

SEQUENCE LISTING

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<120> Vector particles for targeting CD34+ cells

<130> BET 08P0498

<150> EP 07290918.7

<151> 2007-07-23

<160> 15

<170> PatentIn version 3.4

<210> 1

<211> 1692

<212> DNA

<213> Artificial sequence

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<223> Fusion of the transmembrane and extracellular domains of the feline endogenous RD114 virus envelope glycoprotein and the cytoplasmic domain of MLV-A envelope glycoprotein

<220>

<221> CDS

<222> (1)..(1692)

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Pro Pro Asn Ser Ile Gln Gln Val Thr Cys Pro Gly Lys Thr Ala Tyr	
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Ser Met His Ser Ser Cys Tyr Thr Glu Tyr Arg Gln Cys Arg Arg Ile	
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Asn Lys Thr Tyr Tyr Thr Ala Thr Leu Leu Lys Ile Arg Ser Gly Ser	

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Leu Gly Val Ser Val Thr Gln Tyr Thr Lys Leu Ser His Gln Leu Ile	
405 410 415	
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Pro Leu Trp Thr Gly Leu Gln Gly Phe Leu Pro Tyr Leu Leu Pro Leu	
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<213> Artificial sequence

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<223> Fusion of the transmembrane and extracellular domains of the

feline endogenous RD114 virus envelope glycoprotein and the
cytoplasmic domain of MLV-A envelope glycoprotein

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Arg Ala Gly Phe Asp Asp Pro Arg Lys Ala Ile Ala Leu Val Gln Lys
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Gln His Gly Lys Pro Cys Glu Cys Ser Gly Gly Gln Val Ser Glu Ala
35 40 45

Pro Pro Asn Ser Ile Gln Gln Val Thr Cys Pro Gly Lys Thr Ala Tyr
50 55 60

Leu Met Thr Asn Gln Lys Trp Lys Cys Arg Val Thr Pro Lys Ile Ser
65 70 75 80

Pro Ser Gly Gly Glu Leu Gln Asn Cys Pro Cys Asn Thr Phe Gln Asp
85 90 95

Ser Met His Ser Ser Cys Tyr Thr Glu Tyr Arg Gln Cys Arg Arg Ile
100 105 110

Asn Lys Thr Tyr Tyr Thr Ala Thr Leu Leu Lys Ile Arg Ser Gly Ser
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Leu Asn Glu Val Gln Ile Leu Gln Asn Pro Asn Gln Leu Leu Gln Ser
130 135 140

Pro Cys Arg Gly Ser Ile Asn Gln Pro Val Cys Trp Ser Ala Thr Ala
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Pro Ile His Ile Ser Asp Gly Gly Gly Pro Leu Asp Thr Lys Arg Val
165 170 175

Trp Thr Val Gln Lys Arg Leu Glu Gln Ile His Lys Ala Met Thr Pro
180 185 190

Glu Leu Gln Tyr His Pro Leu Ala Leu Pro Lys Val Arg Asp Asp Leu
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Ser Leu Asp Ala Arg Thr Phe Asp Ile Leu Asn Thr Thr Phe Arg Leu
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Leu Gln Met Ser Asn Phe Ser Leu Ala Gln Asp Cys Trp Leu Cys Leu
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Lys Leu Gly Thr Pro Thr Pro Leu Ala Ile Pro Thr Pro Ser Leu Thr
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Tyr Ser Leu Ala Asp Ser Leu Ala Asn Ala Ser Cys Gln Ile Ile Pro
 260 265 270

Pro Leu Leu Val Gln Pro Met Gln Phe Ser Asn Ser Ser Cys Leu Ser
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 290 295 300

Phe Thr Asn Cys Thr Ser Val Ala Asn Val Ser Ser Pro Leu Cys Ala
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Leu Asn Gly Ser Val Phe Leu Cys Gly Asn Asn Met Ala Tyr Thr Tyr
 325 330 335

Leu Pro Gln Asn Trp Thr Arg Leu Cys Val Gln Ala Ser Leu Leu Pro
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Asp Ile Asp Ile Asn Pro Gly Asp Glu Pro Val Pro Ile Pro Ala Ile
 355 360 365

