3512	Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser
		GAG GAG ACG GAC CAA AGC CAC TTG GCC ACT GCG GGC TCT ACT TCA TCG
70		
	3560	His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro
		CAT TCC TTG CAA AAG TAT TAC ATC ACG GGG GAG GCA GAG GGT TTC CCT

Ala Thr Ala \*\*\*  
3608 GCC ACA GCT TGA

SEQ ID NOs: 13 and 14

5 Description of Artificial Sequence: DNA sequence (SEQ ID NO: 13) coding for fusion protein MFas-ER(T2) (SEQ ID NO: 14)

1	Met Leu Trp Ile Trp Ala Val Leu Pro Leu Val Leu Ala Gly Ser Gln
	ATG CTG TGG ATC TGG GCT GTC CTG CCT CTG GTG CTT GCT GGC TCA CAG
10	
49	Leu Arg Val His Thr Thr Ser Asn Thr Asn Cys Arg Lys Gln Ser Pro
	TTA AGA GTT CAT ACT ACC AGC AAT ACA AAC TGC AGG AAA CAA AGT CCC
15	
97	Arg Asn Arg Leu Trp Leu Leu Thr Ile Leu Val Leu Leu Ile Pro Leu
	AGA AAT CGC CTA TGG TTG TTG ACC ATC CTT GTT TTG TTA ATT CCA CTT
20	
145	Val Phe Ile Tyr Arg Lys Tyr Arg Lys Arg Lys Cys Trp Lys Arg Arg
	GTA TTT ATA TAT CGA AAG TAC CGG AAA AGA AAG TGC TGG AAA AGG AGA
25	
193	Gln Asp Asp Pro Glu Ser Arg Thr Ser Ser Arg Glu Thr Ile Pro Met
	CAG GAT GAC CCT GAA TCT AGA ACC TCC AGT CGT GAA ACC ATA CCA ATG
30	
241	Asn Ala Ser Asn Leu Ser Leu Ser Lys Tyr Ile Pro Arg Ile Ala Glu
	AAT GCC TCA AAT CTT AGC TTG AGT AAA TAC ATC CCG AGA ATT GCT GAA
35	
289	Asp Met Thr Ile Gln Glu Ala Lys Lys Phe Ala Arg Glu Asn Asn Ile
	GAC ATG ACA ATC CAG GAA GCT AAA AAA TTT GCT CGA GAA AAT AAC ATC
40	
337	Lys Glu Gly Lys Ile Asp Glu Ile Met His Asp Ser Ile Gln Asp Thr
	AAG GAG GGC AAG ATA GAT GAG ATC ATG CAT GAC AGC ATC CAA GAC ACA
45	
385	Ala Glu Gln Lys Val Gln Leu Leu Leu Cys Trp Tyr Gln Ser His Gly
	GCT GAG CAG AAA GTC CAG CTG CTC CTG TGC TGG TAC CAA TCT CAT GGG
50	
433	Lys Ser Asp Ala Tyr Gln Asp Leu Ile Lys Gly Leu Lys Lys Ala Glu
	AAG AGT GAT GCA TAT CAA GAT TTA ATC AAG GGT CTC AAA AAA GCC GAA
55	
481	Cys Arg Arg Thr Leu Asp Lys Phe Gln Asp Met Val Gln Lys Asp Leu
	TGT CGC AGA ACC TTA GAT AAA TTT CAG GAC ATG GTC CAG AAG GAC CTT
60	
529	Gly Lys Ser Thr Pro Asp Thr Gly Asn Glu Asn Glu Gly Gln Cys Leu
	GGA AAA TCA ACC CCA GAC ACT GGA AAT GAA AAT GAA GGA CAA TGT CTG
65	
577	Val Glu Pro Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser
	GTC GAG CCA TCT GCT GGA GAC ATG AGA GCT GCC AAC CTT TGG CCA AGC
70	
625	Pro Leu Met Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu
	CCG CTC ATG ATC AAA CGC TCT AAG AAG AAC AGC CTG GCC TTG TCC CTG
75	
673	Thr Ala Asp Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile
	ACG GCC GAC CAG ATG GTC AGT GCC TTG TTG GAT GCT GAG CCC CCC ATA
80	
721	Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met
	CTC TAT TCC GAG TAT GAT CCT ACC AGA CCC TTC AGT GAA GCT TCG ATG
85	
769	Met Gly Leu Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile
	ATG GGC TTA CTG ACC AAC CTG GCA GAC AGG GAG CTG GTT CAC ATG ATC
90	
817	Asn Trp Ala Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp
	AAC TGG GCG AAG AGG GTG CCA GGC TTT GTG GAT TTG ACC CTC CAT GAT
95	
865	Gln Val His Leu Leu Glu Cys Ala Trp Leu Glu Ile Leu Met Ile Gly
	CAG GTC CAC CTT CTA GAA TGT GCC TGG CTA GAG ATC CTG ATG ATT GGT
100	
913	Leu Val Trp Arg Ser Met Glu His Pro Val Lys Leu Leu Phe Ala Pro
	CTC GTC TGG CGC TCC ATG GAG CAC CCA GTG AAG CTA CTG TTT GCT CCT
105	
961	Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Met Val
	AAC TTG CTC TTG GAC AGG AAC CAG GGA AAA TGT GTA GAG GGC ATG GTG
110	
1009	Glu Ile Phe Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met
	GAG ATC TTC GAC ATG CTG CTG GCT ACA TCA TCT CGG TTC CGC ATG ATG
	Asn Leu Gln Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu

1057 AAT CTG CAG GGA GAG GAG TTT GTG TGC CTC AAA TCT ATT ATT TTG CTT

5 1105 Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu  
AAT TCT GGA GTG TAC ACA TTT CTG TCC AGC ACC CTG AAG TCT CTG GAA

1153 Glu Lys Asp His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu  
GAG AAG GAC CAT ATC CAC CGA GTC CTG GAC AAG ATC ACA GAC ACT TTG

10 1201 Ile His Leu Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln  
ATC CAC CTG ATG GCC AAG GCA GGC CTG ACC CTG CAG CAG CAG CAC CAG

1249 Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser  
CGG CTG GCC CAG CTC CTC CTC ATC CTC TCC CAC ATC AGG CAC ATG AGT

15 1297 Asn Lys Gly Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val  
AAC AAA GGC ATG GAG CAT CTG TAC AGC ATG AAG TGC AAG AAC GTG GTG

20 1345 Pro Leu Tyr Asp Leu Leu Leu Glu Ala Ala Asp Ala His Arg Leu His  
CCC CTC TAT GAC CTG CTG CTG GAG GCG GCG GAC GCC CAC CGC CTA CAT

1393 Ala Pro Thr Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser  
GCG CCC ACT AGC CGT GGA GGG GCA TCC GTG GAG GAG ACG GAC CAA AGC

25 1441 His Leu Ala Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr  
CAC TTG GCC ACT GCG GGC TCT ACT TCA TCG CAT TCC TTG CAA AAG TAT

1489 Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro Ala Thr Ala \*\*\*  
TAC ATC ACG GGG GAG GCA GAG GGT TTC CCT GCC ACA GCT TGA

30 **SEQ ID NO: 15**  
**Description of Artificial Sequence: primer Casp8ER-A**  
1 CCTTAATTAA TTCCACCATG AGTGAGTCAC GGAATTCAG

35 **SEQ ID NO: 16**  
**Description of Artificial Sequence: primer Casp8ER-B**  
1 GGCTCGAGGG GAGGGAAGAA GAGCTTC

40 **SEQ ID NO: 17**  
**Description of Artificial Sequence: primer myrCasp8ER-A**  
1 CCTTAATTAA TTCCACCATG GGGAGTAGCA AGAGCAAGCC TAAGGACCCC AGCCAGCGCA GTGAGTCACG  
GACTTCAG

45 **SEQ ID NO: 18**  
**Description of Artificial Sequence: vector pCAG-Casp8-ER(T2)-bpa**  
1 TCGCGCGTTT CGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA  
61 CAGCTTGCTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGCGGGTG  
121 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC  
181 ACCATATGCG GTGTGAAATA CCGCACAGAT CCGTAAGGAG AAAATACCGC ATCAGGCGCC  
50 241 ATTGCGCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC TCTTCGCTAT  
301 TACGCCAGCT GCGGAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA ACGCCAGGGT  
361 TTTCCCACTC ACGACGTGT AAAACGACGG CCAGTGAATT CGAGCTCGGT ACCCGGGGGC  
421 GCGCCGGATC TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAATT ACGGGGTGCT  
481 TAGTTCATAG CCCATATATG GAGTTCCGCG TTACATAACT TACGGTAAAT GGCCCGCCTG  
55 541 GCTGACCGCC CAACGACCCC CGCCCATTGA CGTCAATAAT GACGTATGTT CCCATAGTAA  
601 CGCCAATAGG GACTTTCCAT TGACGTCAAT GGGTGGACTA TTTACGGTAA ACTGCCACT  
661 TGGCAGTACA TCAAGTGAT CATATGCCAA GTACGCCCCC TATTGACGTC AATGACGGTA  
721 AATGGCCCCG CTGGCATTAT GCCCAGTACA TGACCTTATG GGAATTTCTT ACTTGGCAGT  
781 ACATCTACGT ATTAGTCATC GCTATTACCA TGGGTGAGG TGAGCCCCAC GTTCTGCTTC  
60 841 ACTCTCCCCA TCTCCCCCCC CTCCCCACCC CCAATTTTGT ATTTATTTAT TTTTAAATTA  
901 TTTTGTGAG CGATGGGGGG GGGGGGGGGG GGGGCGCGCG CCAGCGGGGG CGGGGCGGGG  
961 CGAGGGGGCG GCGGGGGCGA GCGGGAGAGG TGCGGGCGCA GCCAATCAGA GCGGCGCGCT  
1021 CCGAAAGTTT CCTTTTATGG CGAGGCGGCG GCGGCGGCGG CCTATAAAA AGCGAAGCGC  
1081 CCGGCGGGCG GGAGTCGCTG CGTTGCCTTC GCCCGTGCC CCGCTCCGCG CCGCCTCGCG  
65 1141 CCGCCCGCCC CGGCTCTGAC TGACCGGCTT ACTCCACAG GTGAGCGGGG GGGACGGCCC  
1201 TTCTCCTCCG GGTGTAATT AGCGTTGGT TTAATGACGG CTCGTTTCTT TTCTGTGGCT  
1261 GCGTGAAAGC CTTAAAGGGC TCCGGGAGGG CCCTTTGTGC GGGGGGAGC GGCTCGGGGG  
1321 GTGCGTGCGT GTGTGTGTGC GTGGGGAGCG CCGCGTGCGG CCCGCGCTGC CCGGCGGCTG  
1381 TGAGCGCTGC GGGCGCGGCG CGGGGCTTTG TGCGCTCCGC GTGTGCGCGA GGGGAGCGCG  
70 1441 GCCGGGGGCG GTGCCCGCG GTGCGGGGGG GCTGCGAGGG GAACAAAGGC TCGGTGCGGG  
1501 GTGTGTGCGT GGGGGGGTGA GCAGGGGGTG TGGGCGCGGC GGTGCGGCTG TAACCCCCC  
1561 CTGACCCCCC CTCCCCGAGT TGCTGAGCAC GGCCCGGCTT CGGGTGCGGG GCTCCGTGCG  
1621 GGGCGTGCGG CGGGGCTGCG CTGCGCGGCG GGGGGGTGGC GGCAGGTGGG GGTGCCGGG

5	1681	GGGGCGGGGC	CGCCTCGGGC	CGGGGAGGGC	TCGGGGGAGG	GGCGCGGCGG	CCCCGGAGCG
	1741	CCGGCGGCTG	TCGAGGCGCG	GCGAGCCGCA	GCCATTGCCT	TTTATGGTAA	TCGTGCAGAG
	1801	GGGCGCAGGG	ACTTCCTTTG	TCCCAAATCT	GGCGGAGCCG	AAATCTGGGA	GGCGCCGCGG
	1861	CACCCCTCT	AGCGGGCGCG	GGCGAAGCGG	TGCGGCGCCG	GCAGGAAGGA	AATGGGCGGG
	1921	GAGGGCCTTC	GTGCGTCGCC	GCGCCGCCGT	CCCCTTCTCC	ATCTCCAGCC	TCGGGGCTGC
10	1981	CGCAGGGGGA	CGGCTGCCTT	CGGGGGGGAC	GGGGCAGGGC	GGGGTTCGGC	TTCTGGCGTG
	2041	TGACCGGCGG	CTCTAGAGCC	TCTGCTAACC	ATGTTTCATG	CTTCTTCTTT	TTCTACAGA
	2101	TCCTTAATTA	ATTCCACCAT	GAGTGAGTCA	CGGACTTCAG	ACAAAGTTTA	CCAAATGAAG
	2161	AACAAACCTC	GGGGATACTG	TCTGATCATC	AACAATCATG	ATTTCAGCAA	GGCCCGGGAA
	2221	GACATAACCC	AACTCCGAAA	AATGAAGGAC	AGAAAGGAA	CAGACTGTGA	TAAAGAGGCT
15	2281	CTGAGTAAGA	CCTTTAAGGA	GCTTCATTTT	GAGATAGTAT	CTTACGACGA	CTGCACTGCA
	2341	AATGAAATCC	ACGAGATTCT	AGTAAGGCTAC	CAAAGCGCAG	ACCACAAGAA	CAAAGACTGC
	2401	TTCATCTGCT	GTATCCTATC	CCACGGTGAC	AAGGGTGTCG	TCTATGGAAC	GGATGGGAAG
	2461	GAGGCCTCCA	TCTATGACCT	GACATCTTAC	TTCCTGCTGT	CAAAGTGCCC	TTCCCTGTCT
	2521	GGGAAACCCA	AGATCTTTTT	CATTAGGCT	TGCCAAGGAA	GTAACCTCCA	GAAAGGAGTG
20	2581	CCTGATGAGG	CAGGCTTCGA	GCAACAGAAC	CACACTTTAG	AAGTGGATTG	ATCATCTCAC
	2641	AAGAACTATA	TTCGGATGA	GGCAGACTTT	CTGCTGGGAA	TGGCTACGGT	GAAGAACTGC
	2701	GTTCCTTACC	GAGATCCTGT	GAATGGAACC	TGGTATATTC	AGTCACTTTG	CCAGAGCCTG
	2761	AGGGAAGGAT	GCCTCAAGG	AGATGACATT	CTTAGCATCC	TGACTGGCGT	GAAGTATGAC
	2821	GTGAGCAATA	AAGACGACAG	GAGGAACAAG	GGAAGCAGA	TGCCACAGCC	CACCTTCACA
25	2881	CTACGGAAGA	AGCTCTTCTT	CCCTCCCCTC	GAGCCATCTG	CTGGAGACAT	GAGAGCTGCC
	2941	AACCTTTGGC	CAAGCCCGCT	CATGATCAAA	CGCTCTAAGA	AGAACAGCCT	GGCCTTGTC
	3001	CTGACGGCCG	ACCAGATGGT	CAGTGACATT	TTGGATGCTG	AGCCCCCAT	ACTCTATTCC
	3061	GAGTATGATC	CTACCAGACC	CTTCAGTGAA	GCTTCGATGA	TGGGCTTACT	GACCAACCTG
	3121	GCAGACAGGG	AGCTGGTTCA	CATGATCAAC	TGGGCGAAGA	GGGTGCCAGG	CTTGTGTGAT
30	3181	TTGACCTTCC	ATGATCAGGT	CCACCTTCTA	GAATGTGCC	GGCTAGAGAT	CCTGATGATT
	3241	GGTCTCGTCT	GGCGCTCCAT	GGAGCACCCA	GTGAAGCTAC	TGTTTGCTCC	TAACTTGCTC
	3301	TTGGACAGGA	ACCAGGAAA	ATGTGTAGAG	GGCATGGTGG	AGATCTTCGA	CATGCTGCTG
	3361	GCTACATCAT	CTCGGTTCGG	CATGATGAAT	CTGCAGGGAG	AGGAGTTTGT	GTGCCTCAAA
	3421	TCTATTATTT	TGCTTAATTC	TGGAGTGATC	ACATTTCTGT	CCAGCACCC	GAAGTCTCTG
35	3481	GAAGAGAAGG	ACCATATCCA	CCGAGTCTTG	GACAAGATCA	CAGACACTTT	GATCCACCTG
	3541	ATGGCCAAGG	CAGGCCTGAC	CCTGCAGCAG	CAGCACCAGC	GGCTGGCCCA	GCTCCTCCTC
	3601	ATCCTCTCCC	ACATCAGGCA	CATGAGTAAC	AAAGGCATGG	AGCATCTGTA	CAGCATGAAG
	3661	TGCAAGAACG	TGGTGCCCTT	CTATGACCTG	CTGCTGGAGG	CGGCGGACGC	CCACCGCCTA
	3721	CATGCGGCCA	CTAGCCGTGG	AGGGGCATCC	GTGGAGGAGA	CGGACCAAG	CCACTTGCCC
40	3781	ACTGCGGGCT	CTACTTCATC	GCATTCCTTG	CAAAAGTATT	ACATCACGGG	GGAGGCAGAG
	3841	GGTTTCCCTG	CCACAGCTTG	ATGAAGATCT	GAGCTCCCTG	GCGGAATTGC	GTAATGATT
	3901	GCAGATCCAC	TAGTTCTAGA	GTCGCTGAT	CAGCCTCGAC	TGTGCTTCT	AGTTGCCAGC
	3961	CATCTGTGTG	TGCCCCCTCC	CCCGTGCTTT	CCTTGACCTT	GGAAGGTGCC	ACTCCCCTG
	4021	TCCTTTCTCTA	ATAAAATGAG	GAAATTGCAT	CGCATGTGCT	GAGTAGGTGT	CATCTATTTC
45	4081	TGGGGGGTGG	GGTGGGGCAG	GACAGCAAGG	GGGAGGATTG	GGAAGACAAT	AGCAGGCATG
	4141	CTGGGGATCG	GGTGGGCTCT	ATGGCTTCTG	AGGCGGAAAG	AACCAGAAGC	TTGGCGTAAT
	4201	CATGGTCCATA	GCTGTTTCCT	GTGTGAAATT	GTTATCCGCT	CACAATTCCA	CACAACATAC
	4261	GAGCCGGGAG	CATAAAGTGT	AAAGCCTGGG	GTGCCATAATG	AGTGAGCTAA	CTCACATTAA
	4321	TTGCGTTGCG	CTCACTGCCC	GCTTTCCAGT	CGGGAACCT	GTCGTGCCAG	CTGCATTAA
50	4381	GAATCGGCCA	ACGCGCGGGG	AGAGCGGTTT	TGCGTATTGG	GCGCTCTTCC	GCTTCTCGC
	4441	TCACTGACTC	GCTGCGCTCG	GTCGTTCCGG	TGCGGCGAGC	GGTATCAGCT	CACTCAAAGG
	4501	CGGTAATACG	GTTATCCACA	GAATCAGGGG	ATAACGCAGG	AAAGAACATG	TGAGCAAAAG
	4561	GCCAGCAAAA	GGCCAGGAAC	CGTAAAAAGG	CCGCGTTGCT	GGCGTTTTTC	CATAGGCTCC
	4621	GGCCCCCTGA	CAGCATCAC	AAAAATCGAC	GCTCAAGTCA	GAGGTGGCGA	AACCCGACAG
55	4681	GACTATAAAG	ATACCAGGCG	TTTCCCCCTG	GAAGCTCCCT	CGTGCGCTCT	CCTGTTCCGA
	4741	CCCTGCCGCT	TACCGGATAC	CTGTCCGCTT	TTCTCCCTTC	GGGAAGCGTG	GCGCTTTCTC
	4801	ATAGCTCACG	CTGTAGGTAT	CTCAGTTCGG	TGTAGGTCGT	TCGCTCCAAG	CTGGGCTGTG
	4861	TGCACGAACC	CCCCGTTTCA	CCCGACCGCT	GCGCCTTATC	CGGTAACAT	CGTCTTGAGT
	4921	CCAACCCGGT	AAGACACGAC	TTATCGCCAC	TGGCAGCAGC	CACTGGTAAC	AGGATTAGCA
60	4981	GAGCGAGGTA	TGTAGGCGGT	GCTACAGAGT	TCTTGAAGTG	GTGGCCTAAC	TACGGCTACA
	5041	CTAGAAGGAC	AGTATTGGT	ATCTGCGCTC	TGCTGAAGCC	AGTTACCTTC	GGAAAAAGAG
	5101	TTGGTAGCTC	TTGATCCGGC	AAACAAACCA	CCGCTGGTAG	CGGTGGTTTT	TTTGTTCGCA
	5161	AGCAGCAGAT	TACGCGCAGA	AAAAAAGGAT	CTCAAGAAGA	TCCTTTGATC	TTTTCTACGG
	5221	GGTCTGACGC	TCAGTGAAC	GAAAACTCAC	GTTAAGGGAT	TTTGGTCATG	AGATTATCAA
65	5281	AAAGGATCTT	CACCTAGATC	CTTTTAAATT	AAAAATGAAG	TTTTAAATCA	ATCTAAAGTA
	5341	TATATGAGTA	AACCTTGCTT	GACAGTTACC	AATGCTTAAT	CAGTGAGGCA	CCTATCTCAG
	5401	CGATCTGTCT	ATTTCGTTCA	TCCATAGTTG	CCTGACTCCC	CGTCGTGTAG	ATAACTACGA
	5461	TACGGGAGGG	CTTACCATCT	GGCCCCAGTG	CTGCAATGAT	ACCGCGAGAC	CCACGCTCAC
	5521	CGGCTCCAGA	TTTATCAGCA	ATAAACCCAG	CAGCCGGAAG	GGCCGAGCGC	AGAAGTGCTC
70	5581	CTGCAACTTT	ATCCGCTTCC	ATCCAGTCTA	TTAATTGTTG	CCGGGAAGCT	AGAGTAAGTA
	5641	GTTCCGCACT	TAATAGTTTG	CGCAACGTTG	TTGCCATTGC	TACAGGCATC	GTGGTGTAC
	5701	GCTCGTCTGT	TGGTATGGCT	TCATTGACGT	CCGGTTCCCA	ACGATCAAGG	CGAGTTACAT
	5761	GATCCCCCAT	GTTGTGCAAA	AAAGCGGTTA	GCTCCTTCGG	TCCTCCGATC	GTTGTACAGAA
	5821	GTAAGTTGGC	GCCAGTGTTA	TCACTCATGG	TTATGGCAGC	ACTGCATAAT	TCTCTACTG
	5881	TCATGCCATC	CGTAAGATGC	TTTTCTGTGA	CTGGTGAGTA	CTCAACCAAG	TCATTCTGAG
	5941	AATAGTGTAT	GCGGCGACCG	AGTTGCTCTT	GCCCGGCGTC	AATACGGGAT	AATACCGCGC
	6001	CACATAGCAG	AACTTTAAAA	GTGCTCATCA	TTGGAAAACG	TTCTTCGGGG	CGAAAACCTCT

	6061	CAAGGATCTT ACCGGTGTT AGATCCAGTT CGATGTAAACC CACTCGTGCA CCCAATCAT															
	6121	CTTCACGATC TTTTACTTTC ACCAGCGTTT CTGGGTGAGC AAAAACAGGA AGGCAAAATG															
	6181	CCGCCAAAA GGAATAAGG GCGACACGGA AATGTTGAAT ACTCATACTC TTCCTTTTTT															
	6241	AATATTATTG AAGCATTTAT CAGGGTTATT GTCTCATGAG CGGATACATA TTGTAATGTA															
5	6301	TTTAGAAAA TAACAATA GGGGTTCCGC GCACATTTCC CCGAAAAGTG CCACCTGACG															
	6361	TCTAAGAAAC CATATTATC ATGACATTAA CCTATAAAAA TAGGCGTATC ACGAGGCCCT															
	6421	TTCGTC															
	<b>SEQ ID NOS: 19 and 20</b>																
10	<b>Description of Artificial Sequence: DNA sequence (SEQ ID NO: 19) coding for fusion protein Casp8-ER(T2) (SEQ ID NO: 20)</b>																
	Met Ser Glu Ser Arg Thr Ser Asp Lys Val Tyr Gln Met Lys Asn Lys																
	2119	ATG AGT GAG TCA CGG ACT TCA GAC AAA GTT TAC CAA ATG AAG AAC AAA															
15		Pro Arg Gly Tyr Cys Leu Ile Ile Asn Asn His Asp Phe Ser Lys Ala															
	2167	CCT CGG GGA TAC TGT CTG ATC ATC AAC AAT CAT GAT TTC AGC AAG GCC															
		Arg Glu Asp Ile Thr Gln Leu Arg Lys Met Lys Asp Arg Lys Gly Thr															
20	2215	CGG GAA GAC ATA ACC CAA CTC CGA AAA ATG AAG GAC AGA AAA GGA ACA															
		Asp Cys Asp Lys Glu Ala Leu Ser Lys Thr Phe Lys Glu Leu His Phe															
	2263	GAC TGT GAT AAA GAG GCT CTG AGT AAG ACC TTT AAG GAG CTT CAT TTT															
25		Glu Ile Val Ser Tyr Asp Asp Cys Thr Ala Asn Glu Ile His Glu Ile															
	2311	GAG ATA GTA TCT TAC GAC GAC TGC ACT GCA AAT GAA ATC CAC GAG ATT															
		Leu Glu Gly Tyr Gln Ser Ala Asp His Lys Asn Lys Asp Cys Phe Ile															
	2359	CTA GAA GGC TAC CAA AGC GCA GAC CAC AAG AAC AAA GAC TGC TTC ATC															
30		Cys Cys Ile Leu Ser His Gly Asp Lys Gly Val Val Tyr Gly Thr Asp															
	2407	TGC TGT ATC CTA TCC CAC GGT GAC AAG GGT GTC GTC TAT GGA ACG GAT															
		Gly Lys Glu Ala Ser Ile Tyr Asp Leu Thr Ser Tyr Phe Thr Gly Ser															
35	2455	GGG AAG GAG GCC TCC ATC TAT GAC CTG ACA TCT TAC TTC ACT GGT TCA															
		Lys Cys Pro Ser Leu Ser Gly Lys Pro Lys Ile Phe Phe Ile Gln Ala															
	2503	AAG TGC CCT TCC CTG TCT GGG AAA CCC AAG ATC TTT TTC ATT CAG GCT															
40		Cys Gln Gly Ser Asn Phe Gln Lys Gly Val Pro Asp Glu Ala Gly Phe															
	2551	TGC CAA GGA AGT AAC TTC CAG AAA GGA GTG CCT GAT GAG GCA GGC TTC															
		Glu Gln Gln Asn His Thr Leu Glu Val Asp Ser Ser Ser His Lys Asn															
	2599	GAG CAA CAG AAC CAC ACT TTA GAA GTG GAT TCA TCA TCT CAC AAG AAC															
45		Tyr Ile Pro Asp Glu Ala Asp Phe Leu Leu Gly Met Ala Thr Val Lys															
	2647	TAT ATT CCG GAT GAG GCA GAC TTT CTG CTG GGA ATG GCT ACG GTG AAG															
		Asn Cys Val Ser Tyr Arg Asp Pro Val Asn Gly Thr Trp Tyr Ile Gln															
50	2695	AAC TGC GTT TCC TAC CGA GAT CCT GTG AAT GGA ACC TGG TAT ATT CAG															
		Ser Leu Cys Gln Ser Leu Arg Glu Arg Cys Pro Gln Gly Asp Asp Ile															
	2743	TCA CTT TGC CAG AGC CTG AGG GAA AGA TGT CCT CAA GGA GAT GAC ATT															
55		Leu Ser Ile Leu Thr Gly Val Asn Tyr Asp Val Ser Asn Lys Asp Asp															
	2791	CTT AGC ATC CTG ACT GGC GTG AAC TAT GAC GTG AGC AAT AAA GAC GAC															
		Arg Arg Asn Lys Gly Lys Gln Met Pro Gln Pro Thr Phe Thr Leu Arg															
	2839	AGG AGG AAC AAG GGA AAG CAG ATG CCA CAG CCC ACC TTC ACA CTA CGG															
60		Lys Lys Leu Phe Phe Pro Pro Leu Glu Pro Ser Ala Gly Asp Met Arg															
	2887	AAG AAG CTC TTC TTC CCT CCC CTC GAG CCA TCT GCT GGA GAC ATG AGA															
		Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys		</													

	3127	Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe
		AGG GAG CTG GTT CAC ATG ATC AAC TGG GCG AAG AGG GTG CCA GGC TTT
5	3175	Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp
		GTG GAT TTG ACC CTC CAT GAT CAG GTC CAC CTT CTA GAA TGT GCC TGG
	3223	Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro
10		CTA GAG ATC CTG ATG ATT GGT CTC GTC TGG CGC TCC ATG GAG CAC CCA
	3271	Val Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly
		GTG AAG CTA CTG TTT GCT CCT AAC TTG CTC TTG GAC AGG AAC CAG GGA
15	3319	Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr
		AAA TGT GTA GAG GGC ATG GTG GAG ATC TTC GAC ATG CTG CTG GCT ACA
	3367	Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys
		TCA TCT CGG TTC CGC ATG ATG AAT CTG CAG GGA GAG GAG TTT GTG TGC
20	3415	Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser
		CTC AAA TCT ATT ATT TTG CTT AAT TCT GGA GTG TAC ACA TTT CTG TCC
	3463	Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu
25		AGC ACC CTG AAG TCT CTG GAA GAG AAG GAC CAT ATC CAC CGA GTC CTG
	3511	Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu
		GAC AAG ATC ACA GAC ACT TTG ATC CAC CTG ATG GCC AAG GCA GGC CTG
30	3559	Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu
		ACC CTG CAG CAG CAG CAC CAG CGG CTG GCC CAG CTC CTC CTC ATC CTC
	3607	Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser
		TCC CAC ATC AGG CAC ATG AGT AAC AAA GGC ATG GAG CAT CTG TAC AGC
35	3655	Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala
		ATG AAG TGC AAG AAC GTG GTG CCC CTC TAT GAC CTG CTG CTG GAG GCG
	3703	Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser
40		GCG GAC GCC CAC CGC CTA CAT GCG CCC ACT AGC CGT GGA GGG GCA TCC
	3751	Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser
		GTG GAG GAG ACG GAC CAA AGC CAC TTG GCC ACT GCG GGC TCT ACT TCA
45	3799	Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe
		TCG CAT TCC TTG CAA AAG TAT TAC ATC ACG GGG GAG GCA GAG GGT TTC
		Pro Ala Thr Ala ***
	3847	CCT GCC ACA GCT TGA

50 SEQ ID NO: 21

Description of Artificial Sequence: vector pCAG-myrCasp8-ER(T2)

	1	TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA
	61	CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGCGGGTG
	121	TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC
55	181	ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGGCGCC
	241	ATTGCGCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC TCTTCGCTAT
	301	TACGCCAGCT GCGGAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA ACGCCAGGGT
	361	TTTCCCAGTC ACGACGTTGT AAAACGACGG CCAGTGAATT CGAGCTCGGT ACCCGGGGGC
	421	GCGCCGGATC TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAATT ACGGGGTCAT
60	481	TAGTTCATAG CCCATATATG GAGTTCGCG TTACATAACT TACGGTAAAT GGCCCGCTG
	541	GCTGACCGCC CAACGACCCC CGCCCATTGA CGTCAATAAT GACGTATGTT CCCATAGTAA
	601	CGCCAATAGG GACTTTCCAT TGACGTCAAT GGGTGGACTA TTTACGGTAA ACTGCCCCACT
	661	TGGCAGTACA TCAAGTGTAT CATATGCCAA GTACGCCCCC TATTGACGTC AATGACGGTA
	721	AATGGCCCCG CTGGCATTAT GCCCAGTACA TGACCTTATG GGACTTTCCT ACTTGGCAGT
65	781	ACATCTACGT ATTAGTCATC GCTATTACCA TGGGTCGAGG TGAGCCCCAC GTTCTGCTTC
	841	ACTCTCCCCA TCTCCCCCCC CTCCCCACCC CCAATTTTGT ATTTATTTAT TTTTAAATTA
	901	TTTTGTGAG CGATGGGGGG GGGGGGGGGG GGGGGCGCGG CCAGGCGGGG CGGGGCGGGG
	961	CGAGGGGCGG GGGGGGGCGA GGCGGAGAGG TGCGGCGGCA GCCAATCAGA GCGGCGCGCT
	1021	CCGAAAGTTT CCTTTTATGG CGAGGCGGCG GCGGCGGCGG CCCTATAAAA AGCGAAGCGC
70	1081	GCGGCGGGCG GGAGTCGCTG CGTTGCCTTC GCCCGTGCC CCGCTCCGCG CCGCCTCGCG
	1141	CCGCGCGGCC CGGCTCTGAC TGACCGCGTT ACTCCACAG GTAGCGGGG GGGACGGGCC
	1201	TTCTCTCCG GGCTGTAATT AGCGCTTGGT TTAATGACGG CTCGTTTCTT TTCTGTGGCT
	1261	GCGTGAAGC CTAAAGGGC TCCGGGAGG CCCTTTGTGC GGGGGGGAGC GGCTCGGGGG



