

SEQUENCE LISTING

<110> National University of Ireland, Galway

<120> Markers, antibodies and recombinant scFvs for Mesenchymal Stem Cell sub-populations and osteoclasts

<130> PQ008PCT

<160> 18

<170> PatentIn version 3.3

<210> 1

<211> 10

<212> PRT

<213> artificial

<220>

<223> TMSC3 limbin target epitope

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Glu Asp Leu Val Glu Lys Val Arg Gly Glu
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<210> 2

<211> 30

<212> DNA

<213> artificial

<220>

<223> limbin target epitope

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<212> PRT

<213> artificial

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<223> TMSC3

<400> 3

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Glu Ile Thr Cys Ser Gly Gly Ser Gly Ser Tyr Gly Trp Phe Gln Gln
20 25 30

Lys Ser Pro Gly Ser Ala Pro Val Thr Val Ile Tyr Glu Ser Asn Lys
35 40 45

Arg Pro Ser Asp Ile Pro Ser Arg Phe Ser Gly Ser Lys Ser Gly Ser
50 55 60

Thr Gly Thr Leu Thr Ile Thr Gly Val Gln Ala Glu Asp Glu Ala Val
65 70 75 80

Tyr Phe Cys Gly Ser Arg Asp Ser Ser Gly Ser Ala Tyr Ala Phe Ala
85 90 95

Thr Gly Thr Thr Leu Thr Val Leu Gly Gln Ser Ser Arg Ser Ser Thr
100 105 110

Val Thr Leu Asp Glu Ser Gly Gly Gly Leu Gln Ala Pro Gly Gly Ala
115 120 125

Leu Ser Leu Val Cys Lys Ala Ser Gly Phe Thr Phe Ser Ser Tyr Cys
130 135 140

Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Phe Val Ala
145 150 155 160

Gly Ile Asp Asp Asp Gly Ser Trp Thr Ala Tyr Gly Ala Ala Val Lys
165 170 175

Gly Arg Ala Thr Ile Leu Arg Asp Asn Gly Gln Ser Thr Val Arg Leu
180 185 190

Gln Leu Asn Asn Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
195 200 205

Lys Thr Ala Gly Gly Ser Tyr Tyr Gly Cys Glu Asn Ile Asp Ala Trp
210 215 220

Gly His Gly Thr Glu Val Ile Val Ser Ser Thr Ser Gly Gln Ala Gly
225 230 235 240

Gln His His His His His His Gly Ala Tyr Pro Tyr Asp Val Pro Asp
245 250 255

Tyr Ala Ser

<210> 4
<211> 777
<212> DNA
<213> artificial

<220>
<223> TMSC3

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actgtgattt atgaaagcaa caagagaccc tcggacatcc cttcacgatt ctccggttcc 180
aaatccggct ccacgggcac attaaccatc actgggggtcc aagccgagga cgaggtgtc 240
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ctgaccgtcc taggtcagtc ctctagatct tccaccgtga cgttggacga gtccgggggc 360
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agcagttact gcatgcagtg ggtgcgacag gcgccggca aagggtgga gttcgtcgt 480
ggtattgatg atgatgtag ttggacagca tacggggcgg cgggtgaagg ccgtgccacc 540
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gacaccgcca cctactactg cgccaaaact gctggtgta gttactatgg ttgtgaaaat 660
atcgacgcat ggggccacgg gaccgaagtc atcgtctcct ccactagtgg ccaggccggc 720
cagcaccatc accatcacca tggcgcatat ccgtacgacg ttccggacta cgcttct 777

<210> 5
<211> 237
<212> PRT
<213> artificial

<220>
<223> TMSC1

<400> 5

Ala Leu Thr Gln Pro Ser Ser Val Ser Ala Asn Leu Gly Gly Thr Val
1 5 10 15

Glu Ile Thr Cys Ser Gly Gly Asp Ile Tyr Ala Gly Ser His Tyr Tyr
20 25 30

Gly Trp Tyr Gln Gln Lys Ser Pro Gly Ser Ala Pro Val Thr Val Ile
35 40 45

Tyr Asp Asn Thr Asn Arg Pro Ser Asn Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Ala Ser Gly Ser Thr Asn Thr Leu Thr Ile Thr Gly Val Gln Ala
65 70 75 80

