

SEQUENCE LISTING

<110> ENCEFA

BRESSAC Laurence

GUERREIRO Serge

TOULORGE Damien

<120> CD31 COMPETITORS AND USES THEREOF

<130> CV - 1204/PCT

<150> EP19305086.1

<151> 2019-01-23

<160> 43

<170> BiSSAP 1.3.6

<210> 1

<211> 738

<212> PRT

<213> Homo sapiens

<220>

<223> CD31

<400> 1

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

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Arg	Ile	Ile	Ser	Gly	Ile	His	Met	Gln	Thr	Ser	Glu	Ser	Thr	Lys	Ser	210	215	220
Glu	Leu	Val	Thr	Val	Thr	Glu	Ser	Phe	Ser	Thr	Pro	Lys	Phe	His	Ile	225	230	235
Ser	Pro	Thr	Gly	Met	Ile	Met	Glu	Gly	Ala	Gln	Leu	His	Ile	Lys	Cys	245	250	255
Thr	Ile	Gln	Val	Thr	His	Leu	Ala	Gln	Glu	Phe	Pro	Glu	Ile	Ile	Ile	260	265	270
Gln	Lys	Asp	Lys	Ala	Ile	Val	Ala	His	Asn	Arg	His	Gly	Asn	Lys	Ala	275	280	285
Val	Tyr	Ser	Val	Met	Ala	Met	Val	Glu	His	Ser	Gly	Asn	Tyr	Thr	Cys	290	295	300
Lys	Val	Glu	Ser	Ser	Arg	Ile	Ser	Lys	Val	Ser	Ser	Ile	Val	Val	Asn	305	310	315
Ile	Thr	Glu	Leu	Phe	Ser	Lys	Pro	Glu	Leu	Glu	Ser	Ser	Phe	Thr	His	325	330	335
Leu	Asp	Gln	Gly	Glu	Arg	Leu	Asn	Leu	Ser	Cys	Ser	Ile	Pro	Gly	Ala	340	345	350
Pro	Pro	Ala	Asn	Phe	Thr	Ile	Gln	Lys	Glu	Asp	Thr	Ile	Val	Ser	Gln	355	360	365
Thr	Gln	Asp	Phe	Thr	Lys	Ile	Ala	Ser	Lys	Ser	Asp	Ser	Gly	Thr	Tyr	370	375	380
Ile	Cys	Thr	Ala	Gly	Ile	Asp	Lys	Val	Val	Lys	Lys	Ser	Asn	Thr	Val	385	390	395
Gln	Ile	Val	Val	Cys	Glu	Met	Leu	Ser	Gln	Pro	Arg	Ile	Ser	Tyr	Asp	405	410	415
Ala	Gln	Phe	Glu	Val	Ile	Lys	Gly	Gln	Thr	Ile	Glu	Val	Arg	Cys	Glu	420	425	430
Ser	Ile	Ser	Gly	Thr	Leu	Pro	Ile	Ser	Tyr	Gln	Leu	Leu	Lys	Thr	Ser	435	440	445
Lys	Val	Leu	Glu	Asn	Ser	Thr	Lys	Asn	Ser	Asn	Asp	Pro	Ala	Val	Phe	450	455	460
Lys	Asp	Asn	Pro	Thr	Glu	Asp	Val	Glu	Tyr	Gln	Cys	Val	Ala	Asp	Asn	465	470	475
Cys	His	Ser	His	Ala	Lys	Met	Leu	Ser	Glu	Val	Leu	Arg	Val	Lys	Val	485	490	495
Ile	Ala	Pro	Val	Asp	Glu	Val	Gln	Ile	Ser	Ile	Leu	Ser	Ser	Lys	Val	500	505	510
Val	Glu	Ser	Gly	Glu	Asp	Ile	Val	Leu	Gln	Cys	Ala	Val	Asn	Glu	Gly	515	520	525
Ser	Gly	Pro	Ile	Thr	Tyr	Lys	Phe	Tyr	Arg	Glu	Lys	Glu	Gly	Lys	Pro	530	535	540
Phe	Tyr	Gln	Met	Thr	Ser	Asn	Ala	Thr	Gln	Ala	Phe	Trp	Thr	Lys	Gln	545	550	555
Lys	Ala	Ser	Lys	Glu	Gln	Glu	Gly	Glu	Tyr	Tyr	Cys	Thr	Ala	Phe	Asn	565	570	575
Arg	Ala	Asn	His	Ala	Ser	Ser	Val	Pro	Arg	Ser	Lys	Ile	Leu	Thr	Val	580	585	590
Arg	Val	Ile	Leu	Ala	Pro	Trp	Lys	Lys	Gly	Leu	Ile	Ala	Val	Val	Ile	595	600	605
Ile	Gly	Val	Ile	Ile	Ala	Leu	Leu	Ile	Ile	Ala	Ala	Lys	Cys	Tyr	Phe	610	615	620
Leu	Arg	Lys	Ala	Lys	Ala	Lys	Gln	Met	Pro	Val	Glu	Met	Ser	Arg	Pro	625	630	635
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Ala	Val	Pro	Leu	Leu	Asn	Ser	Asn	Asn	Glu	Lys	Met	Ser	Asp	Pro	Asn	
				645					650					655		
Met	Glu	Ala	Asn	Ser	His	Tyr	Gly	His	Asn	Asp	Asp	Val	Arg	Asn	His	
			660					665					670			
Ala	Met	Lys	Pro	Ile	Asn	Asp	Asn	Lys	Glu	Pro	Leu	Asn	Ser	Asp	Val	
		675					680					685				
Gln	Tyr	Thr	Glu	Val	Gln	Val	Ser	Ser	Ala	Glu	Ser	His	Lys	Asp	Leu	
	690					695					700					
Gly	Lys	Lys	Asp	Thr	Glu	Thr	Val	Tyr	Ser	Glu	Val	Arg	Lys	Ala	Val	
705					710					715					720	
Pro	Asp	Ala	Val	Glu	Ser	Arg	Tyr	Ser	Arg	Thr	Glu	Gly	Ser	Leu	Asp	
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Gly	Thr															