5	1321	GTGCGTGCCT	GTGTGTGTGC	GTGGGGAGCG	CCGCGTGC	CCCGCGCTGC	CCGGCGGCTG
	1381	TGAGCGCTGC	GGGCGCGGCG	CGGGGCTTTG	TGCGCTCCGC	GTGTGCGCGA	GGGGAGCGCG
	1441	GGCGGGGGCG	GTGCCCCGCG	GTGCGGGGGG	GCTGCGAGGG	GAACAAAGGC	TGCGTGCGGG
	1501	GTGTGTGCCT	GGGGGGGTGA	GCAGGGGGTG	TGGGCGCGGC	GGTCGGGCTG	TAACCCCCCG
	1561	CTGCACCCCG	CTCCCCGAGT	TGCTGAGCAC	GGCCCCGGCTT	CGGGTGCGGG	GTCCCGTGCG
10	1621	GGGCGTGGCG	CGGGGCTCGC	CGTGCCGGGC	GGGGGGTGGC	GGCAGGTGGG	GGTGCCGGGC
	1681	GGGCGGGGCG	CGCCTCGGGC	CGGGGAGGGC	TCGGGGGAGG	GGCGCGGGCG	CCCCGGAGCG
	1741	CCGGCGGCTG	TCGAGGCGCG	GCGAGCCGCA	GCCATTGCCT	TTTATGGTAA	TCGTGCGAGA
	1801	GGGCGCAGGG	ACTTCCTTTG	TCCCCAATCT	GGCGGAGCCG	AAATCTGGGA	GGCGCCGCCG
	1861	CACCCCTCT	AGCGGGCGCG	GGCGAAGCGG	TGCGGGCGCCG	GCAGGAAGGA	AATGGGCGGG
15	1921	GAGGGCTTTC	GTGCGTCGCC	GCGCCGCCGT	CCCCCTCTCC	ATCTCCAGCC	TCGGGGCTGC
	1981	CGCAGGGGGA	CGGCTGCCTT	CGGGGGGGAC	GGGGCAGGGC	GGGGTTCCGC	TTCTGGCGTG
	2041	TGACCGGCGG	CTCTAGAGCC	TCTGTAAACC	ATGTTTCATGC	CTTCTCTTTT	TTCTTACAGA
	2101	TCCTTAATTA	ATTCCACCAT	GGGGAGTAGC	AAGAGCAAGC	CTAAGGACCC	CAGCCAGCGC
	2161	AGTGAGTCAC	GGACTTCAGA	CAAAAGTTAC	CAAAATGAAGA	ACAAACCTCG	GGGATACCTT
20	2221	CTGATCATCA	ACAATCATGA	TTTCAGCAAG	GCCCCGGAAG	ACATAACCCA	ACTCCGAAAA
	2281	ATGAAGGACA	GAAAAGGAAC	AGACTGTGAT	AAAGAGGCTC	TGAGTAAGAC	CTTTAAGGAG
	2341	CTTCATTTTG	AGATAGTATC	TTACGACGAC	TGCACTGCAA	ATGAAATCCA	CGAGATTCTA
	2401	GAGGGCTTAC	AAAGCGCAGA	CCACAAGAAC	AAAGACTGCT	TCATCTGCTG	TATCCTATCC
	2461	CACGGTGACA	AGGGTGTGCT	CTATGGAACG	GATGGGAAGG	AGGCCCTCCAT	CTATGACCTG
25	2521	ACATCTTACT	TGACTGGTTC	AAAGTGCCCT	TCCCTGTCTG	GGAAACCCAA	GATCTTTTTT
	2581	ATTGAGGCTT	CCCAAGGAAG	TAACCTCCAG	AAAGGAGTGC	CTGATGAGGC	AGGCTTCGAG
	2641	CAACAGAACC	ACACTTTAGA	AGTGGATTCA	TCATCTCACA	AGAACTATAT	TCCGGATGAG
	2701	GCAGACTTTC	TGCTGGGAAT	GGCTACGGTG	AAGAACTGCG	TTTCTTACCG	AGATCCTGTG
	2761	AATGGAACCT	GGTATATTCA	GTCACCTTTC	CAGAGCCTGA	GGGAAAGATG	TCCTCAAGGA
30	2821	GAGCACCCTT	TAGCATCTTC	GACTGGCGTG	AACATGACCG	TGAGCAATAA	AGACGACAGG
	2881	AGGAACAAGG	GAAAGCAGAT	GCCACAGCCC	ACCTTCACAC	TACGGAAGAA	GCTCTTCTTC
	2941	CCTCCCCCTG	AGCCATCTGC	TGGAGACATG	AGAGCTGCCA	ACCTTTGGCC	AAGCCCGCTC
	3001	ATGATCAAA	GCTCTAAGAA	GAACAGCCTG	GCCTTGTCCT	TGACGGCCGA	CCAGATGGTC
	3061	GATGCCCTTG	TGGATGCTGA	GCCCCCATA	CTCTATTCCG	AGTATGATCC	TACCAAGACC
35	3121	TTGAGTGAAG	CTTCGATGAT	GGGCTTACTG	ACCAACCTGG	CAGACAGGGA	GCTGGTTTAC
	3181	ATGATCAACT	GGGCGAAGAG	GGTGCCAGGC	TTTGTGGATT	TGACCCCTCA	TGATCAGGTC
	3241	CACCTTCTAG	AATGTGCTCT	GCTAGAGATC	CTGATGATTG	GTCTCGTCTG	GCGCTCCATG
	3301	GAGTCCCTTG	TGAAGCTACT	GTTTGTCTCT	AACCTGCTCT	TGGACAGGAA	CCAGGGAATA
	3361	TGTTAGAGAG	GCATGGTGGG	GATCTTCGAC	ATGCTGCTGG	CTACATCATC	TCGGTTCCGC
40	3421	ATGATGAATC	TGCAGGGAGA	GGAGTTTGTG	TGCCTCAAAT	CTATATTTTT	GCTTAATTTT
	3481	GGAGTGATCA	CATTTCTGTC	CAGCACCCCTG	AAGTCTCTGG	AAGAGAAGGA	CCATATCCAC
	3541	CGAGTCCCTG	ACAAGATCAC	AGACACTTTG	ATCCACTTGA	TGGCCAAGGC	AGGCCTGACC
	3601	CTGCAGCAGC	AGCACCAGCG	GCTGGCCAGC	CTCCTCTCTA	TCCTCTCCCA	CATCAGGCAC
	3661	ATGAGTAACA	AAGGCATGGA	GCATCTGTAC	AGCATGAAGT	GCAAGAACGT	GGTGCCCTTC
45	3721	TATGACCTGC	TGCTGGAGGC	GGCGGACGCG	CACCGCCTAC	ATGCGCCAC	TAGCCGTGGA
	3781	GGGCACTCCG	TGGAGGAGAC	GGACCAAAGC	CACCTTGGCC	CTGCGGGCTC	TACTTCTATC
	3841	CATTCCTTGC	AAAAGTATTA	CATCACGGGG	GAGGCAGAGG	GTTTCCCTGC	CACAGCTTGA
	3901	TGAAGATCTG	AGCTCCCTGG	CGGAATTGCG	TAAATGATTG	CAGATCCACT	AGTTCTAGAG
	3961	CTCGCTGATC	AGCCTCGACT	GTGCCTTCTA	GTTGCCAGCC	ATCTGTTGTT	TGCCCCCTCC
50	4021	CCGTGCCCTT	CTTGACCCTG	GAAGGTGCCA	CTCCCCTGT	CCTTTCTTAA	TAAATGAGG
	4081	AAATTGCATC	GCATTGTCTG	AGTAGGTGTC	ATTCTATTCT	GGGGGGTGGG	GTGGGGCAGG
	4141	ACAGCAAGGG	GGAGGATTGG	GAAGACAATA	GCAGGCATGC	TGGGGATGCG	GTGGGCTCTA
	4201	TGGCTTCTGA	GGCGAAAGAA	ACCAGAAGCT	TGGCGTAATC	ATGGTCATAG	CTGTTTCCCT
	4261	TGTGAAATTG	TTATCCGCTC	ACAATTCCAC	ACAACATACG	AGCCGGAAGC	ATAAAGTGTA
55	4321	AAGCCTGGGG	TGCCTAATGA	GTGAGCTAAC	TCACATTAAT	TGCGTTGCGC	TCAGTGCCCG
	4381	CTTTCCAGTC	GGGAAACCTG	TCGTGCCAGC	TGCATTAATG	AATCGGCCAA	CGCGCGGGGA
	4441	GAGCGGGTTT	CGGTATTGGG	CGCTCTTCCG	CTTCTCGCT	CACCTGACTCG	CTGCGCTCGG
	4501	TCGTTCGGCT	GCGGCGAGCG	GTATCAGCTC	ACTCAAAGGC	GGTAATACGG	TTATCCACAG
	4561	AATCAGGGGA	TAACGCAGGA	AAGAACATGT	GAGCAAAGG	CCAGCAAAG	GCCAGGAACC
60	4621	GTAAGAAAGC	CGCGTTGCTG	GCGTTTTTTC	ATAGGCTCCG	CCCCCTGAC	GAGCATCACA
	4681	AAAATCGACG	CTCAAGTCAG	AGGTGGCGAA	ACCCGACAGG	ACTATAAAGA	TACCAGGCGT
	4741	TTCCCCCTGG	AAGCTCCCTC	GTGCGCTCTC	CTGTTCCGAC	CCTGCGGCTT	ACCGGATACC
	4801	TGTCGCGCTT	TCTCCCTTCG	GGAAGCGTGG	CGCTTTCTCA	TAGCTCACGC	TGTAGGTATC
	4861	TCAGTTCGGT	GTAGGTCGTT	CGCTCCAAGC	TGGGCTGTGT	GCACGAACCC	CCCGTTTCAG
65	4921	CCGACCGCTG	CGCCTTATCC	GGTAACATAT	GTCCTGAGTC	CAACCCGGTA	AGACACGACT
	4981	TATCGCCACT	GGCAGCAGCC	ACTGGTAACA	GGATTAGCAG	AGCGAGGTAT	GTAGGCGGTG
	5041	CTACAGAGTT	CTTGAAGTGG	TGGCCTAACT	ACGGCTACAC	TAGAAGGACA	GTATTTGGTA
	5101	TCTGCGCTCT	GCTGAAGCCA	GTTACCTTCG	GAAAAAGAGT	TGGTAGCTCT	TGATCCGGCA
	5161	AACAAACACG	CGCTGGTAGC	GTTGGTTTTT	TTGTTTGCAA	GCAGCAGATT	ACGCGCAGAA
70	5221	AAAAAGGATC	TCAAGAAGAT	CCTTTGATCT	TTTCTACGGG	GTCTGACGCT	CAGTGGAACG
	5281	AAAACCTACG	TTAAGGGATT	TTGGTCATGA	GATTATCAAA	AAGGATCTTC	ACCTAGATCC
	5341	TTTTAAATTA	AAAATGAAGT	TTTAAATCAA	TCTAAAGTAT	ATATGAGTAA	ACTTGGTCTG
	5401	ACAGTTACCA	ATGCTTAATC	AGTGAGGCAC	CTATCTCAGC	GATCTGTCTA	TTTCGTTCTA
	5461	CCATAGTTGC	CTGACTCCCC	GTCGTGTAGA	TAACTACGAT	ACGGGAGGGC	TTACCATCTG
	5521	GCCCCAGTGC	TGCAATGATA	CCGCGAGACC	CACGCTCACC	GGCTCCAGAT	TTATCAGCAA
	5581	TAAACCAGCC	AGCCGGAAGG	GCCGAGCGCA	GAAAGTGGTC	TGCAACTTTA	TCCGCTCCCA
	5641	TCCAGTCTAT	TAATTGTTGC	CGGGAAGCTA	GAGTAAGTAG	TTCGCCAGTT	AATAGTTTTG

[illegible]

	3031	Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu Asp Ala	GCC TTG TCC CTG ACG GCC GAC CAG ATG GTC AGT GCC TTG TTG GAT GCT
5	3079	Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro Phe Ser	GAG CCC CCC ATA CTC TAT TCC GAG TAT GAT CCT ACC AGA CCC TTC AGT
	3127	Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg Glu Leu	GAA GCT TCG ATG ATG GGC TTA CTG ACC AAC CTG GCA GAC AGG GAG CTG
10	3175	Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val Asp Leu	GTT CAC ATG ATC AAC TGG GCG AAG AGG GTG CCA GGC TTT GTG GAT TTG
	3223	Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu Glu Ile	ACC CTC CAT GAT CAG GTC CAC CTT CTA GAA TGT GCC TGG CTA GAG ATC
15	3271	Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Val Lys Leu	CTG ATG ATT GGT CTC GTC TGG CGC TCC ATG GAG CAC CCA GTG AAG CTA
20	3319	Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys Cys Val	CTG TTT GCT CCT AAC TTG CTC TTG GAC AGG AAC CAG GGA AAA TGT GTA
	3367	Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser Ser Arg	GAG GGC ATG GTG GAG ATC TTC GAC ATG CTG CTG GCT ACA TCA TCT CGG
25	3415	Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu Lys Ser	TTC CGC ATG ATG AAT CTG CAG GGA GAG GAG TTT GTG TGC CTC AAA TCT
	3463	Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser Thr Leu	ATT ATT TTG CTT AAT TCT GGA GTG TAC ACA TTT CTG TCC AGC ACC CTG
30	3511	Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp Lys Ile	AAG TCT CTG GAA GAG AAG GAC CAT ATC CAC CGA GTC CTG GAC AAG ATC
35	3559	Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr Leu Gln	ACA GAC ACT TTG ATC CAC CTG ATG GCC AAG GCA GGC CTG ACC CTG CAG
	3607	Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser His Ile	CAG CAG CAC CAG CGG CTG GCC CAG CTC CTC CTC ATC CTC TCC CAC ATC
40	3655	Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met Lys Cys	AGG CAC ATG AGT AAC AAA GGC ATG GAG CAT CTG TAC AGC ATG AAG TGC
	3703	Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala Ala Asp Ala	AAG AAC GTG GTG CCC CTC TAT GAC CTG CTG CTG GAG GCG GCG GAC GCC
45	3751	His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val Glu Glu	CAC CGC CTA CAT GCG CCC ACT AGC CGT GGA GGG GCA TCC GTG GAG GAG
50	3799	Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser His Ser	ACG GAC CAA AGC CAC TTG GCC ACT GCG GGC TCT ACT TCA TCG CAT TCC
	3847	Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro Ala Thr	TTG CAA AAG TAT TAC ATC ACG GGG GAG GCA GAG GGT TTC CCT GCC ACA
55	3895	Ala ***	GCT TGA

**SEQ ID NO: 24**

60 **Description of Artificial Sequence: primer Casp9fullER-A**  
 1 CCTTAATTAA TTCCACCATG GACGAGGCGG ACCGGCAGC

**SEQ ID NO: 25**

65 **Description of Artificial Sequence: primer Casp9ER-B**  
 1 GGCTCGACTG AAGTTTTAAA AACAGC

**SEQ ID NO: 26**

70 **Description of Artificial Sequence: primer Casp9truncER-A**  
 1 CCTTAATTAA TTCCACCATG GGTGCGCAAG CAGCCAAGCA GG

**SEQ ID NO: 27**

**Description of Artificial Sequence: vector pCAG-Casp9full-ER(T2)-bpA**  
 1 TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA

61 CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGCGGGTG  
121 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC  
181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGGCGCC  
241 ATTGCCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC TCTTCGTAT  
5 301 TACGCCAGCT GGCGAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA ACGCCAGGGT  
361 TTCCCCAGTC ACGACGTTGT AAAACGACGG CCAGTGAATT CGAGCTCGGT ACCCGGGGGC  
421 GCGCCGGATC TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAATT ACGGGGTCAT  
481 TAGTTCATAG CCCATATATG GAGTTCGCGG TTACATAACT TACGGTAAAT GGCCCGCCTG  
541 GGTGACCGCC CAACGACCCC CGCCCATTGA CGTCAATAAT GACGTATGTT CCCATAGTAA  
10 601 CGCCAATAGG GACTTTCCAT TGACGTCAAT GGGTGGACTA TTTACGGTAA ACTGCCCACT  
661 TGGCAGTACA TCAAGTGTAT CATATGCCAA GTACGCCCC TATTGACGTC AATGACGGTA  
721 AATGGCCCGC CTGGCATTAT GCCCAGTACA TGACCTTATG GGACTTTCCT ACTTGGCAGT  
781 ACATCTAGCT ATTAGTCATC GCTATTACCA TGGGTCGAGG TGAGCCCCAC GTTCTGCTTC  
841 ACTCTCCCCA TCTCCCCCCC CTCCCCACCC CCAATTTTGT ATTTATTTAT TTTTAAATTA  
15 901 TTTTGTGTCG CGATGGGGG GGGGGGGGGG GGGGCGCGC CAGGCGGGG CGGGCGGGG  
961 CGAGGGGCGG GCGGGGGCGA GCGGGAGAGG TGCGGCGGCA GCCAATCAGA GCGGCGCGCT  
1021 CCGAAAGTTT CTTTTTATGG CGAGGCGGCG GCGGCGGCGG CCCTATAAAA AGCGAAGCGC  
1081 GCGGCGGGCG GGAGTCGCTG CGTTGCCTTC GCCCCGTGCC CCGCTCCGCG CCGCCTCGCG  
1141 CCGCCCGCCC CGGCTCTGAC TGACCGCGTT ACTCCACAG GTGAGCGGGC GGGACGGCCC  
20 1201 TTCTCCTCCG GGCTGTAATT AGCGCTTGGT TTAATGACGG CTCGTTTCTT TTCTGTGGCT  
1261 GCGTGAAGAG CTTAAAGGGG TCCGGGAGGG CCCTTGTGTC GGGGGGGAGC GGCTCGGGG  
1321 GTGCGTGCCT GTGTGTGTG GTGGGGAGCG CCGCGTGC GGCGCGCTGC CCGGCGGCTG  
1381 TGAGCGTGC CGGGGCTGCG CGGGGCTTTG TGCGCTCCCG GTGTGCGCGA GGGGAGCGCG  
1441 GCGGGGGGCG GTGCCCCGCG GTGCGGGGGG GCTGCGAGGG GAACAAAGGC TGCGTGCGGG  
25 1501 GTGTGTGCGT GGGGGGGTGA GCAGGGGGTG TGGGCGCGCG GGTGCGGGTG TAACCCCCC  
1561 GTGACCCCC CTCCCCGAGT TGCTGAGCAC GGCCCGGCTT CCGGTGCGGG GCTCCGTGCG  
1621 GGGCGTGGCG CGGGGCTCGC CGTCCCGGGC GGGGGGTGGC GGCAGGTGGG GGTGCCGGGC  
1681 GGGGCGGGGC CGCCTCGGGC CGGGGAGGGC TCGGGGGAGG GGCAGCGCGG CCGCGAGCG  
1741 CCGGCGGGTG TCGAGGCGCG GCGAGCGCGA GCCATTGCCT TTTATGGTAA TCGTGCAGAA  
30 1801 GGGCGCAGGG ACTTCTTTG TCCAAATCT GCGGAGCGG AAATCTGGGA GGCGCCGCGC  
1861 CACCCCCCT AGCGGGGCGG GCGCAAGCGG TGCGGCGCGG GCAGGAAGGA AATGGGCGGG  
1921 GAGGGCCTTC GTGCGTCGCC GCGCCGCGCT CCCCTTCTCC ATCTCCAGCC TCGGGGCTGC  
1981 CGCAGGGGGA CGGCTGCCTT CGGGGGGGAC GGGGCGAGGG GGGGTTGCGC TTCTGGCGTG  
2041 TGACGTGGGG CTTAGAGCC TCTGCTAACC ATGTTTCATG CTTCTTCTTT TTCTACAGA  
35 2101 TCCTTAATTA ATTCCACCAT GGACGAGGCG GACCGGCAGC TCCTGCGGCG ATGACGGGTG  
2161 CGCTAGTGA GCGAGCTGCA AGTCGCGGAG CTCTGGGACG CTCTGCTGAG TCGAGAGCTC  
2221 TTCACGCGCG ACATGATCGA GGATATTACG CAGGCAGGAT CTGGGTCTCG GCGGGATCAG  
2281 GCCAGGCAGC TGGTCACAGA CCTTGAGACC CGAGGGAGGG AGGCCCTTCC TCTCTTCATC  
40 2341 TCCTGCTTAG AGGACACAGG CCAAGGCACC CTGGCTTCAC TCTTGCAAAG CGGTGCGCAA  
2401 GCAGCCAAGC AGGATCCAGA GGCTGTTAAA CCCCTAGACC ACCTGGTGCC TGTGGTCTG  
2461 GGACCAATGG GACTCACAGC AAAGGAGCAG AGAGTAGTGA AGCTGGACCC GTCACAGCCT  
2521 GCGGTGGGAG ACCTCACCCC AGTGGTGCTG GGGCAGAAAG AGCTCTGGCC TGCTCGGCTC  
2581 AAGCCAGAGG TTCTCAGACC AGAAACACCC AGGCCCGTGG ACATTGGTTC TGGCGGAGCT  
2641 CATGATGTCT GTGTTCCAGG GAAGATCAGG GGACATGCAG ATATGGCATA CACCCTGGAT  
45 2701 TCGGATCCCT GTGGCCACTG CCTCATCATC AACAATGTGA ACTTCTGCCC TTCTCGGGG  
2761 CTGCGTCAAC GCACGGGCTC CAACCTGGAC CGTGACAAAC TCGAGCACCG ATTCCGCTGG  
2821 CTGCGCTTCA TGGTGGAGGT GAAGAACGAC CTGACTGCCA AGAAAATGGT CACGGCTTTG  
2881 ATGGAGATGG CACACCGGAA CCACCGTGCC CTGGACTGCT TTGTGGTGGT CATCCTCTCT  
2941 CATGGCTGCC AGGCCAGCCA CCTCCAGTTC CCGGGTGCTG TCTATGGGAC AGATGGATGC  
50 3001 TCCGTGTCCA TGTAGAAAAT TGTGAATATC TTCAACGGGA GCGGCTGCCC CAGCCTGGGA  
3061 GGGAAAGCCA AGCTCTTCTT CATCCAGGCC TGCGGTGGTG AGCAGAAAGA CCATGGCTTT  
3121 GAGGTGGCCT GCACTTCCCT TCAAGGCAGG ACCTTGGACA GTGACTCTGA GCCAGATGCT  
3181 GTCCCCATC AGGAAGGCCC AAGGCCCTTG GACCAGCTGG ATGCTGTGTC AAGTTTGCTT  
3241 ACCCCAGTG ACATCCTTGT GTCCTACTCC ACCTTCCCAG GTTTTGTCTC CTGGAGGGAC  
55 3301 AAGAAAAGTG GCTCCTGGTA CATCGAGACC TTGGATGGCA TTCTGGAGCA GTGGGCTCGC  
3361 TCTGAAGACC TGCAGTCCCT CCTTCTCAGG GTTGCCAATG CTGTTTCTGC GAAAGGGACT  
3421 TACAAGCAGA TTCTTGCTG TTTTAACTTC CTCGGAAAA AGCTGTTTTT TAAACTTCA  
3481 GTCGAGCCAT TCGCTGGAGA CATGAGAGCT GCCAACCTTT GGCCAAGCCC GCTCATGATC  
3541 AAACGCTCTA AGAAGAACAG CCTGGCCTTG TCCCTGACGG CCGACCAGAT GGTCAAGTCC  
60 3601 TTGTTGGATG CTGAGCCCCC CATACTCTAT TCCGAGTATG ATCCTACCAG ACCCTTCAGT  
3661 GAAGCTTCGA TGATGGGCTT ACTGACCAAC CTGGCAGACA GGGAGCTGGT TCACATGATC  
3721 AACTGGGCGA AGAGGGTGCC AGGCTTTGTG GATTGTGACCC TCCATGATCA GGTCCACCTT  
3781 CTAGAATGTG CTTGGCTAGA GATCCTGATG ATTGGTCTCG TCTGGCGCTC CATGGAGCAC  
3841 CCAGTGAAGC TACTGTTTGC TCCTAACTTG CTCTTGGACA GGAACCAGGG AAAATGTGTA  
65 3901 GAGGGCATGG TGGAGATCTT CGACATGCTG CTGGCTACAT CATCTCGGT CCGCATGATG  
3961 AATCTGCAGG GAGAGGAGTT TGTGTGCCTC AAATCTATTA TTTTGCTTAA TTCTGGAGTG  
4021 TACACATTTT TGTCCAGCAC CCTGAAGTCT CTGGAAGAGA AGGACCATAT CCACCGAGTC  
4081 CTGGACAAGA TCACAGACAC TTTGATCCAC CTGATGGCCA AGGCAGGCCCT GACCCTGCAG  
4141 CAGCAGCAC AGCGGCTGGC CAGCTCCTC CTCACTCTCT CCCACATCAG GCACATGAGT  
70 4201 AACAAAGGCA TGGAGCATCT GTACAGCATG AAGTGCAAGA ACGTGGTGCC CCTCTATGAC  
4261 CTGCTGCTGG AGCGGGCGGA CGCCACCGC CTACATGCGC CCACTAGCCG TGAGGGGCA  
4321 TCCGTGGAGG AGACGGACCA AAGCCACTTG GCCACTGCGG GCTCTACTTC ATCGCATTCC  
4381 TTGCAAAAGT ATTACATCAC GGGGGAGGCA GAGGGTTTCC CTGCCACAGC TTGATGAAGA

4441 TCTGAGCTCC CTGGCGGAAT TGCCTAAATG ATTGCAGATC CACTAGTTCT AGAGCTCGCT  
4501 GATCAGCCTC GACTGTGCCT TCTAGTTGCC AGCCATCTGT TGTTCGCCCC TCCCCCGTGC  
4561 CTTCTTTGAC CCTGGAAGGT GCCACTCCCA CTGTCCTTTC CTAATAAAAT GAGGAAATG  
4621 CATCGCATTG TCTGAGTAGG TGTCATTCTA TTCTGGGGGG TGGGGTGGGG CAGGACAGCA  
5 4681 AGGGGGAGGA TTGGGAAGAC AATAGCAGGC ATGCTGGGGA TGCCGTGGGC TCTATGGCTT  
4741 CTGAGGCGGA AAGAACCAGA AGCTTGCGGT AATCATGGTC ATAGCTGTTT CCTGTGTGAA  
4801 ATTGTTATCC GCTCACAATT CCACACAACA TACGAGCCGG AAGCATAAAG TGTAAAGCCT  
4861 GGGGTGCCCTA ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC  
4921 AGTCGGGAAA CTGTCTGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG  
10 4981 GTTTGCGTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGGTCTGTC  
5041 GGCTGCGGCG AGCCGTATCA GCTCACTCAA AGGCGGTAAT ACGGTTATCC ACAGAATCAG  
5101 GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA  
5161 AGGCCGCGTT GCTGGCGTTT TTCCATAGGC TCCGCCCCCC TGACGAGCAT CACAAAAATC  
5221 GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC  
15 5281 CTTGGAAGTC CTCGTGCGC TCTCCTGTTT CGACCTGCGC GCTTACCGGA TACCTGTCCG  
5341 CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCATAGCTC ACGCTGTAGG TATCTCAGTT  
5401 CGGTGTAGGT CTTTCGCTCC AAGCTGGGCT GTGTGCACGA ACCCCCCGTT CAGCCCGACC  
5461 GCTGCGCCTT ATCCGGTAAC TATCGTCTTG AGTCCAACCC GGTAAAGACAC GACTTATCGC  
5521 GACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG  
20 5581 AGTTCTTGAA GTGGTGGCCT AACTACGGCT ACAC TAGAAG GACAGTATTT GGTATCTGCG  
5641 CTCTGCTGAA GCCAGTTACC TTCGGAAAAA GAGTTGGTAG CTCTTGATCC GGCAAACAAA  
5701 CCACCGCTGG TAGCGGTGGT TTTTGTGTTT GCAAGCAGCA GATTACGCGC AGAAAAAAG  
5761 GATCTCAAGA AGATCCTTTG ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAACT  
5821 CACGTAAAGG GATTTTGGTC ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCTTTTAA  
25 5881 ATTAAAAATG AAGTTTAAAA TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT  
5941 ACCAATGCTT AATCAGTAG GCACCTATCT CAGCGATCTG TCTATTTCGT TCATCCATAG  
6001 TTGCTGACTC CCCCCTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA  
6061 GTGTGCAAT GATACCGCGA GACCCACGCT CACCGCTCC AGATTATCA GCAATAAACCC  
6121 AGCCAGCCGG AAGGGCCGAG CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT  
30 6181 CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG  
6241 TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA  
6301 GTCCTGGTTC CCAACGATCA AGCGAGGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG  
6361 TTAGCTCCTT CGGTCTCCG ATCGTTGTCA GAAGTAAGTT GGCCGAGTG TTATCACTCA  
35 6421 TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCTAGCC ATCCGTAAGA TGCCTTTCTG  
6481 TGA CTGTTGA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT  
6541 CTTGCCCGGC GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA  
6601 TCATTGGAAA ACGTTCCTCG GGGCGAAAAA TCTCAAGGAT CTTACCGCTG TTGAGATCCA  
6661 GTTCGATGTA ACCCACTCGT GCACCCAAC GATCTTCAGC ATCTTTTACT TTCACGAGCG  
6721 TTTCTGGGTG AGCAAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC  
40 6781 GGAATGTTG AATACTCATA CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT  
6841 ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTT  
6901 CGCGCACATT TCCCCGAAAA GTGCCACCTG ACGTCTAAGA AACCATTATT ATCATGACAT  
6961 TAACCTATAA AAATAGGCGT ATCACGAGGC CCTTTCGTC

45 **SEQ ID NOS: 28 and 29**

**Description of Artificial Sequence: DNA sequence (SEQ ID NO: 28) coding for fusion protein Casp9full-ER(T2) (SEQ ID NO: 29)**

2119 Met Asp Glu Ala Asp Arg Gln Leu Leu Arg Arg Cys Arg Val Arg Leu  
50 ATG GAC GAG GCG GAC CGG CAG CTC CTG CGG CGA TGC AGG GTG CGC CTA  
  
2167 Val Ser Glu Leu Gln Val Ala Glu Leu Trp Asp Ala Leu Leu Ser Arg  
GTG AGC GAG CTG CAA GTC GCG GAG CTC TGG GAC GCT CTG CTG AGT CGA  
  
2215 Glu Leu Phe Thr Arg Asp Met Ile Glu Asp Ile Gln Gln Ala Gly Ser  
55 GAG CTC TTC ACG CGC GAC ATG ATC GAG GAT ATT CAG CAG GCA GGA TCT  
  
2263 Gly Ser Arg Arg Asp Gln Ala Arg Gln Leu Val Thr Asp Leu Glu Thr  
GGG TCT CGG CGG GAT CAG GCC AGG CAG CTG GTC ACA GAC CTT GAG ACC  
  
2311 Arg Gly Arg Gln Ala Leu Pro Leu Phe Ile Ser Cys Leu Glu Asp Thr  
60 CGA GGG AGG CAG GCC CTT CCT CTC TTC ATC TCC TGC TTA GAG GAC ACA  
  
2359 Gly Gln Gly Thr Leu Ala Ser Leu Leu Gln Ser Gly Arg Gln Ala Ala  
65 GGC CAA GGC ACC CTG GCT TCA CTC TTG CAA AGC GGT CGG CAA GCA GCC  
  
2407 Lys Gln Asp Pro Glu Ala Val Lys Pro Leu Asp His Leu Val Pro Val  
AAG CAG GAT CCA GAG GCT GTT AAA CCC CTA GAC CAC CTG GTG CCT GTG  
  
2455 Val Leu Gly Pro Met Gly Leu Thr Ala Lys Glu Gln Arg Val Val Lys  
70 GTC CTG GGA CCA ATG GGA CTC ACA GCA AAG GAG CAG AGA GTA GTG AAG  
  
2503 Leu Asp Pro Ser Gln Pro Ala Val Gly Asn Leu Thr Pro Val Val Leu  
CTG GAC CCG TCA CAG CCT GCC GTG GGA AAC CTC ACC CCA GTG GTG CTG