Asp Asp Glu Ala Val Tyr Tyr Cys Gly Ser Ile Asp Ser Thr Thr Asp
85 90 95

Val Gly Ile Phe Gly Ala Gly Thr Thr Leu Thr Val Leu Gly Gln Ser
100 105 110

Ser Arg Ser Ser Ala Val Thr Leu Asp Glu Ser Gly Gly Gly Leu Gln
115 120 125

Thr Pro Gly Gly Gly Leu Ser Leu Val Cys Lys Ala Ser Gly Phe Ser
130 135 140

Ile Ser Ser Tyr Pro Met Glu Trp Val Arg Gln Ala Pro Asp Lys Gly
145 150 155 160

Leu Glu Phe Val Ala Gly Ile Gly Gly Ser Gly Ser Gly Thr Lys Tyr
165 170 175

Gly Val Ala Val Lys Gly Arg Ala Thr Ile Ser Arg Asp Asn Gly Gln
180 185 190

Ser Thr Val Arg Leu Gln Leu Asn Asn Leu Arg Ala Glu Asp Thr Ala
195 200 205

Thr Tyr Tyr Cys Ala Arg Ser Gly Cys Tyr Asp Cys Ala Gly Gln Ile
210 215 220

Asp Ala Trp Gly His Gly Thr Glu Val Ile Val Ser Ser
225 230 235

<210> 6
<211> 711
<212> DNA
<213> artificial

<220>

<223> TMS1

<400> 6

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ggcagcgcgcg cggtgaccgt gatattatgat aacaccaacc gcccgagcaa cattccgagc      180
cgcttttagcg gcagcgcgag cggcagcacc aacaccctga ccattaccgg cgtgcaggcg      240
gatgatgaag cgggtgtatta ttgcggcagc attgatagca ccaccgatgt gggcattttt      300
ggcgcggggca ccaccctgac cgtgctgggc cagagcagcc gcagcagcg cgtgaccctg      360
gatgaaagcg gcggcggcct gcagaccccg ggcggcgggc tgagcctggt gtgcaaagcg      420
agcggcttta gcattagcag ctatccgatg gaatgggtgc gccaggcgcc ggataaaggc      480
ctggaatttg tggcgggcat tggcggcagc ggcagcggca ccaaatatgg cgtggcggtg      540
aaaggccgcg cgaccattag ccgcgataac ggccagagca ccgtgcgct gcagctgaac      600
aacctgcgcg cggaagatac cgcgacctat tattgcgcbc gcagcggtg ctatgattgc      660
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<211> 234

<212> PRT

<213> artificial

<220>

<223> TMS2

<400> 7

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Ala Leu Thr Gln Pro Ser Ser Val Ser Ala Asn Pro Gly Glu Thr Val
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Lys Ile Thr Cys Ser Gly Ser Ser Asp Tyr Ala Tyr Gly Trp Tyr Gln
                20              25              30
```

```
Gln Lys Ser Pro Gly Ser Ala Pro Val Thr Val Ile Tyr Asn Asn Asn
              35              40              45
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```
Lys Arg Pro Ser Asp Ile Pro Ser Arg Phe Ser Gly Ser Lys Ser Gly
              50              55              60
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Ser Thr Gly Thr Leu Thr Ile Thr Gly Val Gln Ala Glu Asp Glu Ala
65              70              75              80
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Val Tyr Tyr Cys Gly Ser Val Gly Asp Met Tyr Val Gly Ile Phe Gly
85 90 95

Ala Gly Thr Thr Leu Thr Val Leu Gly Gln Ser Ser Arg Ser Ser Thr
100 105 110

Val Thr Leu Asp Glu Ser Gly Gly Gly Leu Gln Thr Pro Gly Gly Gly
115 120 125

Pro Ser Leu Leu Cys Lys Ala Ser Gly Phe Ser Leu Ser Asp Tyr Gly
130 135 140

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Val Ala
145 150 155 160

Gly Ile Ser Thr Asp Gly Ser Trp Thr Gly Tyr Gly Ser Ala Val Lys
165 170 175

Gly Arg Ala Thr Ile Ser Arg Asp Asn Gly Gln Ser Thr Val Arg Leu
180 185 190

Gln Leu Asn Asp Leu Arg Ala Glu Asp Thr Gly Ile Tyr Phe Cys Ala
195 200 205

Lys Ser Ala Ala Val Gly Gly Trp His Ser Gly Phe Ile Asp Ala Trp
210 215 220

Gly His Gly Thr Glu Val Ile Val Ser Ser
225 230

<210> 8
<211> 702
<212> DNA
<213> artificial

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<223> TMSC2

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agcggcagca gcgattatgc gtatggctgg tatcagcaga aaagcccggg cagcgcgccg 120
gtgaccgtga ttataacaa caacaaacgc ccgagcgata ttccgagccg ctttagcggc 180