Asp His Tyr Ile His Arg Pro Lys Arg Ala Val Gln Phe Ile Pro Leu
 370 375 380

Leu Ala Gly Leu Gly Ile Thr Ala Ala Phe Thr Thr Gly Ala Thr Gly
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Leu Gly Val Ser Val Thr Gln Tyr Thr Lys Leu Ser His Gln Leu Ile
 405 410 415

Ser Asp Val Gln Val Leu Ser Gly Thr Ile Gln Asp Leu Gln Asp Gln
 420 425 430

Val Asp Ser Leu Ala Glu Val Val Leu Gln Asn Arg Arg Gly Leu Asp
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Cys Cys Phe Tyr Ala Asn Lys Ser Gly Ile Val Arg Asn Lys Ile Arg

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Tyr Glu Pro

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<223> Fusion of the SCF cytokine, the N-terminal domain of an influenza
virus hemagglutinin glycoprotein, and a signal peptide
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gac ctt gtg gag tgc gtc aaa gaa aac tca tct aag gat cta aaa aaa Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys 130 135 140	432
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aat ccc cct gga gac tcc agc cta cac gcg gcc gca atc gag gga agg Asn Pro Pro Gly Asp Ser Ser Leu His Ala Ala Ala Ile Glu Gly Arg 225 230 235 240	720
caa gac ctt cca gga aat gac aac agc gac aaa att tgt ctt gga cat Gln Asp Leu Pro Gly Asn Asp Asn Ser Asp Lys Ile Cys Leu Gly His 245 250 255	768
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705					710				715						720	
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 <223> Fusion of the SCF cytokine, the N-terminal domain of an influenza virus hemagglutinin glycoprotein, and a signal peptide

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 100 105 110

 Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp
 115 120 125

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 Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe
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 Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys
 180 185 190

 Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala
 195 200 205

Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys
 210 215 220

Asn Pro Pro Gly Asp Ser Ser Leu His Ala Ala Ala Ile Glu Gly Arg
 225 230 235 240

Gln Asp Leu Pro Gly Asn Asp Asn Ser Asp Lys Ile Cys Leu Gly His
 245 250 255

His Ala Val Ser Asn Gly Thr Lys Val Asn Thr Leu Thr Glu Arg Gly
 260 265 270

Val Glu Val Val Asn Ala Thr Glu Thr Val Glu Arg Thr Asn Ile Pro
 275 280 285

Lys Ile Cys Ser Lys Gly Lys Arg Thr Thr Asp Leu Gly Gln Cys Gly
 290 295 300

Leu Leu Gly Thr Ile Thr Gly Pro Pro Gln Cys Asp Gln Phe Leu Glu
 305 310 315 320

Phe Ser Ala Asp Leu Ile Ile Glu Arg Arg Glu Gly Asn Asp Val Cys
 325 330 335

Tyr Pro Gly Lys Phe Val Asn Glu Glu Ala Leu Arg Gln Ile Leu Arg
 340 345 350

Gly Ser Gly Gly Ile Asp Lys Glu Thr Met Gly Phe Thr Tyr Ser Gly
 355 360 365

Ile Arg Thr Asn Gly Thr Thr Ser Ala Cys Arg Arg Ser Gly Ser Ser
 370 375 380

Phe Tyr Ala Glu Met Glu Trp Leu Leu Ser Asn Thr Asp Asn Ala Ser
 385 390 395 400

Phe Pro Gln Met Thr Lys Ser Tyr Lys Asn Thr Arg Arg Glu Ser Ala
 405 410 415

Leu Ile Val Trp Gly Ile His His Ser Gly Ser Thr Thr Glu Gln Thr
 420 425 430

Lys Leu Tyr Gly Ser Gly Asn Lys Leu Ile Thr Val Gly Ser Ser Lys
 435 440 445

Tyr His Gln Ser Phe Val Pro Ser Pro Gly Thr Arg Pro Gln Ile Asn
 450 455 460

Gly Gln Ser Gly Arg Ile Asp Phe His Trp Leu Ile Leu Asp Pro Asn
 465 470 475 480

Asp Thr Val Thr Phe Ser Phe Asn Gly Ala Phe Ile Ala Pro Asn Arg
 485 490 495

Ala Ser Phe Leu Arg Gly Lys Ser Met Gly Ile Gln Ser Asp Val Gln
 500 505 510

Val Asp Ala Asn Cys Glu Gly Glu Cys Tyr His Ser Gly Gly Thr Ile
 515 520 525

Thr Ser Arg Leu Pro Phe Gln Asn Ile Asn Ser Arg Ala Val Gly Lys
 530 535 540

Cys Pro Arg Tyr Val Lys Gln Glu Ser Leu Leu Leu Ala Thr Gly Met
 545 550 555 560

Lys Asn Val Pro Glu Pro Ser Lys Lys Arg Lys Lys Arg Gly Leu Phe
 565 570 575

Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu Gly Leu Val Asp
 580 585 590

Gly Trp Tyr Gly Phe Arg His Gln Asn Ala Gln Gly Glu Gly Thr Ala
 595 600 605

Ala Asp Tyr Lys Ser Thr Gln Ser Ala Ile Asp Gln Ile Thr Gly Lys
 610 615 620

Leu Asn Arg Leu Ile Glu Lys Thr Asn Gln Gln Phe Glu Leu Ile Asp
 625 630 635 640

Asn Glu Phe Thr Glu Val Glu Lys Gln Ile Gly Asn Leu Ile Asn Trp
 645 650 655

Thr Lys Asp Ser Ile Thr Glu Val Trp Ser Tyr Asn Ala Glu Leu Ile
 660 665 670

Val Ala Met Glu Asn Gln His Thr Ile Asp Leu Ala Asp Ser Glu Met
 675 680 685

Asn Arg Leu Tyr Glu Arg Val Arg Lys Gln Leu Arg Glu Asn Ala Glu

690

695

700

Glu Asp Gly Thr Gly Cys Phe Glu Ile Phe His Lys Cys Asp Asp Asp
 705 710 715 720

Cys Met Ala Ser Ile Arg Asn Asn Thr Tyr Asp His Ser Lys Tyr Arg
 725 730 735

Glu Glu Ala Met Gln Asn Arg Ile Gln Ile Asp Pro Val Lys Leu Ser
 740 745 750

Ser Gly Tyr Lys Asp Val Ile Leu Trp Phe Ser Phe Gly Ala Ser Cys
 755 760 765

Phe Leu Leu Leu Ala Ile Ala Met Gly Leu Val Phe Ile Cys Val Lys
 770 775 780

Asn Gly Asn Met Arg Cys Thr Ile Cys Ile
 785 790

<210> 5

<211> 530

<212> PRT

<213> Artificial sequence

<220>

<223> Transmembrane and extracellular domains of the feline endogenous
 RD114 virus envelope glycoprotein

