SEQUENCE LISTING

<110> Immunwork Inc.

<120> MOLECULAR CONSTRUCTS FOR INHIBITING THE FORMATION OF BLOOD CLOT AND/OR TREATING THROMBOSIS

<130> P2955-PCT

<150> US 62/308,349
<151> 2016-03-15
<150> PCT/CN2016/071184
<151> 2016-01-18
<150> US 62/213,012
<151> 2015-09-01

<160> 35

<170> BiSSAP 1.3

<210> 1
<211> 4
<212> PRT
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<220>
<223> filler sequence-1

<400> 1
Gly Gly Gly Ser
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<210> 2
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<220>
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<400> 2
Gly Ser Gly Ser
1

<210> 3
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<400> 3
Gly Gly Ser Gly
1

<210> 4
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<400> 4
Gly Ser Gly Gly Ser
1   5

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<400> 5
Ser Gly Gly Ser Gly
1   5

<210> 6
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<400> 6
Gly Gly Gly Gly Ser
1   5

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

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<400> 7
Gly Gly Ser Gly Gly Ser
1   5

<210> 8
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<212> PRT
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<400> 8
Gly Gly Ser Gly Gly Ser Gly
1   5

<210> 9
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<212> PRT
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<220>
<223> filler sequence-9

<400> 9
Ser Gly Ser Gly Gly Ser Gly Ser
1   5

<210> 10
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> filler sequence-10

<400> 10
Gly Ser Gly Gly Ser Gly Ser Gly Ser
1   5

<210> 11
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> filler sequence-11

<400> 11
Ser Gly Gly Ser Gly Gly Ser Gly Ser Gly
1   5   10

<210> 12
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> filler sequence-12

<400> 12
Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser
1   5   10

<210> 13
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> filler sequence-13

<400> 13
Ser Gly Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser
1   5   10

<210> 14
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> filler sequence-14

<400> 14
Gly Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser
1   5   10

<210> 15
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> filler sequence-15

<400> 15
Gly Gly Gly Ser Gly Ser Gly Ser Gly Ser Gly Gly Gly Ser
1   5   10

<210> 16
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> filler sequence-16

<400> 16
Ser Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Ser Gly Ser Gly
1   5   10   15

<210> 17
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> ACETYLATION

<220>
<223> polypeptide core

<400> 17
Cys Gly Gly Ser Gly Gly Ser Gly Gly Ser Lys Gly Ser Gly Ser Lys
1   5   10   15

<210> 18
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> ACETYLATION

<220>
<223> polypeptitde core-1

<400> 18
Cys Gly Gly Ser Gly Gly Ser Gly Gly Ser Lys Gly Ser Gly Ser Lys
1   5   10   15
Gly Ser Lys

<210> 19
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> ACETYLATION

<220>
<223> polypeptide core

<400> 19
Cys Gly Ser Lys Gly Ser Lys Gly Ser Lys Gly Ser Lys Gly Ser Lys
1   5   10   15
Gly Ser Lys Gly Ser Lys Gly Ser Lys Gly Ser Lys Gly Ser Lys
            20   25   30

<210> 20
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Xaa is homopropargylglycine

<220>
<221> MOD_RES
<222> 1
<223> ACETYLATION

<220>
<223> polypeptide core

<400> 20

Xaa Gly Gly Ser Gly Gly Ser Gly Gly Ser Lys Gly Ser Gly Ser Lys
1   5   10   15

<210> 21
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Xaa is homopropargylglycine

<220>
<221> MOD_RES
<222> 1
<223> ACETYLATION

<220>
<223> polypeptide core

<400> 21
Xaa Gly Gly Ser Gly Gly Ser Gly Gly Ser Lys Gly Ser Gly Ser Lys
1   5   10   15
Gly Ser Lys

<210> 22
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Xaa is L-azidohomoalanine

<220>
<221> MOD_RES
<222> 1
<223> ACETYLATION

<220>
<223> polypeptide core

<400> 22

Xaa Gly Gly Ser Gly Gly Ser Gly Gly Ser Lys Gly Ser Gly Ser Lys
1 5 10 15
Gly Ser Lys

<210> 23
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Xaa is homopropargylglycine

<220>
<221> MOD_RES
<222> 1
<223> ACETYLATION

<220>
<223> polypeptide core

<400> 23
Xaa Gly Gly Ser Gly Gly Ser Gly Gly Ser Lys Gly Ser Gly Ser Lys
1 5 10 15
Gly Ser Gly Ser Cys
            20

