FIG. 1

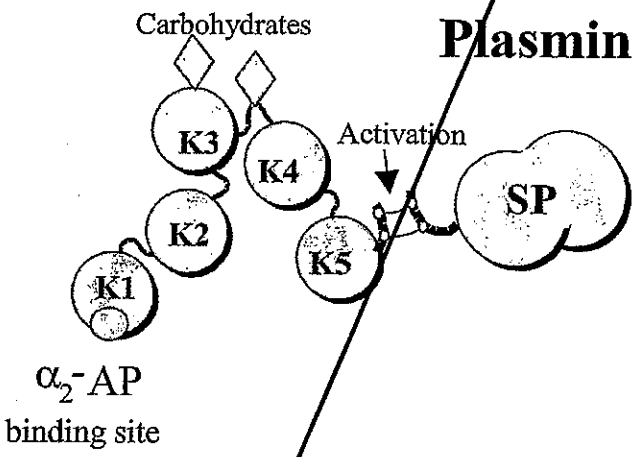

Carbohydrates
Plasmin
K3
K4
Activation
SP
K2
K5
K1
α_2-AP
binding site

FIG. 2

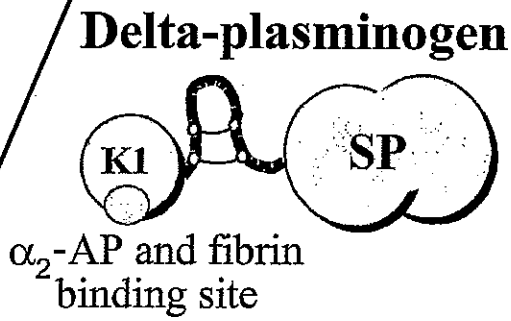

Delta-plasminogen
K1
SP
α_2-AP and fibrin
binding site

FIG. 3

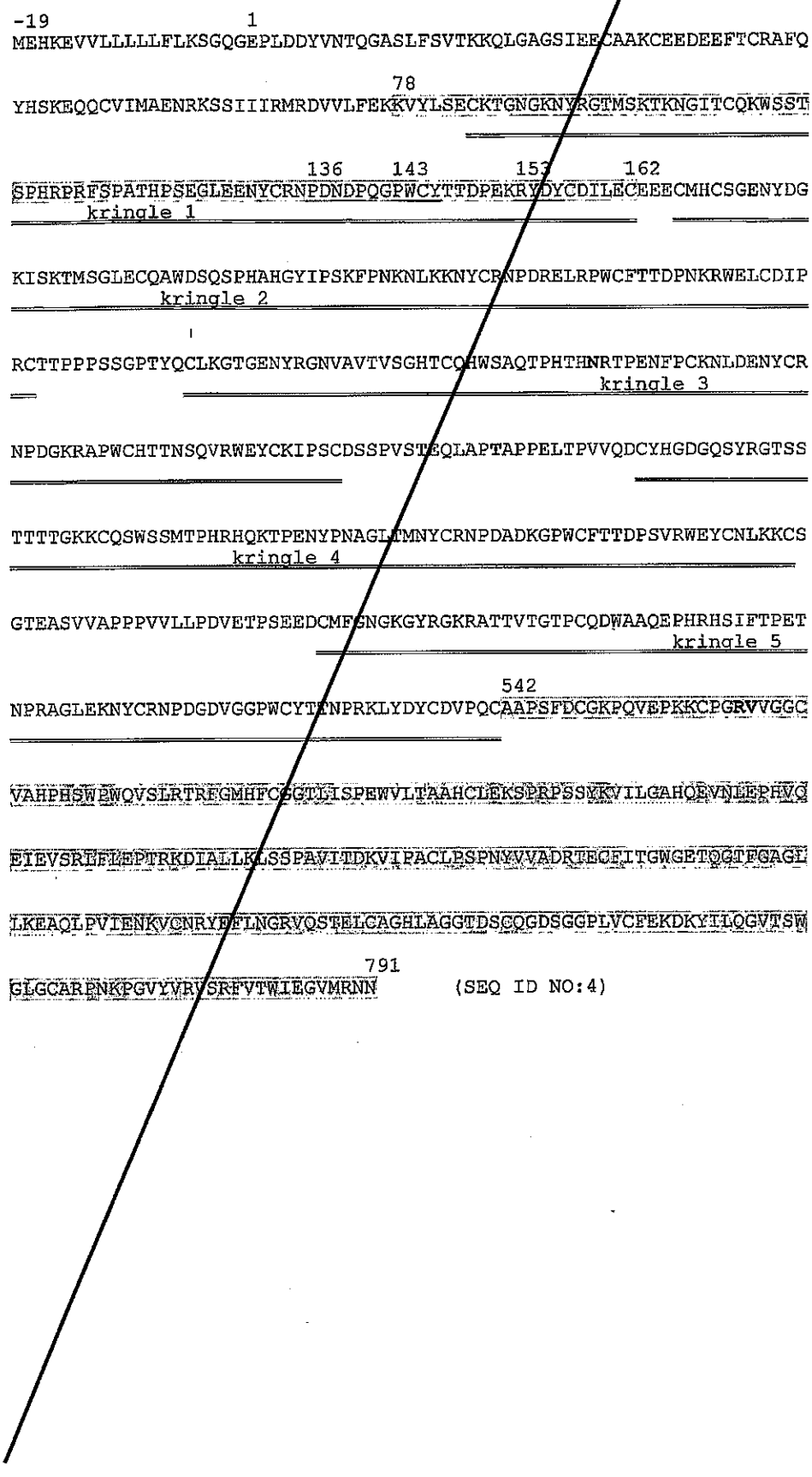

-19
1
MEHKEVVLLLLLFLKSGQGEPLDDYVNTQGASLFSVTKKQLGAGSIEECAAKCEEDEEFTCRAFQ
78
YHSKEQQCVIMAENRKSSIIIRMRDVVLFEKKVYLSECKTGNGKNYRGTMSKTKNGITCQKWSST
136
143
153
162
SPHRPRFSPATHPSEGLEENYCRNPDNDPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDG
kringle 1
KISKTMSGLECQAWDSQSPHAHGYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIP
kringle 2
RCTTPPPSSGPTYQCLKGTGENYRGNVAVTVSGHTCQHWSAQTPHTHNRTPENFPCKNLDENYCR
kringle 3
NPDGKRAPWCHTTNSQVRWEYCKIPSCDSSPVSTEQLAPTAPPELTPVVQDCYHGDGQSYRGTSS
TTTTGKKCQSWSSMTPHRHQKTPENYPNAGLTMNYCRNPDADKGPWCFTTDPSVRWEYCNLKKCS
kringle 4
GTEASVVAPPPVVLLPDVETPSEEDCMFGNGKGYRGKRATTVTGTPCQDWAAQEPHRHSIFTPET
kringle 5
542
NPRAGLEKNYCRNPDGDVGGPWCYTTNPRKLYDYCDVPQCAAPSFDCGKPQVEPKKCPGRVVGGC
VAHPHSWPWQVSLRTREGMHFCGGTLISPEWVLTAAHCLEKSPRPSSYKVILGAHQEVNLEPHVQ
EIEVSRLFLEPTRKDIALLKLSSPAVITDKVIPACLPSPNYVVADRTECFITGWGETQGTFGAGL
LKEAQLPVIENKVCNRYEFLNGRVQSTELCAGHLAGGTDSCQGDSGGPLVCFEKDKYILQGVTSW
791
GLGCARPNKPGVYVRVSRFVTWIEGVMRNN
(SEQ ID NO:4)

FIG. 4

```
HK1   CKTGNGKNYR GTMSKTKNGI TCQKWSSTSP HR-PRFSPAT HPSEGLEENY
HK2   CMHCSGENYD GKISKTMSGL ECQAWDSQSP HA-HGYIPSK FPNKNLKKNY
HK3   CLKGTGENYR GNVAVTVSGH TCQHWSAQTP HT-HNRTPEN FPCKNLDENY
HK4   CYHGDGQSYR GTSSTTTTGK KCQSWSSMTP HR-HQKTPEN YPNAGLTMNY
HK5   CMFGNGKGYR GKRATTVTGT PCQDWAAQEP HRHSIFTPET NPRAGLEKNY

(con't)
HK1   CRNPDNDPQG PWCYTTDPEK RYDYCDILEC  (SEQ ID NO:5)
HK2   CRNPDRE-LR PWCFTTDPNK RWELCDIPRC  (SEQ ID NO:6)
HK3   CRNPDGK-RA PWCHTTNSQV RWEYCKIPSC  (SEQ ID NO:7)
HK4   CRNPDAD-KG PWCFTTDPSV RWEYCNLKKC  (SEQ ID NO:8)
HK5   CRNPDGDVGG PWCYTTNPRK LYDYCDVPQC  (SEQ ID NO:9)
```

