

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

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Gly Gly Gly Ser

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Gly Ser Gly Ser

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Gly Gly Ser Gly

1

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Gly Ser Gly Gly Ser

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Ser Gly Gly Ser Gly

1

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Gly Gly Gly Gly Ser

1

5

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Gly Gly Ser Gly Gly Ser
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Ser Gly Ser Gly Gly Ser Gly Ser
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Gly Ser Gly Gly Ser Gly Ser Gly Ser
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Ser Gly Gly Ser Gly Gly Ser Gly Ser Gly
1 5 10

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Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser
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<223> filler sequence-13

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Ser Gly Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser
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Gly Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser
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16EAP0020CPT-seq1

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<223> filler sequence-16

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Ser Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Ser Gly Ser Gly
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<223> ACETYLATION

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<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

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16EAP0020CPT-seq1

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 Gly Ser Lys

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<222> 1

<223> ACETYLATION

<220>

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<400> 19

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 Gly Ser Lys Gly Ser Lys Gly Ser Lys Gly Ser Lys Gly Ser Lys
 20 25 30

<210> 20

<211> 16

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<223> Xaa is homopropargylglycine

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<223> ACETYLATION

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16EAP0020CPT-seq1

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 1 5 10 15

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 <223> Xaa is homopropargylglycine

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<400> 21
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 1 5 10 15
 Gly Ser Lys

<210> 22
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16EAP0020CPT-seq1

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 1 5 10 15
 Gly Ser Lys

<210> 23
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 <223> Xaa is homopropargylglycine

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<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

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

<400> 24

16EAP0020CPT-seq1

Cys Xaa Lys Xaa Lys Xaa Lys
1 5

<210> 25
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<212> PRT
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<220>
<221> MOD_RES
<222> 1
<223> ACETYLTATION

<220>
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<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

16EAP0020CPT-seq1

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			

16EAP0020CPT-seq1

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

16EAP0020CPT-seq1

<400> 29

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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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

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<210> 30

<211> 599

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 30

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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

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16EAP0020CPT-seq1

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
					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	

16EAP0020CPT-seq1

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 Ser Gly Gly Gly
580 585 590
Gly Ser Gly Gly Gly Ser
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<210> 31

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

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

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Ser Tyr Gln Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr
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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

16EAP0020CPT-seq1

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

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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

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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

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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

<210> 33

<211> 771

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 33

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

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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														

16EAP0020CPT-seq1

<210> 34

<211> 1015

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 34

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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 Lys His Arg Arg Ser Pro Gly Glu Arg
290    295    300

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16EAP0020CPT-seq1

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		

16EAP0020CPT-seq1

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
						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

16EAP0020CPT-seq1

<220>

<223> (TNK-tPA)-(scFv α fibrin)

<400> 35

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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 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

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

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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															