<210> 24
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> ACETYLATION

<220>
<223> polypeptide core

<220>
<221> MOD_RES
<222> 2,4,6
<223> Xaa is PEGylated amino acid with two EG units

<400> 24

Cys Xaa Lys Xaa Lys Xaa Lys
1   5

<210> 25
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> ACETYLATION

<220>
<223> polypeptide core

<220>
<221> MOD_RES
<222> 2,4,6,8,10
<223> Xaa is PEGylated amino acid with six EG units

<400> 25
Cys Xaa Lys Xaa Lys Xaa Lys Xaa Lys Xaa Lys
1   5   10

<210> 26
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide core-2

<400> 26
Cys Gly Ser Lys Gly Ser Lys Gly Ser Lys Gly Ser Lys Gly Ser Lys
1   5   10   15

<210> 27
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-fibrin scFv 102-10

<400> 27

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1               5                  10                  15
Gly Lys Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Lys Tyr
            20                  25                  30
Ile Ala Trp Phe Gln His Lys Pro Gly Lys Gly Pro Arg Leu Leu Ile
        35                  40                  45
His Tyr Thr Ser Thr Leu Gln Pro Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser Asn Leu Glu Pro
65                  70                  75                  80
Glu Asp Leu Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asn Leu Thr Trp
                85                  90                  95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Gly Ser Thr Ser
            100                 105                 110
Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Gln Ile
        115                 120                 125
Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val
    130                 135                 140
Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met
145                 150                 155                 160
Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly Trp
                165                 170                 175
Ile Asn Thr Tyr Thr Gly Glu Ala Thr Tyr Ala Asp Asp Phe Lys Gly
            180                 185                 190
Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Asn Thr Ala Tyr Val Gln
        195                 200                 205
Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg
    210                 215                 220
Leu Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly
225                 230                 235                 240
Gly Gly Gly Ser Gly Gly Gly Gly Ser Cys
                245                 250
```

<210> 28
<211> 366
<212> PRT
<213> Artificial Sequence

<220>
<223> reteplase-Cys

<400> 28

```
Ser Tyr Gln Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr
1               5                  10                  15
Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp
            20                  25                  30
Asn Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser
        35                  40                  45
```

```
Ala Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp
    50                  55                  60
Gly Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr
65                  70                  75                  80
Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln
                85                  90                  95
Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile
            100                 105                 110
Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser
        115                 120                 125
Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp
    130                 135                 140
Ile Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His
145                 150                 155                 160
Leu Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu
                165                 170                 175
Glu Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp
            180                 185                 190
Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp
        195                 200                 205
Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu
    210                 215                 220
Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser
225                 230                 235                 240
Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu
                245                 250                 255
Lys Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln
            260                 265                 270
His Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp
        275                 280                 285
Thr Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly
    290                 295                 300
Asp Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu
305                 310                 315                 320
Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro
                325                 330                 335
Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn
            340                 345                 350
Met Arg Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Cys
        355                 360                 365
```

<210> 29
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Phage-displayed anti-fibrin scFv D10

<400> 29
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Gly Phe Tyr
            20   25   30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Ser Tyr Pro Ser Gly Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Asp Tyr Pro Ile
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Ser Thr Ser
            100   105   110
Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val
        115   120   125
Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
    130   135   140
Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Asn Asp Phe Ser Ile
145   150   155   160
His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly
                165   170   175
Ile Trp Pro Tyr Gly Gly Tyr Thr Phe Tyr Ala Asp Ser Val Lys Gly
            180   185   190
Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu Arg
        195   200   205
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
    210   215   220
Phe Gly Tyr Tyr Ser Phe Gly Asp Tyr Trp Gly Gln Gly Thr Leu Val
225   230   235   240
Thr Val Ser Ser

<210> 30
<211> 599
<212> PRT
<213> Artificial Sequence

<220>
<223> 2-chain IgG4.Fc fusion protein containing reteplase

<400> 30
Ser Tyr Gln Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr
1   5   10   15
Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp
            20   25   30

```
Asn Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser
        35                  40                  45
Ala Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp
    50                  55                  60
Gly Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr
65                  70                  75                  80
Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln
                85                  90                  95
Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile
            100                 105                 110
Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser
        115                 120                 125
Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp
    130                 135                 140
Ile Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His
145                 150                 155                 160
Leu Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu
                165                 170                 175
Glu Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp
            180                 185                 190
Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp
        195                 200                 205
Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu
    210                 215                 220
Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser
225                 230                 235                 240
Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu
                245                 250                 255
Lys Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln
            260                 265                 270
His Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp
        275                 280                 285
Thr Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly
    290                 295                 300
Asp Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu
305                 310                 315                 320
Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro
                325                 330                 335
Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn
            340                 345                 350
Met Arg Pro Ala Ser Gly Gly Ser Pro Pro Cys Pro Ser Cys Pro Ala
        355                 360                 365
Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    370                 375                 380
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
385                 390                 395                 400
Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
                405                 410                 415
```

