FIGURE 1A

cDNA sequence encoding human PLK1 [SEQ. ID No. 1]

```
atgagtgctg cagtgactgc agggaagctg gcacgggcac cggccgaccc tgggaaagcc    60
ggggtccccg gagttgcagc tcccggagct ccggcggcgg ctccaccggc gaaagagatc   120
ccggaggtcc tagtggaccc acgcagccgg cggcgctatg tgcgggccg cttttgggc    180
aagggcggct ttgccaagtg cttcgagatc tcggacgcgg acaccaagga ggtgttcgcg   240
ggcaagattg tgcctaagtc tctgctgctc aagccgcacc agagggagaa gatgtccatg   300
gaaatatcca ttcaccgcag cctcgcccac cagcacgtcg taggattcca cggcttttc    360
gaggacaacg acttcgtgtt cgtggtgttg gagctctgcc gccggaggtc tctcctggag   420
ctgcacaaga ggaggaaagc cctgactgag cctgaggccc gatactacct acggcaaatt   480
gtgcttggct gccagtacct gcaccgaaac cgagttattc atcgagacct caagctgggc   540
aacctttcc tgaatgaaga tctggaggtg aaaatagggg attttggact ggcaaccaaa    600
gtcgaatatg acggggagag gaagaagacc ctgtgtggga ctcctaatta catagctccc   660
gaggtgctga gcaagaaagg gcacagtttc gaggtggatg tgtggtccat tgggtgtatc   720
atgtatacct tgttagtggg caaaccacct tttgagactt cttgcctaaa agagacctac   780
ctccggatca agaagaatga atacagtatt cccaagcaca tcaaccccgt ggccgcctcc   840
ctcatccaga agatgcttca gacagatccc actgcccgcc caaccattaa cgagctgctt   900
aatgacgagt tctttacttc tggctatatc cctgcccgtc tccccatcac ctgcctgacc   960
attccaccaa ggttttcgat tgctcccagc agcctggacc ccagcaaccg gaagcccctc  1020
acagtcctca ataaaggctt ggagaacccc ctgcctgagc gtccccggga aaaagaagaa  1080
ccagtggttc gagagacagg tgaggtggtc gactgccacc tcagtgacat gctgcagcag  1140
ctgcacagtg tcaatgcctc caagccctcg gagcgtgggc tggtcaggca agaggaggct  1200
gaggatcctg cctgcatccc catcttctgg gtcagcaagt gggtggacta ttcggacaag  1260
tacggccttg ggtatcagct ctgtgataac agcgtggggg tgctcttcaa tgactcaaca  1320
cgcctcatcc tctacaatga tggtgacagc ctgcagtaca tagagcgtga cggcactgag  1380
tcctacctca ccgtgagttc ccatcccaac tccttgatga agaagatcac cctccttaaa  1440
tatttccgca attacatgag cgagcacttg ctgaaggcag gtgccaacat cacgccgcgc  1500
gaaggtgatg agctcgcccg gctgccctac ctacggacct ggttccgcac ccgcagcgcc  1560
atcatcctgc acctcagcaa cggcagcgtg cagatcaact tcttccagga tcacaccaag  1620
ctcatcttgt gcccactgat ggcagccgtg acctacatcg acgagaagcg ggacttccgc  1680
acataccgcc tgagtctcct ggaggagtac ggctgctgca aggagctggc cagccggctc  1740
cgctacgccc gcactatggt ggacaagctg ctgagctcac gctcggccag caaccgtctc  1800
aaggcctcc                                                          1809
```

DNA sequence encoding PCR Primer[SEQ. ID No. 2]

```
agtgctgcag tgactgcagg gaagctg                                        27
```

DNA sequence encoding PCR Primer[SEQ. ID No. 3]

```
ttaggaggcc ttgagacggt tgctggccg                                      29
```

DNA sequence encoding PCR Primer[SEQ. ID No. 4]

```
aaatctagag ccaccatgga ctacaaggac gacgatgaca agagtgctgc agtgactgca    60
gggaagctg                                                            69
```

FIGURE 1B

DNA sequence encoding PCR Primer[SEQ. ID No. 5]

```
tggcaactag aaggcacagt cgaggct                                          27
```