<400> 5

Met Lys Leu Pro Thr Gly Met Val Ile Leu Cys Ser Leu Ile Ile Val
 1 5 10 15

Arg Ala Gly Phe Asp Asp Pro Arg Lys Ala Ile Ala Leu Val Gln Lys
 20 25 30

Gln His Gly Lys Pro Cys Glu Cys Ser Gly Gly Gln Val Ser Glu Ala
 35 40 45

Pro Pro Asn Ser Ile Gln Gln Val Thr Cys Pro Gly Lys Thr Ala Tyr
 50 55 60

Leu Met Thr Asn Gln Lys Trp Lys Cys Arg Val Thr Pro Lys Ile Ser
 65 70 75 80

Pro Ser Gly Gly Glu Leu Gln Asn Cys Pro Cys Asn Thr Phe Gln Asp
 85 90 95

Ser Met His Ser Ser Cys Tyr Thr Glu Tyr Arg Gln Cys Arg Arg Ile
 100 105 110

Asn Lys Thr Tyr Tyr Thr Ala Thr Leu Leu Lys Ile Arg Ser Gly Ser
 115 120 125

Leu Asn Glu Val Gln Ile Leu Gln Asn Pro Asn Gln Leu Leu Gln Ser
 130 135 140

Pro Cys Arg Gly Ser Ile Asn Gln Pro Val Cys Trp Ser Ala Thr Ala
 145 150 155 160

Pro Ile His Ile Ser Asp Gly Gly Gly Pro Leu Asp Thr Lys Arg Val
 165 170 175

Trp Thr Val Gln Lys Arg Leu Glu Gln Ile His Lys Ala Met Thr Pro
 180 185 190

Glu Leu Gln Tyr His Pro Leu Ala Leu Pro Lys Val Arg Asp Asp Leu
 195 200 205

Ser Leu Asp Ala Arg Thr Phe Asp Ile Leu Asn Thr Thr Phe Arg Leu
 210 215 220

Leu Gln Met Ser Asn Phe Ser Leu Ala Gln Asp Cys Trp Leu Cys Leu
 225 230 235 240

Lys Leu Gly Thr Pro Thr Pro Leu Ala Ile Pro Thr Pro Ser Leu Thr
 245 250 255

Tyr Ser Leu Ala Asp Ser Leu Ala Asn Ala Ser Cys Gln Ile Ile Pro
 260 265 270

Pro Leu Leu Val Gln Pro Met Gln Phe Ser Asn Ser Ser Cys Leu Ser
 275 280 285

Ser Pro Phe Ile Asn Asp Thr Glu Gln Ile Asp Leu Gly Ala Val Thr
 290 295 300

Phe Thr Asn Cys Thr Ser Val Ala Asn Val Ser Ser Pro Leu Cys Ala
 305 310 315 320

Leu Asn Gly Ser Val Phe Leu Cys Gly Asn Asn Met Ala Tyr Thr Tyr
 325 330 335

Leu Pro Gln Asn Trp Thr Arg Leu Cys Val Gln Ala Ser Leu Leu Pro
 340 345 350

Asp Ile Asp Ile Asn Pro Gly Asp Glu Pro Val Pro Ile Pro Ala Ile
 355 360 365

Asp His Tyr Ile His Arg Pro Lys Arg Ala Val Gln Phe Ile Pro Leu
 370 375 380

Leu Ala Gly Leu Gly Ile Thr Ala Ala Phe Thr Thr Gly Ala Thr Gly
 385 390 395 400

Leu Gly Val Ser Val Thr Gln Tyr Thr Lys Leu Ser His Gln Leu Ile
 405 410 415

Ser Asp Val Gln Val Leu Ser Gly Thr Ile Gln Asp Leu Gln Asp Gln
 420 425 430

Val Asp Ser Leu Ala Glu Val Val Leu Gln Asn Arg Arg Gly Leu Asp
 435 440 445

Leu Leu Thr Ala Glu Gln Gly Gly Ile Cys Leu Ala Leu Gln Glu Lys
 450 455 460

Cys Cys Phe Tyr Ala Asn Lys Ser Gly Ile Val Arg Asn Lys Ile Arg
 465 470 475 480

Thr Leu Gln Glu Glu Leu Gln Lys Arg Arg Glu Ser Leu Ala Ser Asn
 485 490 495

Pro Leu Trp Thr Gly Leu Gln Gly Phe Leu Pro Tyr Leu Leu Pro Leu
 500 505 510

Leu Gly Pro Leu Leu Thr Leu Leu Leu Ile Leu Thr Ile Gly Pro Cys
 515 520 525

Val Phe
 530

<210> 6
 <211> 33
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Cytoplasmic domain of Murine Leukemia Virus-A envelope
 glycoprotein

