SEQUENCE LISTING

<110> INCYTE CORPORATION

<120> CYCLIN-DEPENDENT KINASE 2 BIOMARKERS AND USES THEREOF

<130> 20443-0588WO1

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<150> 62/806,265
<151> 2019-02-15

<160> 8

<170> PatentIn version 3.5

<210> 1
<211> 156
<212> PRT
<213> Homo sapiens

<400> 1

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Met Glu Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
1               5                   10                  15


Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
            20                  25                  30


Glu Ala Gly Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
        35                  40                  45


Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
    50                  55                  60


Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg
65                  70                  75                  80


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


Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg
            100                 105                 110
```

```
Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg
        115                 120                 125


Tyr Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg
    130                 135                 140


Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
145                 150                 155


<210> 2
<211> 410
<212> PRT
<213> Homo sapiens

<400> 2
Met Pro Arg Glu Arg Arg Glu Arg Asp Ala Lys Glu Arg Asp Thr Met
1               5                   10                  15


Lys Glu Asp Gly Gly Ala Glu Phe Ser Ala Arg Ser Arg Lys Arg Lys
            20                  25                  30


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


Ile Asp Arg Thr Ala Arg Asp Gln Cys Gly Ser Gln Pro Trp Asp Asn
    50                  55                  60


Asn Ala Val Cys Ala Asp Pro Cys Ser Leu Ile Pro Thr Pro Asp Lys
65                  70                  75                  80


Glu Asp Asp Asp Arg Val Tyr Pro Asn Ser Thr Cys Lys Pro Arg Ile
                85                  90                  95


Ile Ala Pro Ser Arg Gly Ser Pro Leu Pro Val Leu Ser Trp Ala Asn
            100                 105                 110


Arg Glu Glu Val Trp Lys Ile Met Leu Asn Lys Glu Lys Thr Tyr Leu
        115                 120                 125
```

```
Arg Asp Gln His Phe Leu Glu Gln His Pro Leu Leu Gln Pro Lys Met
    130                 135                 140

Arg Ala Ile Leu Leu Asp Trp Leu Met Glu Val Cys Glu Val Tyr Lys
145                 150                 155                 160

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

Met Ala Thr Gln Glu Asn Val Val Lys Thr Leu Leu Gln Leu Ile Gly
            180                 185                 190

Ile Ser Ser Leu Phe Ile Ala Ala Lys Leu Glu Glu Ile Tyr Pro Pro
        195                 200                 205

Lys Leu His Gln Phe Ala Tyr Val Thr Asp Gly Ala Cys Ser Gly Asp
    210                 215                 220

Glu Ile Leu Thr Met Glu Leu Met Ile Met Lys Ala Leu Lys Trp Arg
225                 230                 235                 240

Leu Ser Pro Leu Thr Ile Val Ser Trp Leu Asn Val Tyr Met Gln Val
                245                 250                 255

Ala Tyr Leu Asn Asp Leu His Glu Val Leu Leu Pro Gln Tyr Pro Gln
            260                 265                 270

Gln Ile Phe Ile Gln Ile Ala Glu Leu Leu Asp Leu Cys Val Leu Asp
        275                 280                 285

Val Asp Cys Leu Glu Phe Pro Tyr Gly Ile Leu Ala Ala Ser Ala Leu
    290                 295                 300

Tyr His Phe Ser Ser Ser Glu Leu Met Gln Lys Val Ser Gly Tyr Gln
305                 310                 315                 320
```

```
Trp Cys Asp Ile Glu Asn Cys Val Lys Trp Met Val Pro Phe Ala Met
                325                 330                 335

Val Ile Arg Glu Thr Gly Ser Ser Lys Leu Lys His Phe Arg Gly Val
            340                 345                 350

Ala Asp Glu Asp Ala His Asn Ile Gln Thr His Arg Asp Ser Leu Asp
        355                 360                 365

Leu Leu Asp Lys Ala Arg Ala Lys Lys Ala Met Leu Ser Glu Gln Asn
    370                 375                 380

Arg Ala Ser Pro Leu Pro Ser Gly Leu Leu Thr Pro Pro Gln Ser Gly
385                 390                 395                 400

Lys Lys Gln Ser Ser Gly Pro Glu Met Ala
                405                 410
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<210> 3
<211> 928
<212> PRT
<213> Homo sapiens