FIG. 5

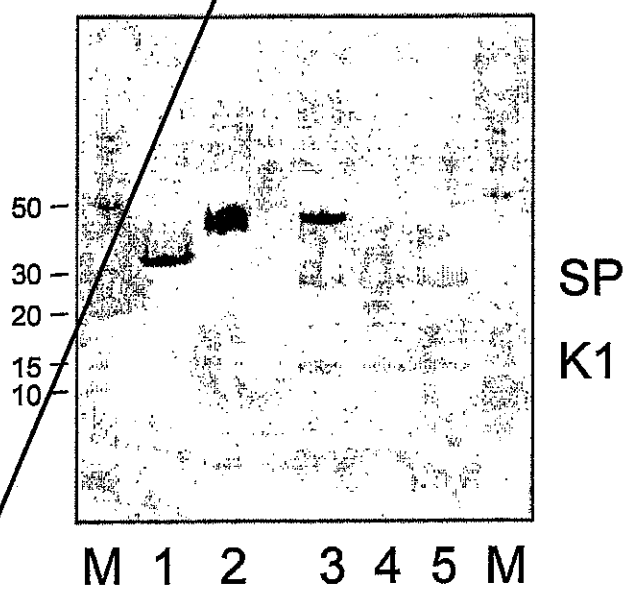


FIG. 6

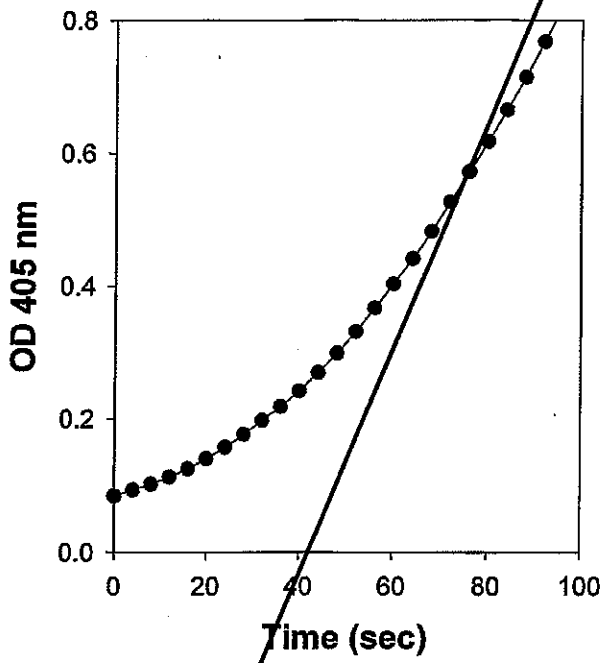

OD 405 nm
0.0
0.2
0.4
0.6
0.8
0
20
40
60
80
100
Time (sec)

FIG. 7

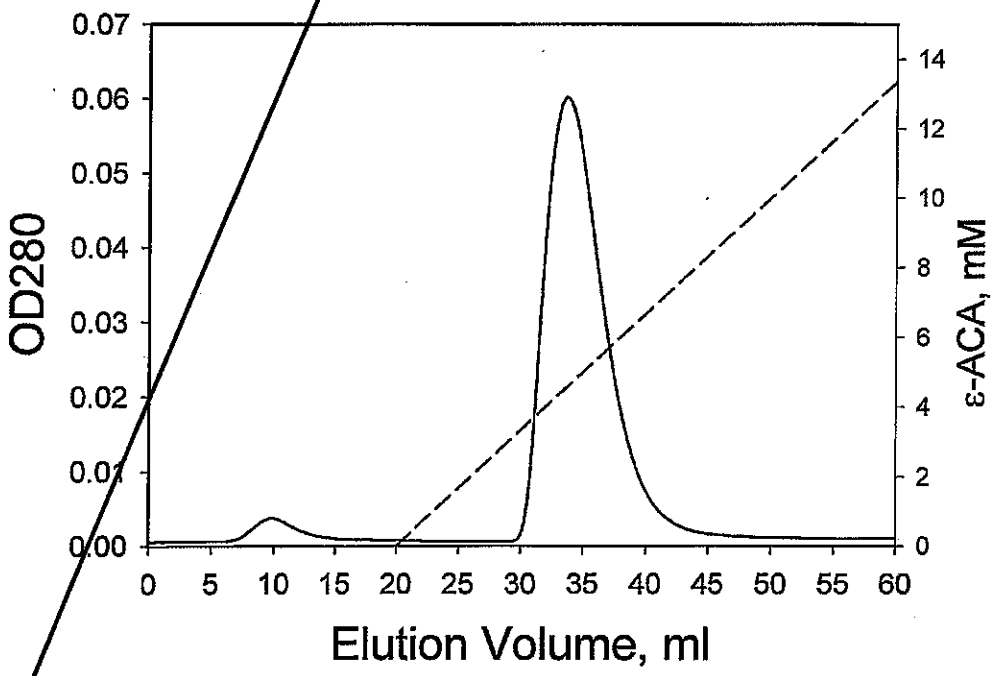

OD280
0.00
0.01
0.02
0.03
0.04
0.05
0.06
0.07
0
2
4
6
8
10
12
14
ε-ACA, mM
0
5
10
15
20
25
30
35
40
45
50
55
60
Elution Volume, ml