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agcaaaagcg gcagcaccgg caccctgacc attaccggcg tgcaggcgga agatgaagcg      240
gtgtattatt gcggcagcgt gggcgatatg tatgtgggca tttttggcgc gggcaccacc      300
ctgaccgtgc tgggccagag cagccgcagc agcaccgtga ccctggatga aagcggcggc      360
ggcctgcaga ccccgggcgg cggcccagc ctgctgtgca aagcgagcgg ctttagcctg      420
agcgattatg gcatgcattg ggtgcgccag gcgcggggca aaggcctgga atatgtggcg      480
ggcattagca ccgatggcag ctggaccggc tatggcagcg cggtgaaagg ccgcgcgacc      540
attagccgcg ataacggcca gagcaccgtg cgctgcagc tgaacgatct gcgcgcggaa      600
gataccggca tttatttttg cgcgaaaagc gcggcggtgg gcggctggca tagcggcttt      660
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<212> PRT
<213> artificial

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<220>
<223> TMS4

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<400> 9

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Ala Leu Thr Gln Pro Ser Ser Val Ser Ala Asn Ser Gly Glu Thr Val
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Glu Ile Thr Cys Ser Gly Ser Gly Gly Ser Tyr Gly Trp Phe Gln Gln
                20              25              30

```

```

Lys Ser Pro Gly Ser Ala Pro Val Thr Leu Ile Tyr Asp Asn Thr Asn
35              40              45

```

```

Arg Pro Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Thr Ser Gly Ser
50              55              60

```

```

Ala Gly Thr Leu Thr Ile Thr Gly Val Gln Ala Glu Asp Glu Ala Val
65              70              75              80

```

```

Tyr Phe Cys Gly Gly Tyr Asp Ser Ser Ser Asn Thr Gly Ile Phe Gly
85              90              95

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Ala Gly Thr Thr Leu Thr Val Leu Ala Val Thr Leu Asp Glu Ser Gly
100             105             110

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Gly Gly Leu Gln Thr Pro Gly Gly Ala Leu Ser Leu Val Cys Lys Gly
115 120 125

Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Phe Trp Val Arg Gln Ala
130 135 140

Pro Gly Lys Gly Leu Glu Phe Val Ala Gly Ile Asp Asn Pro Gly Arg
145 150 155 160

Thr Pro Ser Tyr Gly Ser Ala Val Lys Gly Arg Ala Thr Ile Ser Arg
165 170 175

Asp Asp Trp Gln Ser Thr Val Arg Leu Gln Leu Ser Asn Leu Arg Ala
180 185 190

Glu Asp Thr Ala Thr Tyr Tyr Cys Thr Arg Gly Asp Asn Ile Tyr Cys
195 200 205

Ala Ser Gly Ser Gly Gly Cys Ile Asp Ala Trp Gly His Gly Thr Glu
210 215 220

Val Ile Val Ser Ser
225

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<211> 687
<212> DNA
<213> artificial

<220>
<223> TMS4

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accctgattt atgataacac caaccgcccg agcggcattc cgagccgctt tagcggcagc 180
accagcggca gcgcgggcac cctgaccatt accggcgtgc aggcggaaga tgaagcggtg 240
tatttttgcg gcggctatga tagcagcagc aacaccggca tttttggcgc gggcaccacc 300
ctgaccgtgc tggcggtgac cctggatgaa agcggcgggc gcctgcagac cccggggcggc 360
gcgctgagcc tgggtgtgcaa aggcagcggc tttaccttta gcagctatgc gatgttttgg 420
gtgcgccagg cgccgggcaa aggcctggaa tttgtggcgg gcattgataa cccggggcgc 480

accccgagct atggcagcgc ggtgaaaggc cgcgcgacca ttagccgcga tgattggcag 540
 agcaccgtgc gcctgcagct gagcaacctg cgcgcggaag ataccgcgac ctattattgc 600
 acccgcgggc ataacattta ttgcgcgagc ggcagcggcg gctgcattga tgcgtggggc 660
 catggcaccg aagtgattgt gagcagc 687

<210> 11
 <211> 39
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 <213> artificial

<220>
 <223> CSCVHo-F

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 <212> DNA
 <213> artificial

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 <223> CSCG-B

<400> 12
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 <212> DNA
 <213> artificial

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 <223> CSCVK

<400> 13
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<210> 14
 <211> 33
 <212> DNA
 <213> artificial

<220>
 <223> CKJo-B

<400> 14
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