<400> 3

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Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala
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Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu Glu Asp
            20                  25                  30

Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu
        35                  40                  45

Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu
    50                  55                  60

Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
65                  70                  75                  80
```

```
Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys
                85                  90                  95

Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu
            100                 105                 110

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

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

Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
145                 150                 155                 160

Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln
                165                 170                 175

Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
            180                 185                 190

Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met
        195                 200                 205

Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp
    210                 215                 220

Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys
225                 230                 235                 240

Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly
                245                 250                 255

Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg
            260                 265                 270

Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val
        275                 280                 285
```

```
Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly
    290                 295                 300

Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg
305                 310                 315                 320

Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe
                325                 330                 335

Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu
            340                 345                 350

Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val
        355                 360                 365

Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln
    370                 375                 380

Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu
385                 390                 395                 400

Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu
                405                 410                 415

Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys
            420                 425                 430

Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu
        435                 440                 445

Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu
    450                 455                 460

Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn
465                 470                 475                 480
```

```
Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala
                485                 490                 495

Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu
            500                 505                 510

Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe
        515                 520                 525

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

Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser
545                 550                 555                 560

Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser
                565                 570                 575

Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu
            580                 585                 590

Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser
        595                 600                 605

Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser
    610                 615                 620

Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys
625                 630                 635                 640

Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg
                645                 650                 655

Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu
            660                 665                 670

His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu
        675                 680                 685
```

```
Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met
    690                 695                 700

Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys
705                 710                 715                 720

Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln
                725                 730                 735

Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile
            740                 745                 750

Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile
        755                 760                 765

Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His
    770                 775                 780

Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro
785                 790                 795                 800

Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser
                805                 810                 815

Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu
            820                 825                 830

Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile
        835                 840                 845

Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu
    850                 855                 860

Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu
865                 870                 875                 880
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Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys
885 890 895

Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln
900 905 910

Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
915 920 925

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<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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cggagttgtg tacaaagcca gaaacaagtt gacgggagag gtggtggcgc ttaagaaaat 120

ccgcctggac actgagactg agggtgtgcc cagtactgcc atccgagaga tctctctgct 180

taaggagctt aaccatccta atattgtcaa gctgctggat gtcattcaca cagaaaataa 240

actctacctg gtttttgaat ttctgcacca agatctcaag aaattcatgg atgcctctgc 300

tctcactggc attcctcttc ccctcatcaa gagctatctg ttccagctgc tccagggcct 360

agctttctgc cattctcatc gggtcctcca ccgagacctt aaacctcaga atctgcttat 420

taacacagag ggggccatca agctagcaga ctttggacta gccagagctt ttggagtacc 480

tgttcgtact tacacccatg aagtggtgac cctgtggtac cgagctcctg aaatcctcct 540

gggctgcaaa tattattcca cagctgtgga catctggagc ctgggctgca tctttgctga 600

gatggtgact cgccgggccc tattccctgg agattctgag attgaccagc tctttcggat 660

ctttcggact ctggggaccc cagatgaggt ggtgtggcca ggagttactt ctatgcctga 720

ttacaagcca agtttcccca agtgggcccg gcaagatttt agtaaagttg tacctcccct 780

ggatgaagat ggacggagct tgttatcgca aatgctgcac tacgacccta acaagcggat 840

ttcggccaag gcagccctgg ctcacccttt cttccaggat gtgaccaagc cagtacccca 900

tcttcgactc ggagtgcagg tggaaaccat ctccccagga gacgggcgca ccttccccaa 960

gcgcggccag acctgcgtgg tgcactacac cgggatgctt gaagatggaa agaaagttga 1020

ttcctcccgg gacagaaaca agcccttaa gtttatgcta ggcaagcagg aggtgatccg 1080

aggctgggaa gaaggggttg cccagatgag tgtgggtcag agagccaaac tgactatatc 1140

tccagattat gcctatggtg ccactgggca cccaggcatc atcccaccac atgccactct 1200

cgtcttcgat gtggagcttc taaaactgga aggataccct tacgacgttc ctgattacgc 1260

ttacccttac gacgttcctg attacgctgg atcctaattc gaaagc 1306

<210> 5
<211> 6
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<213> Artificial Sequence

<220>
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gaattc 6

<210> 6
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 6
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<210> 7
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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<400> 7
ttcgaa 6

<210> 8
<211> 18
<212> DNA
<213> Homo sapiens

<400> 8
aagcagagat ctctcgga 18