FIG. 8

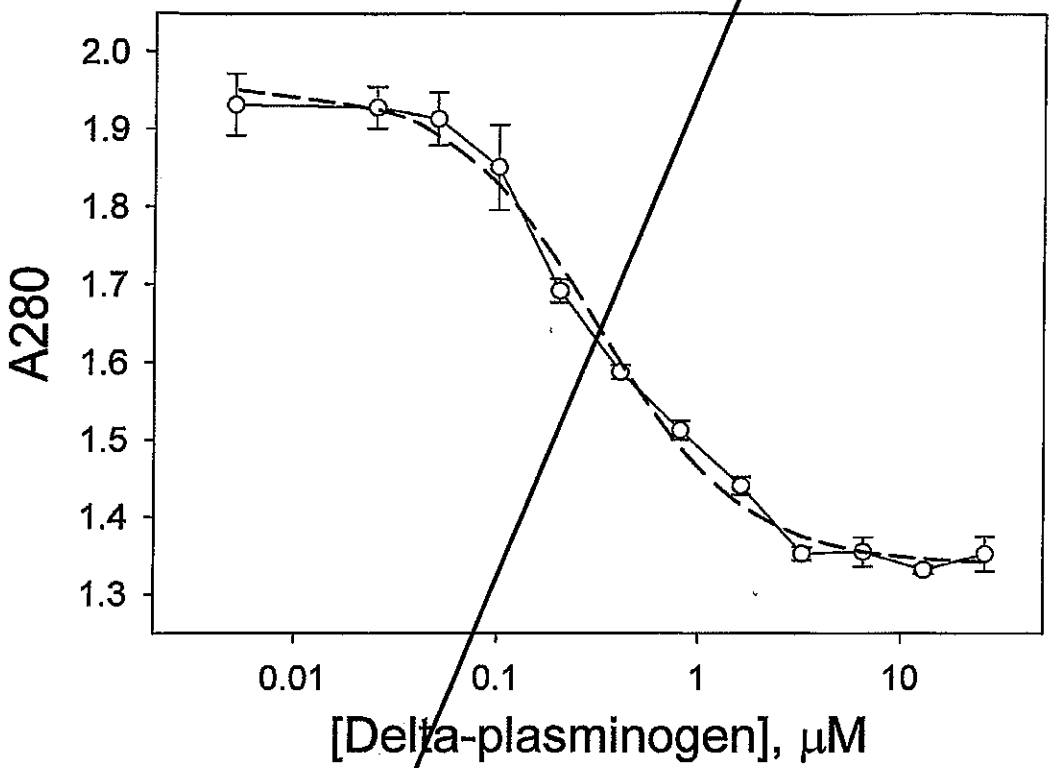

2.0
1.9
1.8
1.7
1.6
1.5
1.4
1.3
A280
0.01
0.1
1
10
[Delta-plasminogen], μM

FIG. 9

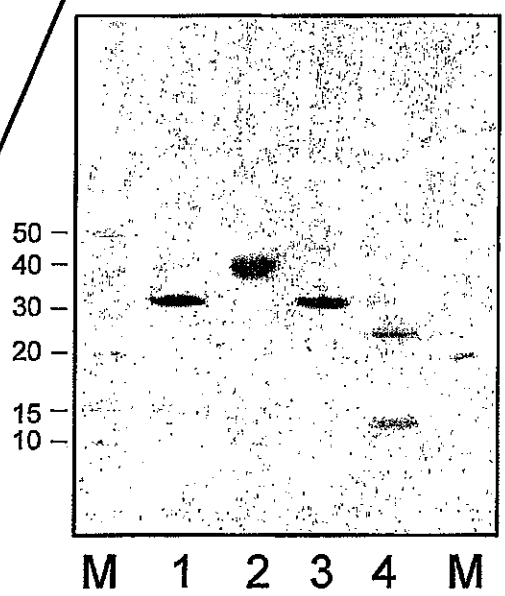
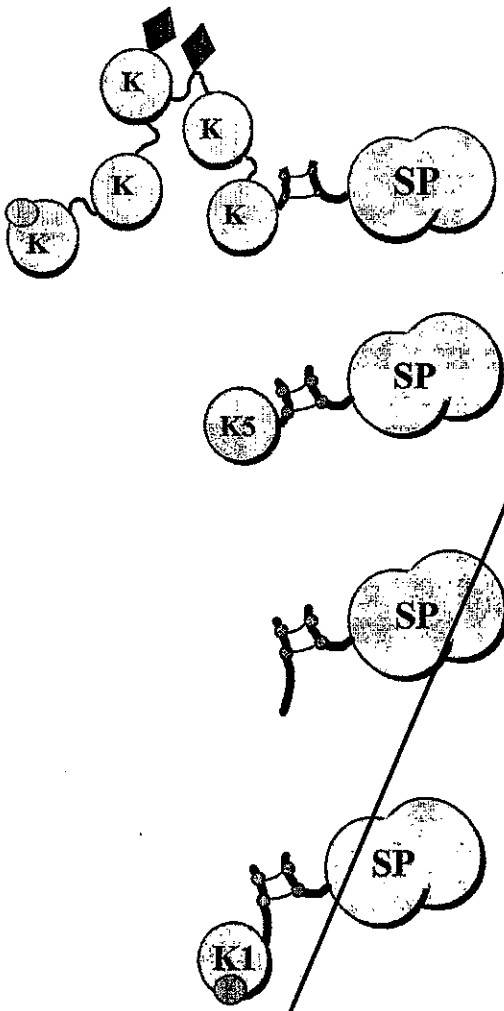

50
40
30
20
15
10
M
1
2
3
4
M

FIG. 10



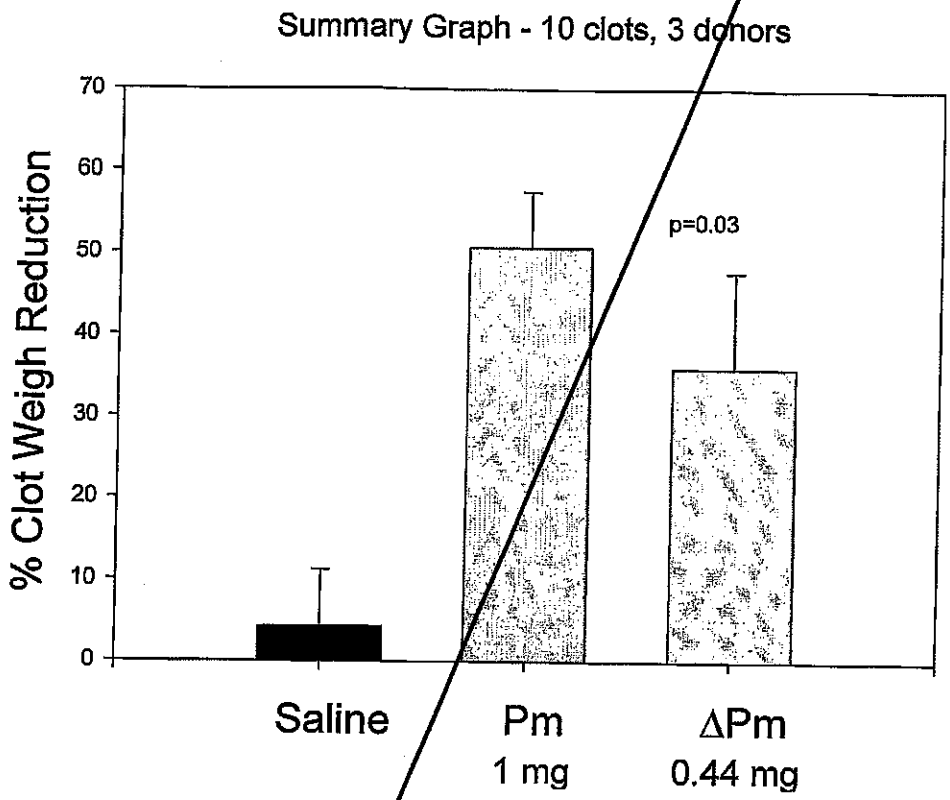
Plasmin:
Km 193 +/- 7 μM
k_{cat}: 760 min^{-1}

Mini-plasmin:
Km 160 +/- 30 μM
k_{cat}: 770 min^{-1}

Micro-plasmin:
Km 145 +/- 13 μM
k_{cat}: 795 min^{-1}

Delta-plasmin:
Km 138 +/- 5 μM
k_{cat}: 755 min^{-1}

FIG. 11


Summary Graph - 10 clots, 3 donors
% Clot Weigh Reduction
70
60
50
40
30
20
10
0
p=0.03
Saline
Pm
1 mg
ΔPm
0.44 mg

B185 1240-PCT(8017).ST25

SEQUENCE LISTING

<110> Talecris Biotherapeutics, Inc.
Hunt, Jennifer A.
Novokhatny, Valery

<120> Recombinantly Modified Plasmin

<130> B185 1240-PCT(8017)

<150> US 60/564,472
<151> 2004-04-22

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1008
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucletoide comprising a nucleotide sequence encoding a polypeptide having a single N-terminal kringle domain homoogous to a kringle domain of native human plasminogen

<400> 1
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aaaacaaaaa acggtatcac ttgtcaaaaa tggtctagca cttcacccca tcgtcctcgt 120
ttctcccctg cgacccatcc ctctgaaggc ctcgaagaaa actactgccg caaccccgat 180
aatgatcctc aaggcccatg gtgttatact accgatcctg aaaaacgtta tgactattgc 240
gatatcttag aatgcgcagc cccttctttt gattgcggca aaccacaagt tgaacccaag 300
aaatgtccag gtcgtgttgt cggcggttgt gttgcgcatc cccacagttg gccgtggcag 360
gtctcattac gtacccggtt tggaatgcac ttttgtggcg gcactctcat ctcgcccgaa 420
tgggttctta cagctgcaca ctgtttggaa aaaagccccc gtccttcttc ttataaagtt 480
atcctcggcg cacatcaaga agtcaattta gaacctcatg tacaagaaat cgaagtatct 540
cgtttattcc tggaaccgac tcgcaagagc atcgcattac ttaaactgtc ctcccccgct 600
gtgatcaccg ataaagtaat tcccgcgtgt ttaccttctc ctaattatgt tgttgcagat 660
cgtacagaat gctttattac cggctggggt gaaactcaag gtacttttgg tgcgggactc 720
ctgaaagaag cacagttacc agtcatcgaa aacaaagtat gtaatcgcta cgaattctta 780
aacggtcgtg ttcaatccac agaattgtgc gcaggtcatt tagcaggtgg cactgatagc 840
tgtcaaggtg attcaggtgg tcctctcgta tgtttcgaaa aagataaata tattctgcaa 900
ggcgtcacct cttggggttt aggttgtgct cgtcccaata aacctggtgt atatgtacgt 960
gtaagtcgtt ttgttacctg gattgaaggt gttatgcgga acaactaa 1008

<210> 2
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<223> a polypeptide having a single N-terminal kringle domain homoogous to a kringle domain of native human plasminogen

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

<210> 3
<211> 2432
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (0)...(0)
<223> Human plasminogen

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ctgggagcag gaagtataga agaatgtgca gcaaaatgtg aggaggacga agaattcacc 180