5	2551	Gly	Pro	Glu	Glu	Leu	Trp	Pro	Ala	Arg	Leu	Lys	Pro	Glu	Val	Leu	Arg
		GGG	CCA	GAA	GAG	CTC	TGG	CCT	GCT	CGG	CTC	AAG	CCA	GAG	GTT	CTC	AGA
10	2599	Pro	Glu	Thr	Pro	Arg	Pro	Val	Asp	Ile	Gly	Ser	Gly	Gly	Ala	His	Asp
		CCA	GAA	ACA	CCC	AGG	CCC	GTG	GAC	ATT	GGT	TCT	GGC	GGA	GCT	CAT	GAT
15	2647	Val	Cys	Val	Pro	Gly	Lys	Ile	Arg	Gly	His	Ala	Asp	Met	Ala	Tyr	Thr
		GTC	TGT	GTT	CCA	GGG	AAG	ATC	AGG	GGA	CAT	GCA	GAT	ATG	GCA	TAC	ACC
20	2695	Leu	Asp	Ser	Asp	Pro	Cys	Gly	His	Cys	Leu	Ile	Ile	Asn	Asn	Val	Asn
		CTG	GAT	TCG	GAT	CCC	TGT	GGC	CAC	TGC	CTC	ATC	ATC	AAC	AAT	GTG	AAC
25	2743	Phe	Cys	Pro	Ser	Ser	Gly	Leu	Gly	Thr	Arg	Thr	Gly	Ser	Asn	Leu	Asp
		TTC	TGC	CCT	TCC	TCG	GGG	CTC	GGC	ACA	CGC	ACG	GGC	TCC	AAC	TTG	GAC
30	2791	Arg	Asp	Lys	Leu	Glu	His	Arg	Phe	Arg	Trp	Leu	Arg	Phe	Met	Val	Glu
		CGT	GAC	AAA	CTC	GAG	CAC	CGA	TTC	CGC	TGG	CTG	CGC	TTC	ATG	GTG	GAG
35	2839	Val	Lys	Asn	Asp	Leu	Thr	Ala	Lys	Lys	Met	Val	Thr	Ala	Leu	Met	Glu
		GTG	AAG	AAC	GAC	CTG	ACT	GCC	AAG	AAA	ATG	GTC	ACG	GCT	TTG	ATG	GAG
40	2887	Met	Ala	His	Arg	Asn	His	Arg	Ala	Leu	Asp	Cys	Phe	Val	Val	Val	Ile
		ATG	GCA	CAC	CGG	AAC	CAC	CGT	GCC	CTG	GAC	TGC	TTT	GTG	GTG	GTC	ATC
45	2935	Leu	Ser	His	Gly	Cys	Gln	Ala	Ser	His	Leu	Gln	Phe	Pro	Gly	Ala	Val
		CTC	TCT	CAT	GGC	TGC	CAG	GCC	AGC	CAC	CTC	CAG	TTC	CCG	GGT	GCT	GTC
50	2983	Tyr	Gly	Thr	Asp	Gly	Cys	Ser	Val	Ser	Ile	Glu	Lys	Ile	Val	Asn	Ile
		TAT	GGG	ACA	GAT	GGA	TGC	TCC	GTG	TCC	ATT	GAG	AAA	ATT	GTG	AAT	ATC
55	3031	Phe	Asn	Gly	Ser	Gly	Cys	Pro	Ser	Leu	Gly	Gly	Lys	Pro	Lys	Leu	Phe
		TTC	AAC	GGG	AGC	GGC	TGC	CCC	AGC	CTG	GGA	GGG	AAG	CCC	AAG	CTC	TTC
60	3079	Phe	Ile	Gln	Ala	Cys	Gly	Gly	Glu	Gln	Lys	Asp	His	Gly	Phe	Glu	Val
		TTC	ATC	CAG	GCC	TGC	GGT	GGT	GAG	CAG	AAA	GAC	CAT	GGC	TTT	GAG	GTG
65	3127	Ala	Cys	Thr	Ser	Ser	Gln	Gly	Arg	Thr	Leu	Asp	Ser	Asp	Ser	Glu	Pro
		GCC	TGC	ACT	TCC	TCT	CAA	GGC	AGG	ACC	TTG	GAC	AGT	GAC	TCT	GAG	CCA
70	3175	Asp	Ala	Val	Pro	Tyr	Gln	Glu	Gly	Pro	Arg	Pro	Leu	Asp	Gln	Leu	Asp
		GAT	GCT	GTC	CCC	TAT	CAG	GAA	GGC	CCA	AGG	CCC	TTG	GAC	CAG	CTG	GAT
75	3223	Ala	Val	Ser	Ser	Leu	Pro	Thr	Pro	Ser	Asp	Ile	Leu	Val	Ser	Tyr	Ser
		GCT	GTG	TCA	AGT	TTG	CCT	ACC	CCC	AGT	GAC	ATC	CTT	GTG	TCC	TAC	TCC
80	3271	Thr	Phe	Pro	Gly	Phe	Val	Ser	Trp	Arg	Asp	Lys	Lys	Ser	Gly	Ser	Trp
		ACC	TTC	CCA	GGT	TTT	GTC	TCC	TGG	AGG	GAC	AAG	AAA	AGT	GGC	TCC	TGG
85	3319	Tyr	Ile	Glu	Thr	Leu	Asp	Gly	Ile	Leu	Glu	Gln	Trp	Ala	Arg	Ser	Glu
		TAC	ATC	GAG	ACC	TTG	GAT	GGC	ATT	CTG	GAG	CAG	TGG	GCT	CGC	TCT	GAA
90	3367	Asp	Leu	Gln	Ser	Leu	Leu	Leu	Arg	Val	Ala	Asn	Ala	Val	Ser	Ala	Lys
		GAC	CTG	CAG	TCC	CTC	CTT	CTC	AGG	GTT	GCC	AAT	GCT	GTT	TCT	GCG	AAA
95	3415	Gly	Thr	Tyr	Lys	Gln	Ile	Pro	Gly	Cys	Phe	Asn	Phe	Leu	Arg	Lys	Lys
		GGG	ACT	TAC	AAG	CAG	ATT	CCT	GGC	TGT	TTT	AAC	TTC	CTC	CGG	AAA	AAG
100	3463	Leu	Phe	Phe	Lys	Thr	Ser	Val	Glu	Pro	Ser	Ala	Gly	Asp	Met	Arg	Ala
		CTG	TTT	TTT	AAA	ACT	TCA	GTC	GAG	CCA	TCT	GCT	GGA	GAC	ATG	AGA	GCT
105	3511	Ala	Asn	Leu	Trp	Pro	Ser	Pro	Leu	Met	Ile	Lys	Arg	Ser	Lys	Lys	Asn
		GCC	AAC	CTT	TGG	CCA	AGC	CCG	CTC	ATG	ATC	AAA	CGC	TCT	AAG	AAG	AAC
110	3559	Ser	Leu	Ala	Leu	Ser	Leu	Thr	Ala	Asp	Gln	Met	Val	Ser	Ala	Leu	Leu
		AGC	CTG	GCC	TTG	TCC	CTG	ACG	GCC	GAC	CAG	ATG	GTC	AGT	GCC	TTG	TTG
115	3607	Asp	Ala	Glu	Pro	Pro	Ile	Leu	Tyr	Ser	Glu	Tyr	Asp	Pro	Thr	Arg	Pro
		GAT	GCT	GAG	CCC	CCC	ATA	CTC	TAT	TCC	GAG	TAT	GAT	CCT	ACC	AGA	CCC
120	3655	Phe	Ser	Glu	Ala	Ser	Met	Met	Gly	Leu	Leu	Thr	Asn	Leu	Ala	Asp	Arg
		TTC	AGT	GAA	GCT	TCG	ATG	ATG	GGC	TTA	CTG	ACC	AAC	CTG	GCA	GAC	AGG

		Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val
3703		GAG CTG GTT CAC ATG ATC AAC TGG GCG AAG AGG GTG CCA GGC TTT GTG
5	3751	Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu
		GAT TTG ACC CTC CAT GAT CAG GTC CAC CTT CTA GAA TGT GCC TGG CTA
	3799	Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Val
		GAG ATC CTG ATG ATT GGT CTC GTC TGG CGC TCC ATG GAG CAC CCA GTG
10	3847	Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys
		AAG CTA CTG TTT GCT CCT AAC TTG CTC TTG GAC AGG AAC CAG GGA AAA
	3895	Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser
15		TGT GTA GAG GGC ATG GTG GAG ATC TTC GAC ATG CTG CTG GCT ACA TCA
	3943	Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu
		TCT CGG TTC CGC ATG ATG AAT CTG CAG GGA GAG GAG TTT GTG TGC CTC
20	3991	Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser
		AAA TCT ATT ATT TTG CTT AAT TCT GGA GTG TAC ACA TTT CTG TCC AGC
	4039	Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp
		ACC CTG AAG TCT CTG GAA GAG AAG GAC CAT ATC CAC CGA GTC CTG GAC
25	4087	Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr
		AAG ATC ACA GAC ACT TTG ATC CAC CTG ATG GCC AAG GCA GGC CTG ACC
	4135	Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser
30		CTG CAG CAG CAG CAC CAG CGG CTG GCC CAG CTC CTC CTC ATC CTC TCC
	4183	His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met
		CAC ATC AGG CAC ATG AGT AAC AAA GGC ATG GAG CAT CTG TAC AGC ATG
35	4231	Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala Ala
		AAG TGC AAG AAC GTG GTG CCC CTC TAT GAC CTG CTG CTG GAG GCG GCG
	4279	Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val
		GAC GCC CAC CGC CTA CAT GCG CCC ACT AGC CGT GGA GGG GCA TCC GTG
40	4327	Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser
		GAG GAG ACG GAC CAA AGC CAC TTG GCC ACT GCG GGC TCT ACT TCA TCG
	4375	His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro
45		CAT TCC TTG CAA AAG TAT TAC ATC ACG GGG GAG GCA GAG GGT TTC CCT
	4423	Ala Thr Ala *** GCC ACA GCT TGA

SEQ ID NO: 30

50 Description of Artificial Sequence: vector pCAG-Casp9trunc-ER(T2)-bpA

1	TCGCGCGTTT	CGGTGATGAC	GGTGAACC	TCTGACACAT	GCAGCTCCCG	GAGACGGTCA
61	CAGCTTGCT	GTAAGCGGAT	GCCGGGAGCA	GACAAGCCCG	TCAGGGCGCG	TCAGCGGGTG
121	TTGGCGGGTG	TCGGGGCTGG	CTTAACATATG	CGGCATCAGA	GCAGATTGTA	CTGAGAGTGC
181	ACCATATGCG	GTGTGAAATA	CCGCACAGAT	GCGTAAGGAG	AAAATACCGC	ATCAGGCGCC
55	241	ATTGCCCAT	CAGGCTGCGC	AACGTGTTGGG	AAGGGCGATC	GGTGGGGGCC
	301	TACGCCAGCT	GGCGAAAGGG	GGATGTGCTG	CAAGGCGATT	AAGTTGGGTA
	361	TTTCCCAGTC	ACGACGTTGT	AAAACGACGG	CCAGTGAATT	CGAGCTCGGT
	421	GCGCCGGATC	TCGACATTGA	TTATTGACTA	GTTATTAATA	GTAATCAATT
	481	TAGTTCATAG	CCCATATATG	GAGTTCCGCG	TTACATAACT	TACGGTAAAT
60	541	GCTGACCGCC	CAACGACCCC	CGCCCATTGA	CGTCAATAAT	GACGTATGTT
	601	CGCCAATAGG	GACTTTCCAT	TGACGTCAAT	GGGTGGACTA	TTTACGGTAA
	661	TGGCAGTACA	TCAAGTGAT	CATATGCCAA	GTACGCCCCC	TATTGACGTC
	721	AATGGCCGCG	CTGGCATTAT	GCCCAGTACA	TGACCTTATG	GGACTTTCCT
	781	ACATCTACGT	ATTAGTCATC	GCTATTACCA	TGGGTGCGAGG	TGAGCCCCAC
65	841	ACTCTCCCCA	TCTCCCCCCC	CTCCCCACCC	CCAATTTTGT	ATTTATTTAT
	901	TTTTGTGCAG	CGATGGGGGC	GGGGGGGGGG	GGGGCGCGCG	CCAGGCGGGG
	961	CGAGGGGGCG	GGCGGGGCGA	GGCGGAGAGG	TGCGGCGGCA	GCCAAACAGA
	1021	CCGAAAGTTT	CCTTTTATGG	CGAGGCGGCG	GCGGCGGCGG	CCCTATAAAA
	1081	GCGGCGGGCG	GGAGTCGCTG	CGTTGCCTTC	GCCCCGTGCC	CCGCTCCGCG
70	1141	CCGCCCCGCC	CGGCTCTGAC	TGACGCGGTT	ACTCCACACG	GTGAGCGGGC
	1201	TTCTCCTCCG	GGCTGTAATT	AGCGCTTGGT	TTAATGACGG	CTCGTTTCTT
	1261	GCGTGAAAGC	CTTAAAGGGC	TCCGGGAGGG	CCCTTTGTGC	GGGGGGGAGC
	1321	GTGCGTGCGT	GTGTGTGTGC	GTGGGGAGCG	CCGCGTGCGG	CCGCGGCTGC

1381 TGAGCGCTGC GGGCGCGGCG CGGGGCTTTG TCGCTCCGC GTGTGCGCGA GGGGAGCGCG  
1441 GCCGGGGGCG GTGCCCCGCG GTGCGGGGGG GCTGCGAGGG GAACAAAGGC TGCGTGCGGG  
1501 GTGTGTGCGT GGGGGGGTGA GCAGGGGGTG TGGGCGCGGC GGTGCGGCTG TAACCCCCC  
1561 CTGCACCCCC CTCCCCAGT TGCTGAGCAC GGCCCGGCTT CGGGTGCGGG GCTCCGTGCG  
5 1621 GGGCGTGCGC CGGGGCTCGC CGTGCCGGGC GGGGGGTGGC GGCAGGTGGG GGTGCCGGGC  
1681 GGGGCGGGGC CGCCTCGGGC CGGGGAGGGC TCGGGGAGG GGCAGCGCGG CCGCGGAGCG  
1741 CCGGCGGCTG TCGAGGCGCG GCGAGCCGCA GCCATTGCCT TTTATGGTAA TCGTGCGAGA  
1801 GGGCGCAGGG ACTTCCTTTG TCCCAAATCT GCGGAGCCG AAATCTGGGA GGCGCCGCGG  
1861 CACCCCTCT AGCGGGCGCG GCGAAGCGG TCGGCGCGCG GCAGGAAGGA AATGGGCGGG  
10 1921 GAGGGCCTTC GTGCGTCGCC GCGCCGCCGT CCCCTTCTCC ATCTCCAGCC TCGGGGCTGC  
1981 CGCAGGGGGA CGGCTGCCTT CGGGGGGGAC GGGGAGGGC GGGGTTGCGC TTCTGGCGTG  
2041 TCGCCGGCGG TCTAGAGCC TCTGCTAACC ATGTTTCATG CTTCTTCTTT TTCTACAGA  
2101 TCCTTAATTA ATTCCACCAT GGGTCGGCAA GCAGCCAAGC AGGATCCAGA GGCTGTTAAA  
2161 CCCCTAGACC ACCTGGTGCC TGTGGTCCTG GGACCAATGG GACTCACAGC AAAGGAGCAG  
15 2221 AGAGTAGTGA AGCTGGAGCC AGATGGATGC GCCGTGGGAA ACCTACCCCG AGTGGTGCTG  
2281 GGGCCAGAA AGCTCTGGCC TGCTCGGCTC AAGCCAGAGG TTCTCAGACC AGAAACACCC  
2341 AGGCCGCTGG ACATTGGTTC TGGCGGAGCT CATGATGTCT GTGTCCAGG GAAGATCAGG  
2401 GGACATGCAG ATATGGCATA CACCCTGGAT TCGGATCCCT GTGGCCACTG CCTCATCATC  
2461 AACATGTGA ACTTCTGCC TTCCTCGGG CTCGCGACAC GCACGGGCTC CAACTTGGAC  
20 2521 CGTGACAAAC TCGAGCACCG ATTCCGCTGG CTGCGCTTCA TGGTGAGAGT GAAGAACGAC  
2581 CTGACTGCCA AGAAAATGGT CACGGCTTTG ATGGAGATGG CACACCGGAA CCACCGTGCC  
2641 CTGGACTGCT TTTGGTGGT CATCCTCTCT CATGGCTGCC AGGCCAGCCA CCTCCAGTTC  
2701 CCGGGTGCTG TCTATGGGAC AGATGGATGC TCCGTGTCCA TTGAGAAAAT TGTGAATATC  
2761 TTCAACGGGA GCGGCTGCCC CAGCCTGGGA GGGAAGCCCA AGCTCTTCTT CATCCAGGCC  
25 2821 TGCGGTGGTG AGCAGAAAGA CCATGGCTTT GAGGTGGCCT GCACCTTCTC TCAAGGCAGG  
2881 ACCTTGACA GTGACTCTGA GCCAGATGCT GTCCCTATC AGGAAGGCCC AAGGCCCTTG  
2941 CTCCGGAAAA AGCTGTTTTT TAAAACTTCA GTGAGCCAT CTGCTGGAGA CATGAGAGCT  
3001 ACCTTCCCAG GTTTTGTCTC CTGGAGGGAC AAGAAAAGTG GCTCCTGGTA CATCGAGACC  
3061 TTGGATGCA TTCTGGAGCA GTGGGCTCGC TCTGAAGACC TGCAGTCCCT CCTTCTCAGG  
30 3121 GTTGCCAATG CTGTTTCTGC GAAAGGGACT TACAAGCAGA TTCCTGGCTG TTTTAAC TTC  
3181 CTCCGGAAAA AGCTGTTTTT TAAAACTTCA GTGAGCCAT CTGCTGGAGA CATGAGAGCT  
3241 GCCAACCTTT GGCCAAGCCC GCTCATGATC AAACGCTCTA AGAAGAACAG CCTGGCCTTG  
3301 TCCTGACGG CCGACCAGAT GGTCACTGCC TTGTTGGATG CTGAGCCCCC CATACTCTAT  
3361 TCCGAGTATG ATCCTACCAG ACCCTTCAGT GAAGCTTCGA TGATGGGCTT ACTGACCAAC  
35 3421 CTGGCAGACA GGGAGCTGGT TCACATGATC AACTGGGCGA AGAGGGTGCC AGGCTTTGTG  
3481 GATTTGACCC TCCATGATCA GGTCCACCTT CTAGAATGTG CCTGGCTAGA GATCCTGATG  
3541 ATTGGTCTCG TCTGGCGCTC CATGGAGCAC CCAAGTGAAG TACTGTTTGC TCCTAACCTG  
3601 CTCTTGACA GGAACACAGG AAAATGTGTA GAGGGCATGG TGGAGATCTT CGACATGCTG  
3661 CTGGCTACAT CATCTCGGTT CCGCATGATG AATCTGCAGG GAGAGGAGTT TGTGTGCTC  
40 3721 AAATCTATTA TTTTGCTTAA TTCTGGAGTG TACACATTTT TGTCCAGCAC CCTGAAGTCT  
3781 CTGGAAGAGA AGGACCATAT CCACCGAGTC CTGGACAAGA TCACAGACAC TTTGATCCAC  
3841 CTGATGGCCA AGGCAGGCTG GACCCTGCAG CAGCAGCACC AGCGGTGGC CCAGCTCCTC  
3901 CTGATCCTCT CCCACATCAG GCACATGAGT AACAAAGGCA TGGAGCATCT GTACAGCATG  
3961 AAGTGCAAGA ACGTGGTGCC CCTCTATGAC CTGCTGCTGG AGGCGGCGGA CGCCACCGC  
45 4021 CTACATGCGC CCACTAGCCG TGGAGGGGCA TCCGTGGAGG AGACGGACCA AAGCCACTTG  
4081 GCCAGTCCGG GCTCTACTTC ATCGCATTC TTGCAAAAGT ATTACATCAC GGGGAGGCA  
4141 GAGGGTTTCC CTGCCACAGC TTGATGAAGA TCTGAGCTCC CTGGCGGAAT TCGTAAATG  
4201 ATTGCAGATC CACTAGTTCT AGAGCTCGCT GATCAGCCTC GACTGTGCTT TCTAGTTGCC  
4261 AGCCATCTGT TGTGTCCTCC TCCCCGTGTC CTTCTTGAC CCTGGAAGGT GCCACTCCCA  
50 4321 CTGTCCTTTC CTAATAAAAT GAGGAAATTG CATCGATTG TCTGAGTAGG TGTCACTCTA  
4381 TTCTGGGGGG TGGGGTGGGG CAGGACAGCA AGGGGGAGGA TTGGGAAGAC AATAGCAGGC  
4441 ATGCTGGGGA TCGGTGGGC TCTATGGCTT CTGAGGCGGA AAGAACCAGA AGCTTGGCGT  
4501 AATCATGGTC ATAGCTGTTT CCTGTGTGAA ATTGTTATCC GCTCACAATT CCACACAACA  
4561 TACGAGCCGG AAGCATAAAG TGTAAGCCTT GGGGTGCCA ATGAGTGAGC TAACTCACAT  
55 4621 TAATTGCGTT GCGCTCACTG CCCGCTTTCC AGTCGGGAAA CCTGTCGTGC CAGCTGCATT  
4681 AATGAATCGG CCAACGCGCG GGGAGAGGCG GTTTGCGTAT TGGGCGCTCT TCCGCTTCTT  
4741 CGCTCACTGA CTCGCTGCGC TCGGTGCTTC GGCTGCGGCG AGCGGTATCA GCTCACTCAA  
4801 AGGCGGTAAT ACGGTTATCC ACAGAATCAG GGGATAACGC AGGAAAGAAC ATGTGAGCAA  
4861 AAGGCCAGCA AAAGGCCAGG AACCGTAAAA AGGCCGCGTT GCTGGCGTTT TTCCATAGGC  
60 4921 TCCGCCCCCC TGACGAGCAT CACAAAATC GACGCTCAAG TCAGAGGTGG CGAAACCCGA  
4981 CAGGACTATA AAGATACCAG GCGTTTCCCC CTGGAAGCTC CCTCGTGCGC TCTCCTGTTT  
5041 CGACCCCTGC GCTTACCGGA TACCTGTCCG CTTTTCTCCC TTCGGGAAGC GTGGCGCTTT  
5101 CTGATAGCTC ACGCTGTAGG TATCTCAGT CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT  
5161 GTGTGCACGA ACCCCCCGTT CAGCCCCACC GCTGCGCCTT ATCCGGTAAC TATCGTCTTG  
65 5221 AGTCCAACCC GGTAAAGACG GACTTATCGC CACTGGCAGC AGCCACTGGT AACAGGATTA  
5281 GCAGAGCGAG GTATGTAGCG GGTGCTACAG AGTTCTTGAA GTGGTGCCCT AACTACGGCT  
5341 AACTAGAAG GACAGTATTT GGTATCTGCG CTCTGCTGAA GCCAGTTACC TTCGGAAGAA  
5401 GAGTTGGTAG CTCTTGATCC GGCAACAAA CCACCGCTGG TAGCGGTGGT TTTTGTGTTT  
5461 CGAAGCAGCA GATTACGCG AGAAAAAAG GATCTCAAGA AGATCCTTTG ATCTTTCTTA  
70 5521 CGGGGTCTGA GCCTCAGTGG AACGAAAAC CAGCTTAAGG GATTTTGGT GATTTTGGT  
5581 CAAAAAGGAT CTTACCTAG ATCCTTTTAA ATTAATAATG AAGTTTAA TCAATCTAAA  
5641 GTATATATGA GTAAACTTGG TCTGACAGT ACCAATGCTT AATCAGTGAG GCACCTATCT  
5701 CAGCGATCTG TCTATTTCTG TCATCCATAG TTGCTGACT CCGGTCGTG TAGATAACTA



5761 CGATACGGGA GGGCTTACCA TCTGGCCCCA GTGCTGCAAT GATACCGCGA GACCCACGCT  
5821 CACCGGCTCC AGATTATCA GCAATAAACC AGCCAGCCGG AAGGGCCGAG CGCAGAAAGTG  
5881 GTCCTGCAAC TTTATCCGCC TCCATCCAGT CTATTAATTG TTGCCGGGAA GCTAGAGTAA  
5941 GTAGTTTCGCC AGTTAATAGT TTGCGCAACG TTGTTGCCAT TGCTACAGGC ATCGTGGTGT  
5 6001 CACGCTCGTC GTTTGGTATG GCTTCATTCA GCTCCGGTTC CCAACGATCA AGGCGAGTTA  
6061 CATGATCCCC CATGTTGTGC AAAAAAGCGG TTAGCTCCTT CGGTCCTCCG ATCGTTGTCA  
6121 GAAGTAAGTT GGCCGAGTG TTATCACTCA TGGTTATGGC AGCACTGCAT AATTCTCTTA  
6181 CTGTCATGCC ATCCGTAAGA TGCTTTTCTG TGACTGGTGA GTACTCAACC AAGTCATTCT  
10 6241 GAGAATAGTG TATGCGGCGA CCGAGTTGCT CTTGCCCGGC GTCAATACGG GATAATACCG  
6301 CGCCACATAG CAGAACTTTA AAAGTGCTCA TCATTGGAAA ACGTTCCTCG GGGCGAAAAAC  
6361 TCTCAAGGAT CTTACCGCTG TTGAGATCCA GTTCGATGTA ACCCACTCGT GCACCAACT  
6421 GATCTTCAGC ATCTTTTACT TTCACCAGCG TTTCTGGGTG AGCAAAAACA GGAAGGCAAA  
6481 ATGCCGAAA AAAGGGAATA AGGGCGACAC GGAAATGTTG AATACTCATA CTCTTCCTTT  
6541 TTCAATATTA TTGAAGCATT TATCAGGGTT ATTGTCTCAT GAGCGGATAC ATATTTGAAT  
15 6601 GTATTTAGAA AAATAAACAA ATAGGGGTTT CGCGCACATT TCCCGGAAAA GTGCCACCTG  
6661 ACGTCTAAGA AACCATATT ATCATGACAT TAACCTATAA AAATAGGCGT ATCACGAGGC  
6721 CCTTTCGTC

SEQ ID NOS: 31 and 32

20 Description of Artificial Sequence: DNA sequence (SEQ ID NO: 31) coding for fusion protein  
Casp9trunc-ER(T2) (SEQ ID NO: 32)

Met Gly Arg Gln Ala Ala Lys Gln Asp Pro Glu Ala Val Lys Pro Leu  
2119 ATG GGT CGG CAA GCA GCC AAG CAG GAT CCA GAG GCT GTT AAA CCC CTA  
25 Asp His Leu Val Pro Val Val Leu Gly Pro Met Gly Leu Thr Ala Lys  
2167 GAC CAC CTG GTG CCT GTG GTC CTG GGA CCA ATG GGA CTC ACA GCA AAG  
Glu Gln Arg Val Val Lys Leu Asp Pro Ser Gln Pro Ala Val Gly Asn  
2215 GAG CAG AGA GTA GTG AAG CTG GAC CCG TCA CAG CCT GCC GTG GGA AAC  
30 Leu Thr Pro Val Val Leu Gly Pro Glu Glu Leu Trp Pro Ala Arg Leu  
2263 CTC ACC CCA GTG GTG CTG GGG CCA GAA GAG CTC TGG CCT GCT CGG CTC  
35 Lys Pro Glu Val Leu Arg Pro Glu Thr Pro Arg Pro Val Asp Ile Gly  
2311 AAG CCA GAG GTT CTC AGA CCA GAA ACA CCC AGG CCC GTG GAC ATT GGT  
Ser Gly Gly Ala His Asp Val Cys Val Pro Gly Lys Ile Arg Gly His  
2359 TCT GGC GGA GCT CAT GAT GTC TGT GTT CCA GGG AAG ATC AGG GGA CAT  
40 Ala Asp Met Ala Tyr Thr Leu Asp Ser Asp Pro Cys Gly His Cys Leu  
2407 GCA GAT ATG GCA TAC ACC CTG GAT TCG GAT CCC TGT GGC CAC TGC CTC  
Ile Ile Asn Asn Val Asn Phe Cys Pro Ser Ser Gly Leu Gly Thr Arg  
2455 ATC ATC AAC AAT GTG AAC TTC TGC CCT TCC TCG GGG CTC GGC ACA CGC  
45 Thr Gly Ser Asn Leu Asp Arg Asp Lys Leu Glu His Arg Phe Arg Trp  
2503 ACG GGC TCC AAC TTG GAC CGT GAC AAA CTC GAG CAC CGA TTC CGC TGG  
Leu Arg Phe Met Val Glu Val Lys Asn Asp Leu Thr Ala Lys Lys Met  
50 2551 CTG CGC TTC ATG GTG GAG GTG AAG AAC GAC CTG ACT GCC AAG AAA ATG  
Val Thr Ala Leu Met Glu Met Ala His Arg Asn His Arg Ala Leu Asp  
2599 GTC ACG GCT TTG ATG GAG ATG GCA CAC CGG AAC CAC CGT GCC CTG GAC  
55 Cys Phe Val Val Val Ile Leu Ser His Gly Cys Gln Ala Ser His Leu  
2647 TGC TTT GTG GTG GTC ATC CTC TCT CAT GGC TGC CAG GCC AGC CAC CTC  
Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys Ser Val Ser Ile  
2695 CAG TTC CCG GGT GCT GTC TAT GGG ACA GAT GGA TGC TCC GTG TCC ATT  
60 Glu Lys Ile Val Asn Ile Phe Asn Gly Ser Gly Cys Pro Ser Leu Gly  
2743 GAG AAA ATT GTG AAT ATC TTC AAC GGG AGC GGC TGC CCC AGC CTG GGA  
Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly Gly Glu Gln Lys  
65 2791 GGG AAG CCC AAG CTC TTC TTC ATC CAG GCC TGC GGT GGT GAG CAG AAA  
Asp His Gly Phe Glu Val Ala Cys Thr Ser Ser Gln Gly Arg Thr Leu  
2839 GAC CAT GGC TTT GAG GTG GCC TGC ACT TCC TCT CAA GGC AGG ACC TTG  
70 Asp Ser Asp Ser Glu Pro Asp Ala Val Pro Tyr Gln Glu Gly Pro Arg  
2887 GAC AGT GAC TCT GAG CCA GAT GCT GTC CCC TAT CAG GAA GGC CCA AGG  
Pro Leu Asp Gln Leu Asp Ala Val Ser Ser Leu Pro Thr Pro Ser Asp

	2935	CCC TTG GAC CAG CTG GAT GCT GTG TCA AGT TTG CCT ACC CCC AGT GAC
5	2983	Ile Leu Val Ser Tyr Ser Thr Phe Pro Gly Phe Val Ser Trp Arg Asp ATC CTT GTG TCC TAC TCC ACC TTC CCA GGT TTT GTC TCC TGG AGG GAC
	3031	Lys Lys Ser Gly Ser Trp Tyr Ile Glu Thr Leu Asp Gly Ile Leu Glu AAG AAA AGT GGC TCC TGG TAC ATC GAG ACC TTG GAT GGC ATT CTG GAG
10	3079	Gln Trp Ala Arg Ser Glu Asp Leu Gln Ser Leu Leu Leu Arg Val Ala CAG TGG GCT CGC TCT GAA GAC CTG CAG TCC CTC CTT CTC AGG GTT GCC
	3127	Asn Ala Val Ser Ala Lys Gly Thr Tyr Lys Gln Ile Pro Gly Cys Phe AAT GCT GTT TCT GCG AAA GGG ACT TAC AAG CAG ATT CCT GGC TGT TTT
15	3175	Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser Val Glu Pro Ser AAC TTC CTC CGG AAA AAG CTG TTT TTT AAA ACT TCA GTC GAG CCA TCT
	3223	Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile GCT GGA GAC ATG AGA GCT GCC AAC CTT TGG CCA AGC CCG CTC ATG ATC
20	3271	Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln AAA CGC TCT AAG AAG AAC AGC CTG GCC TTG TCC CTG ACG GCC GAC CAG
	3319	Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu ATG GTC AGT GCC TTG TTG GAT GCT GAG CCC CCC ATA CTC TAT TCC GAG
25	3367	Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu TAT GAT CCT ACC AGA CCC TTC AGT GAA GCT TCG ATG ATG GGC TTA CTG
	3415	Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys ACC AAC CTG GCA GAC AGG GAG CTG GTT CAC ATG ATC AAC TGG GCG AAG
30	3463	Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu AGG GTG CCA GGC TTT GTG GAT TTG ACC CTC CAT GAT CAG GTC CAC CTT
	3511	Leu Glu Cys Ala Trp Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg CTA GAA TGT GCC TGG CTA GAG ATC CTG ATG ATT GGT CTC GTC TGG CGC
35	3559	Ser Met Glu His Pro Val Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu TCC ATG GAG CAC CCA GTG AAG CTA CTG TTT GCT CCT AAC TTG CTC TTG
	3607	Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp GAC AGG AAC CAG GGA AAA TGT GTA GAG GGC ATG GTG GAG ATC TTC GAC
40	3655	Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly ATG CTG CTG GCT ACA TCA TCT CGG TTC CGC ATG ATG AAT CTG CAG GGA
	3703	Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val GAG GAG TTT GTG TGC CTC AAA TCT ATT ATT TTG CTT AAT TCT GGA GTG
45	3751	Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His TAC ACA TTT CTG TCC AGC ACC CTG AAG TCT CTG GAA GAG AAG GAC CAT
	3799	Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met ATC CAC CGA GTC CTG GAC AAG ATC ACA GAC ACT TTG ATC CAC CTG ATG
50	3847	Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln GCC AAG GCA GGC CTG ACC CTG CAG CAG CAG CAC CAG CGG CTG GCC CAG
	3895	Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly Met CTC CTC CTC ATC CTC TCC CAC ATC AGG CAC ATG AGT AAC AAA GGC ATG
55	3943	Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp GAG CAT CTG TAC AGC ATG AAG TGC AAG AAC GTG GTG CCC CTC TAT GAC
	3991	Leu Leu Leu Glu Ala Ala Asp Ala His Arg Leu His Ala Pro Thr Ser CTG CTG CTG GAG GCG GCG GAC GCC CAC CGC CTA CAT GCG CCC ACT AGC
60	4039	Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr CGT GGA GGG GCA TCC GTG GAG GAG ACG GAC CAA AGC CAC TTG GCC ACT
	4087	Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly GCG GGC TCT ACT TCA TCG CAT TCC TTG CAA AAG TAT TAC ATC ACG GGG