```
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
            420                 425                 430
Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        435                 440                 445
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
    450                 455                 460
Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
465                 470                 475                 480
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr
                485                 490                 495
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            500                 505                 510
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        515                 520                 525
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    530                 535                 540
Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe
545                 550                 555                 560
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                565                 570                 575
Ser Leu Ser Leu Ser Leu Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly
            580                 585                 590
Gly Ser Gly Gly Gly Gly Ser
        595
```

<210> 31
<211> 838
<212> PRT
<213> Artificial Sequence

<220>
<223> (reteplase)-hIgG4.Fc-(scFv α fibrin 102-10)

<400> 31

```
Ser Tyr Gln Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr
1               5                   10                  15
Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp
            20                  25                  30
Asn Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser
        35                  40                  45
Ala Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp
    50                  55                  60
Gly Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr
65                  70                  75                  80
Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln
                85                  90                  95
Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile
            100                 105                 110
```

```
Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser
        115                 120                 125
Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp
    130                 135                 140
Ile Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His
145                 150                 155                 160
Leu Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu
                165                 170                 175
Glu Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp
            180                 185                 190
Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp
        195                 200                 205
Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu
    210                 215                 220
Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser
225                 230                 235                 240
Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu
                245                 250                 255
Lys Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln
            260                 265                 270
His Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp
        275                 280                 285
Thr Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly
    290                 295                 300
Asp Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu
305                 310                 315                 320
Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro
                325                 330                 335
Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn
            340                 345                 350
Met Arg Pro Ala Ser Gly Gly Ser Pro Pro Cys Pro Ser Cys Pro Ala
        355                 360                 365
Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    370                 375                 380
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
385                 390                 395                 400
Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
                405                 410                 415
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
            420                 425                 430
Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        435                 440                 445
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
    450                 455                 460
Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
465                 470                 475                 480
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr
                485                 490                 495
```

```
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            500                 505                 510
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        515                 520                 525
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    530                 535                 540
Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe
545                 550                 555                 560
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                565                 570                 575
Ser Leu Ser Leu Ser Leu Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly
            580                 585                 590
Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
        595                 600                 605
Ser Leu Ser Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala
    610                 615                 620
Ser Gln Asp Ile Asn Lys Tyr Ile Ala Trp Phe Gln His Lys Pro Gly
625                 630                 635                 640
Lys Gly Pro Arg Leu Leu Ile His Tyr Thr Ser Thr Leu Gln Pro Gly
                645                 650                 655
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Phe
            660                 665                 670
Ser Ile Ser Asn Leu Glu Pro Glu Asp Leu Ala Thr Tyr Tyr Cys Leu
        675                 680                 685
Gln Tyr Asp Asn Leu Thr Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
    690                 695                 700
Ile Lys Arg Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu
705                 710                 715                 720
Gly Ser Thr Lys Gly Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu
                725                 730                 735
Lys Lys Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr
            740                 745                 750
Thr Phe Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys
        755                 760                 765
Gly Leu Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Ala Thr
    770                 775                 780
Tyr Ala Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser
785                 790                 795                 800
Ala Asn Thr Ala Tyr Val Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr
                805                 810                 815
Ala Thr Tyr Phe Cys Ala Arg Leu Met Asp Tyr Trp Gly Gln Gly Thr
            820                 825                 830
Ser Val Thr Val Ser Ser
        835
```

<210> 32
<211> 611
<212> PRT

<213> Artificial Sequence

<220>
<223> (reteplase)-(scFv α fibrin 102-10)

<400> 32
Ser Tyr Gln Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr
1   5   10   15
Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp
            20   25   30
Asn Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser
        35   40   45
Ala Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp
    50   55   60
Gly Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr
65   70   75   80
Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln
                85   90   95
Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile
            100   105   110
Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser
        115   120   125
Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp
    130   135   140
Ile Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His
145   150   155   160
Leu Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu
                165   170   175
Glu Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp
            180   185   190
Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp
        195   200   205
Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu
    210   215   220
Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser
225   230   235   240
Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu
                245   250   255
Lys Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln
            260   265   270
His Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp
        275   280   285
Thr Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly
    290   295   300
Asp Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu
305   310   315   320
Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro
                325   330   335