tgcagggcat tccaatatca cagtaaagag caacaatgtg tgataatggc tgaaaacagg 240
aagtcctcca taatcattag gatgagagat gtagttttat ttgaaaagaa agtgtatctc 300
tcagagtgca agactgggaa tggaaagaac tacagaggga cgatgtccaa aacaaaaaat 360
ggcatcacct gtcaaaaatg gagttccact tctccccaca gacctagatt ctcacctgct 420
acacacccct cagagggact ggaggagaac tactgcagga atccagacaa cgatccgcag 480
gggccctggt gctatactac tgatccagaa aagagatatg actactgcga cattcttgag 540
tgtgaagagg aatgtatgca ttgcagtgga gaaaactatg acggcaaaat ttccaagacc 600
atgtctggac tggaatgcca ggcctgggac tctcagagcc cacacgctca tggatacatt 660
ccttccaaat ttccaaacaa gaacctgaag aagaattact gtcgtaaccc cgatagggag 720
ctgcggcctt ggtgtttcac caccgacccc aacaagcgct gggaactttg cgacatcccc 780
cgctgcacaa cacctccacc atcttctggt cccacctacc agtgttctgaa gggaacaggt 840
gaaaactatc gcgggaatgt ggctgttacc gtttccgggc acacctgtca gcactggagt 900
gcacagaccc ctcacacaca taacaggaca ccagaaaact tccctgcaa aaatttggat 960
gaaaactact gccgcaatcc tgacggaaaa agggccccat ggtgccatac aaccaacagc 1020
caagtgcggt gggagtactg taagataccg tcctgtgact cctccccagt atccacggaa 1080
caattggctc ccacagcacc acctgagcta acccctgtgg tccaggactg ctaccatggt 1140
gatggacaga gctaccgagg cacatcctcc accaccacca caggaaagaa gtgtcagtct 1200
tggtcatcta tgacaccaca ccggcaccag aagaccccag aaaactaccc aaatgctggc 1260
ctgacaatga actactgcag gaatccagat gccgataaag gcccctggtg ttttaccaca 1320
gaccccagcg tcaggtggga gtactgcaac ctgaaaaaat gctcaggaac agaagcgagt 1380
gttgtagcac ctccgcctgt tgtcctgctt ccagatgtag agactccttc cgaagaagac 1440
tgtatgtttg ggaatgggaa aggataccga ggcaagaggg cgaccactgt tactgggacg 1500
ccatgccagg actgggctgc ccaggagccc catagacaca gcattttcac tccagagaca 1560
aatccacggg cgggtctgga aaaaaattac tgccgtaacc ctgatggtga tgtaggtggt 1620
ccctggtgct acacgacaaa tccaagaaaa ctttacgact actgtgatgt ccctcagtgt 1680
gcggcccctt catttgattg tgggaagcct caagtggagc cgaagaaatg tcctggaagg 1740
gttgtggggg ggtgtgtggc ccacccacat tcctggccct ggcaagtcag tcttagaaca 1800
aggtttggaa tgcacttctg tggaggcacc ttgatatccc cagagtgggt gttgactgct 1860
gcccactgct tggagaagtc cccaaggcct tcatcctaca aggtcatcct gggtgcacac 1920
caagaagtga atctcgaacc gcatgttcag gaaatagaag tgtctaggct gttcttggag 1980
cccacacgaa aagatattgc cttgctaaag ctaagcagtc ctgccgtcat cactgacaaa 2040
gtaatcccag cttgtctgcc atccccaaat tatgtggtcg ctgaccggac cgaatgtttc 2100
atcactggct ggggagaaac ccaaggtact tttggagctg gccttctcaa ggaagcccag 2160
ctccctgtga ttgagaataa agtgtgcaat cgctatgagt ttctgaatgg aagagtccaa 2220
tccaccgaac tctgtgctgg gcatttggcc ggaggcactg acagttgcca gggtgacagt 2280
ggaggtcctc tggtttgctt cgagaaggac aaatacattt tacaaggagt cacttcttgg 2340
ggtcttggct gtgcacgccc caataagcct ggtgtctatg ttcgtgtttc aaggtttgtt 2400
acttggattg agggagtgat gagaaataat ta 2432

<210> 4
<211> 810
<212> PRT
<213> Homo sapien

<220>
<221> PEPTIDE
<222> (0)...(0)
<223> Human plasminogen

<400> 4

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 1               5                  10                  15
Gly Gln Gly Glu Pro Leu Asp Asp Tyr Val Asn Thr Gln Gly Ala Ser
            20                  25                  30
Leu Phe Ser Val Thr Lys Lys Gln Leu Gly Ala Gly Ser Ile Glu Glu
        35                  40                  45
Cys Ala Ala Lys Cys Glu Glu Asp Glu Glu Phe Thr Cys Arg Ala Phe
    50                  55                  60
Gln Tyr His Ser Lys Glu Gln Gln Cys Val Ile Met Ala Glu Asn Arg
```

```
65                  70                  75                  80
Lys Ser Ser Ile Ile Ile Arg Met Arg Asp Val Val Leu Phe Glu Lys
                85                  90                  95
Lys Val Tyr Leu Ser Glu Cys Lys Thr Gly Asn Gly Lys Asn Tyr Arg
            100                 105                 110
Gly Thr Met Ser Lys Thr Lys Asn Gly Ile Thr Cys Gln Lys Trp Ser
        115                 120                 125
Ser Thr Ser Pro His Arg Pro Arg Phe Ser Pro Ala Thr His Pro Ser
    130                 135                 140
Glu Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Pro Gln
145                 150                 155                 160
Gly Pro Trp Cys Tyr Thr Thr Asp Pro Glu Lys Arg Tyr Asp Tyr Cys
                165                 170                 175
Asp Ile Leu Glu Cys Glu Glu Glu Cys Met His Cys Ser Gly Glu Asn
            180                 185                 190
Tyr Asp Gly Lys Ile Ser Lys Thr Met Ser Gly Leu Glu Cys Gln Ala
        195                 200                 205
Trp Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ser Lys Phe
    210                 215                 220
Pro Asn Lys Asn Leu Lys Lys Asn Tyr Cys Arg Asn Pro Asp Arg Glu
225                 230                 235                 240
Leu Arg Pro Trp Cys Phe Thr Thr Asp Pro Asn Lys Arg Trp Glu Leu
                245                 250                 255
Cys Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Ser Ser Gly Pro Thr
            260                 265                 270
Tyr Gln Cys Leu Lys Gly Thr Gly Glu Asn Tyr Arg Gly Asn Val Ala
        275                 280                 285
Val Thr Val Ser Gly His Thr Cys Gln His Trp Ser Ala Gln Thr Pro
    290                 295                 300
His Thr His Asn Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Asp
305                 310                 315                 320
Glu Asn Tyr Cys Arg Asn Pro Asp Gly Lys Arg Ala Pro Trp Cys His
                325                 330                 335
Thr Thr Asn Ser Gln Val Arg Trp Glu Tyr Cys Lys Ile Pro Ser Cys
            340                 345                 350
Asp Ser Ser Pro Val Ser Thr Glu Gln Leu Ala Pro Thr Ala Pro Pro
        355                 360                 365
Glu Leu Thr Pro Val Val Gln Asp Cys Tyr His Gly Asp Gly Gln Ser
    370                 375                 380
Tyr Arg Gly Thr Ser Ser Thr Thr Thr Thr Gly Lys Lys Cys Gln Ser
385                 390                 395                 400
Trp Ser Ser Met Thr Pro His Arg His Gln Lys Thr Pro Glu Asn Tyr
                405                 410                 415
Pro Asn Ala Gly Leu Thr Met Asn Tyr Cys Arg Asn Pro Asp Ala Asp
            420                 425                 430
Lys Gly Pro Trp Cys Phe Thr Thr Asp Pro Ser Val Arg Trp Glu Tyr
        435                 440                 445
Cys Asn Leu Lys Lys Cys Ser Gly Thr Glu Ala Ser Val Val Ala Pro
    450                 455                 460
Pro Pro Val Val Leu Leu Pro Asp Val Glu Thr Pro Ser Glu Glu Asp
465                 470                 475                 480
Cys Met Phe Gly Asn Gly Lys Gly Tyr Arg Gly Lys Arg Ala Thr Thr
                485                 490                 495
Val Thr Gly Thr Pro Cys Gln Asp Trp Ala Ala Gln Glu Pro His Arg
            500                 505                 510
His Ser Ile Phe Thr Pro Glu Thr Asn Pro Arg Ala Gly Leu Glu Lys
        515                 520                 525
Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Gly Gly Pro Trp Cys Tyr
    530                 535                 540
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Thr Thr Asn Pro Arg Lys Leu Tyr Asp Tyr Cys Asp Val Pro Gln Cys
545                 550                 555                 560
Ala Ala Pro Ser Phe Asp Cys Gly Lys Pro Gln Val Glu Pro Lys Lys
                565                 570                 575
Cys Pro Gly Arg Val Val Gly Gly Cys Val Ala His Pro His Ser Trp
            580                 585                 590
Pro Trp Gln Val Ser Leu Arg Thr Arg Phe Gly Met His Phe Cys Gly
        595                 600                 605
Gly Thr Leu Ile Ser Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu
    610                 615                 620
Glu Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His
625                 630                 635                 640
Gln Glu Val Asn Leu Glu Pro His Val Gln Glu Ile Glu Val Ser Arg
                645                 650                 655
Leu Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala Leu Leu Lys Leu Ser
            660                 665                 670
Ser Pro Ala Val Ile Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser
        675                 680                 685
Pro Asn Tyr Val Val Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp
    690                 695                 700
Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln
705                 710                 715                 720
Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn
                725                 730                 735
Gly Arg Val Gln Ser Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly
            740                 745                 750
Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu
        755                 760                 765
Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys
    770                 775                 780
Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val
785                 790                 795                 800
Thr Trp Ile Glu Gly Val Met Arg Asn Asn
                805                 810
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<210> 5
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<223> kringle domain 1 of native human plasmin(ogen)