Glu Ala Glu Gly Phe Pro Ala Thr Ala \*\*\*  
4135 GAG GCA GAG GGT TTC CCT GCC ACA GCT TGA

5 SEQ ID NO: 33

Description of Artificial Sequence: primer Casp3ER-A

1 CCTTAATTAA TTCCACCATG GAGAACACA AAACCTC

SEQ ID NO: 34

10 Description of Artificial Sequence: primer Casp3ER-B

1 GGCTCGAGGT GATAAAAGTA CAGTTCTTTC

SEQ ID NO: 35

Description of Artificial Sequence: vector pCAG-Casp3-ER(T2)-bpa

15 1 TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA  
61 CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGCGGGTG  
121 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC  
181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGGCGCG  
241 ATTGCCCAT T CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC TCTTCGCTAT  
20 301 TACGCCAGCT GGCGAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA ACGCCAGGGT  
361 TTTCCCACTG ACGACGTGTG AAAACGACGG CCAGTGAATT CGAGCTCGGT ACCCGGGGGC  
421 GCGCCGGATC TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAATT ACGGGGTGCT  
481 TATGTCATAG CCCATATATG GAGTTCCGCG TTACATAACT TACGGTAAAT GGCCCGCTG  
541 GCTGACCGCC CAACGACCCC CGCCCATGTA CGTCAATAAT GACGTATGTT CCCATAGTAA  
25 601 CGCCAATAGG GACTTTTCAT TGACGTCAAT GGGTGGACTA TTTACGGTAA ACTGCCACT  
661 TGGCAGTACA TCAAGTGATG CATATGCCAA GTACGCCCCC TATTGACGTC AATGACGGTA  
721 AATGGCCCCG CTGGCATATG GCCCAGTACA TGACCTTATG GGACTTTTCT ACTTGGCAGT  
781 ACATCTACGT ATTAGTCATC GCTATTACCA TGGGTCGAGG TGAGCCCCAC GTTCTGCTTC  
841 ACTCTCCCCA TCTCCCCCCC CTCCCCACCC CCAATTTTGT ATTTATTTAT TTTTAAATTA  
30 901 TTTTGTGCGC GATGGGGGGG GGGGGGGGGG GGGGCGCGCG CCAGCGGGGG CGGGCGGGG  
961 CGAGGGGCGG GCGGGGCGCA GCGGGAGAGG TGCGGCGGCA GCCAATCAGA GCGGCGCGCT  
1021 CCGAAAGTTT CCTTTTATGG CGAGGCGGCG GCGGCGGCGG CCCTATAAAA AGCGAAGCGC  
1081 CGGGCGGGCG GGAGTCGCTG CGTTGCTTTC GCCCGTGCC CCGCTCCGCG CCGCCTCGCG  
1141 CCGCCCGCCC CGGCTCTGAC TGACCGCGTT ACTCCACAG GTGAGCGGGC GGGACGGGCC  
35 1201 TTCTCCTCCG GGCTGTAATT AGCGCTTGGT TTAATGACGG CTCGTTTCTT TTCTGTGGCT  
1261 GCGTGAAAGC CTTAAAGGGC TCCGGGAGGG CCCTTTGTGC GGGGGGGAGC GGCTCGGGGG  
1321 GTGCGTGCCT GTGTGTGTGC GTGGGGAGCG CCGCGTGCGG CCCGCGCTGC CCGGCGGGTG  
1381 TGAGCGCTGC GCGGCGGCGG CGGGGCTTTG TCGCGCTCCG GTGTGCGCGA GGGGAGCGCG  
1441 GCGGGGGGCG GTGCCCGCGG GTGCGGGGGG GCTGCGAGGG GAACAAAGGC TGCGTGCGGG  
40 1501 GTGTGTGCGT GGGGGGGTGA GCAGGGGGTG TGGGCGCGCG GGTGCGGGTG TAACCCCCC  
1561 GTGACCCCCC CTCCCCGAGT TGCTGAGCAC GGCCCGGCTT CCGGTGCGGG GCTCCGTGCG  
1621 GGGCCCTCTT AGCGGGCGCG GCGGCTTGGG GGGGGGTGGC GGCAGGTGGG GGTGCCGGCG  
1681 GGGGCGGGGC CGCCTCGGGC CGGGGAGGGC TCGGGGAGG GCGCGGGCGG CCGCGGAGCG  
1741 CCGCGGGCTG TCGAGGCGCG GCGAGCCGCA GCCATTGCCT TTTATGGTAA TCGTGCGAGA  
45 1801 GGGCGCAGGG ACTTCCTTTG TCCCAAATCT GGCGGAGCCG AAATCTGGGA GGGCGCCCGC  
1861 CACCCCTCTT AGCGGGCGCG GCGGAAGCGG TGCGGCGCGG GCAGGAAGGA AATGGGCGGG  
1921 GAGGGCCTTC GTGCGTGCCT GCGCCGCGCT CCCCTTCTCC ATCTCCAGCC TCGGGGCTGC  
1981 CGCAGGGGGA CGGCTGCTTT CGGGGGGGAC GGGGCGAGGG GGGGTTCGGC TTCTGGCGTG  
2041 TGACCGGGCG CTCTAGAGCC TCTGCTAACC ATGTTTCATG CTTCTTCTTT TTCTACAGA  
50 2101 TCCTTAATTA ATTCACCAT GGAGAACAA AAAACCTCAG TGGATTCAAA ATCCATTAAT  
2161 AATTTTGAAG TAAAGACCAT ACATGGGAGC AAGTCAGTGG ACTCTGGGAT CTATCTGGAC  
2221 AGTAGTTACA AAATGGATTA TCCTGAAATG GGCATATGCA TAATAATTAA TAATAAGAAC  
2281 TTCCATAAGA GCACTGGAAT GTCATCTCGC TCTGGTACGG ATGTGGACGC AGCCAACCTC  
2341 AGAGAGACAT TCATGGGCCT GAAATACCAA GTCAGGAATA AAAATGATCT TACTCGTGAA  
55 2401 GACATTTTGG AATTAATGGA TAGTGTTCCT AAGGAAGATC ATAGCAAAAG GAGCAGCTTT  
2461 GTGTGTGTGA TTCTAAGCCA TGGTGATGAA GGGGTCATTT ATGGGACAAA TGGGCTGTG  
2521 GAACTGAAAA AGTTGACTAG CTCTTCAGG GCGGACTACT GCCGAGTCT GACTGGAAG  
2581 CCGAACTCTT TCATCATTCA GGCCTGCCGG GGTACGGAGC TGGACTGTGG CATTGAGACA  
2641 GACAGTGGGA CTGATGAGGA GATGGCTTGC CAGAAGATAC CCGTGGAGGC TGACTTCCTG  
60 2701 TATGCTTACT CTACAGCACC TGGTTACTAT TCCTGGAGAA ATTCAAAGGA CGGGTCTGTG  
2761 TTCATCCAGT CCCTTTGCGC CATGCTGAAG CTGTACGCGC ACAAGCTAGA ATTTATGCAC  
2821 ATTCTCACTC GCGTTAACAG GAAGGTGGCA ACGGAATTCT AGTCCTTCTC CTTGGACTCC  
2881 ACTTTCCACG CAAAGAAACA GATCCCCTGT ATTGTGTCCA TGCTCACGAA AGAACTGTAC  
2941 TTTTATCACC TCGAGCCATC TGCTGGAGAC ATGAGAGCTG CCAACCTTTG GCCAAGCCCC  
65 3001 CTATGATACA ACGCTCTAA GAAGAACAGC CTGGCCTTGT CCCTGACGGC CGACCAATG  
3061 GTCAGTGCCT TGTGGATGCG TGAGCCCCC ATACTCTATT CCGAGTATGA TCCTACCAGA  
3121 CCCTTCAGTG AAGCTTCGAT GATGGGCTTA CTGACCAACC TGGCAGACAG GGAGCTGGTT  
3181 CACATGATCA ACTGGGCGAA GAGGGTGCCA GGCTTTGTGG ATTTGACCCT CCATGATCAG  
3241 GTCCACCTTC TAGAATGTGC CTGGCTAGAG ATCCTGATGA TTGGTCTCGT CTGGCGCTCC  
70 3301 ATGGAGCACC CAGTGAAGCT ACTGTTTGCT CCTAATTGCT TCTTGGACAG GAACCAGGGA  
3361 AAATGTGTAG AGGGCATGGT GGAGATCTTC GACATGCTGC TGGCTACATC ATCTCGGTTT  
3421 CGCATGATGA ATCTGCAGGG AGAGGAGTTT GTGTGCCTCA AATCTATTAT TTTGCTTAAT  
3481 TCTGGAGTGT ACACATTTCT GTCCAGCACC CTGAAGTCTC TGGAAGAGAA GGACCATATC

3541 CACCCAGTCC TGGACAAGAT CACAGACACT TTGATCCACC TGATGGCCAA GGCAGGCCTG  
3601 ACCCTGCAGC AGCAGCACCA GCGGCTGGCC CAGCTCCTCC TCATCCTCTC CCACATCAGG  
3661 CACATGAGTA ACAAAGGCAT GGAGCATCTG TACAGCATGA AGTGCAAGAA CGTGGTGCCC  
5 3721 CTCTATGACC TGCTGCTGGA GCGGCGGGAC GCCCACC GCC TACATGCGCC CACTAGCCGT  
3781 GGAGGGGCAT CCGTGGAGGA GACGGACCAA AGCCACTTGG CCACTGCGGG CTCTACTTCA  
3841 TCGCATTCCCT TGCAAAAGTA TTACATCACG GGGGAGGCAG AGGGTTTCCC TGCCACAGCT  
3901 TGATGAAGAT CTGAGCTCCC TGGCGGAATT GCGTAAATGA TTGCAGATCC ACTAGTTCTA  
3961 GAGCTCGCTG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT GTTTGCCCTT  
10 4021 CCCCCGTGCC TTCTTTGACC CTGGAAGGTG CCACTCCAC TGCTCTTTCC TAATAAAATG  
4081 AGGAAATTCG ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT GGGGTGGGGC  
4141 AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT GCGGTGGGCT  
4201 CTATGGCTTC TGAGGCGGAA AGAACCAGAA GCTTGGCGTA ATCATGGTCA TAGCTGTTTC  
4261 CTGTGTGAAA TTGTTATCCG CTCACATTTC CACACAACAT ACGAGCCGGA AGCATAAAGT  
4321 GTAAAGCCTG GGGTGCCTAA TGAGTGAGCT AACTCACATT AATTGCGTTG CGCTCACTGC  
15 4381 CCGCTTTTCCA CTCGGGAAC CTGTCTGCGC AGCTGCATTA ATGAATCGGC CAACGCGCGG  
4441 GGAGAGGCGG TTTGCGTATT GGGCGCTCTT CCGCTTCTC GCTCACTGAC TCGCTGCGCT  
4501 CCGTCTGTCG GGTGCGGCGA GCGGTATCAG CTCACTCAA GGGCGTAATA CCGTTATCCA  
4561 CAGAATCAGG GGATAACGCA GGAAAGAACA TGTGAGCAA AGGCCAGCAA AAGGCCAGGA  
4621 ACCGTAAAAA GCGCGGTTG CTGGCGTTTT TCCATAGGCT CCGCCCCCT GACGAGCATC  
20 4681 ACAAATTCG ACGCTCAAGT CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG  
4741 CGTTTCCCCC TGAAGCTCC CTCGTGCGCT CTCCTGTTCC GACCTGCGG CTTACCGGAT  
4801 ACCTGTCCCG CTTTCTCCCT TCGGGAAGCG TGGCGGTTTC TCATAGCTCA CGCTGAGGT  
4861 ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG TGTGCACGAA CCCCCGTTT  
25 4921 AGCCCGACCG CTGCGCCTTA TCCGGTAACT ATCGTCTTGA GTCCAACCCG GTAAGACACG  
4981 ACTTATCGCC ACTGGCAGCA GCCACTGGTA ACAGGATTAG CAGAGCGAGG TATGTAGGCG  
5041 GTGTCTACGA GTTCTTGAAG TGGTGGCCTA ACTACGGCTA CACTAGAAGG ACAGTATTTG  
5101 GTATCTGCGC TCTGCTGAAG CCAGTTACCT TCGGAAAAAG AGTTGGTAGC TCTTGATCCG  
5161 GCAACAACAC CACCGCTGGT AGCGGTGGTT TTTTGTGTTG CAAGCAGCAG ATTACGCGCA  
5221 GAAAAAAGG ATCTCAAGAA GATCCTTTGA TCTTTTCTAC GGGGTCTGAC GCTCAGTGGA  
30 5281 ACGAAAATC ACGTTAAGGG ATTTTGGTCA TGAGATTATC AAAAAGGATC TTCACCTAGA  
5341 TCCTTTTAAA TTAATAATGA AGTTTAAAT CAATCTAAAG TATATATGAG TAACTTGGT  
5401 CTGACAGTTA CCAATGCTTA ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTCTGT  
5461 CATCCATAGT TGCTGACTC CCCGTCGTGT AGATAACTAC GATACGGGAG GGCTTACCAT  
35 5521 CTGGCCCCAG TGCTGCAATG ATACCGCGAG ACCCAGCTC ACCGCTCCA GATTATCAG  
5581 CAATAAACCA GCCAGCCGGA AGGGCCGAGC GCAGAAGTGG TCCTGCAACT TTATCCGCCT  
5641 CCAATCCAGTC TATTAATTGT TGCCGGGAGG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT  
5701 TCGCAACGCT TGTGTCATT GCTACAGGCA TCGTGGTGTG ACGCTCGTCG TTTGGTATGG  
5761 GTTCATTGCT CTCCGGTTCC CAACGATCAA GGCAGTTAC ATGATCCCCC ATGTTGTGCA  
40 5821 AAAAAGCGGT TAGCTCCTTC GGTCTCCGA TCGTTGTGAG AAGTAAGTTG GCCGCACTGT  
5881 TATCACTCAT GGTATGGA GCACTGCATA ATTCTCTTAC TGTATGCCA TCCGTAAGAT  
5941 GCTTTTCTGT GACTGGTGAG TACTCAACCA AGTCATTCTG AGAATAGTGT ATGCGGCGAC  
6001 CGAGTTGCTC TTGCCCGGCG TCAATACGGG ATAATACCGC GCCACATAGC AGAAGTTTAA  
6061 AAGTGCTCAT CATTGAAAA CGTTCTTCGG GGCGAAAACT CTCAAGGATC TTACCGCTGT  
6121 TGAGATCCAG TTCGATGTAA CCACTCGTG CACCCAACTG ATCTTCAGCA TCTTTTACTT  
45 6181 TCACCAGCGT TTCTGGGTGA GCAAAAACAG GAAGGCAAAA TGCCGCAAAA AAGGGAATAA  
6241 GGGCGACACG GAAATGTTGA ATACTCATAC TCTTCTTTT TCAATATTAT TGAAGCATTT  
6301 ATCAGGGTTA TTGTCTCATG AGCGGATACA TATTTGAATG TATTTAGAAA AATAAACAAA  
6361 TAGGGGTTCC GCGCACATTT CCCCAGAAAG TGCCACCTGA CGTCTAAGAA ACCATTATTA  
50 6421 TCATGACATT AACCTATAAA AATAGGCGTA TCACGAGGCC CTTTCGTC

SEQ ID NOS: 36 and 37

Description of Artificial Sequence: DNA sequence (SEQ ID NO: 36) coding for fusion gene  
Casp3-ER(T2) (SEQ ID NO: 37)

Met Glu Asn Asn Lys Thr Ser Val Asp Ser Lys Ser Ile Asn Asn Phe  
55 2119 ATG GAG AAC AAC AAA ACC TCA GTG GAT TCA AAA TCC ATT AAT AAT TTT  
  
Glu Val Lys Thr Ile His Gly Ser Lys Ser Val Asp Ser Gly Ile Tyr  
2167 GAA GTA AAG ACC ATA CAT GGG AGC AAG TCA GTG GAC TCT GGG ATC TAT  
  
Leu Asp Ser Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Ile Cys Ile  
60 2215 CTG GAC AGT AGT TAC AAA ATG GAT TAT CCT GAA ATG GGC ATA TGC ATA  
  
Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Ser Ser Arg  
2263 ATA ATT AAT AAT AAG AAC TTC CAT AAG AGC ACT GGA ATG TCA TCT CGC  
  
Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Met Gly  
2311 TCT GGT ACG GAT GTG GAC GCA GCC AAC CTC AGA GAG ACA TTC ATG GGC  
  
Leu Lys Tyr Gln Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Asp Ile  
70 2359 CTG AAA TAC CAA GTC AGG AAT AAA AAT GAT CTT ACT CGT GAA GAC ATT  
  
Leu Glu Leu Met Asp Ser Val Ser Lys Glu Asp His Ser Lys Arg Ser  
2407 TTG GAA TTA ATG GAT AGT GTT TCT AAG GAA GAT CAT AGC AAA AGG AGC

5	2455	Ser Phe Val Cys Val Ile Leu Ser His Gly Asp Glu Gly Val Ile Tyr
		AGC TTT GTG TGT GTG ATT CTA AGC CAT GGT GAT GAA GGG GTC ATT TAT
10	2503	Gly Thr Asn Gly Pro Val Glu Leu Lys Lys Leu Thr Ser Phe Phe Arg
		GGG ACA AAT GGG CCT GTT GAA CTG AAA AAG TTG ACT AGC TTC TTC AGA
15	2551	Gly Asp Tyr Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
		GGC GAC TAC TGC CGG AGT CTG ACT GGA AAG CCG AAA CTC TTC ATC ATT
20	2599	Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser
		CAG GCC TGC CGG GGT ACG GAG CTG GAC TGT GGC ATT GAG ACA GAC AGT
25	2647	Gly Thr Asp Glu Glu Met Ala Cys Gln Lys Ile Pro Val Glu Ala Asp
		GGG ACT GAT GAG GAG ATG GCT TGC CAG AAG ATA CCG GTG GAG GCT GAC
30	2695	Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn
		TTC CTG TAT GCT TAC TCT ACA GCA CCT GGT TAC TAT TCC TGG AGA AAT
35	2743	Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ser Met Leu Lys
		TCA AAG GAC GGG TCG TGG TTC ATC CAG TCC CTT TGC AGC ATG CTG AAG
40	2791	Leu Tyr Ala His Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn
		CTG TAC GCG CAC AAG CTA GAA TTT ATG CAC ATT CTC ACT CGC GTT AAC
45	2839	Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Leu Asp Ser Thr Phe
		AGG AAG GTG GCA ACG GAA TTC GAG TCC TTC TCC CTG GAC TCC ACT TTC
50	2887	His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu
		CAC GCA AAG AAA CAG ATC CCG TGT ATT GTG TCC ATG CTC ACG AAA GAA
55	2935	Leu Tyr Phe Tyr His Leu Glu Pro Ser Ala Gly Asp Met Arg Ala Ala
		CTG TAC TTT TAT CAC CTC GAG CCA TCT GCT GGA GAC ATG AGA GCT GCC
60	2983	Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn Ser
		AAC CTT TGG CCA AGC CCG CTC ATG ATC AAA CGC TCT AAG AAG AAC AGC
65	3031	Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu Asp
		CTG GCC TTG TCC CTG ACG GCC GAC CAG ATG GTC AGT GCC TTG TTG GAT
70	3079	Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro Phe
		GCT GAG CCC CCC ATA CTC TAT TCC GAG TAT GAT CCT ACC AGA CCC TTC
75	3127	Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg Glu
		AGT GAA GCT TCG ATG ATG GGC TTA CTG ACC AAC CTG GCA GAC AGG GAG
80	3175	Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val Asp
		CTG GTT CAC ATG ATC AAC TGG GCG AAG AGG GTG CCA GGC TTT GTG GAT
85	3223	Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu Glu
		TTG ACC CTC CAT GAT CAG GTC CAC CTT CTA GAA TGT GCC TGG CTA GAG
90	3271	Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Val Lys
		ATC CTG ATG ATT GGT CTC GTC TGG CGC TCC ATG GAG CAC CCA GTG AAG
95	3319	Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys Cys
		CTA CTG TTT GCT CCT AAC TTG CTC TTG GAC AGG AAC CAG GGA AAA TGT
100	3367	Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser Ser
		GTA GAG GGC ATG GTG GAG ATC TTC GAC ATG CTG CTG GCT ACA TCA TCT
105	3415	Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu Lys
		CGG TTC CGC ATG ATG AAT CTG CAG GGA GAG GAG TTT GTG TGC CTC AAA
110	3463	Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser Thr
		TCT ATT ATT TTG CTT AAT TCT GGA GTG TAC ACA TTT CTG TCC AGC ACC
115	3511	Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp Lys
		CTG AAG TCT CTG GAA GAG AAG GAC CAT ATC CAC CGA GTC CTG GAC AAG
120	3559	Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr Leu
		ATC ACA GAC ACT TTG ATC CAC CTG ATG GCC AAG GCA GGC CTG ACC CTG

		Gln	Gln	Gln	His	Gln	Arg	Leu	Ala	Gln	Leu	Leu	Leu	Ile	Leu	Ser	His
3607		CAG	CAG	CAG	CAC	CAG	CGG	CTG	GCC	CAG	CTC	CTC	CTC	ATC	CTC	TCC	CAC
5	3655	Ile	Arg	His	Met	Ser	Asn	Lys	Gly	Met	Glu	His	Leu	Tyr	Ser	Met	Lys
		ATC	AGG	CAC	ATG	AGT	AAC	AAA	GGC	ATG	GAG	CAT	CTG	TAC	AGC	ATG	AAG
	3703	Cys	Lys	Asn	Val	Val	Pro	Leu	Tyr	Asp	Leu	Leu	Leu	Glu	Ala	Ala	Asp
		TGC	AAG	AAC	GTG	GTG	CCC	CTC	TAT	GAC	CTG	CTG	CTG	GAG	GCG	GCG	GAC
10	3751	Ala	His	Arg	Leu	His	Ala	Pro	Thr	Ser	Arg	Gly	Gly	Ala	Ser	Val	Glu
		GCC	CAC	CGC	CTA	CAT	GCG	CCC	ACT	AGC	CGT	GGA	GGG	GCA	TCC	GTG	GAG
	3799	Glu	Thr	Asp	Gln	Ser	His	Leu	Ala	Thr	Ala	Gly	Ser	Thr	Ser	Ser	His
15		GAG	ACG	GAC	CAA	AGC	CAC	TTG	GCC	ACT	GCG	GGC	TCT	ACT	TCA	TCG	CAT
	3847	Ser	Leu	Gln	Lys	Tyr	Tyr	Ile	Thr	Gly	Glu	Ala	Glu	Gly	Phe	Pro	Ala
		TCC	TTG	CAA	AAG	TAT	TAC	ATC	ACG	GGG	GAG	GCA	GAG	GGT	TTC	CCT	GCC
20	3895	Thr	Ala	***													
		ACA	GCT	TGA													

SEQ ID NO: 38

Description of Artificial Sequence: vector pCAG-Casp3-ED4ER(T2)-bpa

25	1	TCGCGCGTTT	CGGTGATGAC	GGTGAAGACC	TCTGACACAT	GCAGCTCCCG	GAGACGGTCA
	61	CAGCTTGCTT	GTAAGCGGAT	GCCGGGAGCA	GACAAGCCCG	TCAGGGCGCG	TCAGCGGGTG
	121	TTGGCGGGTG	TCGGGGCTGG	CTTAACATATG	CGGCATCAGA	GCAGATTGTA	CTGAGAGTGC
	181	ACCATATGCG	GTGTGAAATA	CCGCACAGAT	GCGTAAGGAG	AAAATACCGC	ATCAGGCGCC
	241	ATTGCCCAT	CAGGCTGCGC	AACTGTTGGG	AAGGGCGATC	GGTGGCGGCC	TCTTCGCTAT
	301	TACGCCAGCT	GGCGAAAGGG	GGATGTGCTG	CAAGGCGATT	AAGTTGGGTA	ACGCCAGGGT
30	361	TTTCCCAGTC	ACGACGTTGT	AAAACGACGG	CCAGTGAATT	CGAGCTCGGT	ACCCGGGGGC
	421	GCGCCGGATC	TCGACATTGA	TTATTGACTA	GTTATTAATA	GTAATCAATT	ACGGGGTCAT
	481	TAGTTCATAG	CCCATATATG	GAGTTCCGCG	TTACATAACT	TACGGTAAAT	GGCCCGCCTG
	541	GCTGACCGCC	CAACGACCCC	CGCCCATTGA	CGTCAATAAT	GACGTATGTT	CCCATAGTAA
	601	ACTCTCCCA	TCTCCCCC	CTCCCCACCC	CCAATTTTGT	ATTTATTTAT	TTTTTAATTA
35	661	TGGCAGTACA	TCAAGTGTAT	CATATGCCAA	GTACGCCCCC	TATTGACGTC	AATGACGGTA
	721	AATGGCCCCG	CTGGCATTAT	GCCCAGTACA	TGACCTTATG	GGACTTTCCT	ACTTGGCAGT
	781	ACATCTACGT	ATTAGTCATC	GCTATTACCA	TGGGTCGAGG	TGAGCCCCAC	GTTCGTCTTC
	841	ACTCTCCCA	TCTCCCCC	CTCCCCACCC	CCAATTTTGT	ATTTATTTAT	TTTTTAATTA
	901	TTTTGTGCAG	CGATGGGGGC	GGGGGGGGGG	GGGGCGCGCG	CCAGGCGGGG	CGGGGCGGGG
40	961	CGAGGGGCGG	GGCGGGGCGA	GGCGGAGAGG	TGCGGCGGCA	GCCATCAGA	GCGGCGCGCT
	1021	CCGAAAGTTT	CCTTTTATGG	CGAGGCGGGC	GCGGCGGGCG	CCCTATAAAA	AGCGAAGCGC
	1081	GCGGCGGGCG	GAGTTCGCTG	CGTTGCCTTC	GCCCGGTGCC	CCGCTCCGCG	CCGCTCCGCG
	1141	CCGCGCGCCC	CGGCTCTGAC	TGACCGCGTT	ACTCCACAG	GTGAGCGGGC	GGGACGGCCC
	1201	TTCTCCTCCG	GGCTGTAATT	AGCGCTTGGT	TTAATGACGG	CTCGTTTCTT	TTCTGTGGCT
45	1261	GCGTGAAAGC	CTTAAAGGGC	TCCGGGAGGG	CCCTTTGTGC	GGGGGGGAGC	GGCTCGGGGG
	1321	GTGCGTGCTT	GTGTGTGTCG	TGGGGGAGCG	CCGCGTGCGG	CCGCGCTGCG	CCGCGGCTG
	1381	TGAGCGCTGC	GGGCGGGCGG	CGGGGCTTTG	TGCGCTCCCG	GTGTGCGCGA	GGGGAGCGCG
	1441	GCCGGGGGCG	GTGCCCCGCG	GTGCGGGGGG	GCTGCGAGGG	GAACAAAGGC	TGCGTGCGGG
50	1501	GTGTGTGCGT	GGGGGGGTGA	GCAGGGGGTG	TGGGCGCGGC	GGTCGGGCTG	TAACCCCCCC
	1561	CTGCACCCCC	CTCCCCGAGT	TGCTGAGCAC	GGCCCGGCTT	CGGGTGCGGG	GCTCCGTGCG
	1621	GGGCGTGCGG	CGGGGCTCGC	CGTGCCGGGC	GGGGGGTGGC	GGCAGGTGGG	GGTGCCGGGC
	1681	GGGCGGGGCG	CGCCTCGGGC	CGGGGAGGGC	TCGGGGGAGG	GGCGCGGGCG	CCCGGAGGCG
	1741	CCGCGGGCTG	TCGAGGCGCG	GCGAGCCGCA	GCCATTGCC	TTTATGGTAA	TCGTGCGAGA
55	1801	GGGCGCAGGG	ACTTCCTTTG	TCCCAAATCT	GGCGGAGCCG	AAATCTGGGA	GGCGCCGCGG
	1861	CACCCCTCT	AGCGGGCGCG	GGCGAAGCGG	TGCGGCGCCG	GCAGGAAGGA	AATGGGCGGG
	1921	GAGGGCCTTC	GTGCGTCGCC	GCGCCGCGCT	CCCCTTCTCC	ATCTCCAGCC	TCGGGGCTGC
	1981	CGCAGGGGGA	CGGCTGCCTT	CGGGGGGGAC	GGGGCAGGGC	GGGGTTCGGC	TTCTGGCGTG
	2041	TGACCGGCGG	CTCTAGAGCC	TCTGCTAACC	ATGTTTCATG	CTTCTTCTTT	TTCTACAGA
60	2101	TCCTTAATTA	ATTCCACCAT	GGAGAACAAC	AAAACCTCAG	TGGATTCAAA	ATCCATTAA
	2161	AATTTTGAAG	TAAAGACCAT	ACATGGGAGC	AAGTCAGTGG	ACTCTGGGAT	CTATCTGGAC
	2221	AGTAGTTACA	AAATGGATTA	TCCTGAAATG	GGCATATGCA	TAATAATTAA	TAATAAGAAC
	2281	TTCCATAAGA	GCACTGGAAT	GTCATCTCGC	TCTGGTACGG	ATGTGGACGC	AGCCAACCTC
	2341	AGAGAGACAT	TCATGGGCCT	GAAATACCAA	GTCAGGAATA	AAAATGATCT	TACTCGTGAA
	2401	GACATTTTGG	AATTAATGGA	TAGTGTCTCT	AAGGAAGATC	ATAGCAAAAG	GAGCAGCTTT
65	2461	GTGTGTGTGA	TTCTAAGCCA	TGGTGATGAA	GGGGTCATTT	ATGGGACAAA	TGGGCTGTT
	2521	GAAGTGAAAA	AGTTGACTAG	CTTCTTCAGA	GGCGACTACT	GCCGGAGTCT	GACTGGAAAG
	2581	CCGAAACTCT	TCATCATTTA	GGCCTGCCGG	GGTACGGAGC	TGGACTGTGG	CATGAGACA
	2641	GACAGTGGGA	CTGATGAGGA	GATGGCTTGC	CAGAAGATAC	CGGTGGAGGC	TGACTTCCTG
	2701	TATGCTTACT	CTACAGCACC	TGGTTACTAT	TCCTGGAGAA	ATTCAAAGGA	CGGGCTGTTG
70	2761	TTTCATCCAGT	CCCTTTGCGG	CATGCTGAAG	CTGTACGCGC	ACAAGCTAGA	ATTTATGCAC
	2821	ATTCTCACTC	GCGTTAACAG	GAAGGTGGCA	ACGGAATTCT	AGTCCTTCTC	CCTGGACTCC
	2881	ACTTTCCACG	CAAAGAAACA	GATCCCCTGT	ATTGTGTCCA	TGCTCACGAA	AGAACTGTAC
	2941	TTTTATCAC	TCGAGAGCCT	GGCCTTGTCC	CTGACGGCCG	ACCAGATGGT	CAGTGCCTTG

