

SEQUENCE LISTING

<110> Mitsubishi Tanabe Pharma Corporation

<120> Mutant RSV F protein and use thereof

<130> 19084-201016

<150> US62/952673

<151> 2019-12-23

<160> 75

<170> PatentIn version 3.5

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<212> PRT

<213> respiratory syncytial virus

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<223> F1 transmembrane and intracellular

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 Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala
 50 55 60
 Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr Pro Pro Thr Asn Asn
 65 70 75 80
 Arg Ala Arg Arg Glu Leu Pro Arg Phe Met Asn Tyr Thr Leu Asn Asn
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 Ala Lys Lys Thr Asn Val Thr Leu Ser Lys Lys Arg Lys Arg Arg Phe
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 Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile Ala Ser Gly Val Ala
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 Ser Val Leu Thr Ser Lys Val Leu Asp Leu Lys Asn Tyr Ile Asp Lys
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 Gln Leu Leu Pro Ile Val Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile
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 Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu Glu Ile
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 Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
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 Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
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 Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
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 Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
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 Gly Ser Ala Ile Ala Ser Gly Val Ala Val Ser Lys Val Leu His Leu
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 165 170 175
 Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val
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Thr	Asp	Arg	Gly	Trp	Tyr	Cys	Asp	Asn	Ala	Gly	Ser	Val	Ser	Phe	Phe
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Tyr	Gly	Lys	Thr	Lys	Cys	Thr	Ala	Ser	Asn	Lys	Asn	Arg	Gly	Ile	Ile
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Thr	Ile	Glu	Leu	Ser	Asn	Ile	Lys	Glu	Asn	Lys	Cys	Asn	Gly	Thr	Asp
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Ala	Lys	Val	Lys	Leu	Ile	Lys	Gln	Glu	Leu	Asp	Lys	Tyr	Lys	Asn	Ala
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Val	Thr	Glu	Leu	Gln	Leu	Met	Gln	Ser	Thr	Pro	Ala	Thr	Asn	Asn	
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Arg	Ala	Arg	Arg	Glu	Leu	Pro	Arg	Phe	Met	Asn	Tyr	Thr	Leu	Asn	Asn
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Val	Ser	Lys	Val	Leu	His	Leu	Glu	Gly	Glu	Val	Asn	Lys	Ile	Lys	Ser
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Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val
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Gln	Leu	Leu	Pro	Ile	Val	Asn	Lys	Gln	Ser	Cys	Ser	Ile	Ser	Asn	Ile
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Ala	Tyr	Val	Val	Gln	Leu	Pro	Leu	Tyr	Gly	Val	Ile	Asp	Thr	Pro	Cys
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Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp				
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			20					25					30		
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Arg	Gln	Gln	Ser	Tyr	Ser	Ile	Met	Ser	Ile	Ile	Lys	Glu	Glu	Val	Leu
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Trp	Lys	Leu	His	Thr	Ser	Pro	Leu	Cys	Thr	Thr	Asn	Thr	Lys	Glu	Gly
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Glu	Val	Asn	Leu	Cys	Asn	Val	Asp	Ile	Phe	Asn	Pro	Lys	Tyr	Asp	Cys
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Lys	Ile	Met	Thr	Ser	Lys	Thr	Asp	Val	Ser	Ser	Ser	Val	Ile	Thr	Ser
	370					375						380			

Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser
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 Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr
 405 410 415
 Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr Leu Tyr
 420 425 430
 Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro
 435 440 445
 Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp
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 Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala
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 Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr Pro Ala Thr Asn Asn

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Arg	Ala	Arg	Arg	Glu	Leu	Pro	Arg	Phe	Met	Asn	Tyr	Thr	Leu	Asn
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Ala	Lys	Lys	Thr	Asn	Val	Thr	Leu	Ser	Lys	Lys	Arg	Lys	Asn	Asn
			100					105					110	Phe
Leu	Gly	Phe	Cys	Leu	Gly	Val	Gly	Ser	Ala	Ile	Ala	Ser	Gly	Val
		115					120					125		Ala
Val	Ser	Lys	Val	Leu	His	Leu	Gly	Glu	Val	Asn	Lys	Ile	Lys	Ser
	130				135					140				
Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val	Ser	Leu	Ser	Asn	Gly
145					150					155				160
Ser	Val	Leu	Val	Val	Lys	Val	Leu	Asp	Leu	Lys	Asn	Tyr	Ile	Asp
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Gln	Leu	Leu	Pro	Ile	Val	Asn	Lys	Gln	Ser	Cys	Ser	Ile	Ser	Asn
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		195					200					205		Ile
Thr	Arg	Glu	Phe	Ser	Val	Asn	Ala	Gly	Val	Thr	Thr	Pro	Val	Ser
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Tyr	Met	Leu	Thr	Asn	Ser	Glu	Leu	Leu	Ser	Leu	Ile	Asn	Asp	Met
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Ile	Thr	Asn	Asp	Gln	Lys	Lys	Leu	Met	Ser	Asn	Asn	Val	Gln	Ile
			245					250					255	Val
Arg	Gln	Gln	Ser	Tyr	Ser	Ile	Met	Ser	Ile	Ile	Lys	Glu	Glu	Val
			260				265						270	Leu
Ala	Tyr	Val	Val	Gln	Leu	Pro	Leu	Tyr	Gly	Val	Ile	Asp	Thr	Pro
		275					280					285		Cys
Trp	Lys	Leu	His	Thr	Ser	Pro	Leu	Cys	Thr	Thr	Asn	Thr	Lys	Glu
	290					295					300			Gly
Ser	Asn	Ile	Cys	Leu	Thr	Arg	Thr	Asp	Arg	Gly	Trp	Tyr	Cys	Asp
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Ala	Gly	Ser	Val	Ser	Phe	Phe	Pro	Gln	Ala	Glu	Thr	Cys	Lys	Val
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Ser	Asn	Arg	Val	Phe	Cys	Asp	Thr	Met	Asn	Ser	Cys	Thr	Leu	Pro
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Glu	Val	Asn	Leu	Cys	Asn	Thr	Asp	Ile	Phe	Asn	Pro	Lys	Tyr	Asp
		355				360					365			Cys
Lys	Ile	Met	Thr	Ser	Lys	Thr	Asp	Val	Ser	Ser	Ser	Val	Ile	Thr
	370					375					380			Ser
Leu	Gly	Ala	Ile	Val	Ser	Cys	Tyr	Gly	Lys	Thr	Lys	Cys	Thr	Ala
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Asn	Lys	Asn	Arg	Gly	Ile	Ile	Lys	Thr	Phe	Ser	Asn	Gly	Cys	Asp
			405						410					415
Val	Ser	Asn	Lys	Gly	Val	Asp	Thr	Val	Ser	Val	Gly	Asn	Thr	Leu
			420					425					430	Tyr
Tyr	Val	Asn	Lys	Gln	Glu	Gly	Lys	Ser	Leu	Tyr	Val	Lys	Gly	Glu
		435				440						445		Pro
Ile	Ile	Asn	Phe	Tyr	Asp	Pro	Leu	Val	Phe	Pro	Ser	Asp	Glu	Phe
	450					455				460				Asp
Ala	Ser	Ile	Ser	Gln	Val	Asn	Glu	Lys	Ile	Asn	Gln	Ser	Leu	Ala
														Phe

465 470 475 480
Ile Arg Lys Ser Asp Glu Leu Leu
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Thr	Ile	Met	Leu	Ser	Asn	Ile	Lys	Glu	Asn	Lys	Cys	Asn	Gly	Thr	Asp
			35				40				45				
Ala	Lys	Val	Lys	Leu	Ile	Lys	Gln	Glu	Leu	Asp	Lys	Tyr	Lys	Asn	Ala
			50				55				60				
Val	Thr	Glu	Leu	Gln	Leu	Leu	Met	Gln	Ser	Thr	Pro	Ala	Thr	Asn	Asn
65				70				75				80			
Arg	Ala	Arg	Arg	Glu	Leu	Pro	Arg	Phe	Met	Asn	Tyr	Thr	Leu	Asn	Asn
			85				90				95				
Ala	Lys	Lys	Thr	Asn	Val	Thr	Leu	Ser	Lys	Lys	Arg	Lys	Asn	Asn	Phe
			100				105				110				
Leu	Gly	Phe	Cys	Leu	Gly	Val	Gly	Ser	Ala	Ile	Ala	Ser	Gly	Val	Ala
			115				120				125				
Val	Ser	Lys	Val	Leu	His	Leu	Glu	Gly	Glu	Val	Asn	Lys	Ile	Lys	Ser
			130				135				140				
Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val
145				150				155				160			

Ser	Val	Leu	Val	Val	Lys	Val	Leu	Asp	Leu	Lys	Asn	Tyr	Ile	Asp	Lys
				165					170					175	
Gln	Leu	Leu	Pro	Ile	Val	Asn	Lys	Gln	Ser	Cys	Ser	Ile	Ser	Asn	Ile
			180					185					190		
Glu	Thr	Val	Ile	Glu	Phe	Gln	Gln	Lys	Asn	Asn	Arg	Leu	Leu	Glu	Ile
		195					200					205			
Thr	Arg	Glu	Phe	Ser	Val	Asn	Ala	Gly	Val	Thr	Thr	Pro	Val	Ser	Thr
	210					215					220				
Tyr	Met	Leu	Thr	Asn	Ser	Glu	Leu	Leu	Ser	Leu	Ile	Asn	Asp	Met	Pro
225					230					235					240
Ile	Thr	Asn	Asp	Gln	Lys	Lys	Leu	Met	Ser	Asn	Asn	Val	Gln	Ile	Val
				245					250					255	
Arg	Gln	Gln	Ser	Tyr	Ser	Ile	Met	Ser	Ile	Ile	Lys	Glu	Glu	Val	Leu
			260					265						270	
Ala	Tyr	Val	Val	Gln	Leu	Pro	Leu	Tyr	Gly	Val	Ile	Asp	Thr	Pro	Cys
		275					280					285			
Trp	Lys	Leu	His	Thr	Ser	Pro	Leu	Cys	Thr	Thr	Asn	Thr	Lys	Glu	Gly
	290					295					300				
Ser	Asn	Ile	Cys	Leu	Thr	Arg	Thr	Asp	Arg	Gly	Trp	Tyr	Cys	Asp	Asn
305					310					315					320
Ala	Gly	Ser	Val	Ser	Phe	Phe	Pro	Gln	Ala	Glu	Thr	Cys	Lys	Val	Gln
				325					330					335	
Ser	Asn	Arg	Val	Phe	Cys	Asp	Thr	Met	Asn	Ser	Cys	Thr	Leu	Pro	Ser
			340					345					350		
Glu	Val	Asn	Leu	Cys	Asn	Thr	Asp	Ile	Phe	Asn	Pro	Lys	Tyr	Asp	Cys
		355					360					365			
Lys	Ile	Met	Thr	Ser	Lys	Thr	Asp	Val	Ser	Ser	Ser	Val	Ile	Thr	Ser
	370					375					380				
Leu	Gly	Ala	Ile	Val	Ser	Cys	Tyr	Gly	Lys	Thr	Lys	Cys	Thr	Ala	Ser
385					390					395					400
Asn	Lys	Asn	Arg	Gly	Ile	Ile	Lys	Thr	Phe	Ser	Asn	Gly	Cys	Asp	Tyr
				405					410					415	
Val	Ser	Asn	Lys	Gly	Val	Asp	Thr	Val	Ser	Val	Gly	Asn	Thr	Leu	Tyr
			420					425					430		
Tyr	Val	Asn	Lys	Gln	Glu	Gly	Lys	Ser	Leu	Tyr	Val	Lys	Gly	Glu	Pro
		435					440					445			
Ile	Ile	Asn	Phe	Tyr	Asp	Pro	Leu	Val	Phe	Pro	Ser	Asp	Glu	Phe	Asp
	450					455					460				
Ala	Ser	Ile	Ser	Gln	Val	Asn	Glu	Lys	Ile	Asn	Gln	Ser	Leu	Ala	Phe
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<223> F1 extracellular

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<223> foldon

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			20					25					30		
Thr	Ile	Glu	Leu	Ser	Asn	Ile	Lys	Glu	Asn	Lys	Cys	Asn	Gly	Thr	Asp
		35				40					45				
Ala	Lys	Val	Lys	Leu	Ile	Lys	Gln	Glu	Leu	Asp	Lys	Tyr	Lys	Asn	Ala
	50					55				60					
Val	Thr	Glu	Leu	Gln	Leu	Leu	Met	Gln	Ser	Thr	Pro	Ala	Thr	Asn	Asn
65					70					75				80	
Arg	Ala	Arg	Arg	Glu	Leu	Pro	Arg	Phe	Met	Asn	Tyr	Thr	Leu	Asn	Asn
			85					90						95	
Ala	Lys	Lys	Thr	Asn	Val	Thr	Leu	Ser	Lys	Lys	Arg	Lys	Asn	Asn	Phe
			100					105					110		
Leu	Gly	Phe	Cys	Leu	Gly	Val	Gly	Ser	Ala	Ile	Ala	Ser	Gly	Val	Ala
		115					120					125			
Val	Ser	Lys	Val	Leu	His	Leu	Glu	Gly	Glu	Val	Asn	Lys	Ile	Lys	Ser
		130				135					140				
Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val
145					150					155				160	
Ser	Val	Leu	Val	Val	Lys	Val	Leu	Asp	Leu	Lys	Asn	Tyr	Ile	Asp	Lys
			165					170						175	
Gln	Leu	Leu	Pro	Ile	Val	Asn	Lys	Gln	Ser	Cys	Ser	Ile	Ser	Asn	Ile
			180					185					190		
Glu	Thr	Val	Ile	Glu	Phe	Gln	Gln	Lys	Asn	Asn	Arg	Leu	Leu	Glu	Ile
		195					200						205		