<400> 6

Asn Arg Leu Val Gln Phe Val Lys Asp Arg Ile Ser Val Val Gln Ala
 1 5 10 15

Leu Val Leu Thr Gln Gln Tyr His Gln Leu Lys Pro Leu Glu Tyr Glu
 20 25 30

Pro

<210> 7

<211> 39

<212> PRT

<213> Artificial sequence

<220>

<223> Signal peptide of the Murine Leukemia Virus-A envelope
 glycoprotein

<400> 7

Met Ala Arg Ser Thr Leu Ser Lys Pro Leu Lys Asn Lys Val Asn Pro
 1 5 10 15

Arg Gly Pro Leu Ile Pro Leu Ile Leu Leu Met Leu Arg Gly Val Ser
 20 25 30

Thr Ala Ser Pro Gly Ser Ser
 35

<210> 8

<211> 976

<212> PRT

<213> Homo sapiens

<400> 8

Met Arg Gly Ala Arg Gly Ala Trp Asp Phe Leu Cys Val Leu Leu Leu
 1 5 10 15

Leu Leu Arg Val Gln Thr Gly Ser Ser Gln Pro Ser Val Ser Pro Gly
 20 25 30

Glu Pro Ser Pro Pro Ser Ile His Pro Gly Lys Ser Asp Leu Ile Val
 35 40 45

Arg Val Gly Asp Glu Ile Arg Leu Leu Cys Thr Asp Pro Gly Phe Val
 50 55 60

Lys Trp Thr Phe Glu Ile Leu Asp Glu Thr Asn Glu Asn Lys Gln Asn

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

Thr Thr Val Phe Val Asn Asp Gly Glu Asn Val Asp Leu Ile Val Glu
325 330 335

Tyr Glu Ala Phe Pro Lys Pro Glu His Gln Gln Trp Ile Tyr Met Asn
340 345 350

Arg Thr Phe Thr Asp Lys Trp Glu Asp Tyr Pro Lys Ser Glu Asn Glu
355 360 365

Ser Asn Ile Arg Tyr Val Ser Glu Leu His Leu Thr Arg Leu Lys Gly
370 375 380

Thr Glu Gly Gly Thr Tyr Thr Phe Leu Val Ser Asn Ser Asp Val Asn
385 390 395 400

Ala Ala Ile Ala Phe Asn Val Tyr Val Asn Thr Lys Pro Glu Ile Leu
405 410 415

Thr Tyr Asp Arg Leu Val Asn Gly Met Leu Gln Cys Val Ala Ala Gly
420 425 430

Phe Pro Glu Pro Thr Ile Asp Trp Tyr Phe Cys Pro Gly Thr Glu Gln
435 440 445

Arg Cys Ser Ala Ser Val Leu Pro Val Asp Val Gln Thr Leu Asn Ser
450 455 460

Ser Gly Pro Pro Phe Gly Lys Leu Val Val Gln Ser Ser Ile Asp Ser
465 470 475 480

Ser Ala Phe Lys His Asn Gly Thr Val Glu Cys Lys Ala Tyr Asn Asp
485 490 495

Val Gly Lys Thr Ser Ala Tyr Phe Asn Phe Ala Phe Lys Gly Asn Asn
500 505 510

Lys Glu Gln Ile His Pro His Thr Leu Phe Thr Pro Leu Leu Ile Gly
515 520 525

Phe Val Ile Val Ala Gly Met Met Cys Ile Ile Val Met Ile Leu Thr
530 535 540

Tyr Lys Tyr Leu Gln Lys Pro Met Tyr Glu Val Gln Trp Lys Val Val
545 550 555 560

Glu Glu Ile Asn Gly Asn Asn Tyr Val Tyr Ile Asp Pro Thr Gln Leu
 565 570 575

Pro Tyr Asp His Lys Trp Glu Phe Pro Arg Asn Arg Leu Ser Phe Gly
 580 585 590

Lys Thr Leu Gly Ala Gly Ala Phe Gly Lys Val Val Glu Ala Thr Ala
 595 600 605

Tyr Gly Leu Ile Lys Ser Asp Ala Ala Met Thr Val Ala Val Lys Met
 610 615 620

Leu Lys Pro Ser Ala His Leu Thr Glu Arg Glu Ala Leu Met Ser Glu
 625 630 635 640

Leu Lys Val Leu Ser Tyr Leu Gly Asn His Met Asn Ile Val Asn Leu
 645 650 655

Leu Gly Ala Cys Thr Ile Gly Gly Pro Thr Leu Val Ile Thr Glu Tyr
 660 665 670

Cys Cys Tyr Gly Asp Leu Leu Asn Phe Leu Arg Arg Lys Arg Asp Ser
 675 680 685

Phe Ile Cys Ser Lys Gln Glu Asp His Ala Glu Ala Ala Leu Tyr Lys
 690 695 700

Asn Leu Leu His Ser Lys Glu Ser Ser Cys Ser Asp Ser Thr Asn Glu
 705 710 715 720

Tyr Met Asp Met Lys Pro Gly Val Ser Tyr Val Val Pro Thr Lys Ala
 725 730 735

Asp Lys Arg Arg Ser Val Arg Ile Gly Ser Tyr Ile Glu Arg Asp Val
 740 745 750

Thr Pro Ala Ile Met Glu Asp Asp Glu Leu Ala Leu Asp Leu Glu Asp
 755 760 765

Leu Leu Ser Phe Ser Tyr Gln Val Ala Lys Gly Met Ala Phe Leu Ala
 770 775 780

Ser Lys Asn Cys Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu
 785 790 795 800

