SEQUENCE LISTING

<110> KONINKLIJKE NEDERLANDSE AKADEMIE VAN WETENSCHAPPEN

<120> IMPROVED CULTURE MEDOD USING INTEGRIN AGONIST

<130> P075582WO

<140>
<141> 2020-05-18

<160> 10

<170> SeqWin2010, version 1.0

<210> 1
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
<223> TS2/16 H-chain

<400> 1
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Met Asp Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val
20 25 30

Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
35 40 45

Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg
50 55 60

Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr
65 70 75 80

Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ala Lys
85 90 95

Asn Thr Leu Tyr Leu Gln Met Gly Ser Leu Lys Ser Glu Asp Thr Ala
100 105 110

Met Tyr Tyr Cys Thr Arg Ile Gly Tyr Asp Glu Asp Tyr Ala Met Asp
115 120 125

His Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145 150 155 160

```
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225                 230                 235                 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
    370                 375                 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445
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Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
450 455 460

Ser Leu Ser Pro Gly Lys
465 470

<210> 2
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> TS2-16 kL-chain

<400> 2
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Glu Ile Val Val Thr Gln Ser Pro Thr Thr Met Ala Ala
20 25 30

Ser Pro Gly Asp Lys Ile Thr Ile Thr Cys Ser Val Ser Ser Ile Ile
35 40 45

Ser Ser Asn Tyr Leu His Trp Tyr Ser Gln Lys Pro Gly Phe Ser Pro
50 55 60

Lys Leu Leu Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Pro
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Gly
85 90 95

Thr Met Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Gly Ser
100 105 110

Asp Ile Pro Leu Thr Phe Gly Asp Gly Thr Lys Leu Asp Leu Lys Arg
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

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His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230
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<210> 3
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanised TS2/16 H-chain

<400> 3

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Met Asp Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly
1               5                   10                  15

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
            20                  25                  30

Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp
        35                  40                  45

Val Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser
    50                  55                  60

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ala Lys Asn Thr Leu
65                  70                  75                  80

Tyr Leu Gln Met Gly Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr
                85                  90                  95

Cys Thr Arg Ile Gly Tyr Asp Glu Asp Tyr Ala Met Asp His Trp Gly
            100                 105                 110

Gln Gly Thr Ser Val Thr Val Ser Ser
        115                 120
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<210> 4
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanised TS2/16 L-chain

<400> 4

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Glu Ile Val Val Thr Gln Ser Pro Thr Thr Met Ala Ala Ser Pro Gly
1               5                   10                  15

Asp Lys Ile Thr Ile Thr Cys Ser Val Ser Ser Ile Ile Ser Ser Asn
            20                  25                  30
```

Tyr Leu His Trp Tyr Ser Gln Lys Pro Gly Phe Ser Pro Lys Leu Leu
        35   40   45

Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Pro Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Gly Thr Met Glu
65   70   75   80

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

Leu Thr Phe Gly Asp Gly Thr Lys Leu Asp Leu Lys
            100   105

<210>   5
<211>   10
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   Humanised TS2/16 H-chain HCDR1

<400>   5
Gly Phe Thr Phe Ser Ser Tyr Thr Met Ser
1   5   10

<210>   6
<211>   17
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   Humanised TS2/16 H-chain HCDR2

<400>   6
Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val Lys
1   5   10   15

Gly

<210>   7
<211>   11
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   Humanised TS2/16 H-chain HCDR3

<400>   7
Ile Gly Tyr Asp Glu Asp Tyr Ala Met Asp His
1   5   10

<210> 8
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanised TS2/16 L-chain LCDR1

<400> 8
Ser Val Ser Ser Ile Ile Ser Ser Asn Tyr Leu His
1   5   10

<210> 9
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanised TS2/16 L-chain LCDR2

<400> 9
Ser Val Ser Ser Ile Ile Ser Ser Asn Tyr Leu His
1   5   10

<210> 10
<211> 9
<212> PRT
<213> Humanised TS2/16 L-chain LCDR3

<400> 10
Gln Gln Gly Ser Asp Ile Pro Leu Thr
1   5