Thr	Arg	Glu	Phe	Ser	Val	Asn	Ala	Gly	Val	Thr	Thr	Pro	Val	Ser	Thr
210						215				220					
Tyr	Met	Leu	Thr	Asn	Ser	Glu	Leu	Leu	Ser	Leu	Ile	Asn	Asp	Met	Pro
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Ile	Thr	Asn	Asp	Gln	Lys	Lys	Leu	Met	Ser	Asn	Asn	Val	Gln	Ile	Val
				245					250					255	
Arg	Gln	Gln	Ser	Tyr	Ser	Ile	Met	Ser	Ile	Ile	Lys	Glu	Glu	Val	Leu
			260				265						270		
Ala	Tyr	Val	Val	Gln	Leu	Pro	Leu	Tyr	Gly	Val	Ile	Asp	Thr	Pro	Cys
	275						280					285			
Trp	Lys	Leu	His	Thr	Ser	Pro	Leu	Cys	Thr	Thr	Asn	Thr	Lys	Glu	Gly
290						295					300				
Ser	Asn	Ile	Cys	Leu	Thr	Arg	Thr	Asp	Arg	Gly	Trp	Tyr	Cys	Asp	Asn
305					310					315					320
Ala	Gly	Ser	Val	Ser	Phe	Phe	Pro	Gln	Ala	Glu	Thr	Cys	Lys	Val	Gln
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Ser	Asn	Arg	Val	Phe	Cys	Asp	Thr	Met	Asn	Ser	Cys	Thr	Leu	Pro	Ser
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Glu	Val	Asn	Leu	Cys	Asn	Val	Asp	Ile	Phe	Asn	Pro	Lys	Tyr	Asp	Cys
		355					360					365			
Lys	Ile	Met	Thr	Ser	Lys	Thr	Asp	Val	Ser	Ser	Ser	Val	Ile	Thr	Ser
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Leu	Gly	Ala	Ile	Val	Ser	Cys	Tyr	Gly	Lys	Thr	Lys	Cys	Thr	Ala	Ser
385					390				395						400
Asn	Lys	Asn	Arg	Gly	Ile	Ile	Lys	Thr	Phe	Ser	Asn	Gly	Cys	Asp	Tyr
			405					410					415		
Val	Ser	Asn	Lys	Gly	Val	Asp	Thr	Val	Ser	Val	Gly	Asn	Thr	Leu	Tyr
		420					425					430			
Tyr	Val	Asn	Lys	Gln	Glu	Gly	Lys	Ser	Leu	Tyr	Val	Lys	Gly	Glu	Pro
	435					440					445				
Ile	Ile	Asn	Phe	Tyr	Asp	Pro	Leu	Val	Phe	Pro	Ser	Asp	Glu	Phe	Asp
	450					455					460				
Ala	Ser	Ile	Ser	Gln	Val	Asn	Glu	Lys	Ile	Asn	Gln	Ser	Leu	Ala	Phe
465					470					475					480
Ile	Arg	Lys	Ser	Asp	Glu	Leu	Leu	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala
			485					490						495	
Pro	Arg	Asp	Gly	Gln	Ala	Tyr	Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu
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 35 40 45
 Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala
 50 55 60
 Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr Pro Ala Thr Asn Asn
 65 70 75 80
 Arg Ala Arg Arg Glu Leu Pro Arg Phe Met Asn Tyr Thr Leu Asn Asn
 85 90 95
 Ala Lys Lys Thr Asn Val Thr Leu Ser Lys Lys Arg Lys Asn Asn Phe
 100 105 110
 Leu Gly Phe Cys Leu Gly Val Gly Ser Ala Ile Ala Ser Gly Val Ala
 115 120 125
 Val Ser Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Lys Ser
 130 135 140
 Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val
 145 150 155 160
 Ser Val Leu Val Val Lys Val Leu Asp Leu Lys Asn Tyr Ile Asp Lys
 165 170 175
 Gln Leu Leu Pro Ile Val Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile
 180 185 190
 Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu Glu Ile
 195 200 205
 Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val Ser Thr
 210 215 220

Tyr	Met	Leu	Thr	Asn	Ser	Glu	Leu	Leu	Ser	Leu	Ile	Asn	Asp	Met	Pro
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Ile	Thr	Asn	Asp	Gln	Lys	Lys	Leu	Met	Ser	Asn	Asn	Val	Gln	Ile	Val
				245					250					255	
Arg	Gln	Gln	Ser	Tyr	Ser	Ile	Met	Ser	Ile	Ile	Lys	Glu	Glu	Val	Leu
			260					265					270		
Ala	Tyr	Val	Val	Gln	Leu	Pro	Leu	Tyr	Gly	Val	Ile	Asp	Thr	Pro	Cys
	275						280					285			
Trp	Lys	Leu	His	Thr	Ser	Pro	Leu	Cys	Thr	Thr	Asn	Thr	Lys	Glu	Gly
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Ser	Asn	Ile	Cys	Leu	Thr	Arg	Thr	Asp	Arg	Gly	Trp	Tyr	Cys	Asp	Asn
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Ala	Gly	Ser	Val	Ser	Phe	Phe	Pro	Gln	Ala	Glu	Thr	Cys	Lys	Val	Gln
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Ser	Asn	Arg	Val	Phe	Cys	Asp	Thr	Met	Asn	Ser	Cys	Thr	Leu	Pro	Ser
			340					345					350		
Glu	Val	Asn	Leu	Cys	Asn	Val	Asp	Ile	Phe	Asn	Pro	Lys	Tyr	Asp	Cys
	355						360					365			
Lys	Ile	Met	Thr	Ser	Lys	Thr	Asp	Val	Ser	Ser	Ser	Val	Ile	Thr	Ser
370						375						380			
Leu	Gly	Ala	Ile	Val	Ser	Cys	Tyr	Gly	Lys	Thr	Lys	Cys	Thr	Ala	Ser
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Asn	Lys	Asn	Arg	Gly	Ile	Ile	Lys	Thr	Phe	Ser	Asn	Gly	Cys	Asp	Tyr
			405					410					415		
Val	Ser	Asn	Lys	Gly	Val	Asp	Thr	Val	Ser	Val	Gly	Asn	Thr	Leu	Tyr
			420					425					430		
Tyr	Val	Asn	Lys	Gln	Glu	Gly	Lys	Ser	Leu	Tyr	Val	Lys	Gly	Glu	Pro
	435						440					445			
Ile	Ile	Asn	Phe	Tyr	Asp	Pro	Leu	Val	Phe	Pro	Ser	Asp	Glu	Phe	Asp
450						455					460				
Ala	Ser	Ile	Ser	Gln	Val	Asn	Glu	Lys	Ile	Asn	Gln	Ser	Leu	Ala	Phe
465					470					475					480
Ile	Arg	Lys	Ser	Asp	Glu	Leu	Leu	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala
			485					490						495	
Pro	Arg	Asp	Gly	Gln	Ala	Tyr	Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu
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 35 40 45
 Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala
 50 55 60
 Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr Pro Ala Thr Asn Asn
 65 70 75 80
 Arg Ala Arg Arg Glu Leu Pro Arg Phe Met Asn Tyr Thr Leu Asn Asn
 85 90 95
 Ala Lys Lys Thr Asn Val Thr Leu Ser Lys Lys Arg Lys Asn Asn Phe
 100 105 110
 Leu Gly Phe Cys Leu Gly Val Gly Ser Ala Ile Ala Ser Gly Val Ala
 115 120 125
 Val Ser Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Lys Ser
 130 135 140
 Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val
 145 150 155 160
 Ser Val Leu Val Val Lys Val Leu Asp Leu Lys Asn Tyr Ile Asp Lys
 165 170 175
 Gln Leu Leu Pro Ile Val Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile
 180 185 190
 Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu Glu Ile
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 Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val Ser Thr
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 Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp Met Pro
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		20					25						30		
Thr	Ile	Met	Leu	Ser	Asn	Ile	Lys	Glu	Asn	Lys	Cys	Asn	Gly	Thr	Asp
	35					40						45			
Ala	Lys	Val	Lys	Leu	Ile	Lys	Gln	Glu	Leu	Asp	Lys	Tyr	Lys	Asn	Ala
50					55						60				
Val	Thr	Glu	Leu	Gln	Leu	Leu	Met	Gln	Ser	Thr	Pro	Ala	Thr	Asn	Asn
65				70					75					80	
Arg	Ala	Arg	Arg	Glu	Leu	Pro	Arg	Phe	Met	Asn	Tyr	Thr	Leu	Asn	Asn
			85					90						95	
Ala	Lys	Lys	Thr	Asn	Val	Thr	Leu	Ser	Lys	Lys	Arg	Lys	Asn	Asn	Phe
			100				105						110		
Leu	Gly	Phe	Cys	Leu	Gly	Val	Gly	Ser	Ala	Ile	Ala	Ser	Gly	Val	Ala
	115				120							125			
Val	Ser	Lys	Val	Leu	His	Leu	Glu	Gly	Glu	Val	Asn	Lys	Ile	Lys	Ser
130					135						140				
Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val
145				150						155				160	
Ser	Val	Leu	Val	Val	Lys	Val	Leu	Asp	Leu	Lys	Asn	Tyr	Ile	Asp	Lys
			165					170						175	
Gln	Leu	Leu	Pro	Ile	Val	Asn	Lys	Gln	Ser	Cys	Ser	Ile	Ser	Asn	Ile
			180					185					190		
Glu	Thr	Val	Ile	Glu	Phe	Gln	Gln	Lys	Asn	Asn	Arg	Leu	Leu	Glu	Ile
	195					200						205			
Thr	Arg	Glu	Phe	Ser	Val	Asn	Ala	Gly	Val	Thr	Thr	Pro	Val	Ser	Thr
	210					215						220			
Tyr	Met	Leu	Thr	Asn	Ser	Glu	Leu	Leu	Ser	Leu	Ile	Asn	Asp	Met	Pro
225					230					235				240	
Ile	Thr	Asn	Asp	Gln	Lys	Lys	Leu	Met	Ser	Asn	Asn	Val	Gln	Ile	Val
			245					250						255	

Arg Gln Gln Ser Tyr Ser Ile Met Ser Ile Ile Lys Glu Glu Val Leu
 260 265 270
 Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys
 275 280 285
 Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly
 290 295 300
 Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys Asp Asn
 305 310 315 320
 Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys Val Gln
 325 330 335
 Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Cys Thr Leu Pro Ser
 340 345 350
 Glu Val Asn Leu Cys Asn Thr Asp Ile Phe Asn Pro Lys Tyr Asp Cys
 355 360 365
 Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile Thr Ser
 370 375 380
 Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser
 385 390 395 400
 Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr
 405 410 415
 Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr Leu Tyr
 420 425 430
 Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro
 435 440 445
 Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp
 450 455 460
 Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu Ala Phe
 465 470 475 480
 Ile Arg Lys Ser Asp Glu Leu Leu Gly Ser Gly Tyr Ile Pro Glu Ala
 485 490 495
 Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
 500 505 510
 Leu Ser Thr Phe Leu
 515

