SEQUENCE LISTING

<110> CNRS
Université de la Méditerranée-Aix Marseille II

<120> Regulation of Glypican 4 activity to modulate the fate of stem cells and uses thereof

<130> BET11P2178

<150> EP 10305836.8
<151> 2010-07-29

<160> 9

<170> PatentIn version 3.5

<210> 1
<211> 556
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> (1)..(18)

<220>
<221> SITE
<222> (16)..(19)
<223> Glycosaminoglycan attachment site

<220>
<221> SITE
<222> (358)..(361)
<223> Glycosaminoglycan attachment site

<220>
<221> SITE
<222> (361)..(364)
<223> Glycosaminoglycan attachment site

<220>
<221> SITE
<222> (491)..(496)
<223> Glycosaminoglycan attachment site

<220>
<221> SITE
<222> (496)..(500)
<223> Glycosaminoglycan attachment site

<220>
<221> SITE
<222> (521)..(524)
<223> Glycosaminoglycan attachment site

<220>
<221> SITE
<222> (528)..(531)
<223> Glycosaminoglycan attachment site

<220>
<221> PROPEP
<222> (530)..(556)

<400> 1

```
Met Ala Arg Phe Gly Leu Pro Ala Leu Leu Cys Thr Leu Ala Val Leu
1               5                  10                  15

Ser Ala Ala Leu Leu Ala Ala Glu Leu Lys Ser Lys Ser Cys Ser Glu
            20                  25                  30

Val Arg Arg Leu Tyr Val Ser Lys Gly Phe Asn Lys Asn Asp Ala Pro
        35                  40                  45

Leu His Glu Ile Asn Gly Asp His Leu Lys Ile Cys Pro Gln Gly Ser
    50                  55                  60

Thr Cys Cys Ser Gln Glu Met Glu Glu Lys Tyr Ser Leu Gln Ser Lys
65                  70                  75                  80

Asp Asp Phe Lys Ser Val Val Ser Glu Gln Cys Asn His Leu Gln Ala
                85                  90                  95

Val Phe Ala Ser Arg Tyr Lys Lys Phe Asp Glu Phe Phe Lys Glu Leu
            100                 105                 110

Leu Glu Asn Ala Glu Lys Ser Leu Asn Asp Met Phe Val Lys Thr Tyr
        115                 120                 125

Gly His Leu Tyr Met Gln Asn Ser Glu Leu Phe Lys Asp Leu Phe Val
    130                 135                 140

Glu Leu Lys Arg Tyr Tyr Val Val Gly Asn Val Asn Leu Glu Glu Met
145                 150                 155                 160

Leu Asn Asp Phe Trp Ala Arg Leu Leu Glu Arg Met Phe Arg Leu Val
                165                 170                 175

Asn Ser Gln Tyr His Phe Thr Asp Glu Tyr Leu Glu Cys Val Ser Lys
            180                 185                 190

Tyr Thr Glu Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys
        195                 200                 205

Leu Gln Val Thr Arg Ala Phe Val Ala Ala Arg Thr Phe Ala Gln Gly
    210                 215                 220

Leu Ala Val Ala Gly Asp Val Val Ser Lys Val Ser Val Val Asn Pro
225                 230                 235                 240

Thr Ala Gln Cys Thr His Ala Leu Leu Lys Met Ile Tyr Cys Ser His
                245                 250                 255

Cys Arg Gly Leu Val Thr Val Lys Pro Cys Tyr Asn Tyr Cys Ser Asn
            260                 265                 270
```

```
Ile Met Arg Gly Cys Leu Ala Asn Gln Gly Asp Leu Asp Phe Glu Trp
        275                 280                 285

Asn Asn Phe Ile Asp Ala Met Leu Met Val Ala Glu Arg Leu Glu Gly
    290                 295                 300

Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile Asp Val Lys Ile Ser
305                 310                 315                 320

Asp Ala Ile Met Asn Met Gln Asp Asn Ser Val Gln Val Ser Gln Lys
                325                 330                 335

Val Phe Gln Gly Cys Gly Pro Pro Lys Pro Leu Pro Ala Gly Arg Ile
            340                 345                 350

Ser Arg Ser Ile Ser Glu Ser Ala Phe Ser Ala Arg Phe Arg Pro His
        355                 360                 365

His Pro Glu Glu Arg Pro Thr Thr Ala Ala Gly Thr Ser Leu Asp Arg
    370                 375                 380

Leu Val Thr Asp Val Lys Glu Lys Leu Lys Gln Ala Lys Lys Phe Trp
385                 390                 395                 400

Ser Ser Leu Pro Ser Asn Val Cys Asn Asp Glu Arg Met Ala Ala Gly
                405                 410                 415

Asn Gly Asn Glu Asp Asp Cys Trp Asn Gly Lys Gly Lys Ser Arg Tyr
            420                 425                 430

Leu Phe Ala Val Thr Gly Asn Gly Leu Ala Asn Gln Gly Asn Asn Pro
        435                 440                 445

Glu Val Gln Val Asp Thr Ser Lys Pro Asp Ile Leu Ile Leu Arg Gln
    450                 455                 460

Ile Met Ala Leu Arg Val Met Thr Ser Lys Met Lys Asn Ala Tyr Asn
465                 470                 475                 480

Gly Asn Asp Val Asp Phe Phe Asp Ile Ser Asp Glu Ser Ser Gly Glu
                485                 490                 495

Gly Ser Gly Ser Gly Cys Glu Tyr Gln Gln Cys Pro Ser Glu Phe Asp
            500                 505                 510

Tyr Asn Ala Thr Asp His Ala Gly Lys Ser Ala Asn Glu Lys Ala Asp
        515                 520                 525

Ser Ala Gly Val Arg Pro Gly Ala Gln Ala Tyr Leu Leu Thr Val Phe
    530                 535                 540
```

Cys Ile Leu Phe Leu Val Met Gln Arg Glu Trp Arg
545 550 555

<210> 2
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> shRNA

<400> 2
ccgggccact ggtttaagca atgttctcga gaacattgct taaaccagtg gctttttg 58

<210> 3
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> shRNA

<400> 3
ccgggcatcc cgttacaaga agtttctcga gaaacttctt gtaacgggat gctttttg 58

<210> 4
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> shRNA

<400> 4
ccgggcagag aaatccctga atgatctcga gatcattcag ggatttctct gctttttg 58

<210> 5
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> shRNA

<400> 5
ccggccttca gagtttgact acaatctcga gattgtagtc aaactctgaa ggttttttg 59

<210> 6
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> shRNA

<400> 6
ccgggcctgc aaagtaaaga tgattctcga gaatcatctt tactttgcag gctttttg 59

<210> 7
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> shRNA

<400> 7
ccgggcaaat tgaagctcca ggttactcga gtaacctgga gcttcaattt gctttttg 59

<210> 8
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> shRNA

<400> 8
ccgggctatt atgaacatgc aggatctcga gatcctgcat gttcataata gctttttg 59

<210> 9
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> shRNA

<400> 9
ccgggcttca cgttacaaga agtttctcga gaaacttctt gtaacgtgaa gctttttg 59