```
Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn
            340                 345                 350
Met Arg Pro Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        355                 360                 365
Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
    370                 375                 380
Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
385                 390                 395                 400
Ile Asn Lys Tyr Ile Ala Trp Phe Gln His Lys Pro Gly Lys Gly Pro
                405                 410                 415
Arg Leu Leu Ile His Tyr Thr Ser Thr Leu Gln Pro Gly Ile Pro Ser
            420                 425                 430
Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser
        435                 440                 445
Asn Leu Glu Pro Glu Asp Leu Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp
    450                 455                 460
Asn Leu Thr Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
465                 470                 475                 480
Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
                485                 490                 495
Lys Gly Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro
            500                 505                 510
Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
        515                 520                 525
Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys
    530                 535                 540
Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Ala Thr Tyr Ala Asp
545                 550                 555                 560
Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Asn Thr
                565                 570                 575
Ala Tyr Val Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr
            580                 585                 590
Phe Cys Ala Arg Leu Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
        595                 600                 605
Val Ser Ser
    610
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<210> 33
<211> 771
<212> PRT
<213> Artificial Sequence

<220>
<223> 2-chain IgG4.Fc fusion protein containing TNK-tPA

<400> 33
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Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln
1               5                   10                  15
```

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Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu
            20                  25                  30
Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser Val Pro Val
        35                  40                  45
Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln
    50                  55                  60
Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu Gly Phe Ala
65                  70                  75                  80
Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu Asp Gln
                85                  90                  95
Gly Ile Ser Tyr Arg Gly Asn Trp Ser Thr Ala Glu Ser Gly Ala Glu
            100                 105                 110
Cys Thr Gln Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly
        115                 120                 125
Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys
    130                 135                 140
Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala
145                 150                 155                 160
Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys Ser Glu Gly
                165                 170                 175
Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg Gly Thr His
            180                 185                 190
Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met Ile
        195                 200                 205
Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu
    210                 215                 220
Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys
225                 230                 235                 240
Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys
                245                 250                 255
Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro
            260                 265                 270
Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala Ser His Pro
        275                 280                 285
Trp Gln Ala Ala Ala Ala Ala Lys His Arg Arg Ser Pro Gly Glu Arg
    290                 295                 300
Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser Ala
305                 310                 315                 320
Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile
                325                 330                 335
Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe
            340                 345                 350
Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr
        355                 360                 365
Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys
    370                 375                 380
Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro Pro Ala Asp
385                 390                 395                 400
```

```
Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly Tyr Gly Lys
                405                 410                 415
His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys Glu Ala His
            420                 425                 430
Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn
        435                 440                 445
Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly
    450                 455                 460
Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly
465                 470                 475                 480
Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile
                485                 490                 495
Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly Val Tyr Thr
            500                 505                 510
Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met Arg Pro Ala
        515                 520                 525
Ser Gly Gly Ser Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu
    530                 535                 540
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
545                 550                 555                 560
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
                565                 570                 575
Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
            580                 585                 590
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
        595                 600                 605
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
    610                 615                 620
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser
625                 630                 635                 640
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
                645                 650                 655
Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val
            660                 665                 670
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
        675                 680                 685
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
    690                 695                 700
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr
705                 710                 715                 720
Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val
                725                 730                 735
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
            740                 745                 750
Ser Leu Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        755                 760                 765
Gly Gly Ser
    770
```

<210> 34
<211> 1015
<212> PRT
<213> Artificial Sequence

<220>
<223> (TNK-tPA)-hIgG4.Fc-(scFv α fibrin D10)

<400> 34
Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln
1   5   10   15
Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu
            20   25   30
Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser Val Pro Val
        35   40   45
Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln
    50   55   60
Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu Gly Phe Ala
65   70   75   80
Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu Asp Gln
                85   90   95
Gly Ile Ser Tyr Arg Gly Asn Trp Ser Thr Ala Glu Ser Gly Ala Glu
            100   105   110
Cys Thr Gln Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly
        115   120   125
Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys
    130   135   140
Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala
145   150   155   160
Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys Ser Glu Gly
                165   170   175
Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg Gly Thr His
            180   185   190
Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met Ile
        195   200   205
Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu
    210   215   220
Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys
225   230   235   240
Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys
                245   250   255
Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro
            260   265   270
Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala Ser His Pro
        275   280   285
Trp Gln Ala Ala Ala Ala Ala Lys His Arg Arg Ser Pro Gly Glu Arg
    290   295   300

```
Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser Ala
305                 310                 315                 320
Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile
                325                 330                 335
Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe
            340                 345                 350
Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr
        355                 360                 365
Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys
    370                 375                 380
Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro Pro Ala Asp
385                 390                 395                 400
Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly Tyr Gly Lys
                405                 410                 415
His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys Glu Ala His
            420                 425                 430
Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn
        435                 440                 445
Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly
    450                 455                 460
Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly
465                 470                 475                 480
Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile
                485                 490                 495
Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly Val Tyr Thr
            500                 505                 510
Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met Arg Pro Ala
        515                 520                 525
Ser Gly Gly Ser Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu
    530                 535                 540
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
545                 550                 555                 560
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
                565                 570                 575
Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
            580                 585                 590
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
        595                 600                 605
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
    610                 615                 620
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser
625                 630                 635                 640
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
                645                 650                 655
Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val
            660                 665                 670
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
        675                 680                 685
```