<210> 14

<211> 1626

<212> DNA

<213> Artificial Sequence

<220>

<223> FH50-foldon-tag coding sequence

<400> 14

atggaactgc	tgatacttaa	ggctaacgcg	ataactacga	tcctcaccgc	cgtgaccttt	60
tgctttgcct	ctggcctaaa	cattactgag	gaattctacc	agtcaacgtg	cagtgcagtg	120
agcaaagggt	atctgtccgc	cctgagaacc	gggtgggtata	cttccgtcat	taccatcgag	180
ctgtccaaca	taaaagagaa	taagtgaac	ggcaccgatg	ctaaagtga	actgatcaaa	240
caggaactcg	ataaatacaa	gaatgcagtt	acagagcttc	agctcctgat	gcagagcact	300

ccggccacca	ataatagggc	aaggagagaa	ttgccacgat	ttatgaatta	cacactcaac	360
aacgcgaaga	aaactaacgt	gactctgtcc	aagaaacgta	agaataactt	cttgggggttc	420
tgtctgggtg	taggtagcgc	cattgcttct	ggggtggccg	tcagcaaagt	gcttcacctg	480
gaaggagagg	tgaacaagat	caagtctgca	ctgctgtcta	caaacaaagc	agtgggtgagc	540
ctgtccaacg	gagtatccgt	tctgggtggc	aaagtcctgg	atctgaagaa	ttatatcgac	600
aaacaactgc	tccccattgt	gaacaagcag	agttgttcaa	tcagcaacat	agaaactgtg	660
attgagttcc	aacagaagaa	caataggctg	ctcgaaatta	ccagagagtt	tagcgtcaat	720
gctgggtgtca	caaccccagt	cagcacttac	atgctgacta	attccgagtt	gcttagcctt	780
attaacgaca	tgctatcac	caatgaccag	aagaagctga	tgagtaataa	tgtgcagatt	840
gtgcgccagc	agagttacag	cattatgagt	attatcaaag	aggaggtatt	ggcttatgtg	900
gttcagcttc	cgctgtatgg	ggcatcgcac	acaccttggt	ggaagttgca	taccagtccc	960
ctgtgtacga	caaacaccaa	ggaaggtagt	aacatctgct	tgacacgtac	cgatcggggg	1020
tggtattgcg	ataacgccgg	gtctgttagt	ttctttcctc	aagccgagac	atgcaaagtc	1080
cagagcaatc	gcgtgttctg	tgacacgatg	aacagctgta	ctttgccatc	agaggttaat	1140
ctgtgcaatg	tagacatctt	caaccccaaa	tacgactgta	agatcatgac	cagcaagact	1200
gatgtcagct	cctccgttat	aacatcactc	ggcgctatcg	tgtcttgcta	tggcaagacc	1260
aagtgtacag	cgtccaataa	gaatcggggc	attatcaaga	cattctccaa	cggatgtgac	1320
tacgtgagca	acaaaggagt	ggacaccgtg	tcagtcggaa	atacactgta	ttacgtgaat	1380
aagcaggagg	gcaaatctct	ttacgtgaag	ggcgaaccaa	tcacactt	ctatgatccc	1440
ctcgtctttc	cttctgatga	gtttgacgcc	tctatttctc	aggttaacga	gaagatcaat	1500
cagtctctgg	cctttatacg	caaaagcgat	gaactcctgg	gatcaggcta	cattcccga	1560
gctccaaggg	acggacaagc	atacgtacga	aaagatggcg	aatgggtact	cctctcaacg	1620
tttctg						1626

<210> 15

<211> 1626

<212> DNA

<213> Artificial Sequence

<220>

<223> FH81-foldon-tag coding sequence

<400> 15

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agcaaagggt	atctgtccgc	cctgagaacc	gggtgggtata	cttccgtcat	taccatcatg	180
ctgtccaaca	taaaagagaa	taagtgaac	ggcaccgatg	ctaaagtga	actgatcaaa	240
caggaactcg	ataaatacaa	gaatgcagtt	acagagcttc	agctcctgat	gcagagcact	300
ccggccacca	ataatagggc	aaggagagaa	ttgccacgat	ttatgaatta	cacactcaac	360
aacgcgaaga	aaactaacgt	gactctgtcc	aagaaacgta	agaataactt	cttgggggttc	420
tgtctgggtg	taggtagcgc	cattgcttct	ggggtggccg	tcagcaaagt	gcttcacctg	480
gaaggagagg	tgaacaagat	caagtctgca	ctgctgtcta	caaacaaagc	agtgggtgagc	540
ctgtccaacg	gagtatccgt	tctgggtggc	aaagtcctgg	atctgaagaa	ttatatcgac	600
aaacaactgc	tccccattgt	gaacaagcag	agttgttcaa	tcagcaacat	agaaactgtg	660
attgagttcc	aacagaagaa	caataggctg	ctcgaaatta	ccagagagtt	tagcgtcaat	720
gctgggtgtca	caaccccagt	cagcacttac	atgctgacta	attccgagtt	gcttagcctt	780
attaacgaca	tgctatcac	caatgaccag	aagaagctga	tgagtaataa	tgtgcagatt	840
gtgcgccagc	agagttacag	cattatgagt	attatcaaag	aggaggtatt	ggcttatgtg	900
gttcagcttc	cgctgtatgg	ggcatcgcac	acaccttggt	ggaagttgca	taccagtccc	960

ctgtgtacga	caaacaccaa	ggaaggtagt	aacatctgct	tgacacgtac	cgatcgggggt	1020
tggtattgcg	ataacgccgg	gtctgttagt	ttctttcctc	aagccgagac	atgcaaagtc	1080
cagagcaatc	gcgtgttctg	tgacacgatg	aacagctgta	ctttgccatc	agaggttaat	1140
ctgtgcaatg	tagacatctt	caaccccaaa	tacgactgta	agatcatgac	cagcaagact	1200
gatgtcagct	cctccgttat	aacatcactc	ggcgctatcg	tgtcttgcta	tggaagacc	1260
aagtgtacag	cgtccaataa	gaatcggggc	attatcaaga	cattctccaa	cggatgtgac	1320
tacgtgagca	acaaaggagt	ggacaccgtg	tcagtcggaa	atacactgta	ttacgtgaat	1380
aagcaggagg	gcaaattctt	ttacgtgaag	ggcgaaccaa	tcatcaactt	ctatgatccc	1440
ctcgtctttc	cttctgatga	gtttgacgcc	tctatttctc	aggttaacga	gaagatcaat	1500
cagtctctgg	cctttatacg	caaaagcgat	gaactcctgg	gatcaggcta	cattcccga	1560
gctccaaggg	acggacaagc	atacgtacga	aaagatggcg	aatgggtact	cctctcaacg	1620
tttctg						1626

<210> 16

<211> 1626

<212> DNA

<213> Artificial Sequence

<220>

<223> FH82-foldon-tag coding sequence

<400> 16

atggaactgc	tgatacttaa	ggctaacgcg	ataactacga	tcctcaccgc	cgtgaccttt	60
tgctttgcct	ctggccaaaa	cattactgag	gaattctacc	agtcaacgtg	cagtgcagtg	120
agccgagggt	atctgtccgc	cctgagaacc	gggtgggtata	cttccgtcat	taccatcgag	180
ctgtccaaca	taaaagagaa	taagtgaac	ggcaccgatg	ctaaagtga	actgatcaaa	240
caggaactcg	ataaatacaa	gaatgcagtt	acagagcttc	agctcctgat	gcagagcact	300
ccggccacca	ataatagggc	aaggagagaa	ttgccacgat	ttatgaatta	cacactcaac	360
aacgcgaaga	aaactaacgt	gactctgtcc	aagaaacgta	agaataactt	cttgggggttc	420
tgtctgggtg	taggtagcgc	cattgcttct	gggggtggccg	tcagcaaagt	gcttcacctg	480
gaaggagagg	tgaacaagat	caagtctgca	ctgctgtcta	caaacaaagc	agtgggtgagc	540
ctgtccaacg	gagtatccgt	tctgggtggc	aaagtcctgg	atctgaagaa	ttatatcgac	600
aaacaactgc	tccccattgt	gaacaagcag	agttgttcaa	tcagcaacat	agaaactgtg	660
attgagttcc	aacagaagaa	caataggctg	ctcgaaatta	ccagagagtt	tagcgtcaat	720
gctgggtgtca	caaccccagt	cagcacttac	atgctgacta	attccgagtt	gcttagcctt	780
attaacgaca	tgccatatcac	caatgaccag	aagaagctga	tgagtaataa	tgtgcagatt	840
gtgcgccagc	agagttacag	cattatgagt	attatcaaa	aggaggattt	ggcttatgtg	900
gttcagcttc	cgctgtatgg	ggatcatcgac	acaccttggt	ggaagttgca	taccagtccc	960
ctgtgtacga	caaacaccaa	ggaaggtagt	aacatctgct	tgacacgtac	cgatcgggggt	1020
tggtattgcg	ataacgccgg	gtctgttagt	ttctttcctc	aagccgagac	atgcaaagtc	1080
cagagcaatc	gcgtgttctg	tgacacgatg	aacagctgta	ctttgccatc	agaggttaat	1140
ctgtgcaata	ccgacatctt	caaccccaaa	tacgactgta	agatcatgac	cagcaagact	1200
gatgtcagct	cctccgttat	aacatcactc	ggcgctatcg	tgtcttgcta	tggaagacc	1260
aagtgtacag	cgtccaataa	gaatcggggc	attatcaaga	cattctccaa	cggatgtgac	1320
tacgtgagca	acaaaggagt	ggacaccgtg	tcagtcggaa	atacactgta	ttacgtgaat	1380
aagcaggagg	gcaaattctt	ttacgtgaag	ggcgaaccaa	tcatcaactt	ctatgatccc	1440
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cagtctctgg	cctttatacg	caaaagcgat	gaactcctgg	gatcaggcta	cattcccga	1560
gctccaaggg	acggacaagc	atacgtacga	aaagatggcg	aatgggtact	cctctcaacg	1620

tttctg

1626

<210> 17

<211> 1626

<212> DNA

<213> Artificial Sequence

<220>

<223> FH85-foldon-tag coding sequence

<400> 17

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tgctttgcct	ctggccaaaa	cattactgag	gaattctacc	agtcaacgtg	cagtgcagtg	120
agccgagggt	atctgtccgc	cctgagaacc	gggtgggtata	cttccgtcat	taccatcatg	180
ctgtccaaca	taaaagagaa	taagtgcac	ggcaccgatg	ctaaagtga	actgatcaaa	240
caggaactcg	ataaatacaa	gaatgcagtt	acagagcttc	agctcctgat	gcagagcact	300
ccggccacca	ataatagggc	aaggagagaa	ttgccacgat	ttatgaatta	cacactcaac	360
aacgcgaaga	aaactaacgt	gactctgtcc	aagaaacgta	agaataactt	cttgggggttc	420
tgtctgggtg	taggtagcgc	cattgcttct	gggggtggccg	tcagcaaagt	gcttcacctg	480
gaaggagagg	tgaacaagat	caagtctgca	ctgctgtcta	caaacaaagc	agtggtgagc	540
ctgtccaacg	gagtatccgt	tctgggtggc	aaagtcctgg	atctgaagaa	ttatatcgac	600
aaacaactgc	tccccattgt	gaacaagcag	agttgttcaa	tcagcaacat	agaaactgtg	660
attgagttcc	aacagaagaa	caataggctg	ctcgaaatta	ccagagagtt	tagcgtcaat	720
gctgggtgtca	caaccccagt	cagcacttac	atgctgacta	attccgagtt	gcttagcctt	780
attaacgaca	tgccatcac	caatgaccag	aagaagctga	tgagtaataa	tgtgcagatt	840
gtgcgccagc	agagttacag	cattatgagt	attatcaaag	aggagggtatt	ggcttatgtg	900
gttcagcttc	cgctgtatgg	ggcatcgcac	acaccttggt	ggaagttgca	taccagtccc	960
ctgtgtacga	caaacaccaa	ggaaggtagt	aacatctgct	tgacacgtac	cgatcgggggt	1020
tgggtattgcg	ataacgccgg	gtctgttagt	ttctttcctc	aagccgagac	atgcaaagtc	1080
cagagcaatc	gcgtgttctg	tgacacgatg	aacagctgta	ctttgccatc	agaggttaat	1140
ctgtgcaata	ccgacatctt	caaccccaaa	tacgactgta	agatcatgac	cagcaagact	1200
gatgtcagct	cctccgttat	aacatcactc	ggcgctatcg	tgtcttgcta	tggcaagacc	1260
aagtgtacag	cgtccaataa	gaatcggggc	attatcaaga	cattctcaa	cggatgtgac	1320
tacgtgagca	acaaaggagt	ggacaccgtg	tcagtcggaa	atacactgta	ttacgtgaat	1380
aagcaggagg	gcaaattctt	ttacgtgaag	ggcgaaccaa	tcatcaactt	ctatgatccc	1440
ctcgtctttc	cttctgatga	gtttgacgcc	tctatctctc	aggttaacga	gaagatcaat	1500
cagtctctgg	cctttatacg	caaaagcgat	gaactcctgg	gatcaggcta	cattccccgaa	1560
gctccaaggg	acggacaagc	atacgtacga	aaagatggcg	aatgggtact	cctctcaacg	1620
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<210> 18

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> GS linker

<400> 18
Gly Ser Gly Ser Gly Ser
1 5

<210> 19
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> GS linker

<400> 19
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 20
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> GS linker

<400> 20
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 21
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> foldon

<400> 21
Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val
1 5 10 15
Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
20 25

<210> 22
<211> 20
<212> PRT
<213> Artificial Sequence

<220>

<223> tag

<400> 22

Leu Val Pro Arg Gly Ser His His His His His His Trp Ser His Pro
1 5 10 15
Gln Phe Glu Lys
20