3001 TTGGATGCTG AGCCCCCAT ACTCTATTCC GAGTATGATC CTACCAGACC CTTCACTGAA  
3061 GCTTCGATGA TGGGCTTACT GACCAACCTG GCAGACAGGG AGCTGGTTCA CATGATCAAC  
3121 TGGGCGAAGA GGGTGCCAGG CTTTGTGGAT TTGACCCTCC ATGATCAGGT CCACCTTCTA  
3181 GAATGTGCCT GGCTAGAGAT CCTGATGATT GGTCTCGTCT GGCGCTCCAT GGAGCACCCA  
5 3241 GTGAAGCTAC TGTTTGCTCC TAACTTGCTC TTGGACAGGA ACCAGGGAAA ATGTGTAGAG  
3301 GGCATGGTGG AGATCTTCGA CATGCTGCTG GCTACATCAT CTCGGTTCGG CATGATGAAT  
3361 CTGCAGGGAG AGGAGTTTGT GTGCCCAAAA TCTATTATTT TGCTTAATTC TGGAGTGATC  
3421 ACATTTCTGT CCAGCACCTT GAAGTCTCTG GAAGAGAAGG ACCATATCCA CCGAGTCTCTG  
3481 GACAAGATCA CAGACACTTT GATCCACCTG ATGGCCAAAG CAGGCCTGAC CCTGCAGCAG  
10 3541 CAGCACCAGC GGCTGGCCCA GCTCCTCCTC ATCCTCTCCC ACATCAGGCA CATGAGTAAC  
3601 AAAGGCATGG AGCATCTGTA CAGCATGAAG TGCAAGAACG TGGTGCCCTT CTATGACCTG  
3661 CTGCTGGAGG CGGCGGACGC CCACCGCCTA CATGCGCCCA CTAGCCGTGG AGGGGCATCC  
3721 GTGGAGGAGA CGGACCAAAG CCACTTGGCC ACTGCGGGCT CTACTTCATC GCATTCCTTG  
3781 CAAAAGTATT ACATCACGGG GGAGGCAGAG GGTTCCTCTG CCACAGCTTG ATGAAGATCT  
15 3841 GAGGACCTTG AGCAATGATT GTAAATGATT GCAGATCCAC TAGTTCTAGA GCTCGCTGAT  
3901 CAGCCTCGAC TGTGCTTCT AGTTGCCAGC CATCTGTTGT TTGCCCTTCC CCCGTGCCCTT  
3961 CCTTGACCTT GGAAGGTGCC ACTCCCACTG TCCTTTCCTA ATAAATGAG GAAATTGCAT  
4021 CGCATTGTCT GAGTAGGTGT CATTCTATTG TGGGGGGTGG GGTGGGGCAG GACAGCAAGG  
4081 AAAGGCATGG GGAAGACAAT AGCAGGCATG CTGGGGATGC GGTGGGCTCT ATGGCTTCTG  
20 4141 AGGCGGAAAG AACCAGAAGC TTGGCGTAAT CATGGTCATA GCTGTTTCTT GTGTGAAATT  
4201 GTTATCCGCT CACAATTCCA CACAACATAC GAGCCGGAAG CATAAAGTGT AAAGCCTGGG  
4261 GTGCCTAATG AGTGAGCTAA CTCACATTA TGGCGTTGCG CTCCTGCCC GCTTCCAGT  
4321 CGGGAACCTT TCGTGCCAG CTGCATTAAT GAATCGGCCA ACGCGCGGGG AGAGGCGGTT  
4381 TGCGTATTGG GCGCTCTTCC GCTTCTCTCG TCACTGACTC GCTGCGCTCG GTCGTTCGGC  
25 4441 TGCGGCGAGC GGTATCAGT CACTCAAAGG CGGTAATACG GTTATCCACA GAATCAGGGG  
4501 ATAACGCAGG AAAGAACATG TGAGCAAAAG GCCAGCAAAA GGCCAGGAAC CGTAAAAAGG  
4561 CCGCGTTGCT GCGGTTTTTC CATAGGCTCC GCCCCCTGA CGAGCATCAC AAAAATCGAC  
4621 GCTCAAGTCA GAGGTGGCGA AACCCGACAG GACTATAAAG ATACCAGGCG TTTCCCTCTG  
4681 GAAGCTCCCT CGTGCGCTCT CCTGTTCCGA CCCTGCGCGT TACCGGATAC CTGTCCGCCT  
30 4741 TTTCCCTTTC GGAAGCGGTG GCGCTTTCTC ATAGCTCACG CTGTAGGTAT CTCAGTTCCG  
4801 TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG TGCACGAACC CCCCCTTCAG CCCGACCGCT  
4861 GCGCCTTATC CGGTAACATAT CGTCTTGAGT CCAACCCGGT AAGACACGAC TTATCGCCAC  
4921 TGGCAGCAGC CACTGGTAAC AGGATTAGCA GAGCGAGGTA TGTAGGCGGT GCTACAGAGT  
4981 TCTTGAAGTG GTGGCCTAAC TACGGCTACA CTAGAAGGAC AGTATTGGT ATCTGCGCTC  
35 5041 TGCTGAAGCC AGTTACCTTC GGAAAAAGAG TTGGTAGCTC TTGATCCGGC AAACAAACCA  
5101 CCCTGGTAGC CGGTGGTTTT TTTGTTTGCA AGCAGCAGAT TACGCGCAGA AAAAAAGGAT  
5161 CTCAGAAGA TCCTTTGATC TTTTCTACGG GGTCTGACGC TCAGTGGAAC GAAAACCTAC  
5221 GTTAAGGATG TTTGGTCATG AGATTATCAA AAAGGATCTT CACCTAGATC CTTTAAATT  
40 5281 AAAAATGAAG TTTTAAATCA ATCTAAAGTA TATATGAGTA AACTTGGTCT GACAGTTACC  
5341 AATGCTTAAT CAGTGAGGCA CCTATCTCAG CGATCTGTCT ATTTCTGTCA TCCATAGTTG  
5401 CCTGACTCCC CGTCGTGTAG ATAACCTACG TACGGGAGGG CTTACCATCT GGCCCCAGTG  
5461 CCGGTTCCGA ACGCGAGAC CCACGCTCAC CGGCTCCAGA TTTATCAGCA ATAAACGACG  
5521 CAGCCGGAAG GGCCGAGCGC AGAAGTGGTC CTGCAACTTT ATCCGCTTCC ATCCAGTCTA  
5581 TTAATTGTTG CCGGGAAGCT AGAGTAAGTA GTTCGCCAGT TAATAGTTTG CGCAACGTTG  
45 5641 TTGCCATTGC TACAGGCATC GTGGTGTCAC GCTCGTCTGT TGGTATGGCT TCATTACGCT  
5701 CCGGTTCCGA ACGATCAAGG CGAGTTACAT GATCCCCCAT GTTGTGCAAA AAAGCGGTTA  
5761 GCTCCTTCGG TCCTCCGATC GTTGTCAGAA GTAAGTTGGC CGCAGTGTTA TCACTCATGG  
5821 TTTATGGCAGC ACTGCATAAT TCTCTTACTG TCATGCCATC CGTAAGATGC TTTTCTGTGA  
5881 CTGGTGAGTA CTCAACCAAG TCATTCTGAG AATAGTGTAT GCGGCGACCG AGTTGCTCTT  
50 5941 GCCCGGCGTC AATACGGGAT AATACCGCGC CACATAGCAG AACTTTAAAA GTGCTCATCA  
6001 TTGGAACACG TTCTTCGGGG CGAAACTCT CAAGGATCTT ACCGCTGTTG AGATCCAGTT  
6061 CGATGTAACC CACTCGTGCA CCCAACTGAT CTTCAGCATC TTTTACTTTC ACCAGCGTTT  
6121 CTGGGTGAGC AAAACAGGA AGGCAAAATG CCGCAAAAAA GGAATAAGG GCGACACGGA  
6181 AATGTTGAAT ACTCATACTC TTCCTTTTTC AATATTATTG AAGCATTTAT CAGGGTTATT  
55 6241 GTCTCATGAG CGGATACATA TTTGAATGTA TTTAGAAAAA TAAACAAATA GGGGTTCCGC  
6301 GCACATTTC CCGAAAAGTG CCACCTGACG TCTAAGAAAC CATTATTATC ATGACATTAA  
6361 CCTATAAAAA TAGGCGTATC ACGAGGCCCT TTCGTC

SEQ ID NO: 39

60 Description of Artificial Sequence: vector pCAG-Cre-ED4ER(T2)-bpA

1 TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGTCCCCG GAGACGGTCA  
61 CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGCGGGTG  
121 TTGGCGGGTG TCGGGGCTGG CTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC  
181 ACCATATGCG GTGTGAAAA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGGCGCC  
65 241 ATTGCGCAAT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC TCTTCGCTAT  
301 TACGCCAGCT GGCGAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA ACGCCAGGGT  
361 TTTCCCACTC ACGACGTGTG AAAACGACGG CCAAGTGAAT CGAGCTCGGT ACCCGGGGGC  
421 GCGCCGGATC TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAATT ACGGGGTCAT  
481 TAGTTCTATG CCCATATATG GAGTTCGCGG TTACATAACT TACGGTAAAT GGCCCGCTAT  
70 541 GCTGACCGCC CAACGACCCC CGCCATTGA CGTCAATAAT GACGTATGTT CCCATAGTAA  
601 CGCCAATAGG GACTTTCCAT TGACGTCAAT GGGTGGACTA TTTACGGTAA ACTGCCACT  
661 TGGCAGTACA TCAAGTGAT CATATGCCAA GTACGCCCCC TATTGACGTC AATGACGGTA  
721 AATGGCCCGC CTGGCATTAT GCCCAGTACA TGACCTTATG GGACTTTCCT ACTTGGCAGT

781 ACATCTACGT ATTAGTCATC GCTATTACCA TGGGTCGAGG TGAGCCCCAC GTTCTGCTTC  
841 ACTCTCCCCA TCTCCCCCCC CTCCCCACCC CCAATTTTGT ATTTATTTAT TTTTAAATTA  
901 TTTTGTGCAG CGATGGGGGG GGGGGGCGCG GGGGCGCGCG CCAGGCGGGG CCGGGCGGGG  
961 CGAGGGGCGG GGGGGGCGCA GCGGAGAGG TCGGGCGGCA GCCAATCAGA GCGGCGCGCT  
5 1021 CCGAAAGTTT CCTTTTATGG CGAGGCGGCG GCGGCGGCGG CCCTATAAAA AGCGAAGCGC  
1081 GCGGCGGGCG GGAGTCGCTG CGTTGCCTTC GCCCGTGCC CCGCTCCGCG CCGCTCGCG  
1141 CCGCCGCCCC CGGCTCTGAC TGACCGCGTT ACTCCACAG GTGAGCGGGC GGGACGGCCC  
1201 TTCTCTCCG GGCTGTAATT AGCGCTTGGT TTAATGACGG CTCGTTTCTT TTCTGTGGCT  
1261 GCGTGAAAGC CTTAAAGGGC TCCGGGAGGG CCCTTTGTGC GGGGGGAGC GGCTCGGGG  
10 1321 GTGCGTGCGT GTGTGTGTGC GTGGGAGCG CCGCGTGCGG CCCGCGCTGC CCGGCGGCTG  
1381 TGAGCGCTGC AGGCGCGGCG GGGGCTTTG TCGCTCCGC GTGTGCGCA GGGGAGCGCG  
1441 GCGGGGGGCG GTGCCCCGCG GTGCGGGGGG GCTGCGAGGG GAACAAAGGC TCGGTGCGGG  
1501 GTGTGTGCGT GGGGGGGTGA GCAGGGGGTG TGGGCGCGCG GGTGCGGCTG TAACCCCCC  
1561 CTGCACCCCC CTCCCCGAGT TGCTGAGCAC GGCCCGGCTT CGGGTGCGGG GCTCCGTGCG  
15 1621 GGGCGTGGCG CGGGCTCGCG CGTCCCGGGC GGGGGTGGC GGCAGGTGGG GGTGCCGGCG  
1681 GGGGCGGGGC CGCCTCGGCG GGGGAGGGC TCGGGGAGG GCGCGGCGG CCGCGGAGCG  
1741 CCGGCGGCTG TCGAGGCGCG GCAGCCGCA GCCATTGCCT TTTATGGTAA TCGTGCGAGA  
1801 GGGCGCAGGG ACTTCCTTTG TCCCAAATCT GGCGGAGCCG AAATCTGGGA GGCGCCCGCG  
1861 CACCCCTCTA AGCTAGAGT GCGTAAGCGG TCGGCGCGCG GCAGGAAGGA AATGGGCGCG  
20 1921 GAGGGCCTTC GTGCGTCGCC GCGCCGCGCT CCCCTTCTCC ATCTCCAGCC TCGGGGCTGC  
1981 CGCAGGGGGA CGGCTGCCTT CCGGGGGGAC GGGGCGAGGG GGGGTTCGCG TTCTGGCGTG  
2041 TGACCGGCGG CTCTAGAGCC TCTGCTAACC ATGTTTCATG CTCTCTCTTT TTCTACAGA  
2101 TCCCTTAATT AGCTAGAGT GCGTATATAT ATTCCACCAT GTCCAATTTA CTGACCGTAC  
2161 ACCAAAATTT GCCTGCATTA CCGGTCGATG CAACGAGTGA TGAGGTTGCG AAGAACCTGA  
25 2221 TGGACATGTT CAGGGATCGC CAGGCGTTT CTGAGCATAC CTGGAATATG CTTCTGTCCG  
2281 TTTGCCGGTC GTGGGCGGCA TGGTGCAAGT TGAATAACCG GAAATGGTTT CCCGCGAAC  
2341 CTGAAGATGT TCGCGATTAT CTCTATATAT TTCAGGCGCG CGGTCTGGCA GTAAAACTA  
2401 TCCAGCAACA TTTGGGCCAG CTAACATGCT TTCATCGTCG GTCCGGGCTG CCACGACCAA  
2461 GTGACAGCAA TGCTGTTTCA CTGGTTATGC GCGGATCCG AAAAGAAAAC GTTGATGCCG  
30 2521 GTGAACGTGC AAAACAGGCT CTAGCGTTTC AACGCACTGA TTTGACCCAG GTTCGTTTAC  
2581 TCATGGAAAA TAGCGATCGC TGCCAGGATA TACGTAATCT GGCATTTCTG GGGATTGCTT  
2641 ATAACACCCT GTTACGTATA GCCGAAATG CAGGATCAG GGTAAAGAT ATCTCACGTA  
2701 CTGACGGTGG GAGAATGTTA ATCCATATG GCAGAACGAA AACGCTGGTT AGCACCGCAG  
2761 GTGTAGAGAA GGCATTAGC CTGGGGGTAA CTAACTGGT CGAGCGATGG ATTTCCGTCT  
35 2821 CTGGGTAGC TGATGATCCG AATAACTACC TGTTTTGCCG GGTACAGAAA AATGGTGTG  
2881 CCGCGCCATC TGCCACCAGC CAGCTATCAA CTCGCGCCCT GGAAGGGATT TTTGAAGCAA  
2941 CTCATCGATT GATTTACGGC GCTAAGGATG ACTCTGGTCA GAGATACCTG GCCTGGTCTG  
3001 GACACAGTGC CCGTGTCCGA GCGCGCGGAG ATATGGCCCG CGCTGGAGTT TCAATACCGG  
40 3061 AGATCATGCA AGCTGGTGGC TGGACCAATG TAAATATTGT CATGAACTAT ATCCGTAACC  
3121 TGGTAGTGA AACAGGGGCA ATGGTGCCG TGCTGGAAGA TGGCGATCTC GAGAGCCTGG  
3181 CTTGTGCCCT GACGGCCGAC CAGATGGTCA GTGCCCTGTT GGATGCTGAG CCCCCATAC  
3241 TCTATTCCGA GTATGATCCT ACCAGACCCT TCAGTGAAGC TTCGATGATG GGCTTACTGA  
3301 CCAACCTGGC AGACAGGGAG CTGGTTTACA TGATCAACTG GCGGAAGAGG GTGCCAGGCT  
3361 TTGTGGATT T GACCTCCAT GATCAGGTCC ACCTTCTAGA ATGTGCTGG CTAGAGATCC  
45 3421 TGATGATTGG TCTCGTCTGG CGCTCCATGG AGCACCCAGT GAAGTACTG TTTGCTCTTA  
3481 ACTTGCTCTT GGACAGGAAC CAGGGAAAAT GTGTAGAGGG CATGGTGGAG ATCTTCGACA  
3541 TGCTGCTGGC TACATCATCT CGGTTCGCA TGATGAATCT GCAGGGAGAG GAGTTTGTGT  
3601 GCCTCAAATC TATTATTTTG CTTAATTCTG GAGTGTACAC ATTTCTGTCC AGCACCTGA  
50 3661 AGTCTCTGGA AGAGAAGGAC CATATCCACC GAGTCTGGA CAAGATCACA GACACTTTGA  
3721 TCCACCTGAT GGCCAAGGCA GGCTGACCC TGCAGCAGCA GCACACGGG CTGGCCAGC  
3781 TCCTCCTCAT CCTCTCCAC ATCAGGCACA TGAGTAACAA AGGCATGGAG CATCTGTACA  
3841 GCATGAAGTG CAAGAACGTG GTGCCCTCT ATGACCTGCT GCTGGAGGGC GCGGACGGCC  
3901 ACCGCTTACA TGCGCCCACT AGCCGTGGAG GGCATCCGT GGAGGAGACG GACCAAAGCC  
3961 ACTTGCCAC TGCGGGCTCT ACTTCATCGC ATTCCTTGCA AAAGTATTAC ATCACGGGGG  
55 4021 AGGAGAGGG TTTCCCTGCC ACAGCTTGAT GAAGATCTGA GCTCCCTGGC GGAATTGCGT  
4081 AAATGATTGC AGATCCACTA GTTCTAGAGC TCGCTGATCA GCCTCGACTG TGCTTCTAG  
4141 TTGCCAGCCA TCTGTTGTTT GCGCTTCCCG CGTGCCTTCC TTGACCTTG AAGGTGCCAC  
4201 TCCCACTGCT CTTTCTTAAT AAAATGAGGA AATTGCATCG CATTGTCTGA GTAGGTGTCA  
60 4261 TTCTATTCTG GGGGTGCGG TGGGCTCTAT GGCTTCTGAG GCGGAAAGAA CCAGCATGCA  
4321 CAGGCATGCT GGGGATGCGG TGGGCTCTAT GGCTTCTGAG GCGGAAAGAA CCAGCATGCA  
4381 AGCTTGCGGT AATCATGGTC ATAGCTGTTT CTTGTGTGAA ATTGTTATCC GCTCACAATT  
4441 CCACACAACA TACGAGCCGG AAGCATAAAG TGTAAGCCTT GGGGTGCCTA ATGAGTGAGC  
4501 TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC AGTCGGGAAA CCTGTCGTGC  
4561 CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG GTTTGCGTAT TGGGCGCTCT  
65 4621 TCCGCTTCTT CGCTCACTGA CTCGCTGCGC TCGGTGCTTC GGCTGCGGCG AGCGGTATCA  
4681 GCTCACTCAA AGGCGGTAAT ACGGTTATCC ACAGAATCAG GGGATAACGC AGGAAAGAAC  
4741 ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCCTAAAA AGGCCGCGTT GCTGGCGTTT  
4801 TTCCATAGGC TCCGCCCCC TGACGAGCAT CACAAAAATC GACGCTCAAG TCAGAGGTGG  
4861 CGAAACCCGA CAGGACTATA AAGATAACCAG GCGTTTCCCC CTGGAAGCTC CCTCGTCCG  
70 4921 TCTCTGTTT CGACCCTGCC GCTTACCGGA TACCTGTCCG CCTTCTCTCC TTCGGGAAGC  
4981 GTGGCGCTTT CTATAGCTC ACGCTGTAGG TATCTCAGTT CGGGTAGAGT CGTTCGCTCC  
5041 AAGCTGGGCT GTGTGCACGA ACCCCCGGTT CAGCCCGACC GCTGCGCCTT ATCCGGTAAC  
5101 TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC CACTGGCAGC AGGCACTGGT



5161 AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG AGTTCTTGAA GTGGTGGCCT  
5221 AACTACGGCT ACACTAGAAG GACAGTATTT GGTATCTGCG CTCTGCTGAA GCCAGTTACC  
5281 TTCGGAAAAA GAGTTGGTAG CTCTTGATCC GGCAACAAAA CCACCGCTGG TAGCGGTGGT  
5341 TTTTTTGTTC GCAAGCAGCA GATTACGCGC AGAAAAAAG GATCTCAAGA AGATCCTTTG  
5401 ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAACT CACGTTAAGG GATTTTGGTC  
5461 ATGAGATTAT CAAAAAGGAT CTTACCTAG ATCCTTTTAA ATTAATAATG AAGTTTAAAA  
5521 TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT ACCAATGCTT AATCAGTGAG  
5581 GCACCTATCT CAGCGATCTG TCTATTTCTG TCTATCCATAG TTGCCTGACT CCCCCTCGTG  
5641 TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA GTGCTGCAAT GATACCGCGA  
5701 GACCCACGCT CACCGGCTCC AGATTATCA GCAATAAACC AGCCAGCCGG AAGGGCCGAG  
5761 CGCAGAAAGT GTCCTGCAAC TTTATCCGCC TCCATCCAGT CTATTAATTG TTGCCGGGAA  
5821 GCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG TTGTTGCCAT TGCTACAGGC  
5881 ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA GCTCCGGTTC CCAACGATCA  
5941 AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG TTAGCTCCTT CGGTCCTCCG  
6001 ATCGTTGTCA GAAGTAAGTT GGCCGCGAGT TTATCACTCA TGGTTATGGC AGCACTGCGT  
6061 AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG TGAAGTGTGA GTACTCAACC  
6121 AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT CTTGCCCGGC GTCAATACGG  
6181 GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA TCATTGGAAA ACGTCTCTCG  
6241 GGCAGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA TGTTCGATGA ACCCACTCGT  
6301 GCACCCAACT GATCTTCAGC ATCTTTTACT TTCACCAGCG TTTCTGGGTG AGCAAAAACA  
6361 GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC GGAATGTTG AATACTCATA  
6421 CTCTTCCCTT TTCAATATTA TTGAAGCATT TATCAGGGTT ATTGTCTCAT GAGCGGATAC  
6481 ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTT CGCGCACATT TCCCCGAAAA  
6541 GTGCCACCTG ACGTCTAAGA AACCATTATT ATCATGACAT TAACCTATAA AAATAGGCGT  
6601 ATCACGAGGC CCTTTCGTC

SEQ ID NOS: 40 and 41

Description of Artificial Sequence: DNA sequence (SEQ ID NO: 40) coding for fusion gene  
Casp3-ED4ER(T2) (SEQ ID NO: 41)

30 Met Glu Asn Asn Lys Thr Ser Val Asp Ser Lys Ser Ile Asn Asn Phe  
2119 ATG GAG AAC AAC AAA ACC TCA GTG GAT TCA AAA TCC ATT AAT AAT TTT  
  
Glu Val Lys Thr Ile His Gly Ser Lys Ser Val Asp Ser Gly Ile Tyr  
2167 GAA GTA AAG ACC ATA CAT GGG AGC AAG TCA GTG GAC TCT GGG ATC TAT  
35  
  
Leu Asp Ser Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Ile Cys Ile  
2215 CTG GAC AGT AGT TAC AAA ATG GAT TAT CCT GAA ATG GGC ATA TGC ATA  
  
Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Ser Ser Arg  
40 2263 ATA ATT AAT AAT AAG AAC TTC CAT AAG AGC ACT GGA ATG TCA TCT CGC  
  
Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Met Gly  
2311 TCT GGT ACG GAT GTG GAC GCA GCC AAC CTC AGA GAG ACA TTC ATG GGC  
45  
  
Leu Lys Tyr Gln Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Asp Ile  
2359 CTG AAA TAC CAA GTC AGG AAT AAA AAT GAT CTT ACT CGT GAA GAC ATT  
  
Leu Glu Leu Met Asp Ser Val Ser Lys Glu Asp His Ser Lys Arg Ser  
50 2407 TTG GAA TTA ATG GAT AGT GTT TCT AAG GAA GAT CAT AGC AAA AGG AGC  
  
Ser Phe Val Cys Val Ile Leu Ser His Gly Asp Glu Gly Val Ile Tyr  
2455 AGC TTT GTG TGT GTG ATT CTA AGC CAT GGT GAT GAA GGG GTC ATT TAT  
  
Gly Thr Asn Gly Pro Val Glu Leu Lys Lys Leu Thr Ser Phe Phe Arg  
55 2503 GGG ACA AAT GGG CCT GTT GAA CTG AAA AAG TTG ACT AGC TTC TTC AGA  
  
Gly Asp Tyr Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile  
2551 GGC GAC TAC TGC CGG AGT CTG ACT GGA AAG CCG AAA CTC TTC ATC ATT  
60  
  
Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser  
2599 CAG GCC TGC CGG GGT ACG GAG CTG GAC TGT GGC ATT GAG ACA GAC AGT  
  
Gly Thr Asp Glu Glu Met Ala Cys Gln Lys Ile Pro Val Glu Ala Asp  
65 2647 GGG ACT GAT GAG GAG ATG GCT TGC CAG AAG ATA CCG GTG GAG GCT GAC  
  
Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn  
2695 TTC CTG TAT GCT TAC TCT ACA GCA CCT GGT TAC TAT TCC TGG AGA AAT  
  
Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ser Met Leu Lys  
70 2743 TCA AAG GAC GGG TCG TGG TTC ATC CAG TCC CTT TGC AGC ATG CTG AAG  
  
Leu Tyr Ala His Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn  
2791 CTG TAC GCG CAC AAG CTA GAA TTT ATG CAC ATT CTC ACT CGC GTT AAC

	2839	Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Leu Asp Ser Thr Phe
		AGG AAG GTG GCA ACG GAA TTC GAG TCC TTC TCC CTG GAC TCC ACT TTC
5	2887	His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu
		CAC GCA AAG AAA CAG ATC CCG TGT ATT GTG TCC ATG CTC ACG AAA GAA
10	2935	Leu Tyr Phe Tyr His Leu Glu Ser Leu Ala Leu Ser Leu Thr Ala Asp
		CTG TAC TTT TAT CAC CTC GAG AGC CTG GCC TTG TCC CTG ACG GCC GAC
	2983	Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
		CAG ATG GTC AGT GCC TTG TTG GAT GCT GAG CCC CCC ATA CTC TAT TCC
15	3031	Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
		GAG TAT GAT CCT ACC AGA CCC TTC AGT GAA GCT TCG ATG ATG GGC TTA
	3079	Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
		CTG ACC AAC CTG GCA GAC AGG GAG CTG GTT CAC ATG ATC AAC TGG GCG
20	3127	Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
		AAG AGG GTG CCA GGC TTT GTG GAT TTG ACC CTC CAT GAT CAG GTC CAC
25	3175	Leu Leu Glu Cys Ala Trp Leu Glu Ile Leu Met Ile Gly Leu Val Trp
		CTT CTA GAA TGT GCC TGG CTA GAG ATC CTG ATG ATT GGT CTC GTC TGG
	3223	Arg Ser Met Glu His Pro Val Lys Leu Leu Phe Ala Pro Asn Leu Leu
		CGC TCC ATG GAG CAC CCA GTG AAG CTA CTG TTT GCT CCT AAC TTG CTC
30	3271	Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Met Val Glu Ile Phe
		TTG GAC AGG AAC CAG GGA AAA TGT GTA GAG GGC ATG GTG GAG ATC TTC
	3319	Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
		GAC ATG CTG CTG GCT ACA TCA TCT CGG TTC CGC ATG ATG AAT CTG CAG
35	3367	Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
		GGA GAG GAG TTT GTG TGC CTC AAA TCT ATT ATT TTG CTT AAT TCT GGA
40	3415	Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
		GTG TAC ACA TTT CTG TCC AGC ACC CTG AAG TCT CTG GAA GAG AAG GAC
	3463	His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
		CAT ATC CAC CGA GTC CTG GAC AAG ATC ACA GAC ACT TTG ATC CAC CTG
45	3511	Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
		ATG GCC AAG GCA GGC CTG ACC CTG CAG CAG CAG CAC CAG CGG CTG GCC
	3559	Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
		CAG CTC CTC CTC ATC CTC TCC CAC ATC AGG CAC ATG AGT AAC AAA GGC
50	3607	Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
		ATG GAG CAT CTG TAC AGC ATG AAG TGC AAG AAC GTG GTG CCC CTC TAT
55	3655	Asp Leu Leu Leu Glu Ala Ala Asp Ala His Arg Leu His Ala Pro Thr
		GAC CTG CTG CTG GAG GCG GCG GAC GCC CAC CGC CTA CAT GCG CCC ACT
	3703	Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
		AGC CGT GGA GGG GCA TCC GTG GAG GAG ACG GAC CAA AGC CAC TTG GCC
60	3751	Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
		ACT GCG GGC TCT ACT TCA TCG CAT TCC TTG CAA AAG TAT TAC ATC ACG
	3799	Gly Glu Ala Glu Gly Phe Pro Ala Thr Ala ***
		GGG GAG GCA GAG GGT TTC CCT GCC ACA GCT TGA