<400> 5

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Cys Lys Thr Gly Asn Gly Lys Asn Tyr Arg Gly Thr Met Ser Lys Thr
 1                5                  10                  15
Lys Asn Gly Ile Thr Cys Gln Lys Trp Ser Ser Thr Ser Pro His Arg
            20                  25                  30
Pro Arg Phe Ser Pro Ala Thr His Pro Ser Glu Gly Leu Glu Glu Asn
        35                  40                  45
Tyr Cys Arg Asn Pro Asp Asn Asp Pro Gln Gly Pro Trp Cys Tyr Thr
    50                  55                  60
Thr Asp Pro Glu Lys Arg Tyr Asp Tyr Cys Asp Ile Leu Glu Cys
65                  70                  75
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<210> 6
<211> 78

<212> PRT
<213> Artificial Sequence

<220>
<223> kringle domain 2 of native human plasmin(ogen)

<400> 6
Cys Met His Cys Ser Gly Glu Asn Tyr Asp Gly Lys Ile Ser Lys Thr
1 5 10 15
Met Ser Gly Leu Glu Cys Gln Ala Trp Asp Ser Gln Ser Pro His Ala
20 25 30
His Gly Tyr Ile Pro Ser Lys Phe Pro Asn Lys Asn Leu Lys Lys Asn
35 40 45
Tyr Cys Arg Asn Pro Asp Arg Glu Leu Arg Pro Trp Cys Phe Thr Thr
50 55 60
Asp Pro Asn Lys Arg Trp Glu Leu Cys Asp Ile Pro Arg Cys
65 70 75

<210> 7
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<223> kringle domain 3 of native human plasmin(ogen)

<400> 7
Cys Leu Lys Gly Thr Gly Glu Asn Tyr Arg Gly Asn Val Ala Val Thr
1 5 10 15
Val Ser Gly His Thr Cys Gln His Trp Ser Ala Gln Thr Pro His Thr
20 25 30
His Asn Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Asp Glu Asn
35 40 45
Tyr Cys Arg Asn Pro Asp Gly Lys Arg Ala Pro Trp Cys His Thr Thr
50 55 60
Asn Ser Gln Val Arg Trp Glu Tyr Cys Lys Ile Pro Ser Cys
65 70 75

<210> 8
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<223> kringle domain 4 of native human plasmin(ogen)

<400> 8
Cys Tyr His Gly Asp Gly Gln Ser Tyr Arg Gly Thr Ser Ser Thr Thr
1 5 10 15
Thr Thr Gly Lys Lys Cys Gln Ser Trp Ser Ser Met Thr Pro His Arg
20 25 30
His Gln Lys Thr Pro Glu Asn Tyr Pro Asn Ala Gly Leu Thr Met Asn
35 40 45
Tyr Cys Arg Asn Pro Asp Ala Asp Lys Gly Pro Trp Cys Phe Thr Thr
50 55 60
Asp Pro Ser Val Arg Trp Glu Tyr Cys Asn Leu Lys Lys Cys
65 70 75

<210> 9
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> kringle domain 5 of native human plasmin(ogen)

<400> 9

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

FIG. 1

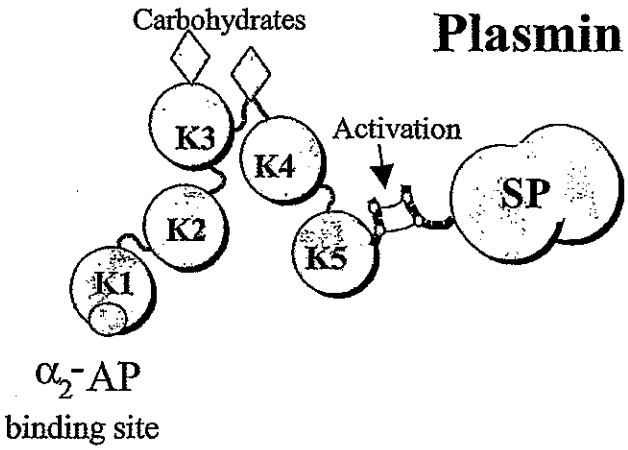

Carbohydrates
Plasmin
K3
K4
Activation
SP
K2
K5
K1
α_2-AP
binding site

FIG. 2

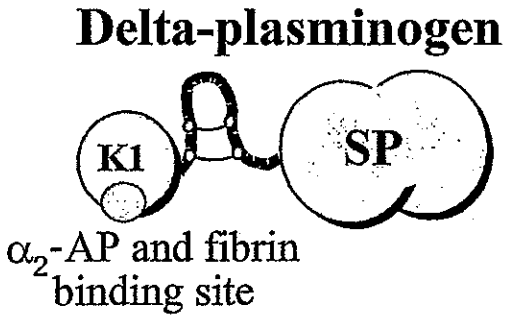

Delta-plasminogen
K1
SP
α_2-AP and fibrin
binding site

FIG. 3


-19
1
MEHKEVVLLLLLFLKSGQGEPLDDYVNTQGASLFSVTKKQLGAGSIEECAAKCEEDEEFTCRAFQ
78
YHSKEQQCVIMAENRKSSIIIRMRDVVLFEKKVYLSECKTGNGKNYRGTMSKTKNGITCQKWSST
136
143
153
162
SPHRPRFSPATHPSEGLEENYCRNPDNDPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDG
kringle 1
KISKTMSGLECQAWDSQSPHAHGYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIP
kringle 2
RCTTPPPSSGPTYQCLKGTGENYRGNVAVTVSGHTCQHWSAQTPHTHNRTPENFPCKNLDENYCR
kringle 3
NPDGKRAPWCHTTNSQVRWEYCKIPSCDSSPVSTEQLAPTAPPELTPVVQDCYHGDGQSYRGTSS
TTTTGKKCQSWSSMTPHRHQKTPENYPNAGLTMNYCRNPDADKGPWCFTTDPSVRWEYCNLKKCS
kringle 4
GTEASVVAPPPVVLLPDVETPSEEDCMFGNGKGYRGKRATTVTGTPCQDWAAQEPHRHSIFTPET
kringle 5
542
NPRAGLEKNYCRNPDGDVGGPWCYTTNPRKLYDYCDVPQCAAPSFDCGKPQVEPKKCPGRVVGGC
VAHPHSWPWQVSLRTRFGMHFCGGTLISPEWVLTAAHCLEKSPRPSSYKVILGAHQEVNLEPHVQ
EIEVSRLFLEPTRKDIALLKLSSPAVITDKVIPACLPSPNYVVADRTECFITGWGETQGTFGAGL
LKEAQLPVIENKVCNRYEFLNGRVQSTELCAGHLAGGTDSCQGDSGGPLVCFEKDKYILQGVTSW
791
GLGCARPNKPGVYVRVSRFVTWIEGVMRNN
(SEQ ID NO:4)

FIG. 4

```
HK1   CKTGNGKNYR GTMSKTKNGI TCQKWSSTSP HR-PRFSPAT HPSEGLEENY
HK2   CMHCSGENYD GKISKTMSGL ECQAWDSQSP HA-HGYIPSK FPNKNLKKNY
HK3   CLKGTGENYR GNVAVTVSGH TCQHWSAQTP HT-HNRTPEN FPCKNLDENY
HK4   CYHGDGQSYR GTSSTTTTGK KCQSWSSMTP HR-HQKTPEN YPNAGLTMNY
HK5   CMFGNGKGYR GKRATTVTGT PCQDWAAQEP HRHSIFTPET NPRAGLEKNY

(con't)
HK1   CRNPDNDPQG PWCYTTDPEK RYDYCDILEC  (SEQ ID NO:5)
HK2   CRNPDRE-LR PWCFTTDPNK RWELCDIPRC  (SEQ ID NO:6)
HK3   CRNPDGK-RA PWCHTTNSQV RWEYCKIPSC  (SEQ ID NO:7)
HK4   CRNPDAD-KG PWCFTTDPSV RWEYCNLKKC  (SEQ ID NO:8)
HK5   CRNPDGDVGG PWCYTTNPRK LYDYCDVPQC  (SEQ ID NO:9)
```