<210> 23

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> DS-Cav1

<400> 23

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

Ala	Gly	Val	Thr	Thr	Pro	Val	Ser	Thr	Tyr	Met	Leu	Thr	Asn	Ser	Glu	
				245					250					255		
Leu	Leu	Ser	Leu	Ile	Asn	Asp	Met	Pro	Ile	Thr	Asn	Asp	Gln	Lys	Lys	
			260					265					270			
Leu	Met	Ser	Asn	Asn	Val	Gln	Ile	Val	Arg	Gln	Gln	Ser	Tyr	Ser	Ile	
		275					280					285				
Met	Cys	Ile	Ile	Lys	Glu	Glu	Val	Leu	Ala	Tyr	Val	Val	Gln	Leu	Pro	
	290					295					300					
Leu	Tyr	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Lys	Leu	His	Thr	Ser	Pro	
305					310					315					320	
Leu	Cys	Thr	Thr	Asn	Thr	Lys	Glu	Gly	Ser	Asn	Ile	Cys	Leu	Thr	Arg	
				325					330						335	
Thr	Asp	Arg	Gly	Trp	Tyr	Cys	Asp	Asn	Ala	Gly	Ser	Val	Ser	Phe	Phe	
			340					345					350			
Pro	Gln	Ala	Glu	Thr	Cys	Lys	Val	Gln	Ser	Asn	Arg	Val	Phe	Cys	Asp	
		355					360					365				
Thr	Met	Asn	Ser	Leu	Thr	Leu	Pro	Ser	Glu	Val	Asn	Leu	Cys	Asn	Val	
	370					375					380					
Asp	Ile	Phe	Asn	Pro	Lys	Tyr	Asp	Cys	Lys	Ile	Met	Thr	Ser	Lys	Thr	
385					390					395					400	
Asp	Val	Ser	Ser	Ser	Val	Ile	Thr	Ser	Leu	Gly	Ala	Ile	Val	Ser	Cys	
				405					410					415		
Tyr	Gly	Lys	Thr	Lys	Cys	Thr	Ala	Ser	Asn	Lys	Asn	Arg	Gly	Ile	Ile	
			420					425					430			
Lys	Thr	Phe	Ser	Asn	Gly	Cys	Asp	Tyr	Val	Ser	Asn	Lys	Gly	Val	Asp	
		435					440					445				
Thr	Val	Ser	Val	Gly	Asn	Thr	Leu	Tyr	Tyr	Val	Asn	Lys	Gln	Glu	Gly	
						455					460					
Lys	Ser	Leu	Tyr	Val	Lys	Gly	Glu	Pro	Ile	Ile	Asn	Phe	Tyr	Asp	Pro	
465					470					475					480	
Leu	Val	Phe	Pro	Ser	Asp	Glu	Phe	Asp	Ala	Ser	Ile	Ser	Gln	Val	Asn	
				485					490					495		
Glu	Lys	Ile	Asn	Gln	Ser	Leu	Ala	Phe	Ile	Arg	Lys	Ser	Asp	Glu	Leu	
			500					505					510			
Leu	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp	Gly	Gln	Ala	Tyr	
		515					520					525				
Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu	Leu	Ser	Thr	Phe	Leu	Leu	Val	
	530					535					540					
Pro	Arg	Gly	Ser	His	His	His	His	His	His	Trp	Ser	His	Pro	Gln	Phe	
545					550					555					560	
Glu	Lys															

<210> 24
 <211> 521
 <212> PRT
 <213> Artificial Sequence

<220>

<223> delta FP furinwt Fecto

<400> 24

Met	Glu	Leu	Leu	Ile	Leu	Lys	Ala	Asn	Ala	Ile	Thr	Thr	Ile	Leu	Thr
1				5					10					15	
Ala	Val	Thr	Phe	Cys	Phe	Ala	Ser	Gly	Gln	Asn	Ile	Thr	Glu	Glu	Phe
		20						25					30		
Tyr	Gln	Ser	Thr	Cys	Ser	Ala	Val	Ser	Lys	Gly	Tyr	Leu	Ser	Ala	Leu
	35					40						45			
Arg	Thr	Gly	Trp	Tyr	Thr	Ser	Val	Ile	Thr	Ile	Glu	Leu	Ser	Asn	Ile
	50					55					60				
Lys	Glu	Asn	Lys	Cys	Asn	Gly	Thr	Asp	Ala	Lys	Val	Lys	Leu	Ile	Lys
65					70					75					80
Gln	Glu	Leu	Asp	Lys	Tyr	Lys	Asn	Ala	Val	Thr	Glu	Leu	Gln	Leu	Leu
				85					90					95	
Met	Gln	Ser	Thr	Pro	Ala	Thr	Asn	Asn	Arg	Ala	Arg	Arg	Glu	Leu	Pro
			100					105					110		
Arg	Phe	Met	Asn	Tyr	Thr	Leu	Asn	Asn	Ala	Lys	Lys	Thr	Asn	Val	Thr
		115					120						125		
Leu	Ser	Lys	Lys	Arg	Lys	Arg	Arg	Ser	Ala	Ile	Ala	Ser	Gly	Val	Ala
	130					135					140				
Val	Ser	Lys	Val	Leu	His	Leu	Glu	Gly	Glu	Val	Asn	Lys	Ile	Lys	Ser
145					150					155					160
Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val
				165					170					175	
Ser	Val	Leu	Thr	Ser	Lys	Val	Leu	Asp	Leu	Lys	Asn	Tyr	Ile	Asp	Lys
			180					185					190		
Gln	Leu	Leu	Pro	Ile	Val	Asn	Lys	Gln	Ser	Cys	Ser	Ile	Ser	Asn	Ile
		195					200					205			
Glu	Thr	Val	Ile	Glu	Phe	Gln	Gln	Lys	Asn	Asn	Arg	Leu	Leu	Glu	Ile
	210					215					220				
Thr	Arg	Glu	Phe	Ser	Val	Asn	Ala	Gly	Val	Thr	Thr	Pro	Val	Ser	Thr
225					230					235					240
Tyr	Met	Leu	Thr	Asn	Ser	Glu	Leu	Leu	Ser	Leu	Ile	Asn	Asp	Met	Pro
				245					250					255	
Ile	Thr	Asn	Asp	Gln	Lys	Lys	Leu	Met	Ser	Asn	Asn	Val	Gln	Ile	Val
		260						265					270		
Arg	Gln	Gln	Ser	Tyr	Ser	Ile	Met	Ser	Ile	Ile	Lys	Glu	Glu	Val	Leu
		275					280					285			
Ala	Tyr	Val	Val	Gln	Leu	Pro	Leu	Tyr	Gly	Val	Ile	Asp	Thr	Pro	Cys
	290					295					300				
Trp	Lys	Leu	His	Thr	Ser	Pro	Leu	Cys	Thr	Thr	Asn	Thr	Lys	Glu	Gly
305					310					315					320
Ser	Asn	Ile	Cys	Leu	Thr	Arg	Thr	Asp	Arg	Gly	Trp	Tyr	Cys	Asp	Asn
				325					330					335	
Ala	Gly	Ser	Val	Ser	Phe	Phe	Pro	Gln	Ala	Glu	Thr	Cys	Lys	Val	Gln
			340					345					350		
Ser	Asn	Arg	Val	Phe	Cys	Asp	Thr	Met	Asn	Ser	Leu	Thr	Leu	Pro	Ser
		355					360					365			
Glu	Val	Asn	Leu	Cys	Asn	Val	Asp	Ile	Phe	Asn	Pro	Lys	Tyr	Asp	Cys

370		375		380
Lys Ile Met Thr Ser	Lys Thr Asp Val Ser	Ser Ser Val Ile Thr Ser		
385	390	395	400	
Leu Gly Ala Ile Val	Ser Cys Tyr Gly Lys Thr	Lys Cys Thr Ala Ser		
	405	410	415	
Asn Lys Asn Arg Gly	Ile Ile Lys Thr Phe Ser	Asn Gly Cys Asp Tyr		
	420	425	430	
Val Ser Asn Lys Gly	Val Asp Thr Val Ser Val	Gly Asn Thr Leu Tyr		
	435	440	445	
Tyr Val Asn Lys Gln	Glu Gly Lys Ser Leu Tyr	Val Lys Gly Glu Pro		
	450	455	460	
Ile Ile Asn Phe Tyr	Asp Pro Leu Val Phe Pro	Ser Asp Glu Phe Asp		
465	470	475	480	
Ala Ser Ile Ser Gln	Val Asn Glu Lys Ile Asn	Gln Ser Leu Ala Phe		
	485	490	495	
Ile Arg Lys Ser Asp	Glu Leu Leu His Asn Val	Asn Ala Gly Lys Ser		
	500	505	510	
Thr Thr Asn His His	His His His His			
	515	520		

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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> His tag

<400> 25
 His His His His His His
 1 5

<210> 26
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Strep-tagII

<400> 26
 Trp Ser His Pro Gln Phe Glu Lys
 1 5

<210> 27
 <211> 5
 <212> PRT

<213> Artificial Sequence

<220>

<223> GS linker

<400> 27

Gly Gly Gly Gly Ser
1 5

<210> 28

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> FLAG tag

<400> 28

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 29

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> GGS+Flag

<400> 29

Gly Gly Ser Asp Tyr Lys Asp Asp Asp Asp Lys
1 5 10

<210> 30

<211> 227

<212> PRT

<213> Artificial Sequence

<220>

<223> Fc

<400> 30

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

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

Tyr	Gln	Ser	Thr	Cys	Ser	Ala	Val	Ser	Arg	Gly	Tyr	Leu	Ser	Ala	Leu	
	35						40					45				
Arg	Thr	Gly	Trp	Tyr	Thr	Ser	Val	Ile	Thr	Ile	Glu	Leu	Ser	Asn	Ile	
	50					55					60					
Lys	Glu	Asn	Lys	Cys	Asn	Gly	Thr	Asp	Ala	Lys	Val	Lys	Leu	Ile	Lys	
65					70					75					80	
Gln	Glu	Leu	Asp	Lys	Tyr	Lys	Asn	Ala	Val	Thr	Glu	Leu	Gln	Leu	Leu	
			85						90					95		
Met	Gln	Ser	Thr	Pro	Ala	Thr	Asn	Asn	Arg	Ala	Arg	Arg	Glu	Leu	Pro	
			100					105					110			
Arg	Phe	Met	Asn	Tyr	Thr	Leu	Asn	Asn	Ala	Lys	Lys	Thr	Asn	Val	Thr	
		115					120						125			
Leu	Ser	Lys	Lys	Arg	Lys	Asn	Asn	Phe	Leu	Gly	Phe	Cys	Leu	Gly	Val	
	130					135					140					
Gly	Ser	Ala	Ile	Ala	Ser	Gly	Val	Ala	Val	Ser	Lys	Val	Leu	His	Leu	
145					150					155					160	
Glu	Gly	Glu	Val	Asn	Lys	Ile	Lys	Ser	Ala	Leu	Leu	Ser	Thr	Asn	Lys	
				165					170					175		
Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val	Ser	Val	Leu	Val	Val	Lys	Val	
			180					185						190		
Leu	Asp	Leu	Lys	Asn	Tyr	Ile	Asp	Lys	Gln	Leu	Leu	Pro	Ile	Val	Asn	
	195						200					205				
Lys	Gln	Ser	Cys	Ser	Ile	Ser	Asn	Ile	Glu	Thr	Val	Ile	Glu	Phe	Gln	
	210					215					220					
Gln	Lys	Asn	Asn	Arg	Leu	Leu	Glu	Ile	Thr	Arg	Glu	Phe	Ser	Val	Asn	
225					230					235					240	
Ala	Gly	Val	Thr	Thr	Pro	Val	Ser	Thr	Tyr	Met	Leu	Thr	Asn	Ser	Glu	
				245					250					255		
Leu	Leu	Ser	Leu	Ile	Asn	Asp	Met	Pro	Ile	Thr	Asn	Asp	Gln	Lys	Lys	
		260					265						270			
Leu	Met	Ser	Asn	Asn	Val	Gln	Ile	Val	Arg	Gln	Gln	Ser	Tyr	Ser	Ile	
		275					280					285				
Met	Ser	Ile	Ile	Lys	Glu	Glu	Val	Leu	Ala	Tyr	Val	Val	Gln	Leu	Pro	
	290					295					300					
Leu	Tyr	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Lys	Leu	His	Thr	Ser	Pro	
305					310					315					320	
Leu	Cys	Thr	Thr	Asn	Thr	Lys	Glu	Gly	Ser	Asn	Ile	Cys	Leu	Thr	Arg	
				325					330					335		
Thr	Asp	Arg	Gly	Trp	Tyr	Cys	Asp	Asn	Ala	Gly	Ser	Val	Ser	Phe	Phe	
			340					345					350			
Pro	Gln	Ala	Glu	Thr	Cys	Lys	Val	Gln	Ser	Asn	Arg	Val	Phe	Cys	Asp	
		355					360					365				
Thr	Met	Asn	Ser	Cys	Thr	Leu	Pro	Ser	Glu	Val	Asn	Leu	Cys	Asn	Thr	
	370					375					380					
Asp	Ile	Phe	Asn	Pro	Lys	Tyr	Asp	Cys	Lys	Ile	Met	Thr	Ser	Lys	Thr	
385					390					395					400	
Asp	Val	Ser	Ser	Ser	Val	Ile	Thr	Ser	Leu	Gly	Ala	Ile	Val	Ser	Cys	
				405					410					415		
Tyr	Gly	Lys	Thr	Lys	Cys	Thr	Ala	Ser	Asn	Lys	Asn	Arg	Gly	Ile	Ile	
			420					425					430			