65 SEQ ID NO: 42  
Description of Artificial Sequence: primer ED4ER-A  
1 ACCTCGAGAG CCTGGCCTTG TCCCTGACG

70 SEQ ID NO: 43  
Description of Artificial Sequence: primer ED4ER-B  
1 TTCCTGGGT GCTCCATGGA GCG

SEQ ID NO: 44

**Description of Artificial Sequence: primer baxER-A**

1 CCTTAATTAA TTCCACCATG GGCGACGGGT CCGGGGAGCA GCTT

**SEQ ID NO: 45**

**Description of Artificial Sequence: primer baxER-B**

1 GGCTCGAGGC CCATCTTCTT CCAGATGG

**SEQ ID NO: 46**

**Description of Artificial Sequence: vector pCAG-Bax-ER(T2)-bpa**

10 1 TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA  
61 CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGCGGGTG  
121 TTGGCGGGTG TCGGGGCTGG CTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC  
181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGGCGCC  
241 ATTCCGCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC TCTTCGCTAT  
15 301 TACGCCAGCT GGCGAAAAGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA ACGCCAGGGT  
361 TTTCACGTC ACGACGTTGT AAAACGACGG CCAAGTAATT CGAGCTCGGT ACCCGGGGGC  
421 GCCCGGATC TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAAT ACGGGGTCAT  
481 TAGTTTCATG CCCATATATG GAGTTCCGCG TTACATAACT TACGGTAAAT GGCCCGCCTG  
541 GCTGACCGCC CACGACCCCG CGCCCATTTGA CGTCAATAAT GACGTATGTT CCCATAGTAA  
20 601 CGCCAATAGG GACTTTCCAT TGACGTCAAT GGGTGGACTA TTTACGGTAA ACTGCCCACT  
661 TGGCAGTACA TCAAGTGAT CATATGCCAA GTACGCCCCC TATTGACGTC AATGACGGTA  
721 AATGGCCCGC CTGGCATTAT GCCCAGTACA TGACCTTATG GGACTTTCCT ACTTGGCAGT  
781 ACATCTACGT ATTAGTCATC GCTATTACCA TGGGTGAGG TGAGCCCCAC GTTCTGCTTC  
841 ACTCTCCCA TCTCCCCCCC CTCCCCACCC CCAATTTTGT ATTTATTTAT TTTTAAATTA  
25 901 TTTTGTGAG CGATGGGGGG GGGGGGGGGG GGGGCGCGCG CCAGCGGGG CCGGGCGGGG  
961 CGAGGGGGCG GCGGGGCGCA GCGCGAGAGG TCGGCGGCGA GCCAATCAGA GCGGCGCGCT  
1021 CCGAAAGTTT CCTTTTATGG CGAGGCGGCG GCGGCGGCGG CCCTATAAAA AGCGAAGCGC  
1081 GCGGCGGGCG GGAGTCGCTG CGTTGCCTTC GCCCGGTGCC CCGCTCCGCG CCGCTCGCG  
1141 CCGCCCGCCC CGGCTCTGAC TGACCGCGTT ACTCCACAG GTGAGCGGGC GGGACGGCCC  
30 1201 TTCTCCTCG GGCTGTAATT AGCGCTTGGT TTAATGACGG CTCGTTTCTT TTCTGTGGCT  
1261 GCGTGAAAGC CTAAAGGGC TCCGGGAGGG CCCTTTGTGC GGGGGGGAGC GGCTCGGGGG  
1321 GTGCGTGCCT GTGTGTGTGC GTGGGGAGCG CCGCGTGCAG CCCGCGCTGC CCGCGGGTGC  
1381 TGAGCGCTGC GGGCGCGGCG CGGGGCTTTG TCGCTCCGCG GTGTGCGCGA GGGGAGCGCG  
1441 GCGGGGGGCG GTGCCCGCG GTGCGGGGGG GCTGCGAGGG GAACAAAGGC TCGGTGCGGG  
35 1501 GTGTGTGCGT GGGGGGGTGA GCAGGGGGTG TGGGCGCGGC GGTGCGGGTG TAACCCCCC  
1561 CTGCACCCCC CTCCCCAGT TGCTGAGCAC GGCCCGGCTT CGGGTGCGGG GCTCCGTGCG  
1621 GGGCGTGGCG CGGGGCTCGC CGTGCCGGGC GGGGGGTGGC GGCAGGTGGG GGTGCCGGGC  
1681 GGGCGGGGCG CGCCTCGGCG CGGGGAGGGC TCGGGGAGGG GCGCGGCGCG CCGCGGAGCG  
1741 CCGGCGGCTG TCGAGGCGCG GCGAGCCGCA GCCATTGCCT TTTATGGTAA TCGTGCGAGA  
40 1801 GGGCGCAGGG ACTTCCTTTG TCCCAATCT GCGGAGCCG AAATCTGGGA GGGCGCGCG  
1861 CACCCCTCT AGCGGGCGCG GGCGAAGCG TCGGCGCGCG GCAGGAAGGA AATGGCGGG  
1921 GAGGCGCTTC GTGCGTCGCC GCGCGCGCGT CCCCTTCTCC ATCTCCAGCC TCGGGGCTGC  
1981 CGCAGGGGGA CGGCTGCCTT CGGGGGGGAC GGGGCGAGGC GGGGTTCGGC TTCTGGCGTG  
2041 TGACCGGCGG CTCTAGAGCC TCTGCTAACC ATGTTTCATG CTCTCTCTTT TTCTACAGA  
45 2101 TCCTTAATTA ATTCCACCAT GGGCGACGG TCCGGGGAGC AGCTTGGGAG CGGCGGGCCC  
2161 ACCAGCTCTG AACAGATCAT GAAGACAGGG GCCTTTTTCG TACAGGGTTT CATCCAGGAT  
2221 CGAGCAGGGA GGATGGCTGG GGAGACACCT GAGCTGACCT TGGAGCAGCC GCGCCAGGAT  
2281 GCGTCCACCA AGAAGCTGAG CGAGTGCTC CGGCGAATTG GAGATGAACT GGACAGCAAT  
50 2341 ATGGAGCTGC AGAGGATGAT TGCTGACGTG GACACGGACT CCCCCGAGA GGTCTTCTTC  
2401 CCGGTGGCAG CTGACATGTT TGCTGATGAA AACTTCAACT GGGGCGCGCT GGTGCGCTTC  
2461 TTCTACTTTG CTAGCAAACT GGTGCTCAAG GCCCTGTGCA CTAAAGTGCC CGAGCTGATC  
2521 AGAACCATCA TGGGCTGGAC ACTGGACTTC CTCCGTGAGC GGCTGCTTGT CTGGATCCAA  
2581 GACCAGGGTG GTGGGAAGG CCTCCTCTCC TACTTCGGGA CCCCCACATG GCAGACAGTG  
2641 ACCATCTTTG TGGCTGGAGT CCTACCGCC TCGCTACCA TCTGGAAGAA GATGGGCTTC  
55 2701 GAGCATCTG CTGGAGACAT GAGAGCTGCC AACCTTTGGC CAAGCCCGCT CATGATCAAA  
2761 CGCTCTAAGA AGAACAGCCT GGCCTTGTC CTGACGGCCG ACCAGATGGT CAGTGCCTTG  
2821 TTGGATGCTG AGCCCCCAT ACTCTATTCC GAGTATGATC CTACCAGACC CTTCAAGTAA  
2881 GCTTCGATGA TGGGCTTACT GACCAACCTG GCAGACAGGG AGCTGGTTCA CATGATCAAC  
2941 TGGGCGAAGA GGTGCGCAGG CTTTGTGGAT TTGACCTCC ATGATCAGGT CCACCTTCTA  
60 3001 GAATGTGCCT GGCTAGAGAT CCTGATGATT GGTCTCGTCT GCGCTCCAT GGAGACCCCA  
3061 GTGAAGCTAC TGTTTGCTCC TAACTTGCTC TTGGACAGGA ACCAGGAAA ATGTGTAGAG  
3121 GGCATGGTGG AGATCTTCGA CATGCTGCTG GCTACATCAT CTCGGTTCCG CATGATGAAT  
3181 CTGAGGGGAG AGGAGTTTGT GTGCCTCAA TCTATTATTT TGCTTAATTC TGGAGTGATC  
3241 ACATTTCTGT CCAGCACCTT GAAGTCTCTG GAAGAGAAGG ACCATATCCA CCGAGTCTCT  
65 3301 GACAAGATCA CAGACACTTT GATCCACCTG ATGGCCAAGG CAGGCTGAC CCTGCAGAG  
3361 CAGCACCAGC GGCTGGCCCA GCTCCTCTC ATCCTCTCCC ACATCAGGCA CATGAGTAAC  
3421 AAAGGCATGG AGCATCTGTA CAGCATGAAG TGCAAGAAGC TGGTCCCCCT CTATGACCTG  
3481 CTGCTGGAGG CGGCGGACGC CCACCGCCTA CATGCGCCCA CTAGCCGTGG AGGGGCATCC  
3541 GTGAGGAGGA CGGACCAAGC CCACCTGGCC ACTGCGGGCT CTACTTCATC GCATCTCTTG  
70 3601 CAAAAGTATT ACATCACGGG GGAGGCAGAG GGTTCCTCTG CCACAGCTTG ATGAAGATCT  
3661 GAGCTCCCTG GCGGAATTGC GTAAATGATT GCAGATCCAC TAGTTCTAGA GCTCGCTGAT  
3721 CAGCCTCGAC TGTGCCTTCT AGTTGCCAGC CATCTGTTGT TTGCCCTCC CCCGTGCCTT  
3781 CCTTGACCTT GGAAGGTGCC ACTCCCACTG TCCTTTCCTA ATAAAATGAG GAAATTGCAT

3841 CGCATTGTCT GAGTAGGTGT CATTCTATTC TGGGGGGTGG GGTGGGGCAG GACAGCAAGG  
3901 GGGAGGATTG GGAAGACAAT AGCAGGCATG CTGGGGATGC GGTGGGCTCT ATGGCTTCTG  
3961 AGGCGGAAG AACAGAAAGC TTGGCGTAAT CATGGTCATA GCTGTTTCCT GTGTGAAAT  
5 4021 GTTATCCGCT CACAATTTCA CACAACATAC GAGCCGGAAG CATAAAGTGT AAAGCCTGGG  
4081 GTGCCTAATG AGTGAGCTAA CTCACATTAA TTGCGTTGCG CTTACTGCCC GCTTTCAGT  
4141 CGGGAAACCT GTCGTGCCAG CTGCATTAAT GAATCGGCCA ACGCGCGGGG AGAGGCGGTT  
4201 TGCCTATTGG GCGCTCTTCC GCTTCTCGC TCACTGACTC GCTGCGCTCG GTCGTTCCGC  
4261 TGCGGCGAGC GGTATCAGCT CACTCAAAGG CGGTAATACG GTTATCCACA GAATCAGGGG  
10 4321 ATAACGCAGG AAAGAACATG TGAGCAAAAG GCCAGCAAAA GGCCAGGAAC CGTAAAAAGG  
4381 CCGCGTTGCT GGCCTTTTTT CATAGGCTCC GCGCCCTTGA CGAGCATCAC AAAAATCGAC  
4441 GCTCAAGTCA GAGGTGGCGA AACCCGACAG GACTATAAAG ATACCAGGCG TTTCCCTCTG  
4501 GAAGCTCCCT CGTGCCTCTT CCTGTTCCGA CCCTGCCGCT TACCGGATAC CTGTCCGCCT  
4561 TTCTCCCTTC GGAAGCGGTG GCGCTTCTCT ATAGCTCAGC CTGTAGGTAT CTCAGTTCCG  
15 4621 TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG TGCACGAACC CCCCGTTCAG CCCGACCGCT  
4681 TCGCTTTATG CCGTAACATG CTGTTTGTG CCAACCCGCT AAGACACGAC TTATCGCCAC  
4741 TGGCAGCAGC CACTGGTAAC AGGATTAGCA GAGCGAGGTA TGTAGGCGGT GCTACAGAGT  
4801 TCTGAAGTG GTGGCCTAAC TACGGCTACA CTAGAAGGAC AGTATTTGGT ATCTGCGCTC  
4861 TGCTGAAGCC AGTTACCTTC GGAAAAAGAG TTGGTAGCTC TTGATCCGGC AAACAAACCA  
10 4921 CCGCTGGTAG CCGTGGTTTT TTTGTTTGA AGCAGCAGAT TACGCGCAGA AAAAAAGGAT  
4981 CTCAAGAAGA TCCTTTGATC TTTTCTACGG GGTCTGACGC TCAGTGGAAC GAAAACTCAC  
5041 GTTAAGGGAT TTTGGTCATG AGATTATCAA AAAGGATCTT CACCTAGATC CTTTAAAT  
5101 AAAAATGAAG TTTTAAATCA ATCTAAAGTA TATATGAGTA AACTTGGTCT GACAGTTACC  
5161 AATGCTTAAT CAGTGAGGCA CCTATCTCAG CGATCTGTCT ATTTCTGTTC TCCATAGTTG  
25 5221 CCTGACTCCC CGTCGTGTAG ATAACACGA TACGGGAGGG CTTACCATCT GGCCCCAGTG  
5281 CTGCAATGAT ACCGCGAGAC CCACGCTCAC CGGCTCCAGA TTTATCAGCA ATAAACCAGC  
5341 CAGCCGGAAG GCGCGAGCGC AGAAGTGCTC CTGCAACTTT ATCCGCTTCC ATCCAGTCTA  
5401 TTAATTGTTG CCGGGAAGCT AGAGTAAGTA GTTCGCCAGT TAATAGTTTG CGCAACGTTG  
5461 TTGCCATTGC TACAGGCATC GTGGTGTAC GCTCGTCGTT TGGTATGGCT TCATTCAGCT  
5521 CCGGTTCCCA ACGATCAAGG CGAGTTACAT GATCCCCCAT GTTGTGCAAA AAAGCGGTTA  
30 5581 GCTCCTTCGG TCCTCCGATC GTTGTACAGG GTAAGTTGGC CGCAGTGTTA TCACTCATGG  
5641 TTATGGCAGC ACTGCATAAT TCTCTTACTG TCATGCCATC CGTAAGATGC TTTTCTGTGA  
5701 CTGGTGAGTA CTCAACCAAG TCATTCTGAG AATAGTGTAT GCGGCGACCG AGTTGCTCTT  
5761 GCGGCGCGTC AATACGGGAT AATACCGCGC CACATAGCAG AACTTTAAAA GTGCTCATCA  
35 5821 TTGGAAAACG TTCTTCGGGG CGAAAACCTCT CAAGGATCTT ACCGCTGTTG AGATCCAGTT  
5881 CGATGTAACC CACTCGTGCA CCCAACTGAT CTTACGATC TTTTACTTTC ACCAGCGTTT  
5941 CTGGGTGAGC AAAAACAGGA AGGCAAAATG CCGCAAAAAA GGAATAAGG GCGACACGGA  
6001 AATGTTGAAT ACTCATACTC TTCCTTTTTC AATATTATTG AAGCATTTAT CAGGGTTATT  
6061 GTCTCATGAG CGGATACATA TTGAATGTA TTTAGAAAAA TAAACAAATA GGGGTTCCGC  
6121 GCACATTTCC CCGAAAAGTG CCACCTGACG TCTAAGAAAC CATTATTATC ATGACATTAA  
40 6181 CCTATAAAAA TAGGCGTATC ACGAGGCCCT TTCGTC

SEQ ID NOS: 47 and 48

Description of Artificial Sequence: DNA sequence (SEQ ID NO: 47) coding for fusion gene Bax-ER(T2) (SEQ ID NO: 48)

45 Met Gly Asp Gly Ser Gly Glu Gln Leu Gly Ser Gly Gly Pro Thr Ser  
2119 ATG GGC GAC GGG TCC GGG GAG CAG CTT GGG AGC GGC GGG CCC ACC AGC  
50 Ser Glu Gln Ile Met Lys Thr Gly Ala Phe Leu Leu Gln Gly Phe Ile  
2167 TCT GAA CAG ATC ATG AAG ACA GGG GCC TTT TTG CTA CAG GGT TTC ATC  
Gln Asp Arg Ala Gly Arg Met Ala Gly Glu Thr Pro Glu Leu Thr Leu  
2215 CAG GAT CGA GCA GGG AGG ATG GCT GGG GAG ACA CCT GAG CTG ACC TTG  
55 Glu Gln Pro Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser Glu Cys Leu  
2263 GAG CAG CCG CCC CAG GAT GCG TCC ACC AAG AAG CTG AGC GAG TGT CTC  
Arg Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met  
2311 CGG CGA ATT GGA GAT GAA CTG GAC AGC AAT ATG GAG CTG CAG AGG ATG  
60 Ile Ala Asp Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val  
2359 ATT GCT GAC GTG GAC ACG GAC TCC CCC CGA GAG GTC TTC TTC CGG GTG  
Ala Ala Asp Met Phe Ala Asp Gly Asn Phe Asn Trp Gly Arg Val Val  
2407 GCA GCT GAC ATG TTT GCT GAT GGC AAC TTC AAC TGG GGC CGC GTG GTT  
65 Ala Leu Phe Tyr Phe Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr  
2455 GCC CTC TTC TAC TTT GCT AGC AAA CTG GTG CTC AAG GCC CTG TGC ACT  
70 Lys Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe  
2503 AAA GTG CCC GAG CTG ATC AGA ACC ATC ATG GGC TGG ACA CTG GAC TTC  
Leu Arg Glu Arg Leu Leu Val Trp Ile Gln Asp Gln Gly Gly Trp Glu  
2551 CTC CGT GAG CGG CTG CTT GTC TGG ATC CAA GAC CAG GGT GGC TGG GAA

	2599	Gly Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile
		GGC CTC CTC TCC TAC TTC GGG ACC CCC ACA TGG CAG ACA GTG ACC ATC
5	2647	Phe Val Ala Gly Val Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met
		TTT GTG GCT GGA GTC CTC ACC GCC TCG CTC ACC ATC TGG AAG AAG ATG
	2695	Gly Leu Glu Pro Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro
10		GGC CTC GAG CCA TCT GCT GGA GAC ATG AGA GCT GCC AAC CTT TGG CCA
	2743	Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser
		AGC CCG CTC ATG ATC AAA CGC TCT AAG AAG AAC AGC CTG GCC TTG TCC
15	2791	Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro
		CTG ACG GCC GAC CAG ATG GTC AGT GCC TTG TTG GAT GCT GAG CCC CCC
	2839	Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser
		ATA CTC TAT TCC GAG TAT GAT CCT ACC AGA CCC TTC AGT GAA GCT TCG
20	2887	Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met
		ATG ATG GGC TTA CTG ACC AAC CTG GCA GAC AGG GAG CTG GTT CAC ATG
	2935	Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His
25		ATC AAC TGG GCG AAG AGG GTG CCA GGC TTT GTG GAT TTG ACC CTC CAT
	2983	Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu Glu Ile Leu Met Ile
		GAT CAG GTC CAC CTT CTA GAA TGT GCC TGG CTA GAG ATC CTG ATG ATT
30	3031	Gly Leu Val Trp Arg Ser Met Glu His Pro Val Lys Leu Leu Phe Ala
		GGT CTC GTC TGG CGC TCC ATG GAG CAC CCA GTG AAG CTA CTG TTT GCT
	3079	Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Met
		CCT AAC TTG CTC TTG GAC AGG AAC CAG GGA AAA TGT GTA GAG GGC ATG
35	3127	Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met
		GTG GAG ATC TTC GAC ATG CTG CTG GCT ACA TCA TCT CGG TTC CGC ATG
	3175	Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu
40		ATG AAT CTG CAG GGA GAG GAG TTT GTG TGC CTC AAA TCT ATT ATT TTG
	3223	Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu
		CTT AAT TCT GGA GTG TAC ACA TTT CTG TCC AGC ACC CTG AAG TCT CTG
45	3271	Glu Glu Lys Asp His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr
		GAA GAG AAG GAC CAT ATC CAC CGA GTC CTG GAC AAG ATC ACA GAC ACT
	3319	Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His
		TTG ATC CAC CTG ATG GCC AAG GCA GGC CTG ACC CTG CAG CAG CAG CAC
50	3367	Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met
		CAG CGG CTG GCC CAG CTC CTC CTC ATC CTC TCC CAC ATC AGG CAC ATG
	3415	Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val
55		AGT AAC AAA GGC ATG GAG CAT CTG TAC AGC ATG AAG TGC AAG AAC GTG
	3463	Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala Ala Asp Ala His Arg Leu
		GTG CCC CTC TAT GAC CTG CTG CTG GAG GCG GCG GAC GCC CAC CGC CTA
60	3511	His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln
		CAT GCG CCC ACT AGC CGT GGA GGG GCA TCC GTG GAG GAG ACG GAC CAA
	3559	Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys
		AGC CAC TTG GCC ACT GCG GGC TCT ACT TCA TCG CAT TCC TTG CAA AAG
65	3607	Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro Ala Thr Ala ***
		TAT TAC ATC ACG GGG GAG GCA GAG GGT TTC CCT GCC ACA GCT TGA

SEQ ID NO: 49

Description of Artificial Sequence: primer ERbax-1

70 1 CCTTAATTAA GTCTAGACCG ATATGAGCCT GGCCTTGTCCT CTGAC

SEQ ID NO: 50

Description of Artificial Sequence: primer ERbax-2

1 AAGCTGCTCC CCGGACCCGT CAGCTGTGGC AGGGAAACCC T

SEQ ID NO: 51

Description of Artificial Sequence: primer ERbax-3

5 1 GACGGGTCCG GGGAGCAGCT T

SEQ ID NO: 52

Description of Artificial Sequence: primer ERbax-4

10 1 CAGTCGACTC TAGATCAGCC CATCTTCTTC CAGA

SEQ ID NO: 53

Description of Artificial Sequence: vector pCAG-ER(T2)-Bax-bpA

1 TCGCGCGTTT CGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCC GAGACGGTCA  
61 CAGCTTGCTT GTAAGCGGAT GCCGGGAGCA GACAAGCCCC TCAGGGCGCG TCAGCGGGTG  
15 121 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC  
181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGGCGCC  
241 ATTCCGCAAT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC TCTTCGCTAT  
301 TACGCCAGCT GCGGAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA ACGCCAGGGT  
361 TTCCCAATAG GACTTTCCAT TGACGTCAT AAAACGACGG CCAGTGAATT CGAGCTCGGT ACCCGGGGCG  
20 421 GCGCCGGATC TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAATT ACGGGGTCTAT  
481 TAGTTTCATG CCCATATATG GAGTTCCGCG TTACATAACT TACGGTAAAT GGCCCGCCTG  
541 GTGACCGGCC CAACGACCCC CGCCCATTGA CGTCAATAAT GACGTATGTT CCCATAGTAA  
601 CGCCAATAGG GACTTTCCAT TGACGTCAT GGGTGGACTA TTTACGGTAA ACTGCCCCACT  
661 TGGCAGTACA TCAAGTGTAT CATATGCCAA GTACGCCCCC TATTGACGTC AATGACGGTA  
25 721 AATGGCCCCG CTGGCATTAT GCCCAGTACA TGACCTTATG GGACTTTCCT ACTTGGCAGT  
781 ACATCTACGT ATTAGTCAT GCTATTACCA TGGGTGAGG TGAGCCCCAC GTTCTGCTTC  
841 ACTCTCCCCA TCTCCCCCCC CTCCCCACCC CCAATTTTGT ATTTATTTAT TTTTAAATTA  
901 TTTTGTGAG CATGCGGGGG GGGGGGGGGG GGGGCGCGCG CCAGCGGGGG CGGGGCGGGG  
961 CGAGGGGCGG GCGGGGGCGA GCGGAGAGG TGCGGCGGCA GCCAATCAGA GCGGCGCGCT  
30 1021 CCGAAAGTTT CTTTATATG CGAGGCGGCG GCGGCGGCGG CCTATAAAA AGCGAAGCGC  
1081 GCGGCGGGCG GGAGTCGCTG CGTTGCCTTC GCCCGTGCC CCGCTCCGCG CCGCCTCGCG  
1141 CCGCCCGCCC CGGCTCTGAC TGACCGGCTT ACTCCACAG GTGAGCGGGC GGGACGGCCC  
1201 TTCTCTCCG GGCTGTAATT AGCGCTTGGT TTAATGACGG CTCGTTTCTT TTCTGTGGCT  
1261 GCTGAAAAGC CTTAAAGGGC TCCGGGAGGG CCCTTGTGCG GGGGGGGAGC GGCTCGGGGG  
35 1321 GTGCGTGCCT GTGTGTGTGC GTGGGGAGCG CCGCGTGCAG CCCGCGCTGC CCGGCGGCTG  
1381 TGAGCGCTGC GGGCGCGGCG CGGGGCTTTG TGCGCTCCCG GTGTGCGCGA GGGGAGCGCG  
1441 CGCGGGGGCG GTGCCCCGCG GTGCGGGGGG GCTGCGAGGG GAACAAAGGC TCGGTGCGGG  
1501 GTGTGTGCGT GGGGGGGTGA GCAGGGGGTG TGGGCGCGCG GGTGCGGGCTG TAACCCCCC  
1561 CTGACCCCCC CTCCCCGAGT TGCTGAGCAC GGCCCGGCTT CGGGTGCGGG GCTCCGTGCG  
40 1621 GGGCGTGCGG CCGGGCTCGC CGTGCCGGG GGGGGGTGGC GGCAGGTGGG GGTGCCGGGG  
1681 GGGGCGGGGG CGCCTCGGGC CGGGGAGGGC TCGGGGAGG GGCAGCGCGG CCGCGGAGCG  
1741 CGCAGGGGCG TCGAGGCGCG GCGAGCCGCA GCCATTGCCT TTTATGGTAA TCGTGCGAGA  
1801 GGGCGCAGGG ACTTCTTTG TCCCAAATCT GGGGAGCCG AAATCTGGGA GGGCGCGCCG  
1861 CACCCCCCTT AGCGGGGCGG GCGGAAGCGG TGCGGCGCGG GCAGGAAGGA AATGGGCGGG  
45 1921 GAGGGCCTTC GTGCGTGCCT GCGCCGCCGT CCCCTTCTCC ATCTCCAGCC TCGGGGCTGC  
1981 CGCAGGGGGA CGGCTGCCTT CCGGGGGGAG GGGGAGGGC GGGGTTTCGG TTCTGGCGTG  
2041 TGACCGGCGG CTCTAGAGCC TCTGCTAACC ATGTTTCATG CTTCTTCTTT TTCTACAGA  
2101 TCCTTAATTA AGTCTAGACC GATATGAGCC TGGCCTTGTC CCTGACGGCC GACCAGATGG  
50 2161 TCACTGCCTT GTTGGATGCT GAGCCCCCA TACTCTATTC CGAGTATGAT CCTACCAGG  
2221 CCTTCAGTGA AGCTTCGATG ATGGGCTTAC TGACCAACCT GGCAGACAGG GAGCTGGTTC  
2281 ACATGATCAA CTGGGCGAAG AGGGTGCCAG GCTTTGTGGA TTTGACCCTC CATGATCAGG  
2341 TCACCTTCTT AGAATGTGCC TGGCTAGAGA TCCTGATGAT TGGTCTCGTC TGGCGCTCCA  
2401 TGGAGCACCC AGTGAAGCTA CTGTTTGCTC CTAAGTGTCT CTTGGACAGG AACAGGGAA  
2461 AATGTGTAGA GGGCATGGTG GAGATCTTCG ACATGCTGCT GGCTACATCA TCTCGGTTCC  
55 2521 GCATGATGAA TCTGCAGGGA GAGGAGTTTG TGTGCCTCAA ATCTATTATT TTGCTTAATT  
2581 CTGGAGTGTA CACATTCTTG TCCAGCACCC TGAAGTCTCT GGAAGAGAAG GACCATATCC  
2641 ACCGAGTCCT GGACAAGATC ACAGACACTT TGATCCACCT GATGGCCAAG CAGGCGCTGA  
2701 CCCTGCAGCA GCAGCACCG CCGCTGGCCC AGCTCCTCCT CATCCTCTCC CACATCAGGC  
2761 ACATGAGTAA CAAAGGCATG GAGCATCTGT ACAGCATGAA GTGCAAGAAC GTGGTGCCCC  
60 2821 TCTATGACCT GCTGCTGGAG GCGGCGGACG CCCACCGCCT ACATGCGCCC ACTAGCCGTG  
2881 GAGGGGCATC CGTGGAGGAG ACGGACCAAA GCCACTTGGC CACTGCGGGC TCTACTTCAT  
2941 CGCATTCCTT GCAAAAGTAT TACATCACGG GGGAGGCAGA GGGTTTCCCT GCCACAGCTG  
3001 ACGGGTCCGG GGAGCAGCTT GGGAGCGGCG GGCCCCACCG CTCTGAACAG ATCATGAAGA  
3061 CAGGGGCTTT TTTGCTACAG GGTTCATCC AGGATCGAGC AGGGAGGATG GCTGGGGAGA  
65 3121 CACCTGAGCT GACCTTGGAG CAGCCGCCCC AGGATGCGTC CACCAAGAAG CTGAGCAGT  
3181 GTCTCCGGCG AATTGGAGAT GAACTGGACA GCAATATGGA GCTGCAGAGG ATGATTGCTG  
3241 ACCTGGACAC GGAATCCCC CGAGAGGTCT TCTTCCGGGT GGCAGCTGAC ATGTTTGTCT  
3301 ATGGCAACTT CAAGTGGGGC CGCGTGGTTG CCCTCTTCTA CTTTGCTAGC AAAGTGGTGC  
3361 TCAAGGCCCT GTGCACTAAA GTGCCGAGC TGATCAGAAC CATCATGGGC TGGACACTGG  
70 3421 ACTTCTCCCG TGAGCGGCTG CTTGTCTGGA TCCAAGACCA GGGTGGCTGG GAAGGCCTCC  
3481 TCTCTACTCT CCGGACCCCC ACATGGCAGA CAGTGACCAT CTTTGTGGCT GGAGTCTCTA  
3541 CCGCCTCGCT CACCATCTGG AAGAAGATGG GCTGATCTAG AGTCGACTGT TTCTAGAGCT  
3601 CGCTGATCAG CCTCGACTGT GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG CCCCCTCCCC

3661 GTGCCTTCCT TGACCCTGGA AGGTGCCACT CCCACTGTCC TTTCTAATA AAATGAGGAA  
3721 ATTGCATCGC ATTGTCTGAG TAGGTGTCAT TCTATTCTGG GGGGTGGGGT GGGGCAGGAC  
3781 AGCAAGGGGG AGGATTGGGA AGACAATAGC AGGCATGCTG GGGATGCGGT GGGCTCTATG  
3841 GCTTCTGAGG CGGAAAGAAC CAGCTGGGGC TCGAGATCCA CTAGTTCTAG CCTCGAGGCT  
5 3901 AGAGCGGCCA AACCTGCAGG CATGCAAGCT TGGCGTAATC ATGGTCATAG CTGTTTCCTG  
3961 TGTGAAATTG TTATCCGCTC ACAATTCAC ACAACATACG AGCCGGAAGC ATAAAGTGTA  
4021 AAGCCTGGGG TGCCTAATGA GTGAGCTAAC TCACATTAAT TGCGTTGCGC TCACTGCCCG  
4081 CTTTCCAGTC GGGAAACCTG TCGTGCCAGC TGCATTAATG AATCGGCCAA CGCGCGGGGA  
4141 GAGGCGGTTT GCGTATTGGG CGCTCTCCG CTTCCTCGCT CACTGACTCG CTGCGCTCGG  
10 4201 TCGTTCGGCT GCGGCGAGCG GTATCAGCTC ACTCAAAGGC GGTAAATACG TTATCCACAG  
4261 AATCAGGGGA TAACGCAGGA AAGAACATGT GAGCAAAAG CCAGCAAAAG GCCAGGAACC  
4321 GTAAAAAGGC CGCGTTGCTG GCGTTTTTTC ATAGGCTCCG CCCCCCTGAC GAGCATCACA  
4381 AAAATCGACG CTCAGTCAG AGGTGCGGAA ACCCGACAGG ACTATAAAGA TACGAGCGCT  
4441 TTCCCCCTGG AAGCTCCCTC GTGCGCTCTC CTGTTCCGAC CCTGCCGCTT ACCGGATACC  
15 4501 TGTCCGCGTT TTTCCCTTCG GGAAGCGTGG CGCTTCTCA TAGCTCACG TGTAGGTATC  
4561 TCAGTTCGGT GTAGGTCGTT CGCTCCAAGC TGGGCTGTGT GCACGAACCC CCCGTTCCAGC  
4621 CCGACCGCTG CGCCTTATCC GGTAACTATC GTCTTGAGTC CAACCCGCTA AGACACGACT  
4681 TATCGCCACT GGCAGCAGCC ACTGGTAACA GGATTAGCAG AGCGAGGTAT GTAGGCGGTG  
4741 CTACAGGTTT TTTGAAGTGG TGGCCTAACT ACGGCTACAC TAGAAGGACA GTATTTGGTA  
20 4801 TCTGCGCTCT GCTGAAGCCA GTTACCTTCG GAAAAAGAGT TGGTAGCTCT TGATCCGGCA  
4861 AACAAACCAC CGCTGGTAGC GGTGGTTTTT TTGTTTGCAA GCAGCAGATT ACGCGCAGAA  
4921 AAAAAGGATC TCAAGAAGAT CCTTTGATCT TTTCTACGGG GTCTGACGCT CAGTGAACG  
4981 AAAACTCAGC TTAAGGGATT TTGGTCATGA GATTATCAAA AAGGATCTTC ACCTAGATCC  
5041 TTTTAAATTA AAAATGAAGT TTTAAATCAA TCTAAAGTAT ATATGAGTAA ACTTGGTCTG  
25 5101 ACAGTTACCA ATGCTTAATC AGTGAGGCAC CTATCTCAGC GATCTGTCTA TTTTCGTTCTG  
5161 CCATAGTTGC CTGACTCCCC GTCGTGTAGA TAACTACGAT ACGGGAGGGC TTACCATCTG  
5221 GCCCCAGTGC TGCAATGATA CCGCGAGACC CACGCTCACC GGCTCCAGAT TTATCAGCAA  
5281 TAAACCAGCC AGCCGGAAGG GCCGAGCGCA GAAGTGGTCC TGCAACTTTA TCCGCCTCCA  
5341 TCCAGTCTAT TAATTGTTGC CGGGAAGCTA GAGTAAGTAG TTCGCCAGTT AATAGTTTGC  
30 5401 GCAACGTTGT TGGTGAAGT TCAAGCAAGT CATTCTGAGA ATAGTGTATG CGGCGACGGA  
5461 CATTACGCTC CGGTTCCCAA CGATCAAGGC GAGTTACATG ATCCCCCATG TTGTGCAAAA  
5521 AAGCGGTTAG CTCCTTCGGT CCTCCGATCG TTGTGAGAAG TAAGTTGGCC GCAGTGTTAT  
5581 CACTCATGGT TATGGCAGCA CTGCATAATT CTCTTACTGT CATGCCATCC GTAAGATGCT  
5641 TTTCTGTGAC TGGTGAGTAC TCAACCAAGT CATTCTGAGA ATAGTGTATG CGGCGACGGA  
35 5701 GTTGCTCTTG CCCGCGCTCA ATACGGGATA ATACCGCGCC ACATAGCAGA ACTTTAAAG  
5761 TGCTCATCAT TGGAAACGT TCTTCGGGGC GAAACTCTC AAGGATCTTA CCCTGTTGA  
5821 GATCCAGTTC GATGTAACCC ACTCGTGCAC CCAACTGATC TTCAGCATCT TTTACTTTCA  
5881 CCAGCGTTTC TGGGTGAGCA AAAACAGGAA GGCAAAATGC CGCAAAAAG GGAATAAGGG  
5941 CGACACGGAA ATGTTGAATA CTCATACTCT TCCTTTTTCA ATATTATTGA AGCATTATATC  
40 6001 AGGGTTATTG TCTCATGAGC GGATACATAT TTGAATGTAT TTAGAAAAAT AAACAAATAG  
6061 GGGTTCCGCG CACATTTCCC CGAAAAGTGC CACCTGACGT CTAAGAAACC ATTATTATCA  
6121 TGACATTAAC CTATAAAAAT AGGCGTATCA CGAGGCCCTT TCGTC

SEQ ID NOS: 54 and 55

45 Description of Artificial Sequence: DNA sequence coding for fusion protein ER(T2)-Bax

Met Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu  
2124 ATG AGC CTG GCC TTG TCC CTG ACG GCC GAC CAG ATG GTC AGT GCC TTG  
  
Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg  
50 2172 TTG GAT GCT GAG CCC CCC ATA CTC TAT TCC GAG TAT GAT CCT ACC AGA  
  
Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp  
2220 CCC TTC AGT GAA GCT TCG ATG ATG GGC TTA CTG ACC AAC CTG GCA GAC  
  
Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe  
55 2268 AGG GAG CTG GTT CAC ATG ATC AAC TGG GCG AAG AGG GTG CCA GGC TTT  
  
Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp  
60 2316 GTG GAT TTG ACC CTC CAT GAT CAG GTC CAC CTT CTA GAA TGT GCC TGG  
  
Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro  
2364 CTA GAG ATC CTG ATG ATT GGT CTC GTC TGG CGC TCC ATG GAG CAC CCA  
  
Val Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly  
65 2412 GTG AAG CTA CTG TTT GCT CCT AAC TTG CTC TTG GAC AGG AAC CAG GGA  
  
Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr  
2460 AAA TGT GTA GAG GGC ATG GTG GAG ATC TTC GAC ATG CTG CTG GCT ACA  
  
Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys  
70 2508 TCA TCT CGG TTC CGC ATG ATG AAT CTG CAG GGA GAG GAG TTT GTG TGC  
  
Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser

2556 CTC AAA TCT ATT ATT TTG CTT AAT TCT GGA GTG TAC ACA TTT CTG TCC

5 2604 Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu  
AGC ACC CTG AAG TCT CTG GAA GAG AAG GAC CAT ATC CAC CGA GTC CTG

2652 Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu  
GAC AAG ATC ACA GAC ACT TTG ATC CAC CTG ATG GCC AAG GCA GGC CTG

10 2700 Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu  
ACC CTG CAG CAG CAG CAC CAG CGG CTG GCC CAG CTC CTC CTC ATC CTC

2748 Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser  
TCC CAC ATC AGG CAC ATG AGT AAC AAA GGC ATG GAG CAT CTG TAC AGC

15 2796 Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala  
ATG AAG TGC AAG AAC GTG GTG CCC CTC TAT GAC CTG CTG CTG GAG GCG

2844 Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser  
GCG GAC GCC CAC CGC CTA CAT GCG CCC ACT AGC CGT GGA GGG GCA TCC

20 2892 Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser  
GTG GAG GAG ACG GAC CAA AGC CAC TTG GCC ACT GCG GGC TCT ACT TCA

25 2940 Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe  
TCG CAT TCC TTG CAA AAG TAT TAC ATC ACG GGG GAG GCA GAG GGT TTC

2988 Pro Ala Thr Ala Asp Gly Ser Gly Glu Gln Leu Gly Ser Gly Gly Pro  
CCT GCC ACA GCT GAC GGG TCC GGG GAG CAG CTT GGG AGC GGC GGG CCC

30 3036 Thr Ser Ser Glu Gln Ile Met Lys Thr Gly Ala Phe Leu Leu Gln Gly  
ACC AGC TCT GAA CAG ATC ATG AAG ACA GGG GCC TTT TTG CTA CAG GGT

3084 Phe Ile Gln Asp Arg Ala Gly Arg Met Ala Gly Glu Thr Pro Glu Leu  
TTC ATC CAG GAT CGA GCA GGG AGG ATG GCT GGG GAG ACA CCT GAG CTG

35 3132 Thr Leu Glu Gln Pro Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser Glu  
ACC TTG GAG CAG CCG CCC CAG GAT GCG TCC ACC AAG AAG CTG AGC GAG

3180 Cys Leu Arg Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln  
TGT CTC CGG CGA ATT GGA GAT GAA CTG GAC AGC AAT ATG GAG CTG CAG

3228 Arg Met Ile Ala Asp Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe  
AGG ATG ATT GCT GAC GTG GAC ACG GAC TCC CCC CGA GAG GTC TTC TTC

45 3276 Arg Val Ala Ala Asp Met Phe Ala Asp Gly Asn Phe Asn Trp Gly Arg  
CGG GTG GCA GCT GAC ATG TTT GCT GAT GGC AAC TTC AAC TGG GGC CGC

3324 Val Val Ala Leu Phe Tyr Phe Ala Ser Lys Leu Val Leu Lys Ala Leu  
GTG GTT GCC CTC TTC TAC TTT GCT AGC AAA CTG GTG CTC AAG GCC CTG

50 3372 Cys Thr Lys Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr Leu  
TGC ACT AAA GTG CCC GAG CTG ATC AGA ACC ATC ATG GGC TGG ACA CTG

3420 Asp Phe Leu Arg Glu Arg Leu Leu Val Trp Ile Gln Asp Gln Gly Gly  
GAC TTC CTC CGT GAG CGG CTG CTT GTC TGG ATC CAA GAC CAG GGT GGC

3468 Trp Glu Gly Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Gln Thr Val  
TGG GAA GGC CTC CTC TCC TAC TTC GGG ACC CCC ACA TGG CAG ACA GTG

60 3516 Thr Ile Phe Val Ala Gly Val Leu Thr Ala Ser Leu Thr Ile Trp Lys  
ACC ATC TTT GTG GCT GGA GTC CTC ACC GCC TCG CTC ACC ATC TGG AAG

3564 Lys Met Gly \*\*\*  
AAG ATG GGC TGA

65

SEQ ID NO: 56

Description of Artificial Sequence: vector pCMV-β-gal-pA

1 GAATTCGAGC TTGCATGCCT GCAGGTCGTT ACATAACTTA CGGTAAATGG CCCGCCTGGC  
61 TGACCGCCCA ACGACCCCG CCCATTGACG TCAATAATGA CGTATGTTCC CATAGTAACG  
70 121 CCAATAGGGA CTTTCCATTG ACGTCAATGG GTGGAGTATT TACGGTAAAC TGCCCACTTG  
181 GCAGTACATC AAGTGTATCA TATGCCAAGT ACGCCCCCTA TTGACGTCAA TGACGGTAAA  
241 TGGCCCGCCT GGCATTATGC CCAGTACATG ACCTTATGGG ACTTTCCTAC TTGGCAGTAC  
301 ATCTACGTAT TAGTCATCGC TATTACCATG GTGATGCGGT TTTGGCAGTA CATCAATGGG



5	361	CGTGGATAGC	GGTTTGACTC	ACGGGGATTT	CCAAGTCTCC	ACCCCATTTGA	CGTCAATGGG
	421	AGTTTGT TTT	GGCACCAAAA	TCAACGGGAC	TTTCCAAAAAT	GTCGTAACAA	CTCCGCCCAA
	481	TTGACGCAAA	TGGGCGGTAG	GCGTGTACGG	TGGGAGGTCT	ATATAAGCAG	AGCTCGTTTA
	541	GTGAACCGTC	AGATCGCCTG	GAGACGCCAT	CCACGCTGTT	TTGACCTCCA	TAGAAGACAC
	601	CGGGACCGAT	CCAGCCTCCG	GACTCTAGAG	GATCCGGTAC	TCGAGGAACT	GAAAAACCAG
10	661	AAAGTAACT	GGTAAGTTTA	GTCTTTTGT	CTTTTATTTC	AGGTCCCAGG	TCCGGTGGTG
	721	GTGCAAAACA	AAGAACTGCT	CCTCAGTGGA	TGTTGCCTTT	ACTTCTAGGC	CTGTACGGAA
	781	GTGTTACTTC	TGCTCTAAAA	GCTGCGGAAT	TGTACCCGCG	GCCGCAATTC	CCGGGGATCG
	841	AAAGAGCCTG	CTAAAGCAAA	AAAGAAGTCA	CCATGTCGTT	TACTTTGACC	AACAAGAACG
	901	TGATTTTCGT	TGCCGGTCTG	GGAGGCATTG	GTCTGGACAC	CAGCAAGGAG	CTGCTCAAGC
15	961	GCGATCCCGT	CGTTTTACAA	CGTCGTGACT	GGGAAAACCC	TGGCGTTACC	CAACTTAATC
	1021	GCCTTGACAG	ACATCCCCCT	TTCGCCAGCT	GGCGTAATAG	CGAAGAGGCC	CGCACCGATC
	1081	GCCTTCCCA	ACAGTTGCGC	AGCCTGAATG	GCGAATGGCG	CTTTGCCTGG	TTTCCGGCAC
	1141	CAGAAGCGGT	GCCGGAAAGC	TGGCTGGAGT	GCGATCTTCC	TGAGGCCGAT	ACTGTCGTCG
	1201	TCCCTCAAA	CTGGCAGATG	CACGGTTACG	ATGCGCCCAT	CTACACCAAC	GTAACCTATC
20	1261	CCATTACGGT	CAATCCGCCG	TTTGTTCCTA	CGGAGAATCC	GACGGGTTGT	TACTCGCTCA
	1321	CATTTAATGT	TGATGAAAGC	TGGCTACAGG	AAGGCCAGAC	GCGAATTAT	TTTGATGGCG
	1381	TTAACTCGGC	GTTTCATCTG	TGGTGCAACG	GGCGCTGGGT	CGGTTACGGC	CAGGACAGTC
	1441	GTTTGCCCGT	TGAATTTGAC	CTGAGCGCAT	TTTTACGCGC	CGGAGAAAAC	CGCCTCGCGG
	1501	TGATGGTGCT	GCGTTGGAGT	GACGGCAGTT	ATCTGGAAGA	TCAGGATATG	TGGCGGATGA
25	1561	GCGGCATTTT	CCGTGACGTC	TGCTTGTGTC	ATAAACCGAC	TACACAAATC	AGCGATTTCC
	1621	ATGTTGCCAC	TCGCTTTAAT	GATGATTTC	GCCGCGCTGT	ACTGGAGGCT	GAAGTTTACA
	1681	TTTGCGCGGA	GTTGCGGTAC	TACCTACGGG	TAACAGTTTC	TTTATGGCAG	GGTGAAACGC
	1741	AGGTCGCCAG	CGGCACCGCG	CCTTTCGGCG	GTGAAATTAT	CGATGAGCGT	GGTGGTTATG
	1801	CCGATCGCGT	CACACTACGT	CTGAACGTCG	AAAACCCGAA	ACTGTGGAGC	GCCGAAATCC
30	1861	CGAATCTCTA	TCGTGCCGTG	GTTGAACGTC	ACACCGCCGA	CGGCACGCTG	ATTGAAGCAG
	1921	AAGCCTGCGA	TGTCGGTTTC	CGCGAGGTGC	GGATTGAAAA	TGGTCTGCTG	CTGCTGAACG
	1981	GCAAGCCGTT	GCTGATTCTG	GGCGTTAACC	GTCACGAGCA	TCATCCTCTG	CATGGTCAGG
	2041	TCATGGATGA	GCAGACGATG	GTGCAGGATA	TCCTGCTGAT	GAAGCAGAAC	AACTTTAACG
	2101	CCGTGCGCTG	TTTCGCATTAT	CCGAACCATC	CGCTGTGGTA	CACGCTGTGC	GACCGCTACG
35	2161	GCCTGTATGT	GGTGGATGAA	GCCAATATTG	AAACCCACGG	CATGGTGCCA	ATGAATCGTC
	2221	TGACCGATGA	TCCGCGCTGG	CTACCGGCGA	TGAGCGAACG	CGTAACGCGA	ATGGTGCAGC
	2281	GCGATCGTAA	TCACCCGAGT	GTGATCATCT	GGTCGCTGGG	GAATGAATCA	GGCCACGGCG
	2341	CTAATCACGA	CCGCGTGTAT	CGCTGGATCA	AATCTGTCTG	TCCTTCCCGC	CCGCTGCAGT
	2401	ATGAAGGCGG	CGGAGCCGAC	ACCACGGCCA	CCGATATTAT	TTGCCCGATG	TACGCGCGCG
40	2461	TGATGAAGA	CCAGCCCTTC	CCGGCTGTGC	CGAAATGGTC	CATCAAAAAA	TGGCTTTCCG
	2521	TACCTGGAGA	GACGCGCCCG	CTGATCCTTT	GCGAATACGC	CCACGCGATG	GGTAACAGTC
	2581	TTGGCGGTTT	CGCTAAATAC	TGGCAGGCGT	TTCTGTAGTA	TCCCGGTTTA	CAGGGCGGCT
	2641	TCGTCTGGGA	CTGGGTGGAT	CAGTCGCTGA	TAAATATGTA	TGAAAACGGC	AACCCGTGGT
	2701	CGGCTTACGG	CGGTGATTTT	GGCGATACGC	CGAACGATCG	CCAGTTCTGT	ATGAACGGTC
45	2761	TGGTCTTTTG	CGACCCGACG	CCGCATCCAG	CGCTGACGGA	AGCAAAACAC	CAGCAGCATC
	2821	TTTTCCAGTC	CCGTTTATCC	GGGCAAAACCA	TCGAAGTGAC	CAGCGAATAC	CTGTTCCGTC
	2881	ATAGCGATAA	CGAGCTCCTG	CACTGGATGG	TGGCGCTGGA	TGGTAAGCCG	CTGGCAAGCG
	2941	GTGAAGTGCC	TCTGGATGTC	GCTCCACAAG	GTAACAGTT	GATTGAACGT	CCTGAACATC
	3001	CGCAGCCGGA	GAGCGCCGGG	CAACTCTGGC	TCACAGTACG	CGTAGTGCAA	CCGAACGCGA
50	3061	CCGCATGGTG	AGAAGCCGGG	CACATCAGCG	CCTGGCAGCA	GTGGCGTCTG	GCGGAAACCC
	3121	TCAGTGTGAC	GCTCCCGGCC	GCGTCCACAG	CCATCCCGCA	TCTGACCACC	AGCGAAATGG
	3181	ATTTTGTGAT	CGAGCTGGGT	AATAAGCGTT	GGCAATTTAA	CCGCCAGTCA	GGCTTTCTTT
	3241	CACAGATGTG	GATTGGCGAT	AAAAACAAC	TGCTGACGCC	GCTGCGCGAT	CAGTTCACCC
	3301	GTGCACCGCT	GGATAACGAC	ATTGGCGTAA	GTGAAGCGAC	CCGCATTGAC	CCTAACGCCT
55	3361	GGGTGGAACG	CTGGAAGGCG	GCGGGCCATT	ACCAGGCCGA	AGCAGCGTTG	TTGCAGTGCA
	3421	CGGCAGATAC	ACTTGCTGAT	GCGGTGCTGA	TTACGACCGC	TCACGCGTGG	CAGCATCAGG
	3481	GGAAAACCTT	ATTTATCAGC	CGGAAAACCT	ACCGGATTGA	TGGTAGTGGT	CAAATGGCGA
	3541	TTACCGTTGA	TGTTGAAGTG	GCGAGCGATA	CACCGCATCC	GGCGCGGATT	GGCCTGAAC
	3601	GCCAGCTGGC	GCAGGTAGCA	GAGCGGGTAA	ACTGGCTCGG	ATTAGGGCCG	CAAGAAAAC
60	3661	ATCCCGACCG	CCTTACTGCG	GCCTGTTTTG	ACCGCTGGGA	TCTGCCATTG	TCAGACATGT
	3721	ATACCCCGTA	CGTCTTCCCG	AGCGAAAACG	GTCCTGCGTG	CGGGACGCGC	GAATTGAATT
	3781	ATGGCCCA	CCAGTGGCGC	GGCGACTTCC	AGTTCAACAT	CAGCCGCTAC	AGTCAACAGC
	3841	AACTGATGGA	AACCAGCCAT	CGCCATCTGC	TGCACGCGGA	AGAAGGCACA	TGGCTGAATA
	3901	TCGACGGTTT	CCATATGGGG	ATTGGTGGCG	ACGACTCCTG	GAGCCCGTCA	GTATCGGCGG
65	3961	AATTACAGCT	GAGCGCCGGT	CGCTACCATT	ACCAGTTGGT	CTGGTGTC	AAATAATAAT
	4021	AACCGGGCAG	GCCATGTCTG	CCCGTATTTT	GCGTAAGGAA	ATCCATTATG	TACTATTTAA
	4081	AAAACACAAA	CTTTTGGATG	TTCGGTTTAT	TCTTTTCTTT	TTACTTTTTT	ATCATGGGAG
	4141	CCTACTTCCC	GTTTTTCCCG	ATTTGGCTAC	ATGACATCAA	CCATATCAGC	AAAAGTGATA
	4201	CGGTATATT	TTTGGCCGCT	ATTTCTCTGT	TCTCGCTATT	ATTCCAACCG	CTGTTTGGTC
70	4261	TGCTTTCTGA	CAAACTCGGC	CTCGACTCTA	GGCGGCCGCG	GGGATCCAGA	CATGATAAGA
	4321	TACATTGATG	AGTTTGGACA	AACCACAAC	AGAATGCAGT	GAAAAAATG	CTTTATTTGT
	4381	GAAATTTGTG	ATGCTATTGC	TTTATTTGTA	ACCATTATAA	GCTGCAATAA	ACAAGTTAAC
	4441	AACAACAATT	GATTTCATTT	TATGTTTCAG	GTTACGGGGG	AGGTGTGGGA	GGTTTTTTCG
	4501	GATCCTCTAG	AGTCGACCTG	CAGGCATGCA	AGCTTGGCGT	AATCATGGTC	ATAGCTGTTT
	4561	CCTGTGTGAA	ATTGTTATCC	GCTCACAAAT	CCACACAACA	TACGAGCCGG	AAGCATAAAG
	4621	TGTAAAGCCT	GGGGTGCCTA	ATGAGTGAGC	TAACCTACAT	TAATTGCGTT	GCGCTCACTG
	4681	CCCGCTTTCC	AGTCGGGAAA	CCTGTCTGTC	CAGCTGCATT	AATGAATCGG	CCAACGCGCG

4741 GGGAGAGGCG GTTTCGCTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC  
4801 TCGGTCGTTC GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT ACGGTTATCC  
4861 ACAGAATCAG GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG  
5 4921 AACCGTAAAA AGGCCGCGTT GCTGGCGTTT TTCCATAGGC TCCGCCCCC TGACGAGCAT  
4981 CACAAAAATC GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAG  
5041 GCGTTTCCCC CTGGAAGCTC CCTCGTGCGC TCTCCTGTTC CGACCCTGCC GCTTACCGGA  
5101 TACCTGTCCG CCTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCATAGCTC ACGCTGTAGG  
5161 TATCTCAGTT CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA ACCCCCCGTT  
10 5221 CAGCCCGACC GCTGCGCCTT ATCCGGTAAC TATCGTCTTG AGTCCAACCC GGTAAGACAC  
5281 GACTTATCGC CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC  
5341 GGTGCTACAG AGTTCCTGAA GTGGTGGCCT AACTACGGCT ACACTAGAAG GACAGTATTT  
5401 GGTATCTGCG CTCTGCTGAA GCCAGTTACC TTCGGAAAAA GAGTTGGTAG CTCTTGATCC  
5461 GGCAAACAAA CCACCGCTGG TAGCGGTGGT TTTTTTGTTC GCAAGCAGCA GATTACGCGC  
5521 AGAAAAAAG GATCTCAAGA AGATCCTTTG ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG  
15 5581 AACGAAACT CACGTTAAGG GATTTTGGTC ATGAGATTAT CAAAAGGAT CTTCACTTAG  
5641 ATCCTTTTAA ATTAATAATG AAGTTTTTAA TCAATCTAAA GTATATATGA GTAAACTTGG  
5701 TCTGACAGTT ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTCTG  
5761 TCATCCATAG TTGCCTGACT CCCCCTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA  
5821 TCTGCCCCA TGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCC AGATTTATCA  
20 5881 GCAATAAACC AGCCAGCCGG AAGGGCCGAG CGCAGAAGTG GTCCTGCAAC TTTATCCGCC  
5941 TCCATCCAGT CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC AGTTAATAGT  
6001 TTGCGCAACG TTTGTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTAGT  
6061 GCTTCATCTA GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC  
25 6121 AAAAAAGCGG TTAGCTCCTT CGGTCTCTCC ATCGTGTGTA GAAGTAAGTT GGCCGAGTGC  
6181 TTATCACTCA TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA  
6241 TGTCTTTCTG TGACTGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGCGCA  
6301 CCGAGTTGCT CTTGCCCGGC GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA  
6361 AAAGTGCTCA TCATTGAAA ACCTTCTTCG GGGCGAAAAC TCTCAAGGAT CTTACCGCTG  
6421 TTGAGATCCA GTTCGATGTA ACCCACTCGT GCACCCAACT GATCTTCAGC ATCTTTTACT  
30 6481 TTTACCGAGG TTTCTGGGTG AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA  
6541 AGGGCGACAC GGAATGTTG AATACTCATA CTCTTCTTTT TTCAATATTA TTGAAGCATT  
6601 TATCAGGGTT ATTGTCTCAT GAGCGGATAC ATATTGTAAT GTATTTAGAA AAATAAACAA  
6661 ATAGGGGTTT CGCGCACATT TCCCCGAAAA GTGCCACCTG ACGTCTAAGA AACCATTTAT  
6721 ATCATGACAT TAACCTATAA AAATAGCGGT ATCACGAGGC CCTTTCGTCT CGCGCGTTTC  
35 6781 GGTGATGACG GTGAAAACCT CTGACACATG CAGCTCCCGG AGACGGTCAC AGCTTGTCTG  
6841 TAAGCGGATG CCGGGAGCAG ACAAGCCCGT CAGGGCGCGT CAGCGGGTGT TGGCGGGTGT  
6901 CGGGGCTGGC TTAACCTATG GGCATCAGAG CAGATTGTAC TGAGAGTGCA CCATATGCGG  
6961 TGTGAAATAC CGCACAGATG CGTAAGGAGA AAATACCGCA TCAGGCGCCA TTCGCCATTC  
40 7021 AGGCTGCGCA ACTGTTGGGA AGGGCGATCG GTGCGGGCCT CTTGCTATT ACGCCAGCTG  
7081 GCGAAAGGGG GATGTGCTGC AAGGCGATTA AGTTGGGTAA CGCCAGGGTT TTCCAGTCA  
7141 CGACGTTGTA AAACGACGGC CAGT

SEQ ID NO: 57

Description of Artificial Sequence: vector pPqk-hygro-pA

45 1 AGATCTGATA TCATCGATGA ATTCTACCGG GTAGGGGAGG CGCTTTTCCC AAGGCAGTCT  
61 GGAGCATGCG CTTTAGCAGC CCCGCTGGGC ACTTGCGGCT ACACAAGTGG CCTCTGGCCT  
121 CGCACACATT CCACATCCAC CGGTAGGCGC CAACCGGCTC CGTTCTTTGG TGGCCCCCTC  
181 GCGCCACCTT CTACTCTCC CTAAGTCAAG AAGTTCCCCC CCGCCCCGCA GCTCGCGTGC  
241 TGCAGGACGT GACAAATGGA AGTACACGT CTCACTAGTC TCGTGCAGAT GGACAGCACC  
50 301 GCTGAGCAAT GGAAGCGGGT AGGCCTTTGG GGCAGCGGCC AATAGCAGCT TTGCTCCTTC  
361 GCTTCTTGGG CTGAGAGGCT GGAAGGGGT GGGTCCGGGG CCGGGCTCAG GGGCGGGCTC  
421 AGGGGCGGGG CCGGCGCCCG AAGGTCCTCC GGAGGCGCGG CATTTCTGCAC GCTTCAAAAG  
481 CGCAGCTGT CCGCGCTGTT CTCTCTTCC TCATCTCCGG GCCTTTCGAC CGATCCAGCC  
541 GCCACCATGA AAAAGCCTGA ACTCACCGCG ACGTCTGTCT AGAAGTTTCT GATCGAAAAG  
55 601 TTGACAGCG TCTCCGACCT GATGACGCTC TCGGAGGGCG AAGAATCTCG TGCTTTCAGC  
661 TTGATGTAG GAGGGCGTGT ATATGTCTCT CGGGTAAATA GCTGCGCCGA TGGTTTCTAC  
721 AAAGATCGTT ATGTTTATCG GCACTTTGCA TCGGCCGCGC TCCCATTCC GGAAGTGCTT  
781 GACATTGGGG AATTACGCGA GAGCCTGACC TATTGCATCT CCCGCCGTGC ACAGGGTGTG  
841 ACGTTGCAAG ACCTGCCTGA AACCGAAGTG CCCGCTGTTC TGCAGCCGGT CGCGGAGGCC  
60 901 ATGGATGCGA TCGCTGCGGC CGATCTTAGC CAGACGAGCG GGTTCGGCCC ATTCCGACCG  
961 CAAGGAATCG GTCAATACAC TACATGGCGT GATTTATAT GCGCGATTGC TGATCCCCAT  
1021 GTGTATCACT GGCAAACTGT GATGGACGAC ACCGTCAAGT CGTCCGTCGC GCAGGCTCTC  
1081 GATGAGCTGA TGCTTTGGGC CGAGGACTGC CCCGAAGTCC GGCACCTCGT GCACGCGGAT  
1141 TTCGGCTCCA ACAATGTCTT GACGGACAAT GGCCGCATAA CAGCGGTCTT TGAATGGAGC  
65 1201 GAGGCGATGT TCGGGGATTC CCAATACGAG GTCGCCAACA CTCTTCTCTG GAGGCCGTGG  
1261 TTGGCTTGTA TGGAGCAGCA GACGCGCTAC TTCGAGCGGA GGCATCCGGA GCTTGCAGGA  
1321 TCGCCGCGGC TCCGGGCGTA TATGCTCCGC ATTGGTCTTG ACCAACTCTA TCAGAGCTTG  
1381 GTTGACGGCA ATTTGATGTA TGCAGCTTGG GCGCAGGGTC GATGCGACGC AATCGTCCGA  
1441 TCCGGAGCCG GAGCTGTGCG GCGTACACAA ATCGCCCGCA GAAGCGCGGC CGTCTGGACC  
70 1501 GATGGCTGTG TAGAAGTACT CGCCGATAGT GGAAACCGAC GCGCCAGCAC TCGTCCGAGG  
1561 GCAAAGGAAT AGTCGAGAAA TTGATGATCT ATTAACAAT AAAGATGTCC ACTAAAATGG  
1621 AAGTTTTTCC TGTCATACTT TGTAAAGAAG GGTGAGAACA GAGTACCTAC ATTTTGAATG  
1681 GAAGGATTGG AGCTACGGGG GTGGGGGTGG GGTGGGATTA GATAAATGCC TGCTCTTTAC

1741 TGAAGGCTCT TTA CTATTGC TTTATGATAA TGTTTCATAG TTGGATATCA TAATTTAAAC  
1801 AAGCAAAACC AAATTAAGGG CCAGCTCATT CCTCCCCTC ATGATCTATA GATCTATAGA  
1861 TCTCTCGTGG GATCATTTGT TTTCTCTTGA TTCCCACTTT GTGGTTCTAA GTACTGTGGT  
1921 TTCCAAATGT GTCAGTTTCA TAGCCTGAAG AACGAGATCA GCAGCCTCTG TTCCACATAC  
5 1981 ACTTCATTCT CAGTATTGTT TTGCCAAGTT CTAATTCAT CAGAAGCTTC AGCTGCTCGA  
2041 GTTCTATAGT GTCACCTAAA TCGTATGTGT ATGATACATA AGGTTATGTA TTAATTGTAG  
2101 CCGCGTTCTA ACGACAATAT GTCCATATGG TGCACCTCA GTACAATCTG CTCTGATGCC  
2161 GCATAGTTAA GCCAGCCCCG ACACCCGCCA ACACCCGCTG ACGCGCCCTG ACGGGCTTGT  
10 2221 CTGCTCCCGG CATCCGCTTA CAGACAAGCT GTGACCGTCT CCGGGAGCTG CATGTGTCAG  
2281 AGGTTTTTAC CGTCATCACC GAAACGCGCG AGACGAAAGG GCCTCGTGAT ACGCCTATTT  
2341 TTATAGGTTA ATGTCATGAT AATAATGGTT TCTTAGACGT CAGGTGGCAC TTTTCGGGGA  
2401 AATGTGCGCG GAACCCCTAT TTGTTTATTT TTCTAAATAC ATTCAAATAT GTATCCGCTC  
2461 ATGAGACAAAT AACCCCTGATA AATGCTTCAA TAATATTGAA AAAGGAAGAG TATGAGTATT  
15 2521 CAACATTTCG GTGTCGCCCT TATTCCTTTT TTTGCGGCAT TTTGCCTTCC TGTTTTGTCT  
2581 CCGCCAGAAA CCGTGGTGAA AGTAAAGAT GCTGAAGATC AGTTGGGTGC ACGAGTGGGT  
2641 TACATCGAAC TGGATCTCAA CAGCGGTAAG ATCCTTGAGA GTTTTCGCCC CGAAGAACGT  
2701 TTTCCAATGA TGAGCACTTT TAAAGTTCTG CTATGTGGCG CGGTATTATC CCGTATTGAC  
2761 GCCGGGCAAG AGCAACTCGG TCGCCGCATA CACTATTCTC AGAATGACTT GGTGAGTAC  
2821 TTACAGATCA CAGAAAAGCA TCTTACGGAT GGCATGACAG TAAGAGAATT ATGCAGTGCT  
20 2881 GCCATAACCA TGAGTGATAA CACTGCGGCC AACTTACTTC TGACAACGAT CGGAGGACCG  
2941 AAGGAGCTAA CCGCTTTTTT GCACAACATG GGGGATCATG TAACTCGCCT TGATCGTTGG  
3001 GAACCGGAGC TGAATGAAGC CATACCAAAC GACGAGCGTG ACACCACGAT GCCTGTAGCA  
3061 ATGGCAACAA CGTTGCGCAA ACTATTAACT GGCGAACTAC TTACTCTAGC TTCCCGGCAA  
3121 CAATTAATAG ACTGGATGGA GCGGATAAA GTTGCAGGAC CACTTCTGCG CTCGCGCCTT  
25 3181 CCGGCTGGCT GGTTTATTGC TGATAAATCT GGAGCCGGTG AGCGTGGGTC TCGCGGTATC  
3241 ATTCAGACAT TGGGGCCAGA TGGTAAGCCC TCCCGTATCG TAGTTATCTA CACGACGGGG  
3301 AGTCAGGCAA CTATGGATGA ACGAAATAGA CAGATCGCTG AGATAGGTGC CTCACTGATT  
3361 AAGCATTTGGT AACTGTGAGA CCAAGTTTAC TCATATATAC TTTAGATTGA TTTAAAACCT  
3421 CATTTTTAAT TTTAAAAGAT CTAGGTGAAG ATCCTTTTTG ATAATCTCAT GACCAAAATC  
30 3481 CCTTAACGTG AGTTTTCGTT CCACTGAGCG TCAGACCCCG TAGAAAAGAT CAAAGGATCT  
3541 TCTTGAGATC CTTTTTTTCT GCGCGTAATC TGCTGCTTGC AAACAAAAAA ACCACCGCTA  
3601 CCAGCGGTGG TTTGTTTGCC GGATCAAGAG CTACCAACTC TTTTCCGAA GGTAACTGGC  
3661 TTCAGCAGAG CGCAGATACC AAATACTGTT CTTCTAGTGT AGCCGTAGTT AGGCCACCAC  
3721 TTCAAGAACT CTGTAGCACC GCCTACATAC CTCGCTCTGC TAATCCTGTT ACCAGTGGT  
35 3781 GCTGCCAGTG GCGATAAGTC GTGTCTTACC GGGTTGGACT CAAGACGATA GTTACCGGAT  
3841 AAGCGCAGAG GGTGCGGCTG AACGGGGGGT TCGTGACAC AGCCAGCTT GGAGCGAACG  
3901 ACCTACACCG AACTGAGATA CCTACAGCGT GAGCTATGAG AAAGCGCCAC GCTTCCCGAA  
3961 GGGAGAAAGC CGGACAGGTA TCCGGTAAGC GGCAGGGTCG GAACAGGAGA CCGCACGAGG  
40 4021 GAGCTTCCAG GGGGAAACGC CTGGTATCTT TATAGTCTTG TCGGGTTTCG CCACCTCTGA  
4081 CTTGAGCGTC GATTTTTGTG ATGCTCGTCA GGGGGGCGGA GCCTATGGAA AAACGCCAGC  
4141 AACCGCGCCT TTTTACGGTT CCTGGCCTTT TGCTGGCCTT TTGCTCATAT GTTCTTTCTT  
4201 GCGTTATCCC CTGATTCTGT GGATAACCGT ATTACCGCTT TTGAGTGAGC TGATACCGCT  
4261 CGCCGACGCC GAACGACCGA GCGCAGCGAG TCAGTGAGCG AGGAAGCGGA AGAGCGCCCA  
4321 ATACGCAAAC CGCCTCTCCC CGCGCGTTGG CCGATTCTAT AATGCAGGTT AACCTGGCTT  
45 4381 ATCGAAATTA ATACGACTCA CTATAGGGAG ACCGGC

SEQ ID NO: 58

Description of Artificial Sequence: amino acid sequence of caspase 3, apoptosis related cysteine protease [Mus musculus]

50 1 MENNKTSVDS KSINNFEVKT IHGSKSVDSG IYLDSSYKMD YPEMGICIII  
51 NNKNFHKSTG MSSRSGTDVD AANLRETFMG LKYQVRNKND LTREDILELM  
101 DSVSKEDHSK RSSFVCVILS HGDEGVIYGT NGPVELKKLT SFFRGDYCRS  
151 LTGKPKLFII QACRGTELDG GIETDSGTDE EMACQKIPVE ADFLYAYSTA  
201 PGYYSWRNSK DGSWFIQSLC SMLKLYAHKL EFMHILTRVN RKVATEFESF  
55 251 SLDSFTHAKK QIPCIVSMLT KELYFYH

SEQ ID NO: 59

Description of Artificial Sequence: amino acid sequence of caspase 3 preproprotein [Homo sapiens]