FIG. 5

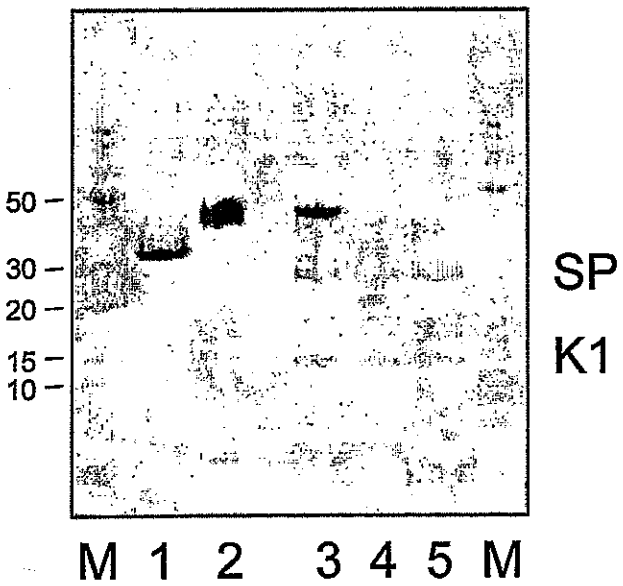


FIG. 6

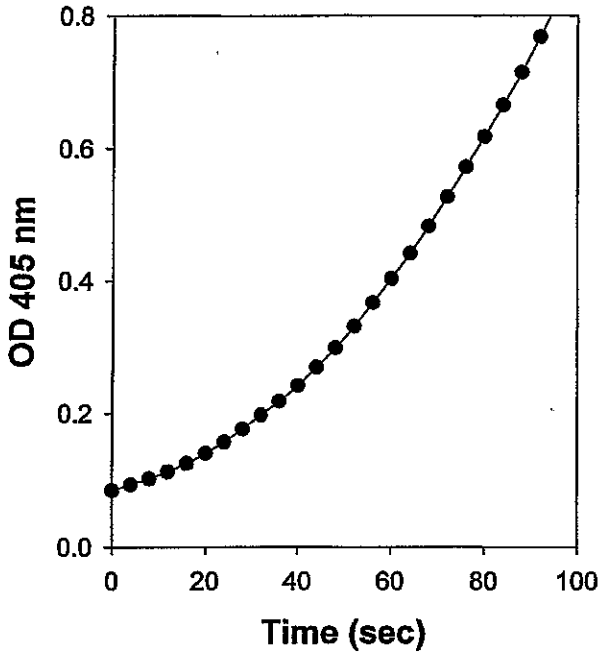

OD 405 nm
0.0
0.2
0.4
0.6
0.8
0
20
40
60
80
100
Time (sec)

FIG. 7

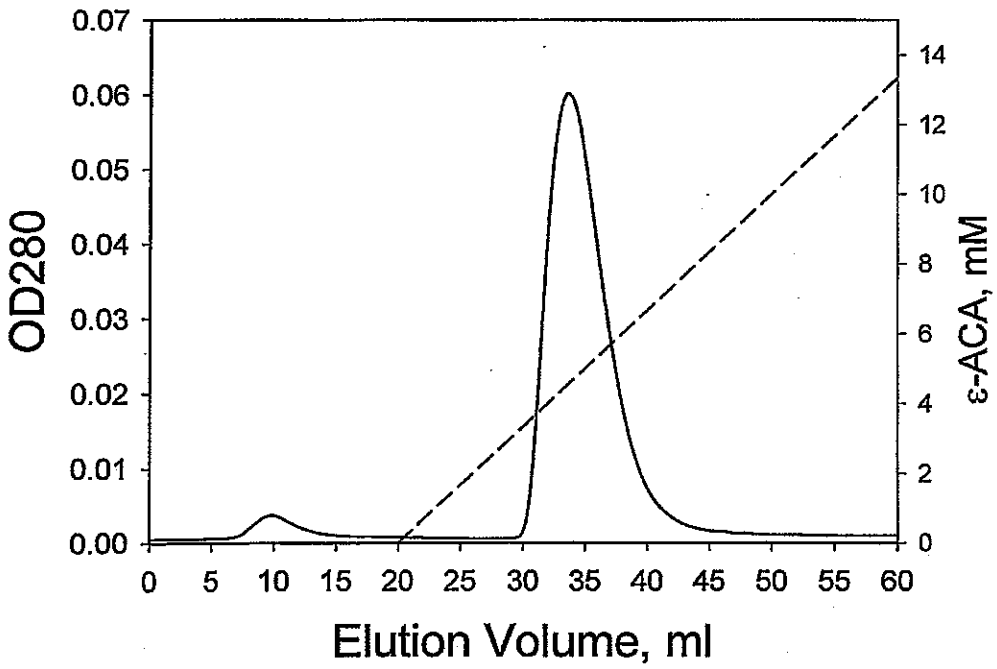

OD280
0.00
0.01
0.02
0.03
0.04
0.05
0.06
0.07
0
5
10
15
20
25
30
35
40
45
50
55
60
Elution Volume, ml
ε-ACA, mM
0
2
4
6
8
10
12
14

FIG. 8

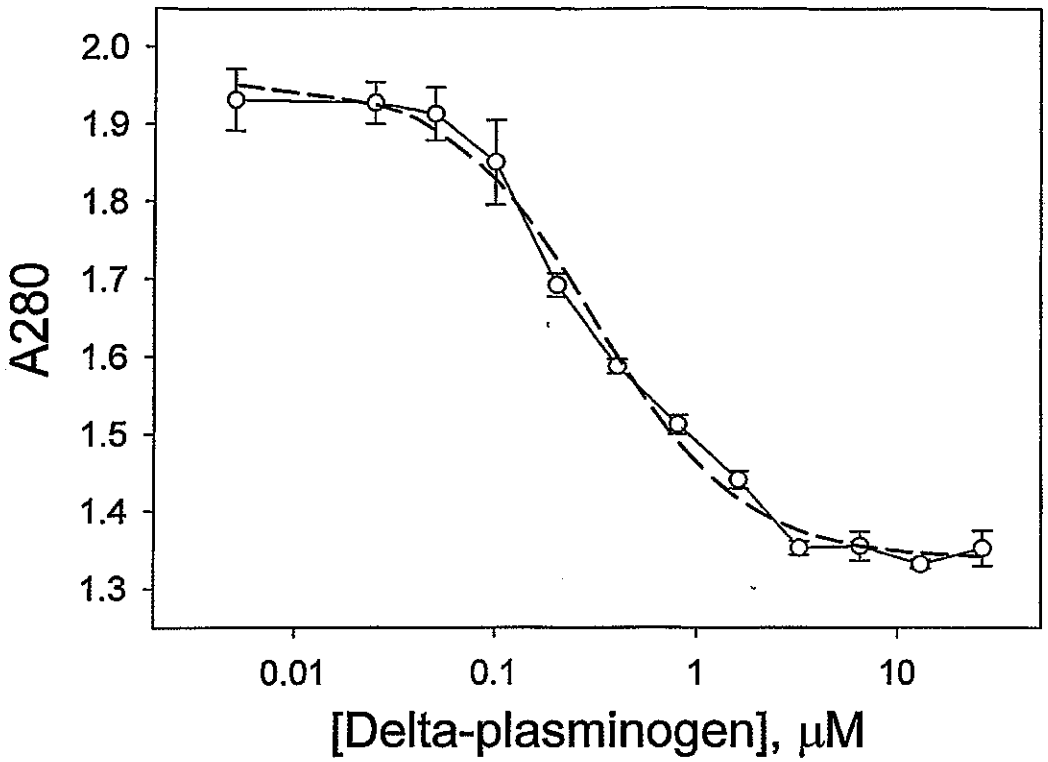

A280
2.0
1.9
1.8
1.7
1.6
1.5
1.4
1.3
0.01
0.1
1
10
[Delta-plasminogen], μM

FIG. 9

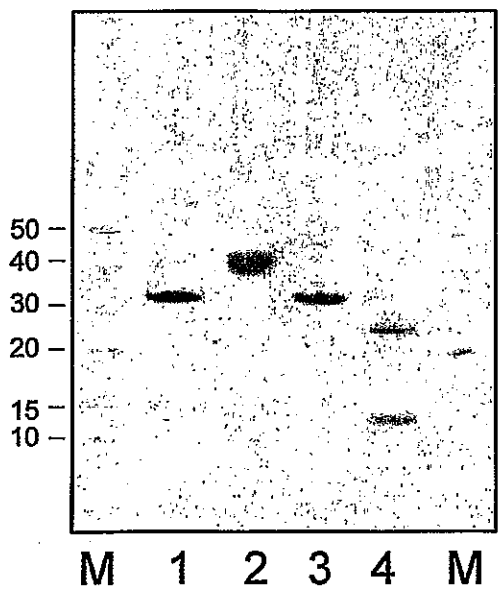
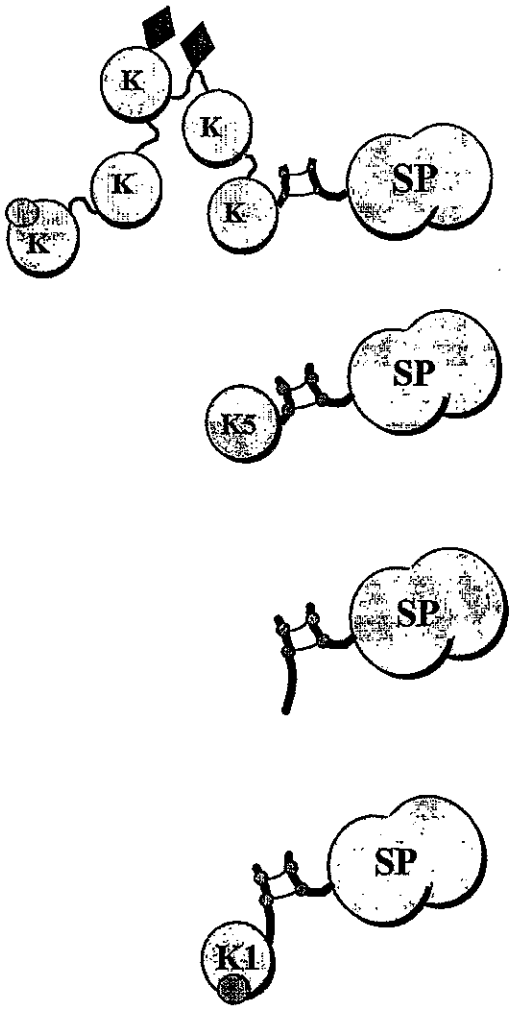