Protein sequence encoding FLAG-tagged PLK1 [SEQ. ID No. 6]

```
Met Asp Tyr Lys Asp Asp Asp Asp Lys Ser Ala Ala Val Thr Ala Gly
                 5                  10                  15
Lys Leu Ala Arg Ala Pro Ala Asp Pro Gly Lys Ala Gly Val Pro Gly
            20                  25                  30
Val Ala Ala Pro Gly Ala Pro Ala Ala Ala Pro Pro Ala Lys Glu Ile
        35                  40                  45
Pro Glu Val Leu Val Asp Pro Arg Ser Arg Arg Arg Tyr Val Arg Gly
    50                  55                  60
Arg Phe Leu Gly Lys Gly Gly Phe Ala Lys Cys Phe Glu Ile Ser Asp
65                  70                  75                  80
Ala Asp Thr Lys Glu Val Phe Ala Gly Lys Ile Val Pro Lys Ser Leu
                85                  90                  95
Leu Leu Lys Pro His Gln Arg Glu Lys Met Ser Met Glu Ile Ser Ile
            100                 105                 110
His Arg Ser Leu Ala His Gln His Val Val Gly Phe His Gly Phe Phe
        115                 120                 125
Glu Asp Asn Asp Phe Val Phe Val Val Leu Glu Leu Cys Arg Arg Arg
    130                 135                 140
Ser Leu Leu Glu Leu His Lys Arg Arg Lys Ala Leu Thr Glu Pro Glu
145                 150                 155                 160
Ala Arg Tyr Tyr Leu Arg Gln Ile Val Leu Gly Cys Gln Tyr Leu His
                165                 170                 175
Arg Asn Arg Val Ile His Arg Asp Leu Lys Leu Gly Asn Leu Phe Leu
            180                 185                 190
Asn Glu Asp Leu Glu Val Lys Ile Gly Asp Phe Gly Leu Ala Thr Lys
        195                 200                 205
Val Glu Tyr Asp Gly Glu Arg Lys Lys Thr Leu Cys Gly Thr Pro Asn
    210                 215                 220
Tyr Ile Ala Pro Glu Val Leu Ser Lys Lys Gly His Ser Phe Glu Val
225                 230                 235                 240
Asp Val Trp Ser Ile Gly Cys Ile Met Tyr Thr Leu Leu Val Gly Lys
                245                 250                 255
Pro Pro Phe Glu Thr Ser Cys Leu Lys Glu Thr Tyr Leu Arg Ile Lys
            260                 265                 270
Lys Asn Glu Tyr Ser Ile Pro Lys His Ile Asn Pro Val Ala Ala Ser
        275                 280                 285
Leu Ile Gln Lys Met Leu Gln Thr Asp Pro Thr Ala Arg Pro Thr Ile
    290                 295                 300
Asn Glu Leu Leu Asn Asp Glu Phe Phe Thr Ser Gly Tyr Ile Pro Ala
305                 310                 315                 320
Arg Leu Pro Ile Thr Cys Leu Thr Ile Pro Pro Arg Phe Ser Ile Ala
                325                 330                 335
```

FIGURE 1C

```
Pro Ser Ser Leu Asp Pro Ser Asn Arg Lys Pro Leu Thr Val Leu Asn
            340                 345                 350
Lys Gly Leu Glu Asn Pro Leu Pro Glu Arg Pro Arg Glu Lys Glu Glu
        355                 360                 365
Pro Val Val Arg Glu Thr Gly Glu Val Val Asp Cys His Leu Ser Asp
    370                 375                 380
Met Leu Gln Gln Leu His Ser Val Asn Ala Ser Lys Pro Ser Glu Arg
385                 390                 395                 400
Gly Leu Val Arg Gln Glu Glu Ala Glu Asp Pro Ala Cys Ile Pro Ile
                405                 410                 415
Phe Trp Val Ser Lys Trp Val Asp Tyr Ser Asp Lys Tyr Gly Leu Gly
            420                 425                 430
Tyr Gln Leu Cys Asp Asn Ser Val Gly Val Leu Phe Asn Asp Ser Thr
        435                 440                 445
Arg Leu Ile Leu Tyr Asn Asp Gly Asp Ser Leu Gln Tyr Ile Glu Arg
    450                 455                 460
Asp Gly Thr Glu Ser Tyr Leu Thr Val Ser Ser His Pro Asn Ser Leu
465                 470                 475                 480
Met Lys Lys Ile Thr Leu Leu Lys Tyr Phe Arg Asn Tyr Met Ser Glu
                485                 490                 495
His Leu Leu Lys Ala Gly Ala Asn Ile Thr Pro Arg Glu Gly Asp Glu
            500                 505                 510
Leu Ala Arg Leu Pro Tyr Leu Arg Thr Trp Phe Arg Thr Arg Ser Ala
        515                 520                 525
Ile Ile Leu His Leu Ser Asn Gly Ser Val Gln Ile Asn Phe Phe Gln
    530                 535                 540
Asp His Thr Lys Leu Ile Leu Cys Pro Leu Met Ala Ala Val Thr Tyr
545                 550                 555                 560
Ile Asp Glu Lys Arg Asp Phe Arg Thr Tyr Arg Leu Ser Leu Leu Glu
                565                 570                 575
Glu Tyr Gly Cys Cys Lys Glu Leu Ala Ser Arg Leu Arg Tyr Ala Arg
            580                 585                 590
Thr Met Val Asp Lys Leu Leu Ser Ser Arg Ser Ala Ser Asn Arg Leu
        595                 600                 605
Lys Ala Ser
    610
```