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

<210> 33
 <211> 769
 <212> PRT
 <213> Artificial Sequence

<220>

<223> FH_85-Fc

<400> 33

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

		355				360				365					
Thr	Met	Asn	Ser	Cys	Thr	Leu	Pro	Ser	Glu	Val	Asn	Leu	Cys	Asn	Thr
	370					375					380				
Asp	Ile	Phe	Asn	Pro	Lys	Tyr	Asp	Cys	Lys	Ile	Met	Thr	Ser	Lys	Thr
385					390					395					400
Asp	Val	Ser	Ser	Ser	Val	Ile	Thr	Ser	Leu	Gly	Ala	Ile	Val	Ser	Cys
				405					410					415	
Tyr	Gly	Lys	Thr	Lys	Cys	Thr	Ala	Ser	Asn	Lys	Asn	Arg	Gly	Ile	Ile
			420					425					430		
Lys	Thr	Phe	Ser	Asn	Gly	Cys	Asp	Tyr	Val	Ser	Asn	Lys	Gly	Val	Asp
		435					440					445			
Thr	Val	Ser	Val	Gly	Asn	Thr	Leu	Tyr	Tyr	Val	Asn	Lys	Gln	Glu	Gly
	450					455					460				
Lys	Ser	Leu	Tyr	Val	Lys	Gly	Glu	Pro	Ile	Ile	Asn	Phe	Tyr	Asp	Pro
465					470					475					480
Leu	Val	Phe	Pro	Ser	Asp	Glu	Phe	Asp	Ala	Ser	Ile	Ser	Gln	Val	Asn
				485					490					495	
Glu	Lys	Ile	Asn	Gln	Ser	Leu	Ala	Phe	Ile	Arg	Lys	Ser	Asp	Glu	Leu
			500					505					510		
Leu	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp	Gly	Gln	Ala	Tyr
		515					520					525			
Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu	Leu	Ser	Thr	Phe	Leu	Asp	Lys
	530					535					540				
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro
545					550					555					560
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser
				565					570					575	
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp
			580					585					590		
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn
		595					600					605			
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val
	610					615						620			
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu
625					630					635					640
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys
				645					650					655	
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr
			660					665					670		
Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr
		675					680					685			
Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu
	690					695					700				
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu
705					710					715					720
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys
				725					730					735	
Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu
			740					745					750		
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly

755
 Lys

760

765

<210> 34
 <211> 789
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> F_DS-Cav1-4GS-Fc

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

Met 290	Cys	Ile	Ile	Lys	Glu	Glu	Val	Leu	Ala	Tyr	Val	Val	Gln	Leu	Pro
Leu 305	Tyr	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Lys	Leu	His	Thr	Ser	Pro
Leu	Cys	Thr	Thr	Asn	Thr	Lys	Glu	Gly	Ser	Asn	Ile	Cys	Leu	Thr	Arg
Thr	Asp	Arg	Gly	Trp	Tyr	Cys	Asp	Asn	Ala	Gly	Ser	Val	Ser	Phe	Phe
Pro	Gln	Ala	Glu	Thr	Cys	Lys	Val	Gln	Ser	Asn	Arg	Val	Phe	Cys	Asp
Thr	Met	Asn	Ser	Leu	Thr	Leu	Pro	Ser	Glu	Val	Asn	Leu	Cys	Asn	Val
Asp 385	Ile	Phe	Asn	Pro	Lys	Tyr	Asp	Cys	Lys	Ile	Met	Thr	Ser	Lys	Thr
Asp	Val	Ser	Ser	Ser	Val	Ile	Thr	Ser	Leu	Gly	Ala	Ile	Val	Ser	Cys
Tyr	Gly	Lys	Thr	Lys	Cys	Thr	Ala	Ser	Asn	Lys	Asn	Arg	Gly	Ile	Ile
Lys	Thr	Phe	Ser	Asn	Gly	Cys	Asp	Tyr	Val	Ser	Asn	Lys	Gly	Val	Asp
Thr	Val	Ser	Val	Gly	Asn	Thr	Leu	Tyr	Tyr	Val	Asn	Lys	Gln	Glu	Gly
Lys 465	Ser	Leu	Tyr	Val	Lys	Gly	Glu	Pro	Ile	Ile	Asn	Phe	Tyr	Asp	Pro
Leu	Val	Phe	Pro	Ser	Asp	Glu	Phe	Asp	Ala	Ser	Ile	Ser	Gln	Val	Asn
Glu	Lys	Ile	Asn	Gln	Ser	Leu	Ala	Phe	Ile	Arg	Lys	Ser	Asp	Glu	Leu
Leu	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp	Gly	Gln	Ala	Tyr
Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu	Leu	Ser	Thr	Phe	Leu	Gly	Gly
Gly 545	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
Gly	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu
Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr
Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val
Glu 625	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu
Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala
Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
 690 695 700
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 705 710 715 720
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 725 730 735
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 740 745 750
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 755 760 765
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 770 775 780
 Leu Ser Pro Gly Lys
 785

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<220>
 <223> F_DS-Cav1-2GS-Fc

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 Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr Glu Glu Phe
 20 25 30
 Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
 35 40 45
 Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
 50 55 60
 Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
 65 70 75 80
 Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
 85 90 95
 Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
 100 105 110
 Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
 115 120 125
 Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
 130 135 140
 Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
 145 150 155 160
 Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
 165 170 175
 Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
 180 185 190
 Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn

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

Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu Gly Gly
 530 535 540
 Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 545 550 555 560
 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 565 570 575
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 580 585 590
 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 595 600 605
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 610 615 620
 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 625 630 635 640
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
 645 650 655
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 660 665 670
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
 675 680 685
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 690 695 700
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 705 710 715 720
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 725 730 735
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 740 745 750
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 755 760 765
 Ser Leu Ser Pro Gly Lys
 770

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 Tyr Gln Ser Thr Cys Ser Ala Val Ser Arg Gly Tyr Leu Ser Ala Leu
 35 40 45
 Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Met Leu Ser Asn Ile

50						55					60				
Lys	Glu	Asn	Lys	Cys	Asn	Gly	Thr	Asp	Ala	Lys	Val	Lys	Leu	Ile	Lys
65					70					75					80
Gln	Glu	Leu	Asp	Lys	Tyr	Lys	Asn	Ala	Val	Thr	Glu	Leu	Gln	Leu	Leu
				85					90					95	
Met	Gln	Ser	Thr	Pro	Ala	Thr	Asn	Asn	Arg	Ala	Arg	Arg	Glu	Leu	Pro
			100				105						110		
Arg	Phe	Met	Asn	Tyr	Thr	Leu	Asn	Asn	Ala	Lys	Lys	Thr	Asn	Val	Thr
	115						120					125			
Leu	Ser	Lys	Lys	Arg	Lys	Asn	Asn	Phe	Leu	Gly	Phe	Cys	Leu	Gly	Val
130						135					140				
Gly	Ser	Ala	Ile	Ala	Ser	Gly	Val	Ala	Val	Ser	Lys	Val	Leu	His	Leu
145					150					155					160
Glu	Gly	Glu	Val	Asn	Lys	Ile	Lys	Ser	Ala	Leu	Leu	Ser	Thr	Asn	Lys
				165					170					175	
Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val	Ser	Val	Leu	Val	Val	Lys	Val
			180					185					190		
Leu	Asp	Leu	Lys	Asn	Tyr	Ile	Asp	Lys	Gln	Leu	Leu	Pro	Ile	Val	Asn
	195						200					205			
Lys	Gln	Ser	Cys	Ser	Ile	Ser	Asn	Ile	Glu	Thr	Val	Ile	Glu	Phe	Gln
210						215					220				
Gln	Lys	Asn	Asn	Arg	Leu	Leu	Glu	Ile	Thr	Arg	Glu	Phe	Ser	Val	Asn
225				230					235						240
Ala	Gly	Val	Thr	Thr	Pro	Val	Ser	Thr	Tyr	Met	Leu	Thr	Asn	Ser	Glu
			245					250						255	
Leu	Leu	Ser	Leu	Ile	Asn	Asp	Met	Pro	Ile	Thr	Asn	Asp	Gln	Lys	Lys
		260				265							270		
Leu	Met	Ser	Asn	Asn	Val	Gln	Ile	Val	Arg	Gln	Gln	Ser	Tyr	Ser	Ile
	275					280						285			
Met	Ser	Ile	Ile	Lys	Glu	Glu	Val	Leu	Ala	Tyr	Val	Val	Gln	Leu	Pro
290						295					300				
Leu	Tyr	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Lys	Leu	His	Thr	Ser	Pro
305				310						315					320
Leu	Cys	Thr	Thr	Asn	Thr	Lys	Glu	Gly	Ser	Asn	Ile	Cys	Leu	Thr	Arg
				325					330					335	
Thr	Asp	Arg	Gly	Trp	Tyr	Cys	Asp	Asn	Ala	Gly	Ser	Val	Ser	Phe	Phe
			340					345					350		
Pro	Gln	Ala	Glu	Thr	Cys	Lys	Val	Gln	Ser	Asn	Arg	Val	Phe	Cys	Asp
	355					360						365			
Thr	Met	Asn	Ser	Cys	Thr	Leu	Pro	Ser	Glu	Val	Asn	Leu	Cys	Asn	Thr
370						375					380				
Asp	Ile	Phe	Asn	Pro	Lys	Tyr	Asp	Cys	Lys	Ile	Met	Thr	Ser	Lys	Thr
385				390						395					400
Asp	Val	Ser	Ser	Ser	Val	Ile	Thr	Ser	Leu	Gly	Ala	Ile	Val	Ser	Cys
			405						410					415	
Tyr	Gly	Lys	Thr	Lys	Cys	Thr	Ala	Ser	Asn	Lys	Asn	Arg	Gly	Ile	Ile
			420					425					430		
Lys	Thr	Phe	Ser	Asn	Gly	Cys	Asp	Tyr	Val	Ser	Asn	Lys	Gly	Val	Asp
	435					440						445			
Thr	Val	Ser	Val	Gly	Asn	Thr	Leu	Tyr	Tyr	Val	Asn	Lys	Gln	Glu	Gly

450		455		460	
Lys Ser Leu Tyr Val	Lys Gly Glu Pro Ile	Ile Asn Phe Tyr Asp	Pro		
465	470	475	480		
Leu Val Phe Pro Ser	Asp Glu Phe Asp	Ala Ser Ile Ser Gln	Val Asn		
	485	490	495		
Glu Lys Ile Asn Gln	Ser Leu Ala Phe	Ile Arg Lys Ser Asp	Glu Leu		
	500	505	510		
Leu Gly Ser Gly Tyr	Ile Pro Glu Ala	Pro Arg Asp Gly	Gln Ala Tyr		
	515	520	525		
Val Arg Lys Asp Gly	Glu Trp Val Leu	Leu Ser Thr Phe	Leu Gly Gly		
	530	535	540		
Gly Gly Ser Gly Gly	Gly Gly Ser Gly	Gly Gly Ser Gly	Gly Gly Gly		
545	550	555	560		
Gly Ser Asp Lys Thr	His Thr Cys Pro	Pro Cys Pro Ala	Pro Glu Leu		
	565	570	575		
Leu Gly Gly Pro Ser	Val Phe Leu Phe	Pro Pro Lys Pro	Lys Asp Thr		
	580	585	590		
Leu Met Ile Ser Arg	Thr Pro Glu Val	Thr Cys Val Val	Val Asp Val		
	595	600	605		
Ser His Glu Asp Pro	Glu Val Lys Phe	Asn Trp Tyr Val	Asp Gly Val		
	610	615	620		
Glu Val His Asn Ala	Lys Thr Lys Pro	Arg Glu Glu Gln	Tyr Asn Ser		
625	630	635	640		
Thr Tyr Arg Val Val	Ser Val Leu Thr	Val Leu His Gln	Asp Trp Leu		
	645	650	655		
Asn Gly Lys Glu Tyr	Lys Cys Lys Val	Ser Asn Lys Ala	Leu Pro Ala		
	660	665	670		
Pro Ile Glu Lys Thr	Ile Ser Lys Ala	Lys Gly Gln Pro	Arg Glu Pro		
	675	680	685		
Gln Val Tyr Thr Leu	Pro Pro Ser Arg	Asp Glu Leu Thr	Lys Asn Gln		
	690	695	700		
Val Ser Leu Thr Cys	Leu Val Lys Gly	Phe Tyr Pro Ser	Asp Ile Ala		
705	710	715	720		
Val Glu Trp Glu Ser	Asn Gly Gln Pro	Glu Asn Asn Tyr	Lys Thr Thr		
	725	730	735		
Pro Pro Val Leu Asp	Ser Asp Gly Ser	Phe Phe Leu Tyr	Ser Lys Leu		
	740	745	750		
Thr Val Asp Lys Ser	Arg Trp Gln Gln	Gly Asn Val Phe	Ser Cys Ser		
	755	760	765		
Val Met His Glu Ala	Leu His Asn His	Tyr Thr Gln Lys	Ser Leu Ser		
	770	775	780		
Leu Ser Pro Gly Lys					
785					