<210> 2
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 <212> PRT
 <213> Homo sapiens

<220>
 <223> CD38

<400> 2

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

225					230					235				240
Trp	Val	Ile	His	Gly	Gly	Arg	Glu	Asp	Ser	Arg	Asp	Leu	Cys	Gln
				245					250				255	
Pro	Thr	Ile	Lys	Glu	Leu	Glu	Ser	Ile	Ile	Ser	Lys	Arg	Asn	Ile
			260					265					270	
Phe	Ser	Cys	Lys	Asn	Ile	Tyr	Arg	Pro	Asp	Lys	Phe	Leu	Gln	Cys
		275					280					285		Val
Lys	Asn	Pro	Glu	Asp	Ser	Ser	Cys	Thr	Ser	Glu	Ile			
	290					295					300			

<210> 3
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 <213> Mus musculus

<220>
 <223> Soluble CD31 (sCD31)

<400> 3

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

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

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<220>

<223> VH-CDR1 - Consensus

<220>

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<223> X is selected from Tyr (Y), Asn (N) and Ser (S)

<400> 4
Gly Phe Thr Phe Ser Asn Xaa
1 5

<210> 5
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<223> X is selected from Ser (S) and Tyr (Y)

<220>
<223> VH-CDR2 - Consensus

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<223> X is selected from Tyr (Y), Asp (D), Asn (N) and Ser (S)

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Xaa Gly Ser Ser Arg Xaa
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<223> X is selected from Ser (S) and an empty position

<220>
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<223> X is selected from Ser (S) and an empty position

<220>
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<223> X is selected from Ser (S) and Tyr (Y)

<220>
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<222> 4
 <223> X is selected from Ser (S) and Asp (D)

<220>
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 <222> 5
 <223> X is selected from Tyr (Y), Ser (S), Asp (D) and Gly (G)

<220>
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 <222> 7
 <223> X being selected from Tyr (Y) and Gly (G)

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 <223> X being selected from Ser (S), Tyr (Y) and Phe (F)

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 <222> 9
 <223> X being selected from Gly (G) and Asp (D)

<220>
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 <223> X being selected from Asn (N), Tyr (Y) and Ser (S)

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 <213> Artificial Sequence

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 1 5

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<220>
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<400> 8
Gly Phe Thr Phe Ser Asn Asn
1 5

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<400> 9
Gly Phe Thr Phe Ser Asn Ser
1 5

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Ser Gly Ser Ser Arg Ser
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Ser Gly Ser Ser Arg Tyr
1 5

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Ser Gly Ser Ser Arg Asn

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Tyr Gly Ser Ser Arg Asp

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Ser Gly Ser Ser Arg Asp

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Ser Ser Ser Ser Tyr Tyr Tyr Ser Gly Asn Gly Met Asp Val

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5

10

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<400> 17
Ser Ser Tyr Ser Ser Tyr Gly Ser Gly Asn Gly Met Asp Val
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<400> 19
Ser Ser Gly Tyr Tyr Phe Gly Tyr Gly Met Asp Val
1 5 10