50
40
30
20
15
10
M
1
2
3
4
M

FIG. 10



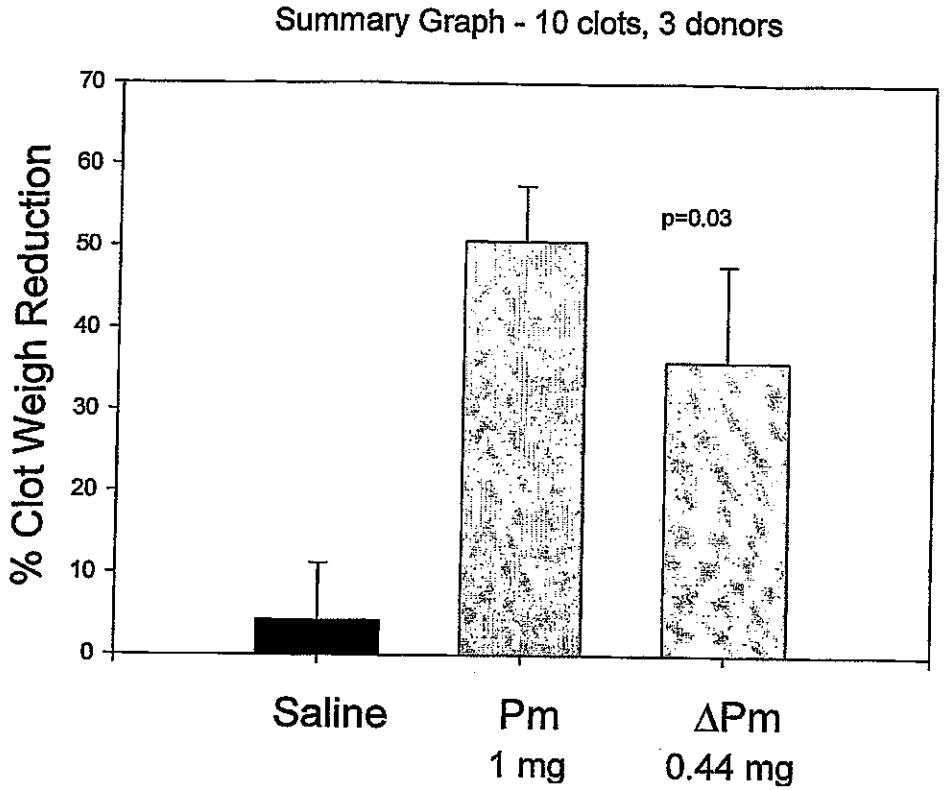
Plasmin:
Km 193 +/- 7 μM
k_{cat}: 760 min^{-1}

Mini-plasmin:
Km 160 +/- 30 μM
k_{cat}: 770 min^{-1}

Micro-plasmin:
Km 145 +/- 13 μM
k_{cat}: 795 min^{-1}

Delta-plasmin:
Km 138 +/- 5 μM
k_{cat}: 755 min^{-1}

FIG. 11


Summary Graph - 10 clots, 3 donors
% Clot Weigh Reduction
70
60
50
40
30
20
10
0
p=0.03
Saline
Pm
1 mg
ΔPm
0.44 mg

SEQUENCE LISTING

<110> Talecris Biotherapeutics, Inc.
Hunt, Jennifer A.
Novokhatny, Valery

<120> Recombinantly Modified Plasmin

<130> B185 1240-PCT(8017)

<150> US 60/564,472
<151> 2004-04-22

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1008
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucletoide comprising a nucleotide sequence encoding a polypeptide having a single N-terminal kringle domain homoogous to a kringle domain of native human plasminogen

<400> 1
aaagtctatt tatctgaatg taaaacaggc aatggtaaaa actatcgcgg taccatgtcc 60
aaaacaaaaa acggtatcac ttgtcaaaaa tggtctagca cttcacccca tcgtcctcgt 120
ttctcccctg cgacccatcc ctctgaaggc ctcgaagaaa actactgccg caacccccgat 180
aatgatcctc aaggcccatg gtgttatact accgatcctg aaaaacgtta tgactattgc 240
gatatcttag aatgcgcagc cccttctttt gattgcggca aaccacaagt tgaacccaag 300
aaatgtccag gtcgtgttgt cggcggttgt gttgcgcatc cccacagttg gccgtggcag 360
gtctcattac gtacccggtt tggaatgcac ttttgtggcg gcactctcat ctcgcccgaa 420
tgggttctta cagctgcaca ctgtttggaa aaaagccccc gtccttcttc ttataaagtt 480
atcctcggcg cacatcaaga agtcaattta gaacctcatg tacaagaaat cgaagtatct 540
cgtttattcc tggaaccgac tcgcaaagac atcgcattac ttaaactgtc ctccccccgct 600
gtgatcaccg ataaagtaat tcccgcgtgt ttaccttctc ctaattatgt tgttgcagat 660
cgtacagaat gctttattac cggctggggt gaaactcaag gtacttttgg tgcgggactc 720
ctgaaagaag cacagttacc agtcatcgaa aacaaagtat gtaatcgcta cgaattctta 780
aacggtcgtg ttcaatccac agaattgtgc gcaggtcatt tagcaggtgg cactgatagc 840
tgtcaaggtg attcaggtgg tcctctcgta tgtttcgaaa aagataaata tattctgcaa 900
ggcgtcacct cttggggttt aggttgtgct cgtcccaata aacctggtgt atatgtacgt 960
gtaagtcgtt ttgttacctg gattgaaggt gttatgcgga acaactaa 1008

<210> 2
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<223> a polypeptide having a single N-terminal kringle domain homoogous to a kringle domain of native human plasminogen

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

<210> 3
<211> 2432
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (0)...(0)
<223> Human plasminogen

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cctctggatg actatgtgaa tacccagggg gcttcactgt tcagtgtcac taagaagcag 120
ctgggagcag gaagtataga agaatgtgca gcaaaatgtg aggaggacga agaattcacc 180