60 1 MENTENSVDK KSIKNLEPKI IHGSESMDSG ISLDNSYKMD YPEMGLCIII  
51 NNKNFHKSTG MTSRSGTDVD AANLRETFRN LKYEVRNKND LTREEIVELM  
101 RDVSKEDHSK RSSFVCVLLS HGEEGIIFGT NGPVDLKKIT NFFRGDRCRS  
151 LTGKPKLFII QACRGTELDG GIETDSGVDD DMACHKIPVE ADFLYAYSTA  
201 PGYYSWRNSK DGSWFIQSLC AMLKQYADKL EFMHILTRVN RKVATEFESF  
65 251 SFDATFTHAKK QIPCIVSMLT KELYFYH

SEQ ID NO: 60

Description of Artificial Sequence: amino acid sequence of caspase 7 [Mus musculus]

70 1 MTDDQDCAAE LEKVDSSSED GVDAPDRSS IISILLKKK RNASAGPVRT  
51 GRDRVPTYLY RMDFOKMGKC IINNKNFDK ATGMDVRNGT DKDAGALFKC  
101 FQNLGFVETV HNDCSCAKMQ DLLRKASEED HSNSACFACV LLSHGEEEDLI  
151 YGKDGVTPIK DLTAHFRGDR CKTLLEKPKL FFIQACRGTE LDDGIQADSG  
201 PINIDIDANPR NKIPVEADFL FAYSTVPGYY SWRNPKGGSW FVQALCSILN

251 EHGKDLEIMQ ILTRVNDRVA RHFESQSDDP RFNEKKQIPC MVSMLTKELY  
301 FSR

SEQ ID NO: 61

5 Description of Artificial Sequence: amino acid sequence of caspase 7 isoform delta [Homo sapiens]

1 MDCVGWPPGR KWHLEKNTSC GGSSGICASY VTQMADDQGC IEEQGVEDSA  
51 NEDSVDAKPD RSSFVPSLFS KKKKNVTMRS IKTTDRVPT YQYNMNFELK  
101 GKCIINNKN FDKVTGMGVR NGTDKDAEAL FKCFRSLGFD VIVYNDSCSA  
10 151 KMQDLLKKAS EEDHTNAACF ACILLSHGEE NVIYGKDGVT PIKDLTAHFR  
201 GDRCKTLLEK PKLFFIQACR GTELDDGIQA DSGPINDTDA NPKYKIPVEA  
251 DFLFAYSTVP GYYSWRSPGR GSWFVQALCS ILEEHGKDLE IMQILTRVND  
301 RVARHFESQS DDPHFHEKKQ IPCVVSMLTK ELYFSQ

15 SEQ ID NO: 62

Description of Artificial Sequence: amino acid sequence of caspase 6 [Mus musculus]

1 MTETDGFYKS REVFDPAEQY KMDHKRRGVA LIFNHERFFW HLTLPERRGT  
51 NADRNLTTR FSDLGFVEVK FNDLRAEELL LKIHVESTSS HIDADCFICV  
101 FLSHGEGNHV YAYDAKIEIQ TLTGLFKGDK CQSLVGKPKI FIIQACRGSQ  
20 151 HDVPVPLDV VDHQTDKLDN VTQVDAASVY TLPAGADFLM CYSVAEGYYS  
201 HRETVNGSWY IQDLCEMLAR YGSSLEFTEL LTLVNRKVSQ RRVDFCKDPP  
251 AIGKKQVPCF ASMLTKKLHF CPKPSK

SEQ ID NO: 63

25 Description of Artificial Sequence: amino acid sequence of caspase 6 isoform alpha preproprotein [Homo sapiens]

1 MSSASGLRRG HPAGGEENMT ETDAFYKREM FDPAEKYKMD HRRRGIALIF  
51 NHERFFWHLT LPERRGTCAD RDNLTTRFSD LGFEVKCFND LKAEELLKI  
101 HEVSTVSHAD ADCFVCVFLS HGEGNHIYAY DAKIEIQTLT GLFKGDKCHS  
30 151 LVGKPKIFII QACRGNQHDV PVIPLDVVDN QTEKLDTNIT EVDAAVSYYTL  
201 PAGADFLMCY SVAEGYYSR ETVNGSWYIQ DLCEMLGKYG SSLEFTELLT  
251 LVNRKVSQRR VDFCKDPSAI GKKQVPCFAS MLTKKLHFFP KSN

SEQ ID NO: 64

35 Description of Artificial Sequence: amino acid sequence of caspase 8 [Mus musculus]

1 MDFQSCLYAI AEELGSEDLA ALKFLCLDYI PHKKQETIED AQKLFLRLRE  
51 KGMLEEGNLS FLKELLFHS RWDLLVNFLD CNREEMVREL RDPDNAQISP  
101 YRVMLFKLSE EVSELELRSF KFLNNEIPK CKLEDDLSLL EIFVEMEKRT  
151 MLAENNLETL KSICDQVNKS LLGKIEDYER SSTERRMSLE GREELPPSVL  
40 201 DEMSLKMAEL CDSPREQDSE SRTSDKVYQM KNKPRGYCLI INNHDPSKAR  
251 EDITQLRKMK DRKGTDCDKE ALSKTFKELH FEIVSYDDCT ANEIHILEG  
301 YQSADHKNKD CFICILSHG DKGVVYGTGD KEASIIDLTS YFTGSKCPSL  
351 SGKPKIFFIQ ACQGSNFQKG VPDEAGFEQQ NHTLEVDSST HKNYIPDEAD  
401 FLLGMATVKN CVSYPDVPNG TWYIQLCQSL LRERCPQGDD ILSILTGVDY  
45 451 DVSNKDDRRN KGKQMPQPTF TLRKKLFFPP

SEQ ID NO: 65

Description of Artificial Sequence: amino acid sequence of caspase 8 isoform B precursor [Homo sapiens]

50 1 MDFSRNLYDI GEQLDSEDLA SLKFLSLDYI PQRKQEPKID ALMLFQRLQE  
51 KRMLEESNLS FLKELLFRIN RLDLLITYLN TRKEEMEREL QTPGRAQISA  
101 YRVMLYQISE EVSRSELRSF KFLNQEEISK CKLDDDMNLL DIFIEMEKRV  
151 ILGEGKLDIL KRVCAQINKS LLKIINDYEE FSKERSSSLE GSPDEFSNGE  
201 ELCGVMTISD SPREQDSESQ TLDKVYQMK KPRGYCLII NNNFAKAREK  
55 251 VPKLHSIRDR NGTHLDAGAL TTTFEELHFE IKPHDDCTVE QIYEILKIYQ  
301 LMDHSNMDCF ICCILSHGDK GIIYGTGDQE APIYELTSQF TGLKCPSLAG  
351 KPKVFFIIQAC QGDNYQKQIP VETDSEEQPY LEMDLSSPQT RYIPDEADFL  
401 LGMATVNNCV SYRNPAEGTW YIQSLCQSLR ERCPRGDDIL TILTEVNYEV  
60 451 SNKDDKKNMG KQMPQPTFTL RKKLVFPPSD

SEQ ID NO: 66

Description of Artificial Sequence: amino acid sequence of caspase 10 isoform d preproprotein [Homo sapiens]

65 1 MKSQGQHWYS SSDKNCKVSF REKLLIIDS N LGVQDVENLK FLCIGLVPNK  
51 KLEKSSASD VFEHLLAEDL LSEEDPFFLA ELLYIIRQKK LLQHLNCTKE  
101 EVERLLPTRQ RVSLFRNLLY ELSEGIDSEN LKDMIFLLKD SLPKTEMTSL  
151 SFLAFLEKQG KDEDNLCTCL EDLCKTVVPK LLRNIEKYKR EKAIQIVTPP  
201 VDKEAESYQG EEELVSQTDV KTFLEALPQE SWQNKHAGSN GNRATNGAPS  
251 LVSRGMQGAS ANTLNSETST KRAAVYRMNR NHRGLCVIVN NHTSFTSLKDR  
70 301 QGTHKDAEIL SHVFQWLGFV VHIHNNVTKV EMEMVLQKQK CNPAHADGDC  
351 FVFCILTHGR FGAVYSSDEA LIPIREIMSH FTALQCPRLA EKPKLFFIIQA  
401 CQGEIIPQSV SIEADALNPE QAPTSIQDSI PAEADFLGL ATVPGYVSFR  
451 HVEEGSWYIQ SLCNHLKKLV PRHEDILSIL TAVNDDVSRR VDKQGTQKQM

501 PQPAFTLRKK LVFPVPLDAL SL

**SEQ ID NO: 67**

**Description of Artificial Sequence: amino acid sequence of caspase 9 [Mus musculus]**

5 1 MDEADRQLLR RCRVRLVSEL QVAELWDALL SRELFTRDMI EDIQQAGSGS  
51 RRDQARQLVT DLETRGRQAL PLFISCLEDT GQGTLASLLQ SGRQAAKQDP  
101 EAVKPLDLHV PVVLGPMGLT AKEQRVVKLD PSQPAVGNLT PVVLGPEELW  
151 PARLKPEVLR PETPRPVDIG SSGAHDVCVP GKIRGHADMA YTLSDSPCGH  
201 CLIINNUNFC PSSGLGTRTG SNLDRDKLEH RFRWLRFMVE VKNDLTAKKM  
10 251 VTALMEMAHR NHRALDCFVV VILSHGCQAS HLQFPGAVYG TDGCSVSIEK  
301 IVNIFNGSGC PSLGGKPKLF FIQACGGEQK DHGFEVACTS SQGRTLDSDS  
351 EPDAVPYQEG PRPLDQLDAV SSLPTPSDIL VSYSTFPGFV SWRDKKSGSW  
401 YIETLDGILE QWARSEDLQS LLLRVANAVS AKGTYKQIPG CFNFLRKKLF  
451 FKTS

**SEQ ID NO: 68**

**Description of Artificial Sequence: amino acid sequence of caspase 9 isoform alpha preproprotein [Homo sapiens]**

20 1 MDEADRRLLR RCRLRLVEEL QVDQLWDALL SRELFPRHMI EDIQRAGSGS  
51 RRDQARQLII DLETRGSQAL PLFISCLEDT GQDMLASFLR TNRQAAKLSK  
101 PTLENLTPVV LRPEIRKPEV LRPETPRPVD IGSGGFGDVG ALESRLGNAD  
151 LAYILSMEPC GHCLIIINNVN FCRESGLRTR TGSNIDCEKL RRRFSSSLHFM  
201 VEVKGDLTAK KMVLLALLELA QQDHGALDCC VVVILSHGCQ ASHLQFPGAV  
25 251 YGTGDCPVSV EKIVNIFNGT SCPSLGGKPK LFFIQACGGE QKDHGFEVAS  
301 TSPEDESPGS NPEPDATPFQ EGLRTFDQLD AISSLPTPSD IFVSYSTFPG  
351 FVSWRDPKSG SWYVETLDDI FEQWAHSEDL QSLLLRVANA VSVKGIYKQM  
401 PGCNFLRKK LFFKTS

**SEQ ID NO: 69**

**Description of Artificial Sequence: amino acid sequence of caspase 2 [Mus musculus]**

30 1 MAAPSGRSQS SLHRKGLMAA DRRSRILAVC GMHPDHQETL KKNRVVLAKQ  
51 LLLSELLEHL LEKDIITLEM RELIQAKGGS FSQNVELLNL LPKRGPQAFD  
101 AFCEALRETR QGHLEDLLLT TSLDIQHVP LSCDYDTSL PFSVCESCPL  
151 HKQLRLSTDA TEHSLDNGDG PPCLLVKPCT PEFYQAHYQL AYRLQSQPRG  
35 201 LALVLSNVHF TGEKDLEFRS GGDVDHTTLV TLFKLLGYNV HVLHDQTAQE  
251 MQEKLQNFQA LPAHRVTDSC VVALLSHGVE GGIYGVGDKL LQLQEVFRLF  
301 DNANCPSLQN KPKMFFIQAC RGETDRGVD QQDGKNHTQS PGCEESDAGK  
351 EELMKMRLPT RSDMICGYAC LKGNAAMRNT KRGSWYIEAL TQVFSERACD  
40 401 MHVADMLVKV NALIKEREGY APGTEFHRCK EMSEYCSTLC QQLYLFPGYP  
451 PT

**SEQ ID NO: 70**

**Description of Artificial Sequence: amino acid sequence of caspase 2 isoform 1 preproprotein [Homo sapiens]**

45 1 MAAPSAGSWS TFQHKELMAA DRGRRILGVC GMHPHHQETL KKNRVVLAKQ  
51 LLLSELLEHL LEKDIITLEM RELIQAKVGS FSQNVELLNL LPKRGPQAFD  
101 AFCEALRETK QGHLEDMLLT TSLGLQHVP LSCDYDLSL PFPVCESCPL  
151 YKKLRLSTDT VEHSLDNKDG PVCLQVKPCT PEFYQTHFQL AYRLQSRPRG  
201 LALVLSNVHF TGEKELEFRS GGDVDHSTLV TLFKLLGYDV HVLCDQTAQE  
50 251 MQEKLQNFQA LPAHRVTDSC IVALLSHGVE GAIYGVGDKL LQLQEVFQLF  
301 DNANCPSLQN KPKMFFIQAC RGETDRGVD QQDGKNHAGS PGCEESDAGK  
351 EKLPMKRLPT RSDMICGYAC LKGTAAMRNT KRGSWYIEAL AQVFSERACD  
401 MHVADMLVKV NALIKDREGY APGTEFHRCK EMSEYCSTLC RHLYLFPGHP  
451 PT

**SEQ ID NO: 71**

**Description of Artificial Sequence: amino acid sequence of caspase 12 [Mus musculus]**

60 1 MAARRTHERD PIYKIKGLAK DMLDGVFDDL VEKNVLNGDE LLKIGESASF  
51 ILLNAENLVE NFLEKTMAG KIFAGHIANS QEQLSLQFSN DEDDGPQKIC  
101 TPSSPSESKE KVEDDEMEVN AGLAHESHLM LTAPHGLQSS EVQDTLKLCP  
151 RDQFCKIKTE RAKEIYPVME KEGRTLALI ICNKKFDYLF DRDNADTDIL  
201 NMQELLENLG YSVVLKENLT AQEMETELMQ FAGRPEHQSS DSTFLVFMSH  
251 GILEGICGVK HRNKKPDVLH DDTIFKIFNN SNCRSLRNKP KILIMQACRG  
301 RYNGTIWVST NKGIATADTD EERVLSCKWN NSITKAHVET DFIAFKSSTP  
65 351 HNISWKVGKT GSLFISKLV DCFKKYCWCYH LEEIFRKVQH SFEVPGELTQ  
401 MPTIERVSMT RYFYLFPGN

**SEQ ID NO: 72**

**Description of Artificial Sequence: amino acid sequence of mouse Estrogen receptor (ER) (Estradiol receptor) (ER-alpha)1-599**

70 1 MTMTLHTKAS GMALLHQIQG NELEPLNRQP LKMPMERALG EVYVDNSKPT  
51 VFNYPEGAA YEFNAAAAA AASAPVYGQS GIAYGPGSEA AAFSANSLSGA  
101 FPQLNSVSPS PELMLHPPQ LSPFLHPHQ QVPYYLENEP SAYAVRDTGP

5 151 PAFYRSNSDN RRQNGRERLS SSNEKGNMIM ESAKETRYCA VCNDYASGYH  
201 YGVWSCEGCK AFFKRSIQGH NDYMCPATNQ CTIDKNRRKS CQACRLRKCY  
251 EVGMMKGGIR KDRRGGRMLK HKRQRDDLEG RNEMGASGDM RAANLWPSPL  
301 VIKHTKKNSP ALSLTADQMV SALLDAEPPM IYSEYDPSRP FSEASMMGLL  
351 TNLADREL VH MINWAKRVPG FGDLNLHDQV HLLCAWLEI LMIGLVWRSM  
401 EHPGKLLFAP NLLLDNRNQG CVEGMVEIFD MLLATSSRFR MMNLQGEFV  
451 CLKSIILLNS GVTFLSSTL KSLEEKDHIH RVLDKITDTL IHLMAKAGLT  
501 LQQQHRRLAQ LLLILSHIRH MSNKGMEHLY NMCKKNVVPL YDLLLEMLDA  
10 551 HRLHAPASRM GVPPEEPSQT QLATTSSSTA HSLQTYIIPP EAEGFPNTI

**SEQ ID NO: 73**

**Description of Artificial Sequence: amino acid sequence of human Estrogen receptor (ER) (Estradiol receptor) (ER-alpha)1-595**

15 1 MTMTLHTKAS GMALLHQIQG NELEPLNRPO LKIPLERPLG EYVLDSSKPA  
51 VYNYPEGAA Y EFNAAAAANA QVYQGTGLPY GPGSEAAAFG SNGLGGFPPPL  
101 NSVSPSPML LHPPPQLSPF LQPHGQQVPY YLENEPSGYT VREAGPPAFY  
151 RPNSDNRRQG GRERLASTND KGSMAMESAK ETRYCAVCND YASGYHYGVW  
201 SCEGCKAFFK RSIQGHNDYM CPATNQCTID KNRRKSCQAC RLRKCYEVMG  
251 MKGGIRKDRR GGRMLKHKRQ RDDGEGRGEV GSAGDMRAAN LWPSPLMIKR  
20 301 SKKNSLALS L TADQMVSA L DAEPPILYSE YDPTRPFSEA SMMGLLTNLA  
351 DREL VHMINW AKRVPGFVDL TLHDQVHLL CAWLEILMIG LVWRSMEHPG  
401 KLLFAPNLLL DRNQKCEVG MVEIFDMLLA TSSRFRMMNL QGEFVCLKS  
451 ILLNSGVYT FLSTLKSLE EKDHHRVLD KITDTLIHLM AKAGLTQQQ  
501 HQRLAQLLLI LSHIRHMSNK GMEHLYSMKC KNVVPLYDLL LEMDLAHLRH  
25 551 APTSRGGASV EETDQSHLAT AGSTSSHSLQ KYYITGEAEG FPATV

**SEQ ID NO: 74**

**Description of Artificial Sequence: amino acid sequence of progesterone receptor B form - mouse 1-923**

30 1 MTELQAKDPQ VLHTSGASPS PPHIGSPLLA RLDSPGFQGS QHSDVSSVVS  
51 PIPISLDGLL FPRSCRGPPEL PDGKTGDQOS LSDVEGAFSG VEATHREGGR  
101 NSRPPEKDSR LLDVLDL SLL TSPGPEQSHA SPPACEAITS WCLFGPELPE  
151 DPRSVPATKG LLSPLMSRPE IKVGDQSGTG RGQKVLPKGL SPPRQLLLPT  
201 SSGAHWPAGG VKPSQPAAAG EVEEDSGLET EGSASPLLKS KPRALEGTGQ  
35 251 GGGVAANAPS AAPGGVTLVP KEDSRFSAPR VSLEQDSPIA PGRSPLATTV  
301 VDFIHVPILP LNHALLAART RQLLEGESYD GGATAGPFCEP PRSPSAPSTP  
351 VPRGDFPDCT YPLEGDPKED VFPLYGDFQT PGLKIKEEEE GADAAVRSPR  
401 PYLSAGASS TFPDFPLAPA PQAAPSSRPG EAAVAGGPSS AAVSPASSSG  
451 SALECILYKA EAPPTQGSFA PLPCKPPAAA SCLLPRDSL P AAPGTAAAPA  
40 501 IYQPLGLNGL PQLGYQAAVL KDSL PQVYYP YLNYLRPDSE ASQSPQYGF  
551 SLPQKICLIC GDEASGCHYG VLTGSGCKVF FKAMEGQHN YLCAGRNDI  
601 YLCAGRNDI ACRLRKCCQA GMVLGGRKFK KFNKVRVVRM LDGVALPQSV  
651 GLPNESQALS QRITFSPNQE IQLVPLINL LMSIEPDVIY AGHDNTKPD  
701 SSSLLTSLNQ LGERQLLSV KWSKSLPGFR NLHIDDQITL IQYSWMSLMV  
45 751 FGLGWSYKH VSGQMLYFAP DLILNEQRMK ELSFYSLCLT MWQIPQEFVK  
801 LQVTHEEFLC MKVLLLLNTI PLEGLRSQS FEEMRSSYIR ELIKAIGLRQ  
851 KGVVPTSQR F YQLTKLLDSL HDLVKQLHLY CLNTFIQSRT LAVEFPFEMMS  
901 EVIAAQLPKI LAGMVKPLLF HKK

**SEQ ID NO: 75**

**Description of Artificial Sequence: amino acid sequence of progesterone receptor form B - human 1-933**

55 1 MTELKAKGPR APHVAGGPPS PEVGSPLLCR PAAGPFPGSQ TSDTLPEVSA  
51 IPISLDGLLF PRPCQQQDPS DEKTQDQQL SDVEGAYSRA EATRAGAGSS  
101 SSPPEKDSGL LDSVLDTLA PSGPGSQSPS PPACEVTSSW CLFGPELPE  
151 PPAAPATQRV LSPMSRSGC KVGDSGGTAA AHKVLPRGLS PARQLLLPAS  
201 ESPHWSGAPV KPSQPAAAVE VEEEDSSESE ESAGPLLK GK PRALGGAAAG  
251 GGAAACPPGA AAGGVALVPK EDSRFSAPRV ALVEQDAPMA PGRSPLATTV  
301 MDFIHVPILP LNHALLAART RQLLEDES YD GGAGAASAF A PPRSSPCASS  
60 351 TPVAVGDFPD CAYPPDAEPK DDAYPLYSD F QPPALKIKEE EEGAEASARS  
401 PRSYLVAGAN PAAFPDFPLG PPPPLPPRAT PSRPGEA AVT AAPASASVSS  
451 ASSSGSTLEC ILYKAEGAPP QQGPFAPPPC KAPGASGCLL PRDGLPSTSA  
501 SAAAAGAAPA LYPALGLNGL PQLGYQAAVL KEGLPQVYYP YLNYLRPDSE  
551 ASQSPQYSFE SLPQKICLIC GDEASGCHYG VLTGSGCKVF FKAMEGQHN  
65 601 YLCAGRNDI YDKIRRNCP ACRLRKCCQA GMVLGGRKFK KFNKVRVVR A  
651 LDAVALPQPL GVPNESQALS QRITFSPGQD IQLIPPLINL LMSIEPDVIY  
701 AGHDNTKPD SSSLLTSLNQ LGERQLLSV KWSKSLPGFR NLHIDDQITL  
751 IQYSWMSLMV FGLGWSYKH VSGQMLYFAP DLILNEQRMK ESSFYSLCLT  
801 MWQIPQEFVK LQVSQEEFLC MKVLLLLNTI PLEGLRSQS FEEMRSSYIR  
70 851 ELIKAIGLRQ KGVVSSSRF YQLTKLLDNL HDLVKQLHLY CLNTFIQSRA  
901 LSVEFPFEMMS EVIAAQLPKI LAGMVKPLLF HKK

**SEQ ID NO: 76**

**Description of Artificial Sequence: amino acid sequence of mouse Glucocorticoid receptor (GR)**

1 MDSKESLAPP GRDEVPSLL GRGRGSVMDL YKTLRGGATV KVSASSPSVA  
5 51 AASQADSKQQ RILLDFSKGS ASNAQQQQQQ QQPQPDLSKA VSLSMGLYMG  
101 ETETKVMGND LGYPQQGQLG LSSGETDFRL LEESIANLNR STSRPENPKS  
151 STPAAGCATP TEKEFPQTHS DPSSEQQNRK SQPGTNGGSV KLYTTDQSTF  
201 DILQDLEFSA GSPGKETNES PWRSDLLIDE NLLSPLAGED DPFLLEGDVN  
251 EDCKPLILPD TKPKIQDTGD TILSSPSSVA LPQVKTEKDD FIELCTPGVI  
301 KQEKLGPIYC QASFSGTNII GNKMSAISVH GVSTSGGQMY HYDMNTASLS  
10 351 QQDQKPVFN VIPPIPVGSE NWNRCQSGE DNLTSLGAMN FAGRSVFSNG  
401 YSSPGMRPDV SSPSSSSTA TGPPPKLCLV CSDEASVCHY GVLTCGSCKV  
451 FFKRAVEGQH NYLCAGRND IIDKIRKNC PACRYRKCLQ AGMNLEARKT  
501 KKKIKGIQQA TAGVSQDTSE NANKTIVPAA LPQLTPTLV LLEVIEPEVL  
551 YAGYDSSVPD SAWRIMTTLN MLGGRQVIAA VKWAKAIPGF RNLHLDQDMT  
15 601 LLQYSWMLFM AFALGWSYR QASGNLLCFA PDLIINEQRM TPCMYDQCK  
651 HMLFISTELQ RLQVSYEYEL CMKTLTLLSS VPKEGLKSQE LFDEIRMTYI  
701 KELGKAIVKR EGNSSQNWR FYQLTKLLDS MHDVVENLLS YCFQTFLDKS  
751 MSIEFPEMLA EIITNQIPKY SNGNIKKLLF HQK

**SEQ ID NO: 77**

**Description of Artificial Sequence: amino acid sequence of human Glucocorticoid receptor (GR)**

1 MDSKESLTPG REENPSSVLA QERGDVMDFY KTLRGGATVK VSASSPSLAV  
51 ASQSDSKQRR LLVDFPKGSV SNAQQPDLSK AVSLSMGLYM GETETKVMGN  
25 101 DLGFPQQGQI SLSSGETDLK LLEESIANLN RSTSVPENPK SSASTAVSAA  
151 PTEKEFPKTH SDVSEQQHL KGQTGTNGGN VKLYTTDQST FDILQDLEFS  
201 SGSPGKETNE SPWRSDLLID ENCLLSPLAG EDDSFLLGN SNEDCKPLIL  
251 PDTKPKIKDN GDLVLSSPSN VTLPOVKTEK EDFIELCTPG VIKQEKLGTV  
301 YCQASFPGAN IIGNKMSAIS VHGVSTSGGQ MYHYDMNTAS LSQQDQDKPI  
30 351 FNVIPPIPVG SENWNRQGS GDNLTSLGT LNFPGRTVFS NGYSSPSMRP  
401 DVSSPPSSSS TATTGPPPKL CLVCSDEASG CHYGVLTCSG CKVFFKRAVE  
451 GQHNYLCAGR NDCIIDKIRR KNCPACRYRK CLQAGMNLEA RKTKKKIKGI  
501 QOATGVQSQE TSENPNGNTI VPATLPQLTP TLVSLLEVIE PEVLYAGYDS  
551 SVPDSTWRIM TFLNMLGGRQ VIAAVKWAKA IPGFRNLHLD DQMTLLQYSW  
35 601 MFLMAFALGW RSYRQSSANL LCFAPDLIIN EQRMTPCMY DQCKHMLYVS  
651 SELHRLQVSY EYLYCMKTL LSSVPKDLG KSQELFDEIR MTYIKELGKA  
701 IVKREGNSSQ NWQRFYQLTK LLDSMHVVVE NLLNYCFQTF LDKTMSIEFP  
751 EMLAEIITNQ IPKYSNGNIK KLLFHQK

**SEQ ID NO: 78**

**Description of Artificial Sequence: amino acid sequence of androgen receptor - mouse**

1 MEVQLGLGRV YRPPSKTYR GAFQNLFSQV REAIQNPGRP HPEAANIAPP  
51 GACLQQRQET SPRRRRRQQH TEDGSPQAH I RGPTGYLALE EEQQPSQQQA  
101 ASEGHPESSC LPEPGAATAP GKGLPQPPA PPDQDDSAAP STLTLGPTF  
45 151 PGLSSCSADI KDILNEAGTM QLLQQQQQQQ QHQQQHQHQ QQQEIVSEGS  
201 SARAREATGA PSSSKDSYLG GNSTISDAK ELCKAVSVSM GLGVEALEHL  
251 SPGEQLRGDC MYASLLGGPP AVRPTPCAPL PECKGLPLDE GPGKSTEETA  
301 EYSSFKGGYA KGLEGESLGC SGSSEAGSSG TLEIPSSLSL YKSGALDEAA  
351 AYQNRDYYNF PLALSGPPHP PPTTHPHARI KLENPLDYGS AAAAAAQCR  
50 401 YGDLGSLHGG SVAGPSTGSP PATTSSSWHT LFTAEEGLY GPGGGGGSSS  
451 PSDAGPVAPY GYTRPPQGLT SQESDYSASE VWYPGGVNR VPYPSPNCVK  
501 SEMGPWMENY SGPYGDMRLD STRDHVLPID YFFPPQKTCL ICGDEASGCH  
551 YGALTCGSCK VFFKRAAEGK QKYLCASTRND CTIDKFRKN CPSCLRKCXY  
601 EAGMTLGARK LKGLGNLKLQ EEGENSAGS PTEDPSQKMT VSHIEGYECQ  
55 651 PIFLNVLEAI EPGVVCAGHD NNQPDFAAL LSSLNELGER QLVHVVKWAK  
701 ALPGFRNLHV DDQMAVIQYS WMGLMVFAMG WRSFTNVNSR MLYFAPDLVF  
751 NEYRMHKS RM YSQVVRMRHL SQEFGWLQIT PQEFLCMKAL LLFSIIPVDG  
801 LKNQKFFDEL RMNYIKELDR IACKRKNP SCSRRFYQLT KLLDSVQPIA  
851 RELHQFTFDL LKSHMVSVD FPEMMAEII S VQVPKILSGK VKPIYFHTQ

**SEQ ID NO: 79**

**Description of Artificial Sequence: amino acid sequence of androgen receptor - human**

1 MEVQLGLGRV YRPPSKTYR GAFQNLFSQV REVIQNPGRP HPEAASAAPP  
51 GASLLLLQQQ QQQQQQQQQQ QQQQQQQQET SPRQQQQQQG EDGSPQAHRR  
65 101 GPTGYLVLDE EQQPSQPQSA LECHPERGCV PEPGAAVAAS KGLPQQLPAP  
151 PDEDDSAAPS TLLSLGPTFP GLSSCSADLK DILSEASTMQ LLQQQQQEAV  
201 SEGSSSGRAR EASGAPTSSK DNYLGGTSTI SDNAKELCKA VSVSMGLGVE  
251 ALEHLSPGEG LRGDCEMYAPL LGVPPAVRPT PCAPLAECKG SLLDSDAGKS  
301 TEDTAEYSPF KGGYTKLEG ESLGCSGSAA AGSSGTLELP STLSTLYKSGA  
70 351 LDEAAAYQSR DYYNFPLALA GPPPPPPPPH PHARIKLENP LDYGSAAAAA  
401 AAQCRYGLA SLHGAGAAGP GSGSPSAAAS SSWHTLFTA EGGLYGPGCGG  
451 GGGGGGGGGG GGGGGGGGGG GGEAGAVAPY GYTRPPQGLA QGESDFTAPD  
501 VWYPGGMVSR VPYPSPCTCVK SEMGPWMSY SGPYGDMRLE TARDHVLPID

551 YYFPPQKTCL ICGDEASGCH YGALTCGSCK VFFKRAAEGK QKYL CASRND  
601 CTIDKFRRKN CPSCRLRKCY EAGMTLGARK LKKLGNLKLQ EEGEASSTTS  
651 PTEETTQKLT VSHIEGYECQ PIFLNVLEAI EPGVVCAGHD NNQPD SFAAL  
701 LSSLNELGER QLVHVVKWAK ALPGFRNLHV DDQMAVIQYS WMGLMVFAMG  
5 751 WRSFTNVNSR MLYFAPDLVF NEYRMHKSRM YSQCVMRHL SQEFGWLQIT  
801 PQEFLCMKAL LLFSIIPVDG LKNQKFFDEL RMNYIKELDR IIACKRKNPT  
851 SCSRRFYQLT KLDSVQPIA RELHQFTFDL LIKSHMVSVD FPEMMAEIIIS  
901 VQVPKILSGK VKPIYFHTQ

10 **SEQ ID NO: 80**  
**Description of Artificial Sequence: amino acid sequence of ER(T2) human ER triple mutant LBD, 314 aa**  
1 SAGDMRAANL WPSPLMIKRS KKNSLALS LT ADQMVSA LLD AEPPILYSEY  
51 DPTRPFSEAS MMGLLTNLAD RELVHMINWA KRVPGFVDLT LHDQVH LLEC  
15 101 AWLEILMIGL VWRSM EHPVK LLFAPN LLLD RNQGKCVEGM VEIFDMLLAT  
151 SSRFRMMNLQ GEEFVCLKSI ILLNSGVYTF LSSTLKSLEE KDHIHRVLDK  
201 ITDTLIHLMA KAGLT LQQQH QRLAQL LLLI L SHIRHMSNKG MEHLYSMKCK  
251 NVVPLYD LLL EAADAHRLHA PTSRGGASVE ETDQSHLATA GSTSSHSLQK  
301 YYITGEAEGF PATA

20 **SEQ ID NO: 81**  
**Description of Artificial Sequence: amino acid sequence of influenza virus hemagglutinin epitope, 9 aa**  
1 YPYDVPDYA

25 **SEQ ID NO: 82**  
**Description of Artificial Sequence: amino acid sequence of myristoylation signal sequence, 13 aa**  
1 GSSKSKPKDPSQR