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<400> 20
Ser Ser Ser Ser Tyr Tyr Tyr Ser Gly Ser Gly Met Asp Val
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<220>
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<222> 10
<223> X being selected from Ser (S) and Asn (N)

<220>
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<223> X being selected from Ser (S) and Tyr (Y)

<220>
<221> SITE
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<223> X being selected from Tyr (Y), and Ser (S)

<400> 21
Ala Gly Thr Ser Ser Asp Val Gly Gly Xaa Xaa Xaa Val Ser
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<212> PRT
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<220>
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<223> X being selected from Tyr (Y), Ser (S) and Asp (D)

<220>
<223> VL-CDR2 - Consensus

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<222> 4
<223> X being selected from Tyr (Y) and Asn (N)

<400> 22
Xaa Asp Ser Xaa Arg Pro Ser
1 5

<210> 23
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<400> 23
Ser Thr Arg Val Phe Gly Gly Gly Thr
1 5

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<211> 14
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<400> 24
Ala Gly Thr Ser Ser Asp Val Gly Gly Ser Tyr Ser Val Ser
1 5 10

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<400> 25
Ala Gly Thr Ser Ser Asp Val Gly Gly Ser Ser Tyr Val Ser
1 5 10

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<210> 27
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<400> 27
Ala Gly Thr Ser Ser Asp Val Gly Gly Ser Tyr Tyr Val Ser
1 5 10

<210> 28
<211> 14
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<223> VL-CDR1

<400> 28
Ala Gly Thr Ser Ser Asp Val Gly Gly Asn Ser Tyr Val Ser
1 5 10

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<212> PRT
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<400> 29
Asp Asp Ser Asn Arg Pro Ser
1 5

<210> 30
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<400> 30
Tyr Asp Ser Tyr Arg Pro Ser
1 5

<210> 31
<400> 31
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<210> 32
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<223> VL-CDR2

<400> 32
Ser Asp Ser Tyr Arg Pro Ser
1 5

<210> 33
<211> 122
<212> PRT
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<220>
<223> HCVR B08

<400> 33

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

<210> 34
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 <212> PRT
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<220>
 <223> HCVR C05

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

<210> 35
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HCVR C06

<400> 35

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

<210> 36

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> HCVR D06

<400> 36

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

<210> 37

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> HCVR D07

<400> 37

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

<210> 38

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> HCVR D10

<400> 38

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

<210> 39

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> LCVR B08

<400> 39

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

<210> 40

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> LCVR C05/C06

<400> 40

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

<210> 41

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> LCVR D06

<400> 41

Gln	Ser	Val	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln
1				5					10					15	
Ser	Ile	Thr	Ile	Ser	Cys	Ala	Gly	Thr	Ser	Ser	Asp	Val	Gly	Gly	Ser
			20					25					30		

Tyr	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu
		35					40					45			
Met	Ile	Tyr	Ser	Asp	Ser	Tyr	Arg	Pro	Ser	Gly	Val	Ser	Asn	Arg	Phe
	50					55					60				
Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu
65					70					75					80
Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ser	Ser	Asn	Thr	Ala	Tyr
			85						90					95	
Ser	Thr	Arg	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu					
			100					105							

<210> 42
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LCVR D07/D10

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

<210> 43
 <211> 609
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Serum albumin

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

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

Val	Thr	Lys	Cys	Cys	Thr	Glu	Ser	Leu	Val	Asn	Arg	Arg	Pro	Cys	Phe
			500					505					510		
Ser	Ala	Leu	Glu	Val	Asp	Glu	Thr	Tyr	Val	Pro	Lys	Glu	Phe	Asn	Ala
		515				520						525			
Glu	Thr	Phe	Thr	Phe	His	Ala	Asp	Ile	Cys	Thr	Leu	Ser	Glu	Lys	Glu
		530				535						540			
Arg	Gln	Ile	Lys	Lys	Gln	Thr	Ala	Leu	Val	Glu	Leu	Val	Lys	His	Lys
545				550						555				560	
Pro	Lys	Ala	Thr	Lys	Glu	Gln	Leu	Lys	Ala	Val	Met	Asp	Asp	Phe	Ala
				565				570						575	
Ala	Phe	Val	Glu	Lys	Cys	Cys	Lys	Ala	Asp	Asp	Lys	Glu	Thr	Cys	Phe
		580						585				590			
Ala	Glu	Glu	Gly	Lys	Lys	Leu	Val	Ala	Ala	Ser	Gln	Ala	Ala	Leu	Gly
		595				600						605			
Leu															