<210> 38
 <211> 779
 <212> PRT
 <213> Artificial Sequence

<220>

<223> FH_85-2GS-Fc

<400> 38

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

Thr	Met	Asn	Ser	Cys	Thr	Leu	Pro	Ser	Glu	Val	Asn	Leu	Cys	Asn	Thr
	370					375					380				
Asp	Ile	Phe	Asn	Pro	Lys	Tyr	Asp	Cys	Lys	Ile	Met	Thr	Ser	Lys	Thr
385					390					395					400
Asp	Val	Ser	Ser	Ser	Val	Ile	Thr	Ser	Leu	Gly	Ala	Ile	Val	Ser	Cys
				405					410					415	
Tyr	Gly	Lys	Thr	Lys	Cys	Thr	Ala	Ser	Asn	Lys	Asn	Arg	Gly	Ile	Ile
			420					425					430		
Lys	Thr	Phe	Ser	Asn	Gly	Cys	Asp	Tyr	Val	Ser	Asn	Lys	Gly	Val	Asp
	435						440					445			
Thr	Val	Ser	Val	Gly	Asn	Thr	Leu	Tyr	Tyr	Val	Asn	Lys	Gln	Glu	Gly
	450					455					460				
Lys	Ser	Leu	Tyr	Val	Lys	Gly	Glu	Pro	Ile	Ile	Asn	Phe	Tyr	Asp	Pro
465					470					475					480
Leu	Val	Phe	Pro	Ser	Asp	Glu	Phe	Asp	Ala	Ser	Ile	Ser	Gln	Val	Asn
				485					490					495	
Glu	Lys	Ile	Asn	Gln	Ser	Leu	Ala	Phe	Ile	Arg	Lys	Ser	Asp	Glu	Leu
			500					505					510		
Leu	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp	Gly	Gln	Ala	Tyr
	515						520					525			
Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu	Leu	Ser	Thr	Phe	Leu	Gly	Gly
	530					535					540				
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro
545					550					555					560
Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro
				565					570					575	
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
			580					585					590		
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn
	595						600				605				
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
	610					615					620				
Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val
625					630					635					640
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
				645					650					655	
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
			660					665					670		
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp
	675						680						685		
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
	690					695					700				
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
705					710					715					720
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
				725					730					735	
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
			740					745					750		
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
	755						760					765			

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 770 775

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<220>
 <223> FH_85-1GS-Fc

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

690		695		700	
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr					
705		710		715	720
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys					
	725		730		735
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys					
	740		745		750
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu					
	755		760		765
Ser Leu Ser Pro Gly Lys					
770					

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<220>
 <223> CC02

<400>	40
Ile Ala Leu Ala Leu Glu Lys Ile Ala Leu Ala Leu Glu Lys Ile Ala	
1	5 10 15
Leu Ala Leu Glu Lys	
	20

<210> 41
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CC03

<400>	41
Ile Lys Leu Glu Leu Glu Lys Ile Lys Leu Glu Leu Glu Lys Ile Lys	
1	5 10 15
Leu Glu Leu Glu Lys	
	20

<210> 42
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<220>
 <223> CC07

<400> 42

Leu His Leu His Ile Glu Lys Leu His Leu His Ile Glu Lys Leu His
1 5 10 15
Leu His Ile Glu Lys
20

<210> 43

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> CC008

<400> 43

Leu Lys Leu Glu Ile His His Leu Lys Leu Glu Ile His His Leu Lys
1 5 10 15
Leu Glu Ile His His
20

<210> 44

<211> 571

<212> PRT

<213> Artificial Sequence

<220>

<223> F_DS-Cav1-CC02

<400> 44

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15
Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr Glu Glu Phe
20 25 30
Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45
Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60
Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80
Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
85 90 95
Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110
Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
115 120 125
Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
130 135 140

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

Leu Ala Leu Glu Lys Ile Ala Leu Ala Leu Glu Lys Ile Ala Leu Ala
 545 550 555 560
 Leu Glu Lys Asp Tyr Lys Asp Asp Asp Asp Lys
 565 570

<210> 45
 <211> 571
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> F_DS-Cav1-CC03

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

Ala	Val	Thr	Phe	Cys	Phe	Ala	Ser	Gly	Gln	Asn	Ile	Thr	Glu	Glu	Phe	
			20					25					30			
Tyr	Gln	Ser	Thr	Cys	Ser	Ala	Val	Ser	Lys	Gly	Tyr	Leu	Ser	Ala	Leu	
		35					40					45				
Arg	Thr	Gly	Trp	Tyr	Thr	Ser	Val	Ile	Thr	Ile	Glu	Leu	Ser	Asn	Ile	
	50					55					60					
Lys	Glu	Asn	Lys	Cys	Asn	Gly	Thr	Asp	Ala	Lys	Val	Lys	Leu	Ile	Lys	
65					70					75					80	
Gln	Glu	Leu	Asp	Lys	Tyr	Lys	Asn	Ala	Val	Thr	Glu	Leu	Gln	Leu	Leu	
				85					90					95		
Met	Gln	Ser	Thr	Pro	Ala	Thr	Asn	Asn	Arg	Ala	Arg	Arg	Glu	Leu	Pro	
			100					105					110			
Arg	Phe	Met	Asn	Tyr	Thr	Leu	Asn	Asn	Ala	Lys	Lys	Thr	Asn	Val	Thr	
		115					120					125				
Leu	Ser	Lys	Lys	Arg	Lys	Arg	Arg	Phe	Leu	Gly	Phe	Leu	Leu	Gly	Val	
	130					135					140					
Gly	Ser	Ala	Ile	Ala	Ser	Gly	Val	Ala	Val	Cys	Lys	Val	Leu	His	Leu	
145					150					155					160	
Glu	Gly	Glu	Val	Asn	Lys	Ile	Lys	Ser	Ala	Leu	Leu	Ser	Thr	Asn	Lys	
				165					170					175		
Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val	Ser	Val	Leu	Thr	Phe	Lys	Val	
			180					185					190			
Leu	Asp	Leu	Lys	Asn	Tyr	Ile	Asp	Lys	Gln	Leu	Leu	Pro	Ile	Leu	Asn	
	195						200					205				
Lys	Gln	Ser	Cys	Ser	Ile	Ser	Asn	Ile	Glu	Thr	Val	Ile	Glu	Phe	Gln	
	210					215					220					
Gln	Lys	Asn	Asn	Arg	Leu	Leu	Glu	Ile	Thr	Arg	Glu	Phe	Ser	Val	Asn	
225					230					235					240	
Ala	Gly	Val	Thr	Thr	Pro	Val	Ser	Thr	Tyr	Met	Leu	Thr	Asn	Ser	Glu	
				245					250					255		
Leu	Leu	Ser	Leu	Ile	Asn	Asp	Met	Pro	Ile	Thr	Asn	Asp	Gln	Lys	Lys	
			260				265						270			
Leu	Met	Ser	Asn	Asn	Val	Gln	Ile	Val	Arg	Gln	Gln	Ser	Tyr	Ser	Ile	
	275						280					285				
Met	Cys	Ile	Ile	Lys	Glu	Glu	Val	Leu	Ala	Tyr	Val	Val	Gln	Leu	Pro	
	290					295					300					
Leu	Tyr	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Lys	Leu	His	Thr	Ser	Pro	
305					310					315					320	
Leu	Cys	Thr	Thr	Asn	Thr	Lys	Glu	Gly	Ser	Asn	Ile	Cys	Leu	Thr	Arg	
				325					330					335		
Thr	Asp	Arg	Gly	Trp	Tyr	Cys	Asp	Asn	Ala	Gly	Ser	Val	Ser	Phe	Phe	
			340					345					350			
Pro	Gln	Ala	Glu	Thr	Cys	Lys	Val	Gln	Ser	Asn	Arg	Val	Phe	Cys	Asp	
		355					360					365				
Thr	Met	Asn	Ser	Leu	Thr	Leu	Pro	Ser	Glu	Val	Asn	Leu	Cys	Asn	Val	
	370					375					380					
Asp	Ile	Phe	Asn	Pro	Lys	Tyr	Asp	Cys	Lys	Ile	Met	Thr	Ser	Lys	Thr	
385					390					395					400	
Asp	Val	Ser	Ser	Ser	Val	Ile	Thr	Ser	Leu	Gly	Ala	Ile	Val	Ser	Cys	
				405					410					415		

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

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 <211> 571
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> F_DS-Cav1-CC08

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 1 5 10 15
 Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr Glu Glu Phe
 20 25 30
 Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
 35 40 45
 Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
 50 55 60
 Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
 65 70 75 80
 Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
 85 90 95
 Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
 100 105 110
 Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
 115 120 125
 Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
 130 135 140
 Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu

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

545 550 555 560
Ile His His Asp Tyr Lys Asp Asp Asp Asp Lys
565 570

<210>	48
<211>	571
<212>	PRT
<213>	Artificial Sequence

<220>
<223> FH 82-CC07

<400>	48														
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Ala	Val	Thr	Phe	Cys	Phe	Ala	Ser	Gly	Gln	Asn	Ile	Thr	Glu	Glu	Phe
			20					25					30		
Tyr	Gln	Ser	Thr	Cys	Ser	Ala	Val	Ser	Arg	Gly	Tyr	Leu	Ser	Ala	Leu
		35					40					45			
Arg	Thr	Gly	Trp	Tyr	Thr	Ser	Val	Ile	Thr	Ile	Glu	Leu	Ser	Asn	Ile
	50					55					60				
Lys	Glu	Asn	Lys	Cys	Asn	Gly	Thr	Asp	Ala	Lys	Val	Lys	Leu	Ile	Lys
65					70					75					80
Gln	Glu	Leu	Asp	Lys	Tyr	Lys	Asn	Ala	Val	Thr	Glu	Leu	Gln	Leu	Leu
				85					90					95	
Met	Gln	Ser	Thr	Pro	Ala	Thr	Asn	Asn	Arg	Ala	Arg	Arg	Glu	Leu	Pro
			100					105					110		
Arg	Phe	Met	Asn	Tyr	Thr	Leu	Asn	Asn	Ala	Lys	Lys	Thr	Asn	Val	Thr
		115					120					125			
Leu	Ser	Lys	Lys	Arg	Lys	Asn	Asn	Phe	Leu	Gly	Phe	Cys	Leu	Gly	Val
	130					135					140				
Gly	Ser	Ala	Ile	Ala	Ser	Gly	Val	Ala	Val	Ser	Lys	Val	Leu	His	Leu
145					150					155					160
Glu	Gly	Glu	Val	Asn	Lys	Ile	Lys	Ser	Ala	Leu	Leu	Ser	Thr	Asn	Lys
				165					170					175	
Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val	Ser	Val	Leu	Val	Val	Lys	Val
			180					185					190		
Leu	Asp	Leu	Lys	Asn	Tyr	Ile	Asp	Lys	Gln	Leu	Leu	Pro	Ile	Val	Asn
		195					200					205			
Lys	Gln	Ser	Cys	Ser	Ile	Ser	Asn	Ile	Glu	Thr	Val	Ile	Glu	Phe	Gln
	210					215					220				
Gln	Lys	Asn	Asn	Arg	Leu	Leu	Glu	Ile	Thr	Arg	Glu	Phe	Ser	Val	Asn
225					230					235					240
Ala	Gly	Val	Thr	Thr	Pro	Val	Ser	Thr	Tyr	Met	Leu	Thr	Asn	Ser	Glu
				245					250					255	
Leu	Leu	Ser	Leu	Ile	Asn	Asp	Met	Pro	Ile	Thr	Asn	Asp	Gln	Lys	Lys
			260					265					270		
Leu	Met	Ser	Asn	Asn	Val	Gln	Ile	Val	Arg	Gln	Gln	Ser	Tyr	Ser	Ile
		275					280					285			

Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
 290 295 300
 Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
 305 310 315 320
 Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
 325 330 335
 Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
 340 345 350
 Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
 355 360 365
 Thr Met Asn Ser Cys Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Thr
 370 375 380
 Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
 385 390 395 400
 Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
 405 410 415
 Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
 420 425 430
 Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
 435 440 445
 Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
 450 455 460
 Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
 465 470 475 480
 Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
 485 490 495
 Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
 500 505 510
 Leu Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr
 515 520 525
 Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu Leu His
 530 535 540
 Leu His Ile Glu Lys Leu His Leu His Ile Glu Lys Leu His Leu His
 545 550 555 560
 Ile Glu Lys Asp Tyr Lys Asp Asp Asp Asp Lys
 565 570

<210> 49
 <211> 571
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FH_85-CC07

<400> 49
 Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
 1 5 10 15
 Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr Glu Glu Phe

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<210> 51
 <211> 175
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> GS+Self-assembly domain of HBcAg+His