Thr His Gly Arg Ile Thr Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp
 805 810 815

Ile Lys Asn Asp Ser Asn Tyr Val Val Lys Gly Asn Ala Arg Leu Pro
 820 825 830

Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Cys Val Tyr Thr Phe
 835 840 845

Glu Ser Asp Val Trp Ser Tyr Gly Ile Phe Leu Trp Glu Leu Phe Ser
 850 855 860

Leu Gly Ser Ser Pro Tyr Pro Gly Met Pro Val Asp Ser Lys Phe Tyr
 865 870 875 880

Lys Met Ile Lys Glu Gly Phe Arg Met Leu Ser Pro Glu His Ala Pro
 885 890 895

Ala Glu Met Tyr Asp Ile Met Lys Thr Cys Trp Asp Ala Asp Pro Leu
 900 905 910

Lys Arg Pro Thr Phe Lys Gln Ile Val Gln Leu Ile Glu Lys Gln Ile
 915 920 925

Ser Glu Ser Thr Asn His Ile Tyr Ser Asn Leu Ala Asn Cys Ser Pro
 930 935 940

Asn Arg Gln Lys Pro Val Val Asp His Ser Val Arg Ile Asn Ser Val
 945 950 955 960

Gly Ser Thr Ala Ser Ser Ser Gln Pro Leu Leu Val His Asp Asp Val
 965 970 975

<210> 9

<211> 189

<212> PRT

<213> Artificial sequence

<220>

<223> Extracellular domain of the human SCF cytokine

<400> 9

Glu Gly Ile Cys Arg Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr
 1 5 10 15