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Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
    690                 695                 700
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr
705                 710                 715                 720
Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val
                725                 730                 735
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
            740                 745                 750
Ser Leu Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        755                 760                 765
Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
    770                 775                 780
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val
785                 790                 795                 800
Gly Phe Tyr Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
                805                 810                 815
Leu Leu Ile Ser Tyr Pro Ser Gly Leu Tyr Ser Gly Val Pro Ser Arg
            820                 825                 830
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
        835                 840                 845
Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Asp
    850                 855                 860
Tyr Pro Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly
865                 870                 875                 880
Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys
                885                 890                 895
Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
            900                 905                 910
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Asn Asp
        915                 920                 925
Phe Ser Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
    930                 935                 940
Val Ala Gly Ile Trp Pro Tyr Gly Gly Tyr Thr Phe Tyr Ala Asp Ser
945                 950                 955                 960
Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala
                965                 970                 975
Tyr Leu Arg Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
            980                 985                 990
Cys Ala Arg Phe Gly Tyr Tyr Ser Phe Gly Asp Tyr Trp Gly Gln Gly
        995                 1000                1005
Thr Leu Val Thr Val Ser Ser
    1010                1015
```

<210> 35
<211> 788
<212> PRT
<213> Artificial Sequence

<220>
<223> (TNK-tPA)-(scFv α fibrin)

<400> 35
Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln
1   5   10   15
Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu
            20   25   30
Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser Val Pro Val
        35   40   45
Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln
    50   55   60
Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu Gly Phe Ala
65   70   75   80
Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu Asp Gln
                85   90   95
Gly Ile Ser Tyr Arg Gly Asn Trp Ser Thr Ala Glu Ser Gly Ala Glu
            100   105   110
Cys Thr Gln Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly
        115   120   125
Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys
    130   135   140
Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala
145   150   155   160
Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys Ser Glu Gly
                165   170   175
Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg Gly Thr His
            180   185   190
Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met Ile
        195   200   205
Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu
    210   215   220
Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys
225   230   235   240
Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys
                245   250   255
Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro
            260   265   270
Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala Ser His Pro
        275   280   285
Trp Gln Ala Ala Ala Ala Ala Lys His Arg Arg Ser Pro Gly Glu Arg
    290   295   300
Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser Ala
305   310   315   320
Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile
                325   330   335
Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe
            340   345   350

```
Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr
        355                 360                 365
Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys
    370                 375                 380
Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro Pro Ala Asp
385                 390                 395                 400
Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly Tyr Gly Lys
                405                 410                 415
His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys Glu Ala His
            420                 425                 430
Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn
        435                 440                 445
Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly
    450                 455                 460
Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly
465                 470                 475                 480
Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile
                485                 490                 495
Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly Val Tyr Thr
            500                 505                 510
Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met Arg Pro Ala
        515                 520                 525
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    530                 535                 540
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
545                 550                 555                 560
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Gly Phe Tyr
                565                 570                 575
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
            580                 585                 590
Ser Tyr Pro Ser Gly Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
        595                 600                 605
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
    610                 615                 620
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Asp Tyr Pro Ile
625                 630                 635                 640
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Ser Thr Ser
                645                 650                 655
Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val
            660                 665                 670
Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
        675                 680                 685
Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Asn Asp Phe Ser Ile
    690                 695                 700
His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly
705                 710                 715                 720
Ile Trp Pro Tyr Gly Gly Tyr Thr Phe Tyr Ala Asp Ser Val Lys Gly
                725                 730                 735
```

```
Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu Arg
            740                 745                 750
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
        755                 760                 765
Phe Gly Tyr Tyr Ser Phe Gly Asp Tyr Trp Gly Gln Gly Thr Leu Val
    770                 775                 780
Thr Val Ser Ser
785
```