<400> 51
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15
 Gly Gly Gly Ser Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser
 20 25 30
 Val Glu Leu Leu Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Ile Arg
 35 40 45
 Asp Leu Leu Asp Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser
 50 55 60
 Pro Glu His Cys Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu
 65 70 75 80
 Cys Trp Gly Glu Leu Met Asn Leu Ala Thr Trp Val Gly Ser Asn Leu
 85 90 95
 Glu Asp Pro Ala Ser Arg Glu Leu Val Val Ser Tyr Val Asn Val Asn
 100 105 110
 Met Gly Leu Lys Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu
 115 120 125
 Thr Phe Gly Arg Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val
 130 135 140
 Trp Ile Arg Thr Pro Pro Ala Ala Arg Pro Pro Asn Ala Pro Ile Leu
 145 150 155 160
 Ser Thr Leu Pro Glu Thr Thr Val Val His His His His His His
 165 170 175

<210> 52
 <211> 70
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> C term side of Self-assembly domain of HBcAg

<400> 52
 Ala Ser Arg Glu Leu Val Val Ser Tyr Val Asn Val Asn Met Gly Leu
 1 5 10 15
 Lys Ile Arg Gln Leu Leu Trp Phe His Ile Ser Ala Leu Thr Phe Gly
 20 25 30
 Arg Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg
 35 40 45

Thr Pro Pro Ala Ala Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu
50 55 60
Pro Glu Thr Thr Val Val
65 70

<210> 53
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<223> N term side of Self-assembly domain of HBcAg

<400> 53
Gly Ala Ser Val Glu Leu Leu Ser Phe Leu Pro Ser Asp Phe Phe Pro
1 5 10 15
Ser Ile Arg Asp Leu Leu Asp Thr Ala Ser Ala Leu Tyr Arg Glu Ala
20 25 30
Leu Glu Ser Pro Glu His Ser Ser Pro His His Thr Ala Leu Arg Gln
35 40 45
Ala Ile Leu Cys Trp Gly Glu Leu Met Asn Leu Ala Thr Trp Val Gly
50 55 60
Ser
65

<210> 54
<211> 186
<212> PRT
<213> Artificial Sequence

<220>
<223> HBcCN

<400> 54
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15
Gly Gly Gly Ser Ala Ser Arg Glu Leu Val Val Ser Tyr Val Asn Val
20 25 30
Asn Met Gly Leu Lys Ile Arg Gln Leu Leu Trp Phe His Ile Ser Ala
35 40 45
Leu Thr Phe Gly Arg Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly
50 55 60
Val Trp Ile Arg Thr Pro Pro Ala Ala Arg Pro Pro Asn Ala Pro Ile
65 70 75 80
Leu Ser Thr Leu Pro Glu Thr Thr Val Val Gly Gly Gly Gly Ser Gly
85 90 95
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ala
100 105 110

Ser Val Glu Leu Leu Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Ile
 115 120 125
 Arg Asp Leu Leu Asp Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu
 130 135 140
 Ser Pro Glu His Ser Ser Pro His His Thr Ala Leu Arg Gln Ala Ile
 145 150 155 160
 Leu Cys Trp Gly Glu Leu Met Asn Leu Ala Thr Trp Val Gly Ser Gly
 165 170 175
 Gly Ser Asp Tyr Lys Asp Asp Asp Asp Lys
 180 185

<210> 55
 <211> 728
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> F_DC-Cav1-HBcCN

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

225					230					235				240	
Ala	Gly	Val	Thr	Thr	Pro	Val	Ser	Thr	Tyr	Met	Leu	Thr	Asn	Ser	Glu
				245					250					255	
Leu	Leu	Ser	Leu	Ile	Asn	Asp	Met	Pro	Ile	Thr	Asn	Asp	Gln	Lys	Lys
			260					265					270		
Leu	Met	Ser	Asn	Asn	Val	Gln	Ile	Val	Arg	Gln	Gln	Ser	Tyr	Ser	Ile
		275					280					285			
Met	Cys	Ile	Ile	Lys	Glu	Glu	Val	Leu	Ala	Tyr	Val	Val	Gln	Leu	Pro
	290					295					300				
Leu	Tyr	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Lys	Leu	His	Thr	Ser	Pro
305					310					315					320
Leu	Cys	Thr	Thr	Asn	Thr	Lys	Glu	Gly	Ser	Asn	Ile	Cys	Leu	Thr	Arg
				325					330					335	
Thr	Asp	Arg	Gly	Trp	Tyr	Cys	Asp	Asn	Ala	Gly	Ser	Val	Ser	Phe	Phe
			340					345					350		
Pro	Gln	Ala	Glu	Thr	Cys	Lys	Val	Gln	Ser	Asn	Arg	Val	Phe	Cys	Asp
		355					360					365			
Thr	Met	Asn	Ser	Leu	Thr	Leu	Pro	Ser	Glu	Val	Asn	Leu	Cys	Asn	Val
	370					375					380				
Asp	Ile	Phe	Asn	Pro	Lys	Tyr	Asp	Cys	Lys	Ile	Met	Thr	Ser	Lys	Thr
385					390					395					400
Asp	Val	Ser	Ser	Ser	Val	Ile	Thr	Ser	Leu	Gly	Ala	Ile	Val	Ser	Cys
				405					410					415	
Tyr	Gly	Lys	Thr	Lys	Cys	Thr	Ala	Ser	Asn	Lys	Asn	Arg	Gly	Ile	Ile
			420					425					430		
Lys	Thr	Phe	Ser	Asn	Gly	Cys	Asp	Tyr	Val	Ser	Asn	Lys	Gly	Val	Asp
		435					440					445			
Thr	Val	Ser	Val	Gly	Asn	Thr	Leu	Tyr	Tyr	Val	Asn	Lys	Gln	Glu	Gly
	450					455				460					
Lys	Ser	Leu	Tyr	Val	Lys	Gly	Glu	Pro	Ile	Ile	Asn	Phe	Tyr	Asp	Pro
465					470					475					480
Leu	Val	Phe	Pro	Ser	Asp	Glu	Phe	Asp	Ala	Ser	Ile	Ser	Gln	Val	Asn
				485					490					495	
Glu	Lys	Ile	Asn	Gln	Ser	Leu	Ala	Phe	Ile	Arg	Lys	Ser	Asp	Glu	Leu
			500					505					510		
Leu	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp	Gly	Gln	Ala	Tyr
	515						520					525			
Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu	Leu	Ser	Thr	Phe	Leu	Gly	Gly
	530					535					540				
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
545					550					555					560
Gly	Ser	Ala	Ser	Arg	Glu	Leu	Val	Val	Ser	Tyr	Val	Asn	Val	Asn	Met
				565					570					575	
Gly	Leu	Lys	Ile	Arg	Gln	Leu	Leu	Trp	Phe	His	Ile	Ser	Ala	Leu	Thr
			580					585					590		
Phe	Gly	Arg	Glu	Thr	Val	Leu	Glu	Tyr	Leu	Val	Ser	Phe	Gly	Val	Trp
		595					600					605			
Ile	Arg	Thr	Pro	Pro	Ala	Ala	Arg	Pro	Pro	Asn	Ala	Pro	Ile	Leu	Ser
	610					615					620				
Thr	Leu	Pro	Glu	Thr	Thr	Val	Val	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly

625					630					635				640
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Ala	Ser Val
				645					650					655
Glu	Leu	Leu	Ser	Phe	Leu	Pro	Ser	Asp	Phe	Phe	Pro	Ser	Ile	Arg Asp
			660					665					670	
Leu	Leu	Asp	Thr	Ala	Ser	Ala	Leu	Tyr	Arg	Glu	Ala	Leu	Glu	Ser Pro
		675					680					685		
Glu	His	Ser	Ser	Pro	His	His	Thr	Ala	Leu	Arg	Gln	Ala	Ile	Leu Cys
	690					695					700			
Trp	Gly	Glu	Leu	Met	Asn	Leu	Ala	Thr	Trp	Val	Gly	Ser	Gly	Gly Ser
705					710					715				720
Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys							
				725										

<210> 56
 <211> 728
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FH_85-HBcCN

<400> 56

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

Lys	Gln	Ser	Cys	Ser	Ile	Ser	Asn	Ile	Glu	Thr	Val	Ile	Glu	Phe	Gln
210						215					220				
Gln	Lys	Asn	Asn	Arg	Leu	Leu	Glu	Ile	Thr	Arg	Glu	Phe	Ser	Val	Asn
225					230					235					240
Ala	Gly	Val	Thr	Thr	Pro	Val	Ser	Thr	Tyr	Met	Leu	Thr	Asn	Ser	Glu
				245					250					255	
Leu	Leu	Ser	Leu	Ile	Asn	Asp	Met	Pro	Ile	Thr	Asn	Asp	Gln	Lys	Lys
			260				265						270		
Leu	Met	Ser	Asn	Asn	Val	Gln	Ile	Val	Arg	Gln	Gln	Ser	Tyr	Ser	Ile
		275					280					285			
Met	Ser	Ile	Ile	Lys	Glu	Glu	Val	Leu	Ala	Tyr	Val	Val	Gln	Leu	Pro
		290				295					300				
Leu	Tyr	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Lys	Leu	His	Thr	Ser	Pro
305					310					315					320
Leu	Cys	Thr	Thr	Asn	Thr	Lys	Glu	Gly	Ser	Asn	Ile	Cys	Leu	Thr	Arg
				325					330						335
Thr	Asp	Arg	Gly	Trp	Tyr	Cys	Asp	Asn	Ala	Gly	Ser	Val	Ser	Phe	Phe
			340					345						350	
Pro	Gln	Ala	Glu	Thr	Cys	Lys	Val	Gln	Ser	Asn	Arg	Val	Phe	Cys	Asp
		355					360					365			
Thr	Met	Asn	Ser	Cys	Thr	Leu	Pro	Ser	Glu	Val	Asn	Leu	Cys	Asn	Thr
		370				375					380				
Asp	Ile	Phe	Asn	Pro	Lys	Tyr	Asp	Cys	Lys	Ile	Met	Thr	Ser	Lys	Thr
385					390					395					400
Asp	Val	Ser	Ser	Ser	Val	Ile	Thr	Ser	Leu	Gly	Ala	Ile	Val	Ser	Cys
				405					410					415	
Tyr	Gly	Lys	Thr	Lys	Cys	Thr	Ala	Ser	Asn	Lys	Asn	Arg	Gly	Ile	Ile
			420					425					430		
Lys	Thr	Phe	Ser	Asn	Gly	Cys	Asp	Tyr	Val	Ser	Asn	Lys	Gly	Val	Asp
		435					440					445			
Thr	Val	Ser	Val	Gly	Asn	Thr	Leu	Tyr	Tyr	Val	Asn	Lys	Gln	Glu	Gly
						455					460				
Lys	Ser	Leu	Tyr	Val	Lys	Gly	Glu	Pro	Ile	Ile	Asn	Phe	Tyr	Asp	Pro
465					470					475					480
Leu	Val	Phe	Pro	Ser	Asp	Glu	Phe	Asp	Ala	Ser	Ile	Ser	Gln	Val	Asn
				485					490					495	
Glu	Lys	Ile	Asn	Gln	Ser	Leu	Ala	Phe	Ile	Arg	Lys	Ser	Asp	Glu	Leu
			500					505					510		
Leu	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp	Gly	Gln	Ala	Tyr
		515					520					525			
Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu	Leu	Ser	Thr	Phe	Leu	Gly	Gly
						535					540				
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
545					550					555					560
Gly	Ser	Ala	Ser	Arg	Glu	Leu	Val	Val	Ser	Tyr	Val	Asn	Val	Asn	Met
				565					570					575	
Gly	Leu	Lys	Ile	Arg	Gln	Leu	Leu	Trp	Phe	His	Ile	Ser	Ala	Leu	Thr
			580					585					590		
Phe	Gly	Arg	Glu	Thr	Val	Leu	Glu	Tyr	Leu	Val	Ser	Phe	Gly	Val	Trp
		595					600					605			

aagcaggaag	gaaagtcact	ctatgtgaaa	ggagagccga	tcatcaactt	ctacgatccc	1440
ctgggtgtttc	ccagtgatga	gttcgacgcc	tctatcagcc	aggtgaatga	aaagatcaac	1500
caatccctgg	ccttcatacg	gaaatcagat	gagctgttag	gctcaggcta	catacccgaa	1560
gcaccgagag	atgggtcaagc	gtatgtgcgg	aaggatggag	agtgggtcct	tctgtcaact	1620
ttcctggaca	aaactcacac	ttgtccgcct	tgtcccgctc	cagagctcct	tggcggaccc	1680
tccgttttcc	tgtttcctcc	gaaacccaag	gatacgctga	tgatttcacg	cacaccagaa	1740
gtgacatgtg	tgggtggtaga	tgtgtcccat	gaagatccgg	aggtgaagtt	taactggtat	1800
gtcgatgggtg	tggaggttca	taacgctaag	acgaaaccac	gggaggagca	gtacaattcc	1860
acctaccgtg	tagtctctgt	gctgaccgtt	ttgcatcagg	attggctgaa	tggtaaagag	1920
tataagtgc	aagtgtccaa	caaggctctg	ccagccccta	tcgaaaagac	catcagtaaa	1980
gccaaaggac	agcctagaga	accccagggtc	tatacgctgc	caccctctcg	ggacgagctg	2040
accaagaatc	aggtgtcact	gacttgtctg	gtgaagggct	tctaccctag	cgacattgcc	2100
gtcgaatggg	agtctaattgg	gcaacccgag	aataactaca	aaaccacacc	gcccgtcttg	2160
gacagcgatg	gcagtttctt	cctgtactcc	aaactgactg	tggacaaaag	ccggtggcag	2220
caaggcaatg	tgttctcatg	ctctgtcatg	cacgaagccc	tgcacaacca	ttacacccaa	2280
aagtcactga	gcctgagccc	tggaaag				2307