Lys Leu Val Ala Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr
 20 25 30

Val Pro Gly Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met
 35 40 45

Val Val Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser
 50 55 60

Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val
 65 70 75 80

Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser Lys
 85 90 95

Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe Thr Pro
 100 105 110

Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp
 115 120 125

Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu
 130 135 140

Ser Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu
 145 150 155 160

Pro Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn
 165 170 175

Arg Lys Ala Lys Asn Pro Pro Gly Asp Ser Ser Leu His
 180 185

<210> 10
 <211> 558
 <212> PRT
 <213> Artificial sequence

<220>
 <223> N-terminal domain of the Fowl Plague Virus hemagglutinin
 <400> 10

Ile Glu Gly Arg Gln Asp Leu Pro Gly Asn Asp Asn Ser Asp Lys Ile
 1 5 10 15

Cys Leu Gly His His Ala Val Ser Asn Gly Thr Lys Val Asn Thr Leu
 20 25 30

Thr Glu Arg Gly Val Glu Val Val Asn Ala Thr Glu Thr Val Glu Arg
 35 40 45

Thr Asn Ile Pro Lys Ile Cys Ser Lys Gly Lys Arg Thr Thr Asp Leu
 50 55 60

Gly Gln Cys Gly Leu Leu Gly Thr Ile Thr Gly Pro Pro Gln Cys Asp
 65 70 75 80

Gln Phe Leu Glu Phe Ser Ala Asp Leu Ile Ile Glu Arg Arg Glu Gly
 85 90 95

Asn Asp Val Cys Tyr Pro Gly Lys Phe Val Asn Glu Glu Ala Leu Arg
 100 105 110

Gln Ile Leu Arg Gly Ser Gly Gly Ile Asp Lys Glu Thr Met Gly Phe
 115 120 125

Thr Tyr Ser Gly Ile Arg Thr Asn Gly Thr Thr Ser Ala Cys Arg Arg
 130 135 140

Ser Gly Ser Ser Phe Tyr Ala Glu Met Glu Trp Leu Leu Ser Asn Thr
 145 150 155 160

Asp Asn Ala Ser Phe Pro Gln Met Thr Lys Ser Tyr Lys Asn Thr Arg
 165 170 175

Arg Glu Ser Ala Leu Ile Val Trp Gly Ile His His Ser Gly Ser Thr
 180 185 190

Thr Glu Gln Thr Lys Leu Tyr Gly Ser Gly Asn Lys Leu Ile Thr Val
 195 200 205

Gly Ser Ser Lys Tyr His Gln Ser Phe Val Pro Ser Pro Gly Thr Arg
 210 215 220

Pro Gln Ile Asn Gly Gln Ser Gly Arg Ile Asp Phe His Trp Leu Ile
 225 230 235 240

Leu Asp Pro Asn Asp Thr Val Thr Phe Ser Phe Asn Gly Ala Phe Ile
 245 250 255

Ala Pro Asn Arg Ala Ser Phe Leu Arg Gly Lys Ser Met Gly Ile Gln
 260 265 270

Ser Asp Val Gln Val Asp Ala Asn Cys Glu Gly Glu Cys Tyr His Ser
 275 280 285

Gly Gly Thr Ile Thr Ser Arg Leu Pro Phe Gln Asn Ile Asn Ser Arg
 290 295 300

Ala Val Gly Lys Cys Pro Arg Tyr Val Lys Gln Glu Ser Leu Leu Leu
 305 310 315 320

Ala Thr Gly Met Lys Asn Val Pro Glu Pro Ser Lys Lys Arg Lys Lys
 325 330 335

Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu
 340 345 350

Gly Leu Val Asp Gly Trp Tyr Gly Phe Arg His Gln Asn Ala Gln Gly
 355 360 365

Glu Gly Thr Ala Ala Asp Tyr Lys Ser Thr Gln Ser Ala Ile Asp Gln
 370 375 380

Ile Thr Gly Lys Leu Asn Arg Leu Ile Glu Lys Thr Asn Gln Gln Phe
 385 390 395 400

Glu Leu Ile Asp Asn Glu Phe Thr Glu Val Glu Lys Gln Ile Gly Asn
 405 410 415

Leu Ile Asn Trp Thr Lys Asp Ser Ile Thr Glu Val Trp Ser Tyr Asn
 420 425 430

Ala Glu Leu Ile Val Ala Met Glu Asn Gln His Thr Ile Asp Leu Ala
 435 440 445

Asp Ser Glu Met Asn Arg Leu Tyr Glu Arg Val Arg Lys Gln Leu Arg
 450 455 460

Glu Asn Ala Glu Glu Asp Gly Thr Gly Cys Phe Glu Ile Phe His Lys
 465 470 475 480

Cys Asp Asp Asp Cys Met Ala Ser Ile Arg Asn Asn Thr Tyr Asp His
 485 490 495

Ser Lys Tyr Arg Glu Glu Ala Met Gln Asn Arg Ile Gln Ile Asp Pro
 500 505 510

Val Lys Leu Ser Ser Gly Tyr Lys Asp Val Ile Leu Trp Phe Ser Phe
 515 520 525

Gly Ala Ser Cys Phe Leu Leu Leu Ala Ile Ala Met Gly Leu Val Phe
 530 535 540

Ile Cys Val Lys Asn Gly Asn Met Arg Cys Thr Ile Cys Ile
 545 550 555

<210> 11
 <211> 6907
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Plasmid encoding the fusion protein of SEQ ID NO: 2

<400> 11
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 aatagtaatc aattacgggg tcattagttc atagcccata tatggagttc cgcgttacat 180
 aacttacggg aaatggcccc cctggctgac cgcccaacga ccccgccca ttgacgtcaa 240
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 tatgggactt tcctacttgg cagtacatct acgtattagt catcgctatt accatgggtga 480
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 caaaatgtcg taacaactcc gcccattga cgcaaattgg cggtaggcgt gtacgggtggg 660
 aggtctatat aagcagagct cgttttagtga accgtcagat cgctggaga cgccatccac 720
 gctgttttga cctccataga agacaccggg accgatccag cctccgggtcg accgatcctg 780
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 tgtatcacca tggaccctca tgataatttt gtttctttca ctttctactc tgttgacaac 960
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