tgcagggcat tccaatatca cagtaaagag caacaatgtg tgataatggc tgaaaacagg 240
aagtcctcca taatcattag gatgagagat gtagttttat ttgaaaagaa agtgtatctc 300
tcagagtgca agactgggaa tggaaagaac tacagaggga cgatgtccaa aacaaaaaat 360
ggcatcacct gtcaaaaatg gagttccact tctccccaca gacctagatt ctcacctgct 420
acacacccct cagagggact ggaggagaac tactgcagga atccagacaa cgatccgcag 480
gggccctggt gctatactac tgatccagaa aagagatatg actactgcga cattcttgag 540
tgtgaagagg aatgtatgca ttgcagtgga gaaaactatg acggcaaaat ttccaagacc 600
atgtctggac tggaatgcca ggcctgggac tctcagagcc cacacgctca tggatacatt 660
ccttccaaat ttccaaacaa gaacctgaag aagaattact gtcgtaaccc cgatagggag 720
ctgcggcctt ggtgtttcac caccgacccc aacaagcgct gggaactttg cgacatcccc 780
cgctgcacaa cacctccacc atcttctggt cccacctacc agtgtctgaa gggaacaggt 840
gaaaactatc gcgggaatgt ggctgttacc gtttccgggc acacctgtca gcactggagt 900
gcacagaccc ctcacacaca taacaggaca ccagaaaact tcccctgcaa aaatttggat 960
gaaaactact gccgcaatcc tgacggaaaa agggccccat ggtgccatac aaccaacagc 1020
caagtgcggt gggagtactg taagataccg tcctgtgact cctccccagt atccacggaa 1080
caattggctc ccacagcacc acctgagcta acccctgtgg tccaggactg ctaccatggt 1140
gatggacaga gctaccgagg cacatcctcc accaccacca caggaaagaa gtgtcagtct 1200
tggtcatcta tgacaccaca ccggcaccag aagaccccag aaaactaccc aaatgctggc 1260
ctgacaatga actactgcag gaatccagat gccgataaag gcccctggtg ttttaccaca 1320
gaccccagcg tcaggtggga gtactgcaac ctgaaaaaat gctcaggaac agaagcgagt 1380
gttgtagcac ctccgcctgt tgtcctgctt ccagatgtag agactccttc cgaagaagac 1440
tgtatgtttg ggaatgggaa aggataccga ggcaagaggg cgaccactgt tactgggacg 1500
ccatgccagg actgggctgc ccaggagccc catagacaca gcattttcac tccagagaca 1560
aatccacggg cgggtctgga aaaaaattac tgccgtaacc ctgatggtga tgtaggtggt 1620
ccctggtgct acacgacaaa tccaagaaaa ctttacgact actgtgatgt ccctcagtgt 1680
gcggcccctt catttgattg tgggaagcct caagtggagc cgaagaaatg tcctggaagg 1740
gttgtggggg ggtgtgtggc ccacccacat tcctggccct ggcaagtcag tcttagaaca 1800
aggtttggaa tgcacttctg tggaggcacc ttgatatccc cagagtgggt gttgactgct 1860
gcccactgct tggagaagtc cccaaggcct tcatcctaca aggtcatcct gggtgcacac 1920
caagaagtga atctcgaacc gcatgttcag gaaatagaag tgtctaggct gttcttggag 1980
cccacacgaa aagatattgc cttgctaaag ctaagcagtc ctgccgtcat cactgacaaa 2040
gtaatcccag cttgtctgcc atccccaaat tatgtggtcg ctgaccggac cgaatgtttc 2100
atcactggct ggggagaaac ccaaggtact tttggagctg gccttctcaa ggaagcccag 2160
ctccctgtga ttgagaataa agtgtgcaat cgctatgagt ttctgaatgg aagagtccaa 2220
tccaccgaac tctgtgctgg gcatttggcc ggaggcactg acagttgcca gggtgacagt 2280
ggaggtcctc tggtttgctt cgagaaggac aaatacattt tacaaggagt cacttcttgg 2340
ggtcttggct gtgcacgccc caataagcct ggtgtctatg ttcgtgtttc aaggtttgtt 2400
acttggattg agggagtgat gagaaataat ta 2432

<210> 4
<211> 810
<212> PRT
<213> Homo sapien

<220>
<221> PEPTIDE
<222> (0)...(0)
<223> Human plasminogen

<400> 4
Met Glu His Lys Glu Val Val Leu Leu Leu Leu Phe Leu Lys Ser
 1   5   10   15
Gly Gln Gly Glu Pro Leu Asp Asp Tyr Val Asn Thr Gln Gly Ala Ser
            20   25   30
Leu Phe Ser Val Thr Lys Lys Gln Leu Gly Ala Gly Ser Ile Glu Glu
        35   40   45
Cys Ala Ala Lys Cys Glu Glu Asp Glu Glu Phe Thr Cys Arg Ala Phe
    50   55   60
Gln Tyr His Ser Lys Glu Gln Gln Cys Val Ile Met Ala Glu Asn Arg

65 70 75 80
Lys Ser Ser Ile Ile Ile Arg Met Arg Asp Val Val Leu Phe Glu Lys
85 90 95
Lys Val Tyr Leu Ser Glu Cys Lys Thr Gly Asn Gly Lys Asn Tyr Arg
100 105 110
Gly Thr Met Ser Lys Thr Lys Asn Gly Ile Thr Cys Gln Lys Trp Ser
115 120 125
Ser Thr Ser Pro His Arg Pro Arg Phe Ser Pro Ala Thr His Pro Ser
130 135 140
Glu Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Pro Gln
145 150 155 160
Gly Pro Trp Cys Tyr Thr Thr Asp Pro Glu Lys Arg Tyr Asp Tyr Cys
165 170 175
Asp Ile Leu Glu Cys Glu Glu Glu Cys Met His Cys Ser Gly Glu Asn
180 185 190
Tyr Asp Gly Lys Ile Ser Lys Thr Met Ser Gly Leu Glu Cys Gln Ala
195 200 205
Trp Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ser Lys Phe
210 215 220
Pro Asn Lys Asn Leu Lys Lys Asn Tyr Cys Arg Asn Pro Asp Arg Glu
225 230 235 240
Leu Arg Pro Trp Cys Phe Thr Thr Asp Pro Asn Lys Arg Trp Glu Leu
245 250 255
Cys Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Ser Ser Gly Pro Thr
260 265 270
Tyr Gln Cys Leu Lys Gly Thr Gly Glu Asn Tyr Arg Gly Asn Val Ala
275 280 285
Val Thr Val Ser Gly His Thr Cys Gln His Trp Ser Ala Gln Thr Pro
290 295 300
His Thr His Asn Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Asp
305 310 315 320
Glu Asn Tyr Cys Arg Asn Pro Asp Gly Lys Arg Ala Pro Trp Cys His
325 330 335
Thr Thr Asn Ser Gln Val Arg Trp Glu Tyr Cys Lys Ile Pro Ser Cys
340 345 350
Asp Ser Ser Pro Val Ser Thr Glu Gln Leu Ala Pro Thr Ala Pro Pro
355 360 365
Glu Leu Thr Pro Val Val Gln Asp Cys Tyr His Gly Asp Gly Gln Ser
370 375 380
Tyr Arg Gly Thr Ser Ser Thr Thr Thr Thr Gly Lys Lys Cys Gln Ser
385 390 395 400
Trp Ser Ser Met Thr Pro His Arg His Gln Lys Thr Pro Glu Asn Tyr
405 410 415
Pro Asn Ala Gly Leu Thr Met Asn Tyr Cys Arg Asn Pro Asp Ala Asp
420 425 430
Lys Gly Pro Trp Cys Phe Thr Thr Asp Pro Ser Val Arg Trp Glu Tyr
435 440 445
Cys Asn Leu Lys Lys Cys Ser Gly Thr Glu Ala Ser Val Val Ala Pro
450 455 460
Pro Pro Val Val Leu Leu Pro Asp Val Glu Thr Pro Ser Glu Glu Asp
465 470 475 480
Cys Met Phe Gly Asn Gly Lys Gly Tyr Arg Gly Lys Arg Ala Thr Thr
485 490 495
Val Thr Gly Thr Pro Cys Gln Asp Trp Ala Ala Gln Glu Pro His Arg
500 505 510
His Ser Ile Phe Thr Pro Glu Thr Asn Pro Arg Ala Gly Leu Glu Lys
515 520 525
Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Gly Gly Pro Trp Cys Tyr
530 535 540

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

<210> 5
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<223> kringle domain 1 of native human plasmin(ogen)

<400> 5

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

<210> 6
<211> 78

<212> PRT
<213> Artificial Sequence

<220>
<223> kringle domain 2 of native human plasmin(ogen)

<400> 6
Cys Met His Cys Ser Gly Glu Asn Tyr Asp Gly Lys Ile Ser Lys Thr
1 5 10 15
Met Ser Gly Leu Glu Cys Gln Ala Trp Asp Ser Gln Ser Pro His Ala
20 25 30
His Gly Tyr Ile Pro Ser Lys Phe Pro Asn Lys Asn Leu Lys Lys Asn
35 40 45
Tyr Cys Arg Asn Pro Asp Arg Glu Leu Arg Pro Trp Cys Phe Thr Thr
50 55 60
Asp Pro Asn Lys Arg Trp Glu Leu Cys Asp Ile Pro Arg Cys
65 70 75

<210> 7
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<223> kringle domain 3 of native human plasmin(ogen)

<400> 7
Cys Leu Lys Gly Thr Gly Glu Asn Tyr Arg Gly Asn Val Ala Val Thr
1 5 10 15
Val Ser Gly His Thr Cys Gln His Trp Ser Ala Gln Thr Pro His Thr
20 25 30
His Asn Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Asp Glu Asn
35 40 45
Tyr Cys Arg Asn Pro Asp Gly Lys Arg Ala Pro Trp Cys His Thr Thr
50 55 60
Asn Ser Gln Val Arg Trp Glu Tyr Cys Lys Ile Pro Ser Cys
65 70 75

<210> 8
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<223> kringle domain 4 of native human plasmin(ogen)

<400> 8
Cys Tyr His Gly Asp Gly Gln Ser Tyr Arg Gly Thr Ser Ser Thr Thr
1 5 10 15
Thr Thr Gly Lys Lys Cys Gln Ser Trp Ser Ser Met Thr Pro His Arg
20 25 30
His Gln Lys Thr Pro Glu Asn Tyr Pro Asn Ala Gly Leu Thr Met Asn
35 40 45
Tyr Cys Arg Asn Pro Asp Ala Asp Lys Gly Pro Trp Cys Phe Thr Thr
50 55 60
Asp Pro Ser Val Arg Trp Glu Tyr Cys Asn Leu Lys Lys Cys
65 70 75

<210> 9
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> kringle domain 5 of native human plasmin(ogen)

<400> 9

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