<210> 58

<211> 2307

<212> DNA

<213> Artificial Sequence

<220>

<223> FH_82-Fc

<400> 58

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tgctttgcct	ctggccaaaa	cattactgag	gaattctacc	agtcaacgtg	cagtgcagtg	120
agccgagggt	atctgtccgc	cctgagaacc	gggtggtata	cttccgtcat	taccatcgag	180
ctgtccaaca	taaaagagaa	taagtgcac	ggcaccgatg	ctaaagtga	actgatcaaa	240
caggaactcg	ataaatacaa	gaatgcagtt	acagagcttc	agctcctgat	gcagagcact	300
ccggccacca	ataatagggc	aaggagagaa	ttgccacgat	ttatgaatta	cacactcaac	360
aacgcgaaga	aaactaacgt	gactctgtcc	aagaaacgta	agaataactt	cttgggggttc	420
tgtctgggtg	taggtagcgc	cattgcttct	gggggtggccg	tcagcaaagt	gcttcacctg	480
gaaggagagg	tgaacaagat	caagtctgca	ctgctgtcta	caaacaaagc	agtggtgagc	540
ctgtccaacg	gagtatccgt	tctgggtggc	aaagtcctgg	atctgaagaa	ttatatcgac	600
aaacaactgc	tccccattgt	gaacaagcag	agttgttcaa	tcagcaacat	agaaactgtg	660
attgagttcc	aacagaagaa	caataggctg	ctcgaaatta	ccagagagtt	tagcgtcaat	720
gctgggtgtca	caaccccagt	cagcacttac	atgctgacta	attccgagtt	gcttagcctt	780
attaacgaca	tgcttatcac	caatgaccag	aagaagctga	tgagtaataa	tgtgcagatt	840
gtgcgccagc	agagttacag	cattatgagt	attatcaaag	aggagggtatt	ggcttatgtg	900
gttcagcttc	cgctgtatgg	ggcatcgac	acaccttggt	ggaagttgca	taccagtccc	960
ctgtgtacga	caaacaccaa	ggaaggtagt	aacatctgct	tgacacgtac	cgatcgggggt	1020
tgggtattgcg	ataacgccgg	gtctgttagt	ttctttcctc	aagccgagac	atgcaaagtc	1080
cagagcaatc	gcgtgttctg	tgacacgatg	aacagctgta	ctttgccatc	agaggttaat	1140
ctgtgcaata	ccgacatctt	caaccccaaa	tacgactgta	agatcatgac	cagcaagact	1200
gatgtcagct	cctccgttat	aacatcactc	ggcgctatcg	tgtcttgcta	tggcaagacc	1260
aagtgtacag	cgtccaataa	gaatcggggc	attatcaaga	cattctccaa	cggatgtgac	1320
tacgtgagca	acaaaggagt	ggacaccgtg	tcagtcggaa	atacactgta	ttacgtgaat	1380

aagcaggagg	gcaaattctt	ttacgtgaag	ggcgaaccaa	tcatcaactt	ctatgatccc	1440
ctcgtctttc	cttctgatga	gtttgacgcc	tctatttctc	aggttaacga	gaagatcaat	1500
cagtctctgg	cctttatacg	caaaagcgat	gaactcctgg	gctcaggcta	catacccgaa	1560
gcaccgagag	atgggtcaagc	gtatgtgcgg	aaggatggag	agtgggtcct	tctgtcaact	1620
ttcctggaca	aaactcacac	ttgtccgcct	tgtcccgctc	cagagctcct	tggcggaccc	1680
tccgttttcc	tgtttcctcc	gaaacccaag	gatacgctga	tgatttcacg	cacaccagaa	1740
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gtcgatggtg	tggaggttca	taacgctaag	acgaaaccac	gggaggagca	gtacaattcc	1860
acctaccgtg	tagtctctgt	gctgaccgtt	ttgcatcagg	attggctgaa	tggtaaagag	1920
tataagtgca	aagtgtccaa	caaggctctg	ccagccccta	tcgaaaagac	catcagtaaa	1980
gccaaaggac	agcctagaga	accccagggtc	tatacgctgc	caccctctcg	ggacgagctg	2040
accaagaatc	aggtgtcact	gacttgtctg	gtgaagggct	tctaccctag	cgacattgcc	2100
gtcgaatggg	agtctaattgg	gcaacccgag	aataactaca	aaaccacacc	gcccgtcttg	2160
gacagcgatg	gcagtttctt	cctgtactcc	aaactgactg	tggacaaaag	ccggtggcag	2220
caaggcaatg	tgttctcatg	ctctgtcatg	cacgaagccc	tgcacaacca	ttacacccaa	2280
aagtcactga	gcctgagccc	tggaaag				2307

<210> 59

<211> 2307

<212> DNA

<213> Artificial Sequence

<220>

<223> FH_85-Fc

<400> 59

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tgctttgcct	ctggccaaaa	cattactgag	gaattctacc	agtcaacgtg	cagtgcagtg	120
agccgagggt	atctgtccgc	cctgagaacc	gggtgggtata	cttccgtcat	taccatcatg	180
ctgtccaaca	taaaagagaa	taagtgcac	ggcaccgatg	ctaaagtga	actgatcaaa	240
caggaactcg	ataaatacaa	gaatgcagtt	acagagcttc	agctcctgat	gcagagcact	300
ccggccacca	ataatagggc	aaggagagaa	ttgccacgat	ttatgaatta	cacactcaac	360
aacgcgaaga	aaactaacgt	gactctgtcc	aagaaacgta	agaataactt	cttgggggttc	420
tgtctgggtg	taggtagcgc	cattgcttct	gggggtggccg	tcagcaaagt	gcttcacctg	480
gaaggagagg	tgaacaagat	caagtctgca	ctgctgtcta	caaacaaagc	agtggtgagc	540
ctgtccaacg	gagtatccgt	tctgggtggc	aaagtcctgg	atctgaagaa	ttatatcgac	600
aaacaactgc	tccccattgt	gaacaagcag	agttgttcaa	tcagcaacat	agaaactgtg	660
attgagttcc	aacagaagaa	caataggctg	ctcgaaatta	ccagagagtt	tagcgtcaat	720
gctgggtgtca	caaccccagt	cagcacttac	atgctgacta	attccgagtt	gcttagcctt	780
attaacgaca	tgcttatcac	caatgaccag	aagaagctga	tgagtaataa	tgtgcagatt	840
gtgcgccagc	agagttacag	cattatgagt	attatcaaag	aggagggtatt	ggcttatgtg	900
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<211> 2367

<212> DNA

<213> Artificial Sequence

<220>

<223> F_DS-Cav1-4GS-Fc

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<220>
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 <212> DNA
 <213> Artificial Sequence

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 <223> FH_85-4GS-Fc

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<211> 2337

<212> DNA

<213> Artificial Sequence

<220>

<223> FH_85-2GS-Fc

<400> 64

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<211> 2322

<212> DNA

<213> Artificial Sequence

<220>

<223> FH_85-1GS-Fc

<400> 65

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 <213> Artificial Sequence

<220>
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<220>
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<220>
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<212> DNA

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<220>

<223> FH_82-CC07

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gatgtcagct	cctccgttat	aacatcactc	ggcgctatcg	tgtcttgcta	tggaagacc	1260
aagtgtacag	cgtccaataa	gaatcggggc	attatcaaga	cattctccaa	cggatgtgac	1320
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cagtctctgg	cctttatacg	caaaagcgat	gaactcctgg	gatcaggcta	cattcccgaa	1560
gctccaaggg	acggacaagc	atacgtacga	aaagatggcg	aatgggtctt	actgagcacc	1620
ttcttgctcc	atctgcacat	tgagaagcta	cacctccata	tcgagaaact	gcattctcac	1680
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<210> 71
 <211> 1713
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> FH_85-CC07

<400> 71						
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ctgtccaaca	taaaagagaa	taagtgaac	ggcaccgatg	ctaaagtga	actgatcaaa	240
caggaactcg	ataaatacaa	gaatgcagtt	acagagcttc	agctcctgat	gcagagcact	300
ccggccacca	ataatagggc	aaggagagaa	ttgccacgat	ttatgaatta	cacactcaac	360
aacgcgaaga	aaactaacgt	gactctgtcc	aagaaacgta	agaataactt	cttgggggttc	420
tgtctgggtg	taggtagcgc	cattgcttct	gggggtggccg	tcagcaaagt	gcttcacctg	480
gaaggagagg	tgaacaagat	caagtctgca	ctgctgtcta	caaacaaagc	agtggtgagc	540
ctgtccaacg	gagtatccgt	tctgggtggc	aaagtcctgg	atctgaagaa	ttatatcgac	600
aaacaactgc	tccccattgt	gaacaagcag	agttgttcaa	tcagcaacat	agaaactgtg	660
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<210> 72
 <211> 2184
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> F_DC-Cav1-HBcCN

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tctaaggggt	acttgtctgc	gcttcgcact	ggctgggtaca	cctcggttat	taccattgag	180
ctgtccaaca	tcaaagagaa	caagtgaac	ggcaccgacg	ccaaagtga	actgattaaa	240
caggagctcg	acaaatacaa	aaatgctgtg	acagagttgc	agttgctcat	gcagtctacc	300
cctgctacga	acaaccgagc	aaggcgagaa	ctaccaagat	tcatgaacta	caccttgaat	360
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gaaggggagg	tgaataagat	caagagtgcc	ctgctgtcca	caaacaaagc	agtagtgtcg	540
cttagcaatg	gggtgtccgt	tctgaccttc	aaggttctag	atctcaaaaa	ctacatcgat	600
aagcagcttc	tgccaatcct	caacaagcag	tcttgagta	ttagcaatat	cgagacggtg	660
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gtccaacttc	ccttatatgg	cgtcatagac	acgccctgtt	ggaaactgca	caccagtcct	960
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cagtcgaatc	gggtgttttg	tgacacaatg	aactcactga	ctcttccttc	cgaagtgaac	1140
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<210> 73
 <211> 2184
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> FH_85-HBcCN

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ctgtccaacg	600
aaacaactgc	660
attgagttcc	720
gctgggtgtca	780
attaacgaca	840
gtgcgccagc	900
gttcagcttc	960
ctgtgtacga	1020
tggtattgcg	1080
cagagcaatc	1140
ctgtgcaata	1200
gatgtcagct	1260
aagtgtacag	1320
tacgtgagca	1380
aagcaggagg	1440
ctcgtctttc	1500
cagtctcttg	1560
gctccaaggg	1620
ttcctgggcg	1680
ggcagcgctt	1740
cgtcagttgc	1800
tacctggtgt	1860
cctatcctgt	1920

ggatctggcg	gaggtggcag	tgggggcggt	ggaagtggcg	ctagcgtcga	gttgctcagc	1980
ttccttcct	cggacttctt	tccgtccatc	agggatctgc	tggacacagc	cagtgccttc	2040
tatcgggaag	cactggaatc	ttccgaacac	agctctcctc	accatacagc	ccttcgacaa	2100
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<210> 74
 <211> 1722
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> RSV_F

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agcaaaggct	atcttagtgc	tctgagaact ggttgggtata ccagtgttat aactatagaa 180
ttaagtaata	tcaaggaaaa	taagtgtaat ggaacagatg ctaaggtaaa attgataaaa 240
caagaattag	ataaatataa	aaatgctgta acagaattgc agttgctcat gcaaagcaca 300
ccaccaacaa	acaatcgagc	cagaagagaa ctaccaaggt ttatgaatta tacactcaac 360
aatgccaaaa	aaaccaatgt	aacattaagc aagaaaagga aaagaagatt tcttggtttt 420
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ttatcaaatg	gagttagtgt	cttaaccagc aaagtgttag acctcaaaaa ctatatagat 600
aaacaattgt	tacctattgt	gaacaagcaa agctgcagca tatcaaatat agaaactgtg 660
atagagttcc	aacaaaagaa	caacagacta ctagagatta ccagggaatt tagtgtaaat 720
gcagggtgtaa	ctacacctgt	aagcacttac atgttaacta atagtgaatt attgtcatta 780
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tccaccacaa	atatcatgat	aactactata attatagtga ttatagtaat attgttatca 1620
ttaattgctg	ttggactgtc	cttatactgt aaggccagaa gcacaccagt cacactaagc 1680
aaagatcaac	tgagtgggtat	aaataatatt gcatttagta ac 1722

<210> 75
 <211> 20
 <212> PRT

<213> Artificial Sequence

<220>

<223> GS linker

<400> 75

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Gly	Gly	Gly	Ser												
			20												